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GLOSSARY OF NOTATION AND SYMBOLS

symbol, name (article denoting transition in notation) [Chapter transition]

z, phenotypic trait value [1]

$\bar{z}$, average phenotypic trait value

$p(z)$, phenotypic trait distribution before selection

$w(z)$, relative fitness as a function of trait value

$\bar{w}$, average relative fitness

$W(z)$, absolute fitness as a function of trait value

$\bar{W}$, average absolute fitness

$p^*(z)$, phenotypic trait distribution after selection

$\int p^*(z)dz$, integral, area under the curve, $p^*(z)$

P, phenotypic trait variance before selection

$\bar{z}^*$, average phenotypic trait value after selection

s, directional selection differential

s', variance-standardized directional selection differential

i, selection intensity

z_{1-p}, phenotypic trait value used as a truncation selection point

$Cov(x, y)$, covariance between random variables x and y

$Cov(w, z)$, covariance between relative fitness and phenotypic trait value

P^*, phenotypic trait variance after selection

C, nonlinear selection differential

$\boldsymbol{z}$, vector of phenotypic trait values for an individual [2]

m, the number of traits

$\bar{\mathbf{z}}$, vector of phenotypic trait means for the population

$p(\boldsymbol{z})$, multivariate distribution of vector of phenotypic trait values before selection

$\boldsymbol{P}$, phenotypic trait variance-covariance matrix before selection

$\boldsymbol{P}^{-1}$, the matrix inverse of $\boldsymbol{P}$

$|\boldsymbol{P}^{-1}|$, the determinant of $\boldsymbol{P}^{-1}$

$p^*(\boldsymbol{z})$, multivariate distribution of vector of phenotypic trait values after selection

$w(\boldsymbol{z})$, relative fitness as a function of the vector of phenotypic trait values

$W(\boldsymbol{z})$, absolute fitness as a function of the vector of phenotypic trait values

$\boldsymbol{s}$, vector of directional selection differentials

$\boldsymbol{\beta}$, vector of directional selection gradients

$\boldsymbol{C}$, matrix of nonlinear selection differentials

$\boldsymbol{P}^*$, phenotypic trait variance-covariance matrix after selection

$\boldsymbol{s}^{\mathrm{T}}$, transpose of $\boldsymbol{s}$, the elements of $\boldsymbol{s}$ are arranged in column, $\boldsymbol{s}^{\mathrm{T}}$ has the same elements arranged in a row

$\boldsymbol{\gamma}$, matrix of nonlinear selection gradients

$\boldsymbol{\Lambda}$, canonical form of $\boldsymbol{\gamma}$ with the eigenvalues of $\boldsymbol{\gamma}$, λ_i, on its main diagonal

$\boldsymbol{M}$, matrix with columns that are the eigenvectors of $\boldsymbol{\gamma}$

$\partial w(z)/\partial z$, first derivative of $w(z)$ with respect to z [3]

$\partial^2 w(z)/\partial z^2$, second derivative of $w(z)$ with respect to z

α, elevation of a linear or quadratic approximation to the individual selection surface (ISS)

ε, deviation of an individual trait value from a linear or quadratic approximation to the ISS

$ln\overline{W}$, natural logarithm of average absolute fitness in the population

θ, optimum of a Gaussian individual selection surface or the peak of a Gaussian adaptive landscape

ω, variance-like width of a Gaussian individual selection surface

Ω, variance-like width of a Gaussian adaptive landscape

$\partial\ ln\,\overline{W}/\partial\bar{z}$, first derivative of the adaptive landscape evaluated at the trait mean, slope

$\partial^2 \ ln \, \overline{W} / \partial \bar{z}^2$, second derivative of the adaptive landscape evaluated at the trait mean, curvature

θ_t, position of the optimum at time t in the Chevin et al. (2015) model

x_t, environmental variable at time t that governs the movement of the optimum

ϵ_t, stochastic contribution to the position of the optimum at time t

σ_ϵ^2, the variance of the stochastic variable ϵ_t

β', variance-standardized directional selection gradient

β_μ, mean-standardized directional selection gradient

$\beta_{i,j}$, the directional selection gradient for the ith trait in the jth temporal period

$\partial w(\boldsymbol{z}) / \partial z_1$, partial derivative of $w(\boldsymbol{z})$ with respect to z_1[4]

$\partial^2 w(\boldsymbol{z}) / \partial z_1^2$, partial second derivative of $w(\boldsymbol{z})$ with respect to z_1

$\partial^2 w(\boldsymbol{z}) / \partial z_1 \partial z_2$, partial second derivative $w(\boldsymbol{z})$ with respect to z_1 and z_2

$\boldsymbol{m_i}$, the *ith* eigenvector of $\boldsymbol{\gamma}$, *ith* column of $\boldsymbol{M}$, corresponding to the *ith* eigenvalue, λ_i

$\boldsymbol{z}_0$, stationary point on a fitted quadratic approximation to the individual selection surface; a fitness maximum, minimum, or saddle point

w_0, value of relative fitness at the stationary point

$\boldsymbol{\gamma_{min}}$, eigenvector of $\boldsymbol{\gamma}$ with the smallest eigenvalue, selective line of least resistance

$\partial\ ln\overline{W}/\partial\bar{\mathbf{z}}$, vector of first derivatives of the adaptive landscape evaluated at the vector of trait means

$\partial^2 ln\overline{W}/\partial\bar{\mathbf{z}}^2$, matrix of second derivatives of the adaptive landscape evaluated at the vector of trait means

$\boldsymbol{\omega}$, matrix of Gaussian nonlinear selection gradients, ω-matrix

$\boldsymbol{\theta}$, vector of optima for a Gaussian ISS

$\boldsymbol{\Omega}$, matrix of Gaussian nonlinear curvature coefficients for a Gaussian adaptive landscape, Ω- matrix

$\boldsymbol{\omega_{max}}$, the eigenvector of $\boldsymbol{\omega}$ with the largest eigenvalue, selective line of least resistance

$\boldsymbol{\Omega_{max}}$, the eigenvector of $\boldsymbol{\Omega}$ with the largest eigenvalue, selective line of least resistance

$\boldsymbol{\Lambda}_{\boldsymbol{\omega}}$, canonical form of $\boldsymbol{\omega}$

$\mathbf{M}_{\boldsymbol{\omega}}$, eigenvectors of $\boldsymbol{\Lambda}_{\boldsymbol{\omega}}$

$\boldsymbol{\Lambda}_{\boldsymbol{\Omega}}$, canonical form of $\boldsymbol{\Omega}$

$\mathbf{M}_{\boldsymbol{\Omega}}$, eigenvectors of $\boldsymbol{\Lambda}_{\boldsymbol{\Omega}}$

$f(\boldsymbol{z})$, projection pursuit approximation of the true ISS in the formulation of Schluter and Nychka (1994)

f_i, single-variable regression coefficient (ridge function)

$\boldsymbol{a}_i$, projection that identify a direction in a cross-section of $f(\boldsymbol{z})$

x, additive genetic or breeding trait value of an individual [5]

e, environmental trait value of an individual

$\bar{x}$, mean additive genetic value for a trait in a population

$\bar{e}$, mean environmental value for for a trait in a population

G, additive genetic variance of a trait within a population

E, environmental variance of a trait within a population

h^2, heritability of a trait within a population

y, dominance value of a trait for an individual

i, epistasis value of a trait for an individual

i_{AA}, contribution of additive by additive interactions across all loci

i_{AD}, contribution of additive by dominance interactions across all loci

i_{DD}, contribution of dominance by dominance interactions across all loci

r, coefficient of relationship, the probability that relatives X and Y have the same allele through identity by descent

u, coefficient of consanguinity, the probability that two alleles at a locus drawn at random, one each from relative X and relative Y, will be identical by descent

G_D, genetic variance arising from dominance, variance of dominance deviations

G_{AA}, genetic variance arising from additive by additive epistasis

G_{AD}, genetic variance arising from additive by dominance epistasis

a, trait value of a single locus homozygous genotype

d, trait value of a single locus heterozygote

α_1, average effect of substituting one allele (A_1) at a locus for another (A_2)

α_2, the average effect of substituting one allele (A_2) at a locus for another (A_1)

α, the average effect of allelic substitution at a locus

p, the number of fixed effects in the animal model of Henderson (1984)

q, the number of individuals in the pedigree in the animal model

n, the number of individuals with phenotypic scores in the animal model

$\boldsymbol{z}$, column vector of phenotypic values of all individuals in a sample

z_i, phenotypic trait value of the *ith* individual in a sample

μ_j, contribution of fixed effect j to z_i

u_k, contribution of random effect k to z_i

e_i, contribution of a residual effect to z_i

$\boldsymbol{b}$, fixed, usually unknown column vector of length p, giving the contributions of the fixed effect to $\boldsymbol{z}$

$\boldsymbol{u}$, random, unknown column vector of additive values of length q, with zero means, giving the contribution of the random effect to $\boldsymbol{z}$

$\boldsymbol{e}$, random, unknown column vector of length n, with zero means, giving the residual contribution to $\boldsymbol{z}$

$\boldsymbol{X}$, known n xp design matrix (with zero and one entries) which assigns the fixed effects to individuals

$\boldsymbol{Z}$, known n xq design matrix (with zero and one entries) which assigns the random effects to individuals

$\boldsymbol{F}$, q xq symmetric variance-covariance matrix matrix that is usually nonsingular (has a matrix inverse), $Var(\boldsymbol{u})$

$\boldsymbol{R}$, n xn diagonal matrix with each individual's error on the diagonal and zeros elsewhere, $Var\ (\boldsymbol{e})$

n, number of freely-recombining loci affecting the trait in Kimura's (1965) model

μ, mutation rate per haploid locus per generation

α^2, variance of mutant allele effects (i.e., variance of average effects, α) at a locus

ζ, total genomic mutation rate

U, per generation input from mutation to genetic variance in a trait

M, variance in mutational effects summed across all loci

$\Delta_s G$, reduction in genetic variance each generation due to stabilizing selection

$\hat{G}$, equilibrium genetic variance at mutation-selection balance

$\boldsymbol{G}$, additive genetic variance-covariance matrix for m traits before selection [6]

$\boldsymbol{z}$, vector of phenotypic values for m traits

$\boldsymbol{x}$, vector of additive genetic (breeding) values for m traits

$\boldsymbol{e}$, vector of environmental values for m traits

$\bar{\boldsymbol{z}}$, vector phenotypic means for m traits

$\bar{\boldsymbol{x}}$, vector of additive genetic means for m traits

$\bar{\boldsymbol{e}}$, vector of environmental means for m traits

$\boldsymbol{P}$, phenotypic variance-covariance matrix before selection

$\boldsymbol{E}$, environmental variance-covariance matrix before selection

r_g, additive genetic correlation between two traits

z_{oi}, phenotypic value of the *ith* trait in an offspring of a mother exerting maternal effects in the Kirkpatric and Lande (1989) model

x_{0i}, additive genetic value of the *ith* trait in an offspring of a mother exerting maternal effects

e_{oi}, environmental value of the *ith* trait in an offspring of a mother exerting maternal effects

m_{ij}, maternal effect of the *jth* maternal trait on the *ith* offspring trait

$\boldsymbol{m}$, matrix of maternal effect coefficients with elements m_{ij}

z_{ij}^{*}, phenotypic value of the *jth* maternal trait after selection

$\boldsymbol{C_{az}}$, matrix of covariances between additive genetic and phenotypic values

$\boldsymbol{M}$, mutational effects matrix, a variance-covariance matrix for per locus effects of mutation on m traits in the multivariate version of Kimura's (1965) model

r_{μ}, mutational correlation, the correlation between per locus effects of mutation on two traits

$\boldsymbol{U}$, the total genomic mutational input matrix for m traits

$\widehat{\boldsymbol{G}}_{ii}$, the equilibrium contribution of the *ith* locus to the G-matrix at mutation-selection balance

$\Delta_S \boldsymbol{G}$, the change in the G-matrix within a generation due to multivariate Gaussian selection

f, performance in the Arnold (1983) model [7]

$\beta_{f_j z_i}$, linear performance gradient for the *ith* phenotypic trait via the *jth* measure of performance

ε_f, residual performance not explained by performance gradients

ε_w, residual fitness not explained by fitness gradients

$\beta_{w f_j}$, fitness gradient for the *jth* measure of performance

$\gamma_{f z_i^2}$, nonlinear performance gradient for the *ith* phenotypic trait

$\gamma_{f z_i z_j}$, correlational performance gradients for the *ith* and *jth* phenotypic traits

$\boldsymbol{\beta_f}$, column vector of linear performance gradients for m phenotypic traits

$\boldsymbol{\beta_w}$, column vector of linear fitness gradients for a set of performance measures

$\boldsymbol{\gamma_f}$, matrix of nonlinear performance gradients for m phenotypic traits

$\boldsymbol{\gamma_w}$, matrix of nonlinear fitness gradients for a set of performance measures

$\boldsymbol{m_i}$, *ith* eigenvector of the γ–matrix

N_e, the effective size of a population [8]

n, number of demes in Wright's (1939) island model

$\bar{N}$, average effective size of the demes in Wright' island model

F_{ST}, among deme component of variance in gene frequency

$Var(\vartheta)$, variance in the eventual contributions of demes to the effective size of the whole population in the Whitlock and Barton (1997) model of effective size of a metapopulation

N_i, the effective size of the *ith* deme

F_{STi}, the average of pair-wise $F_{ST}s$ for the ith deme

$\boldsymbol{m}$, n x n migration matrix in which the element m_{ij} represents the per generation migration rate from deme j to deme i (the proportion of individuals in deme i newly arrived from deme j)

$Var(\bar{z}_0)$, variance in mean trait values at generation 0 of replicate lineages evolving by a stochastic process (e.g., drift) in Lande's (1976) model

$\Phi(\bar{z}_t)$, probability distribution of mean trait values at generation t of replicate lineages evolving by a stochastic process (e.g., drift)

$D(t)$, variance in mean trait values at generation t of replicate lineages evolving by a stochastic process (e.g., drift)

$\boldsymbol{T}$, phylogeny of a set of r taxa represented by an r x r shared ancestry matrix in which the off-diagonal $ijth$ element is the time (in generations) from the root of the tree to the most recent common ancestor of taxon i and taxon j, and the diagonal elements are the time from the root to extant taxon i in the Hansen and Martins (1996) model

$\boldsymbol{A}$, an r x r matrix analog of $D(t)$, in which the off-diagonal, $ijth$ element of is the expected covariance in trait mean values between two taxa, i and j, with a shared coancestry equal to the $ijth$ element of $\boldsymbol{T}$. Similarly, the diagonal, $iith$ element of $\boldsymbol{A}$ is the expected variance in mean trait values after an elapsed time given by the $iith$ element of $\boldsymbol{T}$

$\Phi(\bar{\boldsymbol{z}})$, probability distribution of a vector of mean trait values of replicate lineages at the tips of a phylogeny specified by $\boldsymbol{A}$ and evolving by a stochastic process (e.g., drift)

$\hat{G}$, equilibrium within-population genetic variance for a populations differentiating by the Lande (1992) model for mutation-migration-drift balance in a metapopulation

$\hat{G}_a$, equilibrium among-population genetic variance corresponding to $\hat{G}$

Q_{ST}, among-population genetic variance expressed as a fraction of the total genetic variance for a trait

$Var(\bar{\boldsymbol{z}}_1)$, variance in the vector of trait means at generation 1 of replicate lineages evolving by a stochastic process (e.g., drift) [9]

$\Phi(\bar{\boldsymbol{z}}_t)$, distribution of replicate lineage means for m traits at generation t evolving by a stochastic process (e.g., drift)

$\boldsymbol{D}(t)$**,** variance-covariance (dispersion) matrix for the vector trait means at generation t of replicate lineages evolving by a stochastic process (e.g., drift), D-matrix

$\Phi(\bar{\bar{\boldsymbol{z}}})$, probability distribution of the stacked column vector of mean trait values of replicate lineages, $\bar{\bar{\boldsymbol{z}}}$, at the tips of a phylogeny specified by $\boldsymbol{A}$ and evolving by a stochastic process (e.g., drift) in the account by Hohenlohe and Arnold (2008)

$\otimes$, Kronecker product, a rule for multiplying two matrices

$\boldsymbol{p_{max}}$**,** leading eigenvector of the within-locality phenotypic matrix in the study by Hunt (2007)

$\boldsymbol{g_{max}}$, leading eigenvector of the G–matrix

$\boldsymbol{\omega_{max}}$, leading eigenvector of the ω – matrix

$\boldsymbol{\gamma_{min}}$, trailing eigenvector of the γ – matrix

$\boldsymbol{d_{max}}$, leading eigenvector of the D–matrix

$\boldsymbol{d^*_{max}}$, phyologeny-corrected version analog of $\boldsymbol{d_{max}}$

R-matrix, a trait dispersion matrix in Houle et al. (2017) equivalent to the observed D–matrix

$\boldsymbol{\widehat{G}}$, equilibrium within-population additive genetic variance-covariance matrix in the model of Kremer et al. (1997)

$\boldsymbol{\widehat{G}_a}$, equilibrium among-population additive genetic variance-covariance matrix

$\boldsymbol{Q_{ST}}$, matrix of among-population components of additive genetic variance and covariance corrected for genetic covariance among m traits

$\Delta\bar{z}$, deterministic response to selection, change of the trait mean after one generation of directional selection [10]

$\Delta\bar{z}_t$, change of the trait mean after t generations of directional selection

I_A, square of the additive genetic coefficient of variation

CV_A, additive genetic coefficient of variation

$\beta(x)$, directional selection gradient at spatial position x in the model of Slatkin (1978)

L, characteristic length, the minimum length over which the geographic pattern in the trait mean will respond to geographic differences in selection and not be swamped by gene flow between populations

l, standard deviation of dispersal distance

$\partial^2\bar{z}/\partial x^2$, curvature of the geographic variation surface that relates the trait mean to spatial position, curvature of geographic variation

$\bar{z}_{ii}$, phenotypic trait mean of population i grown in its native environment

$\bar{z}_{icg}$, phenotypic trait mean of population i grown in a common environment (cg)

$\bar{g}_i$, genotypic trait mean of population i

$\bar{e}_{cg}$, average environmental contribution of the common garden to the phenotypic trait mean

$\bar{e}_i$, average contribution of the environment of population i to the phenotypic trait mean

$\bar{z}_{ij}$, phenotypic trait mean of population i grown in the environment of population j

δ_{ij}, interaction effect resulting from rearing genotypes from population i in environment j

b, the trait truncation point corresponding to a level of minimum selective mortality in Lande's (1976) model

P_1, one of two parental generations in a cross

P_2, the other parental generation

F_1, first filial generation, first generation of progeny in a cross between two parental populations (P_1 and P_2)

F_2, second filial generation, second generation of progeny produced by crossing individuals of the F_1

BC1, a backcross generation produced by crossing the F_1 and P_1

BC2, a backcross generation produced by crossing the F_1 and P_2

δ_i, difference in average effects at locus i on a phenotypic trait in two parental populations in the model of Lande (1981)

σ_δ^2, variance in δ_i across all loci

$mean(P_{i2})$, average effect of locus i on a phenotypic trait in population j

$\bar{\delta}$, mean value of δ_i average across all relevant loci

σ_s^2, segregational variance, the extra genetic variance appearing in the F_2 progeny beyond that in the F_1 progeny

$Var(F_k)$, trait phenotypic variance in the $k\,th$ filial generation of a Mendelian cross

$mean(P_i)$, trait mean of the ith parental generation

n, the actual number of factors (loci) contributing to the mean trait difference between samples of the two parental populations raised in a common environment under the Wright (1968) model

n_E, the effective number of factors with equal magnitudes of effect and producing the same pattern of segregation as observed in a Mendelian cross

$Var(n_E)$, sampling variance of n_E

$Var(\sigma_s^2)$, sampling variance of σ_s^2

QTL, quantitative trait locus

b, an unknown parameter that represents the phenotypic effect of a single allele substitution at a putative QTL in the Lander and Botstein (1989) model

g_i, an indicator variable that denotes the number of alleles from P_2 (0 or 1) at a marker locus

ε, normally-distributed error contribution (with a mean of 0 and variance σ^2) to the phenotypic trait value of an individual in a backcross progeny

$\prod_i x_i$, product of variables x_i, where i=1,2,3, ...

$L(a, b, \sigma^2)$, probability of the observed data, likelihood

$L(\hat{a}, \hat{b}, \hat{\sigma}^2)$, the likelihood that maximizes $L(a, b, \sigma^2)$, where $\hat{a}$, $\hat{b}$, and $\hat{\sigma}^2$ are the parameter values that give this maximum

LOD, log10 of the ratio of the unconstrained, $L\left(\hat{a}, \hat{b}, \hat{\sigma}^2\right)$, and constrained likelihoods, $L(\bar{z}_1, 0, \sigma^2_{B1})$; evidence for a QTL

$\boldsymbol{\Delta\bar{z}}$, change in the vector of phenotypic trait mean from one generation to the next [11]

$\boldsymbol{I}$, desired gains index

PC 1, first principal component in a principal component analysis, the eigenvector with the largest eigenvalue

$\boldsymbol{net\beta}$, net selection gradient

$\boldsymbol{I}$, selection index

$\Delta ln\overline{W}$, change in the natural log of mean fitness arising from response to selection in the trait mean [12]

$Var(\bar{z}_t)$, variance in trait means among replicate lineages evolving according to a stochastic process (e.g., OU) after t generations

$Var(\bar{z}_\infty)$, equilibrium variance in trait means among replicate lineages evolving according to a stochastic process (e.g., OU)

$\Phi(\bar{z}_\infty)$, equilibrium probability distribution of trait means among replicate lineages evolving according to a stochastic process (e.g., OU)

$\bar{z}_t$, phenotypic trait mean at generation t

T, the expected time for the trait mean, initially situated between two peaks, to evolve to either of the peaks (Lande 1985)

$\bar{W}_a$, height of the first of two adaptive peaks

$\bar{W}_v$, height of the valley between the two peaks

$E(\bar{z}_t)$, expected value of phenotypic trait mean at generation t

$\partial ln\bar{W}/\partial\,\bar{\mathbf{z}}$, direction of steepest uphill slope on the adaptive landscape from a point given by the vector of trait means [13]

$\boldsymbol{\Delta\bar{z}}^2$, generalized phenotypic distance

$\Delta ln\bar{W}$, approximately equal to generalized genetic distance

$\boldsymbol{\Omega_{min}}$, trailing eigenvector of the Ω-matrix

$\boldsymbol{\Omega_{max}}$, leading eigenvector of the Ω-matrix

G_m, additive genetic variance of a sex-limited, male trait (Lande 1980)

G_f, additive genetic variance of a sex-limited, female trait

B, additive genetic covariance between a sex-limited, male trait and a sex-limited, female trait

β_m, directional selection gradient for a male trait, z

β_f, directional selection gradient for a male trait, y

θ_m, natural selection optimum for a sex-limited, male trait

θ_f, natural selection optimum for a sex-limited, female trait

Ω_m, width of Gaussian adaptive landscape for a sex-limited, male trait

Ω_f, width of Gaussian adaptive landscape for a sex-limited, female trait

ω_m, width of a Gaussian ISS for a sex-limited, male trait

ω_f, width of a Gaussian ISS for a sex-limited, female trait

c_m, constant directional sexual selection gradient acting on a sex-limited, male trait

c_f, constant directional sexual selection gradient acting on a sex-limited, female trait

a, average of the mean of a sex-limited, male trait and the mean of a sex-limited, female trait; sexual average

d, difference between the mean of a sex-limited, male trait and the mean of a sex-limited, female trait; sexual dimorphism

Δa, change in a from one generation to the next

Δd, change in d from one generation to the next

$\bar{\mathbf{z}}_t$, vector of phenotypic trait means at generation t , in elaboration of models by Lande (1976) and Hansen and Martin (1996)

$Var(\bar{\mathbf{z}}_t)$, variance-covariance matrix for the vector of phenotypic trait means at generation t

$Var(\bar{\mathbf{z}}_\infty)$, equilibrium variance-covariance matrix for the vector of phenotypic trait means at generation t

$\Phi(\bar{\mathbf{z}}_\infty)$, equilibrium probability distribution for the vector of phenotypic trait means

P_m, phenotypic variance for a sex-limited male trait, before selection (Lande 1981)

P_m^*, phenotypic variance for a sex-limited male trait, after selection

$\bar{z}^*$, phenotypic male trait (ornament) mean after natural selection

$\bar{z}^{**}$, phenotypic male trait (ornament) mean after natural and sexual selection

$\psi(z|y)$, tendency of the female with preference value y to mate with a male with ornament value z

$\psi(z)$, overall probability of females mating as a function of male ornament value, z

y, normally distributed, female preference trait

$\bar{y}$, mean female preference before selection

τ^2, phenotypic variance in female preference trait

ν^2, 'variance' of the Gaussian function $\psi(z|y)$

λ, eigenvalue of the matrix in Lande's (1981) re-parameterized response to selection equations

H, additive genetic variance for female mating preference

$N[\boldsymbol{m}, \boldsymbol{V}]$, a draw of a vector from a multivariate normal distribution with mean vector, $\boldsymbol{m}$, and variance-covariance matrix, $\boldsymbol{V}$

$\boldsymbol{\beta_z}$, two-element vector total (natural and sexual)selection gradients for the two male ornament traits (Arnold and Houck 2016)

$\boldsymbol{\beta_y}$, two-element vector of natural selection gradients for the two female preference traits

$\boldsymbol{B}$, 2 x 2 between-sex additive genetic covariance matrix

$\boldsymbol{G}$**,** 2 x 2 additive genetic variance-covariance matrix for male ornament traits

$\boldsymbol{H}$, 2 x 2 additive genetic variance-covariance matrix for female preference traits

α, OU selection parameter estimated by OUwie (Beaulieu et al. 2012)

σ^2, Brownian motion parameter estimated by OUwie

θ_t, position of the optimum of a Gaussian ISS at generation t (Hansen et al. 2008)[14]

σ_θ^2, variance in the position of the optimum, θ_t

$N(m, V)$, a draw from a normal distribution with a mean of m and a variance of V

$Var[\theta_t]$, variance among replicate lineages in the position of the optimum at generation t

$E(\bar{z}_t)$, expected value for the trait mean of a lineage at generation t (Lynch and Lande 1993)

$E(\bar{z}_\infty)$, expected equilibrium value for the trait mean of a lineage at generation t

$Var(\bar{z}_\infty)$, expected equilibrium variance among lineages for the trait mean

L, distance between the optimum at generation t and the trait mean at generation t (lag)

X_i, partially measured variable in visible layer i (Reitan et al. 2012)

$dX_i(t)$, small change in X_i at time t

W_i, white noise variable in visible layer i

$W_i(t)$, white noise variable at time t

$dW_i(t)$, small change in W_i at time t

α_1, strength of pulling force towards the optimum in layer 1, viz., X_2

α_2, strength of pulling force towards the optimum in layer 2

μ_0, optimum in layer 2

σ_i, standard deviation of W_i

t_i, characteristic time of the pulling force towards the optimum in layer i

$E(X_1)$, expected value of X_1 as time goes to infinity

$Var(X_1)$, variance in the means of X_1 in replicate lineages as time goes to infinity

$\theta(t)$, optimum of trait z at time t

Ψ, optimum of $\theta(t)$

Υ, variance-like width of a Gaussian function that governs change in $\theta(t)$

λ, constant representing the rate of occurrence displacement in a Poisson model for the occurrence of displacement in the position of a trait optimum (Uyeda et al 2011)

σ_θ^2, variance in white noise contributions to the position of the optimum

d, magnitude of a displacement in the optimum

σ_d^2, variance in d

n, number of optimum displacement events

$p_n(t)$, probability of observing n displacement events in some time interval of length t

$K[\bar{z}(t)]$, excess kurtosis in the distribution of replicate lineage trait means at generation t (Landis and Schraiber 2017)

$\hat{G}(N)$, expected value of G at equilibrium under drift-mutation balance (Lynch and Hill 1986) [15]

$Var\left[\hat{G}(N)\right]$, expected equilibrium variance in G among replicate populations under drift-mutation balance

$\hat{G}(SHC)$, Stochastic house-of-cards approximation for the expected value of G at equilibrium under mutation-drift-selection

$Var(G)_B$, expected equilibrium variance in G among replicate populations under drift-mutation-selection balance

F , inbreeding coefficient for a population [16]

$\hat{\boldsymbol{G}}$, equilibrium $\boldsymbol{G}$ under mutation-drift balance

$\boldsymbol{U}$, matrix of genetic variance and covariance inputs to the G-matrix each generation from mutation

$\Delta_s \boldsymbol{G}$, change in the G–matrix within a generation due to multivariate selection

Σ, size of a G–matrix, sum of its eigenvalues (Jones et al. 2003)

ε, eccentricity of a G–matrix, the ratio of the smallest eigenvalue to the largest

φ, orientation of a G–matrix, the angle of the leading eigenvector to the axis of the first trait, z_1

$\partial ln\bar{W}/\partial r_\mu$, directional selection gradient for the mutational correlation, r_μ

ξ_0, value of an arbitrary reference genotype in the multilinear model of epistasis (Hansen and Wagner 2001)

$y^{(i)}$, the reference effect on an individual's genotype at locus i

$\varepsilon^{(i,j)}$,epistatic coefficient that determines the nature of the interaction between locus i and locus j

${}_{a}x$, individual's genotypic value for trait a in the multivariate multilinear model of epistasis (Jones et al. 2014)

${}_{a}\xi_0$,value of the reference genotype (zero)

${}_{a}y^{(i)}$, individual's reference genotypic value for trait a at locus i

${}_{abc}\varepsilon^{(i,j)}$, epistatic effect on trait a of the interaction between the effects of locus *i* on trait b and locus *j* on trait c

σ_{ε}^{2}, variance of epistatic coefficients

D, difference in trait means between two populations with no migration between them (Hendry et al. 2007)

D^{*}, difference in trait means between two populations, taking migration into account

LoD, expected line of divergence in trait means between an island and a mainland population (Guillaume and Whitlock 2007)

$\boldsymbol{\beta}_t$, vector of directional selection gradients at generation t (Jones et al. 2004) [17]

$\bar{\boldsymbol{z}}_t$, vector of phenotypic trait means at generation t.

$\boldsymbol{\theta}_t$, vector of trait optima (peaks) at generation t

$\Delta\boldsymbol{\theta}$, vector of rates of peak movement

$\Delta\theta_i$, rate of peak movement for phenotypic trait mean $\bar{z}_i$

$\boldsymbol{L}$, vector of equilibrium lags, distances of trait means from their adaptive peaks

$E_t[\boldsymbol{\theta}_t - \bar{\boldsymbol{z}}_t]$, expected lag in a finite population at generation t in a set of replicate lineages

●, a stationary adaptive peak

→, peak movement towards larger values of $\bar{z}_1$ and an unchanging value of $\bar{z}_1$

↗, peak movement towards larger values of $\bar{z}_1$ and $\bar{z}_2$

↘, peak movement towards smaller values of $\bar{z}_1$ and $\bar{z}_2$

σ_θ^2, stochastic variance in position of an adaptive peak

r_ω, correlation in ω –values, selectional correlation

$\sigma^2(r_\omega)$, stochastic variance in r_ω (Revell 2007)

$\boldsymbol{Wi}$, matrix of within-module stabilizing and correlational selection coefficients, ω_{ii} and ω_{ij} (Melo and Marroig 2015)

$\boldsymbol{Bt}$, matrix of between-module stabilizing and correlational selection coefficients, ω_{ii} and ω_{ij}

$\boldsymbol{Br}$, Brownian motion orientation matric with elements giving stochastic variances and covariances for positions of the adaptive peak [18]

$\sigma_{\theta i}^2$, stochastic variance in position of an adaptive peak in direction of trait mean $\bar{z}_i$

$\sigma_{\theta ij}$, stochastic covariance in position of an adaptive peak in directions of trait means $\bar{z}_i$ and $\bar{z}_j$

$\boldsymbol{D}(\bar{\boldsymbol{z}}_{t+1})$, variance-covariance matrix for a vector of trait means at generation t

$\boldsymbol{D}(\boldsymbol{\theta}_t)$, variance-covariance matrix for a vector of adaptive peak positions at generation t

$\boldsymbol{Br_{max}}$, leading eigenvector of $\boldsymbol{Br}$

r_Ω, correlation in nonlinear selection imposed by the Gaussian adaptive landscape

r_{Br}, correlation in Brownian motion of an adaptive peak

a, elevation (intercept) in an expression for allometry

b, allometric slope (scaling exponent)

Y_0, intercept in an allometric plot

B, average metabolic rate in an allometric plot

M, average body mass in an allometric plot

I, intercept in an allometric plot

k, Boltzmann's constant

T, temperature

E_i, average activation energy for the rate-limiting enzyme-catalyzed biochemical reactions of metabolism

$n(\bar{z}, t)$, distribution of the number of species with trait mean $\bar{z}$, at time t in the Slatkin (1981) model [19]

$E(\Delta\bar{z})$, the expected value of $\Delta\bar{z}$

$Var(\Delta\bar{z})$, the among species variance in $\Delta\bar{z}$

$M_o(\bar{z})$, expected per generation change in $\bar{z}$ due to ordinary within-lineage evolution

$V_o(\Delta\bar{z})$, input to variance among species in $\Delta\bar{z}$ arising from stochastic processes within-lineages

$s(\bar{z})\Delta t$, probability that a species with trait mean $\bar{z}$ produces a new species in the time interval Δt

Δy, random variable representing the amount that the new species trait means deviates from its parental species.

$M_s(\bar{z})\Delta t$, expected value of Δy

$V_s(\bar{z})\Delta t$, stochastic change in the trait mean at speciation

$e(\bar{z})\Delta t$, probability that a species with trait mean $\bar{z}$ goes extinct in time interval Δt

$\partial n(\bar{z}, t)$, small change in $n(\bar{z}, t)$

∂t, small interval of time

$\delta(\bar{z} - \bar{z}_0)$, Dirack delta function giving the initial value of the trait mean

s, constant value for the speciation rate, $s(\bar{z})\Delta t$

e, constant rate for the extinction rate, $e(\bar{z})\Delta t$

n, constant number of species with trait mean $\bar{z}$

$Var(\bar{z}_t)$, variance among species in trait mean at time t, arising from within-lineage processes, speciation, and extinction.

π_{AB}, probability of mating between a randomly drawn female from population A and a randomly drawn male from population B (Arnold et al. 1996)

JI, Index of Joint Isolation between two populations

$\boldsymbol{D}(t)$, 2x2 variance-covariance matrix giving the dispersion of replicate lineage trait means (ornament and preference) at generation t during drift along the line of equilibria in the Lande (1981) model

$D_z(t)$, first element of $\boldsymbol{D}(t)$, variance among replicate lineages in ornament means at generation t

$f_{\pi_{AB}}(x)$, probability that π_{AB} takes the value x at generation t (Uyeda et al. 2009)

$E[\,JI(t)]$, the expected value of JI at generation t

$E[\pi_{AB}]$, the expected valued of π_{AB} at generation t

d_{AB}, Euclidean distance between the preference means of females from population A and the ornament means of males from population B

$\boldsymbol{N}$, interaction (matching) matrix, rows represent female traits and columns represent male traits, elements are Gaussian coefficients, such that the ν_{pq} element is the width of a Gaussian function that gives the probability of mating with a male when the trait difference is between her preference value, y_p, and his ornament value, z_q (Hohenlohe and Arnold 2010)

$\boldsymbol{z}_j$, vector of hypothetical male traits in population j with vector of means, $\bar{\boldsymbol{z}}_j$, and variance-covariance matrix, $\boldsymbol{P}_j$

$\boldsymbol{y}_i$, vector of hypothetical female traits in population i with vector of means, $\bar{\boldsymbol{y}}_i$, and variance-covariance matrix, $\boldsymbol{Q}_i$

$\boldsymbol{Z}$, a column vector of hypothetical male trait observations that will account for the π_{ij} observations

$\boldsymbol{Y}$, a column vector of hypothetical female trait observations that will account for the $\boldsymbol{Y}$ observations

$\ln L\ (\boldsymbol{Z}, \boldsymbol{Y})$, the log likelihood that the $\boldsymbol{Z}$ and $\boldsymbol{Y}$ trait vectors will produce the observed table of π_{ij} values

$\boldsymbol{\theta}_{\boldsymbol{z}}$, vector of optima for multiple male ornaments (Arnold and Houck 2016)

$\boldsymbol{\omega}_{\boldsymbol{z}}$, matrix of Gaussian stabilizing selection for multiple male ornaments

$\boldsymbol{\theta}_{\boldsymbol{y}}$, vector of optima for multiple female preferences

$\boldsymbol{\omega}_{\boldsymbol{y}}$, matrix of Gaussian stabilizing selection for multiple female preferences

S_{yi}, directional natural selection differential for the *ith* female preference

S_{zi}, directional natural selection differential for the *ith* male ornament

$\bar{y}_i^*$, mean of the *ith* female preference after natural selection

$Var[\bar{\boldsymbol{z}}\ (t)]$, the equilibrium variance among replicates in the vector of ornaments means in the absence of sexual selection, $t = 10{,}000$ generations

$Var[\bar{\mathbf{z}}\ (t)]$, the equilibrium variance among replicates in the vector of preference means in the absence of sexual selection, $t = 10{,}000$ generations

β_{zi}, directional selection gradient for the *ith* male habitat trait

β_{yi}, directional selection gradient for the *ith* female habitat trait

π_{AB}, probability that a female from population A encounters a male from population B as a function of their habitat traits

EI, Index of Ecological Isolation, a function of π_{ij} values

z_{ij}, phenotypic trait value for the tendency to untilize ecological resources i and j

β_{zij}, directional selection gradient for z_{ij}

θ_{zij}, peak of a Gaussian landscape

$p(z_{Ai}, z_{Bi})$, strength of an interaction between species A and B mediated by the values of the *ith* phenotypic trait

β_{Ai}, total directional selection gradient for the *ith* trait in species A

β_{zFAi}, functional selection gradient for the *ith* trait in species A

β_{zIAi}, interaction selection gradient for the *ith* trait in species A

k, a function that converts trait values into fitness

$d\bar{x}$, a small change in the mean of phenotypic trait, x, in the Kiester et al. (1984) model [20]

dt, a small interval of time

τ_x, generation time of a species with trait x

η, a parameter denoting sex-limitation of the trait and diploidy versus haplodiploidy of the species

$\psi(x|y)$, a matching Gaussian function (with width ν) that gives strength of the interaction between phenotype x in one species and phenotype y in the other species

$w_x(x)$, relative fitness for plants with floral phenotype x

S_x, directional selection differential for a floral trait, x

S_y, directional selection differential for a pollinator trat, y

$\boldsymbol{M}$, matrix of selection and inheritance parameters that governs the evolution of the trait means, $\bar{x}$ and $\bar{y}$

$\Delta\bar{x}$, change the mean of an insect trait, x, from one generation to the next (Nuismer 2017)

$\Delta\bar{y}$, change the mean of an plant trait, y, from one generation to the next

$p(x, y)$, strength of the difference interaction between the insect trait and the plant trait

α, constant that translates interaction success into fitness

$W_{XI}(x, y)$, change in insect fitness as a consequence of interaction with the plant

$W_{YI}(x, y)$, change in plant fitness as a consequence of interaction with the insect

W_{XF}, functional component fitness of the insect as a function of deviation from its trait optimum, θ_x

W_{YF}, functional component fitness of the plant as a function of deviation from its trait optimum, θ_y

$W_X(x, y)$, fitness of the insect as a function of stabilizing selection (with width ω_x) on trait value x, and interaction with a plant with trait value y

$W_Y(x, y)$, fitness of the plant as a function of stabilizing selection (with width ω_y) on trait value y, and interaction with an insect with trait value x

β_{xI}, interaction selection gradient for the insect trait x

β_{yI}, interaction selection gradient for the plant trait y

β_{xF}, functional selection gradient for insect trait x

β_{yF}, functional selection gradient for plant trait y

$\hat{x}$, equilibrium value for $\bar{x}$

$\hat{y}$, equilibrium value for $\bar{y}$

m_x, proportion of individuals that moves from its natal population to another population after selection

$\bar{x}_i^*(t)$, trait mean at locality i after selection response and migration

μ_x, average of trait means at two localities

δ_x, difference between trait means at two localities

$\bar{\beta}_{xI}$, average of interaction selection gradients among localities

$\delta_{\beta_{xI}}$, difference between interaction selection gradients at two localities

$\Delta\mu_x$, change in geographic trait average from one generation to the next

$\Delta\delta_x$, change in geographic trait differences from one generation to the next

$\bar{p}_{i,j}$, average probability that a predator from population i successfully ingests a prey from population j

A_x, measure of local adaptation, a function of $\bar{p}_{i,j}$ values

$s_{x,1}$, sensitivity coefficient that is a function of a constant that translates costs and benefits of interaction into fitness (α), the frequencies of the two host species (f_Y and f_Z), and the fitness benefits to the parasites from the interaction (s_{XY} and s_{XZ}).

$\overline{W}_X$, the average fitness of a predator species X

$\overline{W}_Y$, the average fitness of a prey species, Y

κ_X, a sensitivity coefficient that puts interaction effects and effects of stabilizing selection into register (the same currency)

I, interaction efficiency, a measure of connectivity in the community network

$E\left(\bar{z}_{i,\tau_1}\right)$, the expected value of the trait mean of species i at the instant of speciation

D_{i,τ_1}, within-lineage variance of the trait in lineage i at the instant of speciation

D_{12,τ_1}, the covariance between the trait means of two sister species at the instant of speciation

W_i, fitness of an individual of species *i* as a function of a trait-mediated interaction with another species

$\bar{W}_i$, average fitness of an individual of species *i* as a function of a trait-mediated interaction with another species, and the distributions of trait values in both species

D_{i,τ_2}, within-lineage variance of the trait in lineage i at time τ_2

$\hat{A}_{ij}$, equilibrium value for an index of asymmetry in competitive ability, a function of drift and elapsed time

N_i, number of individuals of the *ith* species

lnW_i, log$_e$ absolute fitness of an individual of the *ith* species

$n_i(z_i)$, number of individuals with phenotype z_i

$p_i(z_i)$, proportion of individuals with phenotype z_i

$lnW_N(z_N)$, log$_e$ absolute fitness of an individual consumer with phenotype z_N (McPeek 2017) [21]

$lnW_R(z_R)$, log$_e$ absolute fitness of an individual resource with phenotype z_R

N, number of consumer individuals

R, number of resource individuals

N_{z_N}, number of consumer individuals with phenotype z_N

N_{z_R}, number of resource individuals with phenotype z_R

b, conversion efficiency for a particular consumer phenotype feeding on a particular resource phenotype

$a(\bar{z}_R, z_N)$, attack coefficient for consumer phenotype z_N feeding on resource phenotype $\bar{z}_R$; the rate at which a consumer kills a resource (Holling 1959)

a_0, maximum value of attack success

ω_a, width parameter for the Gaussian attack function

$f(z_n)$, intrinsic death rate of the consumer with phenotype z_N

f_0, minimum value of the consumer's intrinsic death rate

γ_f, stabilizing selection coefficient for the consumer's intrinsic death rate

θ_f, value of z_R that minimizes consumer's intrinsic death rate

g, density-dependent rate of increase in the consumer's death rate

$c(z_R)$, intrinsic birth rate of resource species with phenotype z_R

$c_{0,}$ maximum value of the resource intrinsic birth rate

γ_c, stabilizing selection coefficient for the intrinsic birth rate of the resource species

θ_c, value of z_N that minimizes the death rate of the resource species

d, density-dependent rate of decrease in the birth rate of the resource

h, handling time for a particular consumer phenotype feeding on a particular resource phenotype

dN/Ndt, per capita growth rate of the consumer species

dR/Rdt, per capita growth rate of the resource species

$d\bar{z}_N/dt$, evolutionary change in $\bar{z}_N$, continuous time version of $\Delta\bar{z}_N$

G_{z_N}, additive genetic variance for the phenotypic trait of the consumer species, z_N

$\beta_{z_N b}$, the birth selection gradient for z_N, reflects the contribution of trait values to the birth component of fitness in the consumer species

$\beta_{z_N d}$, death selection gradient for z_N, reflects the contribution of trait values to the death component of fitness in the consumer species

dN/dt, population growth rate of the consumer species

dR/dt, population growth rate of the resource species