

Module 4: Quantitative traits and local adaptation

Olivier Cotto
Frédéric Guillaume
Max Schmid

DPPS-303 – Tvärminne Zoological Station – University of Helsinki

March 2023

Module 4

Modelling quantitative trait variation and local adaptation

OUTLINE

- Genetic architecture of quantitative traits
- Selection on quantitative traits: the adaptive landscape
- Modelling local adaptation
- Eco-evolutionary dynamics: adaptation to environmental variation
- Adaptation to a shifting environmental gradient

Quantitative traits



Quantitative traits are traits that are influenced by their genes and the environment.

Phenotypic value:

$$\mathbf{P} = \mathbf{G} + \mathbf{E}$$

Phenotype (**P**) = Genotype effect (**G**) + Environmental effect (**E**)

$$\mathbf{G} = \sum_{i=1}^L (a_{X,i} + a_{Y,i} + d_{XY,i}) + \xi$$

The genotype is the sum over *all loci* of the **additive** *a*, **dominance** *d* and **epistatic** ξ effects.

Trait variation

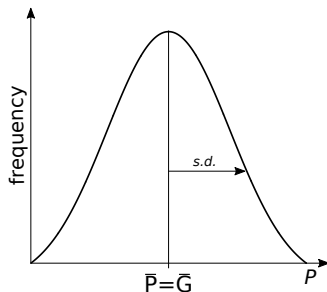


Quantitative traits are continuously distributed in a population. The **phenotypic distribution** of the a trait is often *Normal* on some scale: $\sim N(\bar{\mathbf{P}}, \sqrt{V_P})$, with average $\bar{\mathbf{P}}$ and variance V_P .

$$\bar{\mathbf{P}} = \bar{\mathbf{G}} + \bar{\mathbf{E}} = \bar{\mathbf{G}}$$

where $\mathbf{E} \sim N(0, \sigma_E)$ is a random deviation caused by the environment with mean of $\bar{\mathbf{E}} = 0$ when evaluated across all individuals.

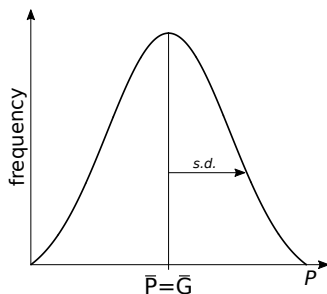
Trait variation



Because environmental effects contribute to the *phenotypic* variation among individuals, they also contribute to the *variance* of the phenotypic distribution.

$$V_P = V_G + V_E$$

Trait variation



Phenotypic variance:

$$V_P = V_G + V_E + 2\text{cov}(\mathbf{G}, \mathbf{E})$$

under the assumption of no plasticity, no $\mathbf{G} \times \mathbf{E}$ and no correlation between genotypes and environments (\mathbf{G} and \mathbf{E} are independent):

$$\text{cov}(\mathbf{G}, \mathbf{E}) = 0$$

Decomposition of the genetic variance

Genetic variance:

$$V_G = V_A + V_D + V_I$$

with:

V_A : **additive** genetic variance, contributed by additive effects of loci

V_D : **dominance** variance (from dominance effects within loci)

V_I : **epistatic** variance (from epistatic effects between loci)

Decomposition of the genetic variance

Genetic variance:

$$V_G = V_A + V_D + V_I$$

with:

V_A : **additive** genetic variance, contributed by additive effects of loci

V_D : **dominance** variance (from dominance effects within loci)

V_I : **epistatic** variance (from epistatic effects between loci)

⇒ V_A is the most important genetic component because inherited.

⇒ V_D and V_I are not, or only partially inherited (in closely related ind.)

Genetic architecture of quantitative traits

Additive genetic variance:

$$V_A = \sum_{i=1}^L \text{var}(a_i) + 2 \sum_{i=1}^L \sum_{j \neq i}^L \text{cov}(a_i, a_j)$$

where $\text{var}(a_i)$ is the *genic* variance at locus i ($= 2a_i^2$ if a_i is the additive effect of the locus), and $\text{cov}(a_i, a_j)$ is the covariance between the additive allelic effects at locus i and j . The covariance is contributed by *linkage disequilibrium* between loci.

Genetic architecture of quantitative traits

Additive genetic variance:

$$V_A = \sum_{i=1}^L \text{var}(a_i) + 2 \sum_{i=1}^L \sum_{j \neq i}^L \text{cov}(a_i, a_j)$$

where $\text{var}(a_i)$ is the *genic* variance at locus i ($= 2a_i^2$ if a_i is the additive effect of the locus), and $\text{cov}(a_i, a_j)$ is the covariance between the additive allelic effects at locus i and j . The covariance is contributed by *linkage disequilibrium* between loci.

Two ways of encoding additive loci contributing to continuous traits:

- infinitely large number of (diallelic) loci of infinitesimally small effects (Fisher's infinitesimal model, 1918)
- finite number of multi-allelic loci with normally distributed effects (continuum-of-allele model of Kimura & Crow, 1964)

Genetic architecture of quantitative traits

In Nemo: trait `quant`

- `diallelic` model: symmetrical $\pm a_i$ additive effects, set for each locus i , or asymmetrical $\{a_i, b_i\}$ effects. Mutation swaps alleles between $\pm a_i$ or $\{a_i, b_i\}$
- `continuous` model: alleles/mutations are drawn from a normal distribution $N(0, \sigma_{a,i})$, with $\sigma_{a,i}^2$ the effect size of the mutation at locus i . Mutations are either added to the existing allele (default) or replace the existing allele (`continuous_in_place` model).

Genetic architecture of quantitative traits

In Nemo: trait `quant`

- `diallelic` model: symmetrical $\pm a_i$ additive effects, set for each locus i , or asymmetrical $\{a_i, b_i\}$ effects. Mutation swaps alleles between $\pm a_i$ or $\{a_i, b_i\}$
- `continuous` model: alleles/mutations are drawn from a normal distribution $N(0, \sigma_{a,i})$, with $\sigma_{a,i}^2$ the effect size of the mutation at locus i . Mutations are either added to the existing allele (default) or replace the existing allele (`continuous_in_place` model).

In SLiM:

- ⇒ re-interpretation of selection coefficient of mutations as an additive effect. Needs additional scripting to compute phenotypes and change the fitness function. It is thus only a di-allelic model with alleles $\{0, a_i\}$ where a_i is the mutational effect.

Parameterization of quant trait

Key quantities:

Mutational variance: V_m = per generation mutational input into V_A

$$V_m = 2L\mu\sigma_a^2$$

with L number of loci, μ the per allele mutation rate, σ_a^2 the variance of mutational effects (assumed constant across loci).

Environmental variance: V_E

will be set relative to the *heritability* of the trait.

Heritability: $h^2 = \frac{V_A}{V_P}$

with $V_P = V_G + V_E$. h^2 is the regression coefficient between parent and offspring genetic values. Thus, $h^2 = 1$ if only additive effects are modeled and $V_E = 0$.

Parameterization of quant trait

Key quantities:

Mutational variance: V_m = per generation mutational input into V_A

$$V_m = 2L\mu\sigma_a^2$$

with L number of loci, μ the per allele mutation rate, σ_a^2 the variance of mutational effects (assumed constant across loci).

Environmental variance: V_E

will be set relative to the *heritability* of the trait.

Heritability: $h^2 = \frac{V_A}{V_P}$

with $V_P = V_G + V_E$. h^2 is the regression coefficient between parent and offspring genetic values. Thus, $h^2 = 1$ if only additive effects are modeled and $V_E = 0$.

It is generally assumed that $V_m \simeq 10^{-4}$ to $10^{-3} \times V_E$. We often set $V_m \simeq 10^{-4}$ to 10^{-3} as a general baseline, even if $V_E = 0$.

Parameterization of quant trait

Basic scaling:

Mutational variance: $V_m = 2L\mu\sigma_a^2 \simeq 10^{-4}$ to 10^{-3}

Environmental variance: $V_E = 0$

Heritability: $h^2 = \frac{V_A}{V_P} = 1$

Continuous loci: one locus spans a whole sequence block, e.g. $>1\text{kb}$, then $\mu \geq 10^{-4}$, which allows for the following scaling: $\sigma_a^2 \simeq 1/2L$ to $10/2L$ to reach $V_m \simeq 10^{-4}$ to 10^{-3} . Thus for $L = 100$, $\sigma_a^2 = \{0.005, 0.05\}$.

Parameterization of quant trait

Basic scaling:

Mutational variance: $V_m = 2L\mu\sigma_a^2 \simeq 10^{-4}$ to 10^{-3}

Environmental variance: $V_E = 0$

Heritability: $h^2 = \frac{V_A}{V_P} = 1$

Continuous loci: one locus spans a whole sequence block, e.g. $>1\text{kb}$, then $\mu \geq 10^{-4}$, which allows for the following scaling: $\sigma_a^2 \simeq 1/2L$ to $10/2L$ to reach $V_m \simeq 10^{-4}$ to 10^{-3} . Thus for $L = 100$, $\sigma_a^2 = \{0.005, 0.05\}$.

Diallelic loci: one locus is a nucleotide (SNP), then $\mu \simeq 10^{-8}$ to 10^{-6} . Remembering that for additive effects $\pm a$ (or scaled $\{0, 2a\}$), $\sigma_a^2 \simeq 2a^2$, then for $\mu = 10^{-6} \mapsto a \simeq \sqrt{10^2/2L}$ to $\sqrt{10^3/2L}$, which for $L = 10000$ would give $a \sim \in [0.07, 0.22]$.

Parameterization of quant trait

Further scaling:

Mutational variance: $V_m = 2L\mu\sigma_a^2 \simeq 10^{-4}$

Gaussian model: assumes many mutations of small effects, for instance $\mu = 10^{-3}$ and $\sigma_a^2 = 0.001$ for $L = 100$ (Lande).

House-of-Cards model: assumes few mutations of larger effects, for instance $\mu = 10^{-5}$ and $\sigma_a^2 = 0.1$ for $L = 100$ (Turelli).

Parameterization of quant trait

Further scaling:

Mutational variance: $V_m = 2L\mu\sigma_a^2 \simeq 10^{-4}$

Gaussian model: assumes many mutations of small effects, for instance $\mu = 10^{-3}$ and $\sigma_a^2 = 0.001$ for $L = 100$ (Lande).

House-of-Cards model: assumes few mutations of larger effects, for instance $\mu = 10^{-5}$ and $\sigma_a^2 = 0.1$ for $L = 100$ (Turelli).

⇒ It is recommended to match the House-of-Card model rather than the Gaussian model.

Validation of quant trait

Expectations:

mutation-drift equilibrium all models:

$$2V_m N_e$$

mutation-(drift)-selection equilibrium: depends on mutational model

Gaussian model: no drift

$$2L\sqrt{\mu\sigma_a^2 V_S}$$

House-of-Cards model: with drift

$$\frac{2V_m N_e}{1 + N_e \sigma_a^2 / V_S}$$

$\Rightarrow V_S$ is the *inverse* of the strength of stabilizing selection.

Validation of quant trait

Expectations:

mutation-drift equilibrium all models:

$$2V_m N_e$$

mutation-(drift)-selection equilibrium: depends on mutational model

Gaussian model: no drift

$$2L\sqrt{\mu\sigma_a^2 V_S}$$

House-of-Cards model: with drift

$$\frac{2V_m N_e}{1 + N_e \sigma_a^2 / V_S}$$

⇒ V_S is the *inverse* of the strength of stabilizing selection.

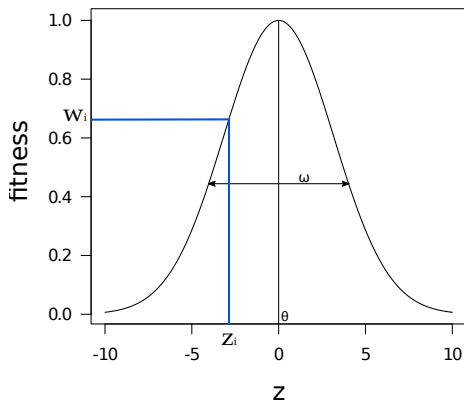
⇒ The stochastic House-of-Card expectation is more general than the Gaussian model.

Selection on quantitative traits

The Gaussian model:

$$W(z_i) = \exp\left[-\frac{(z_i - \theta_j)^2}{2\omega^2}\right],$$

with z_i the phenotypic value of individual i , θ_j the phenotypic *optimum* in patch j , ω^2 the width (variance) of the selection surface. Note that $V_S = \omega^2 + V_E$. The *strength* of selection is *inversely* proportional to ω^2 (V_S).



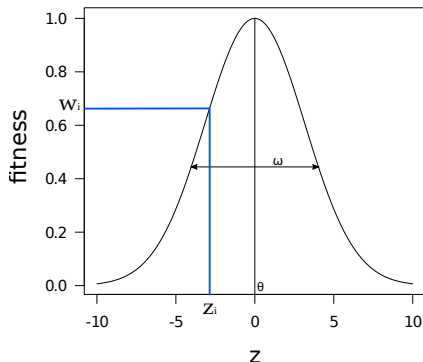
Selection on quantitative traits

The Gaussian model:

$$W(z_i) = \exp\left[-\frac{(z_i - \theta_j)^2}{2\omega^2}\right],$$

with z_i the phenotypic value of individual i , θ_j the phenotypic *optimum* in patch j , ω^2 the width (variance) of the selection surface. Note that $V_S = \omega^2 + V_E$. The *strength* of selection is *inversely* proportional to ω^2 (V_S).

- With this model of *stabilizing selection* on an optimum trait value, we can simulate *local adaptation* within a patch.



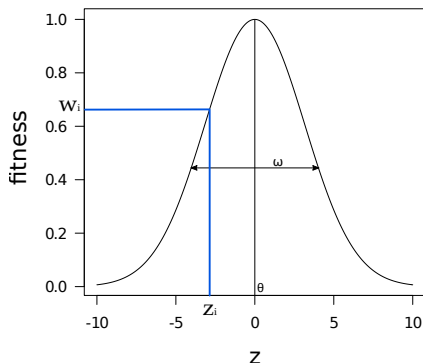
Selection on quantitative traits

The Gaussian model:

$$W(z_i) = \exp\left[-\frac{(z_i - \theta_j)^2}{2\omega^2}\right],$$

with z_i the phenotypic value of individual i , θ_j the phenotypic *optimum* in patch j , ω^2 the width (variance) of the selection surface. Note that $V_S = \omega^2 + V_E$. The *strength* of selection is *inversely* proportional to ω^2 (V_S).

- With this model of *stabilizing selection* on an optimum trait value, we can simulate *local adaptation* within a patch.
- By setting different optimum values in different patches, we can also simulate adaptation to variable environments.



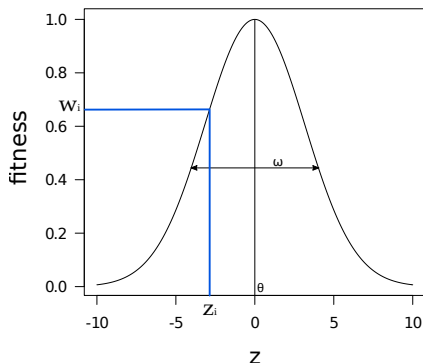
Selection on quantitative traits

The Gaussian model:

$$W(z_i) = \exp\left[-\frac{(z_i - \theta_j)^2}{2\omega^2}\right],$$

with z_i the phenotypic value of individual i , θ_j the phenotypic *optimum* in patch j , ω^2 the width (variance) of the selection surface. Note that $V_S = \omega^2 + V_E$. The *strength* of selection is *inversely* proportional to ω^2 (V_S).

- With this model of *stabilizing selection* on an optimum trait value, we can simulate *local adaptation* within a patch.
- By setting different optimum values in different patches, we can also simulate adaptation to variable environments.
- We can also vary the optimum values through time to simulate adaptation to changing environmental conditions.



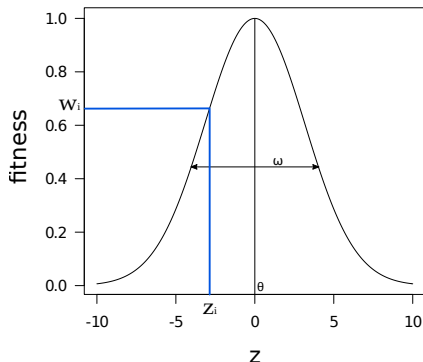
Selection on quantitative traits

The Gaussian model:

$$W(z_i) = \exp\left[-\frac{(z_i - \theta_j)^2}{2\omega^2}\right],$$

with z_i the phenotypic value of individual i , θ_j the phenotypic *optimum* in patch j , ω^2 the width (variance) of the selection surface. Note that $V_S = \omega^2 + V_E$. The *strength* of selection is *inversely* proportional to ω^2 (V_S).

- With this model of *stabilizing selection* on an optimum trait value, we can simulate *local adaptation* within a patch.
- By setting different optimum values in different patches, we can also simulate adaptation to variable environments.
- We can also vary the optimum values through time to simulate adaptation to changing environmental conditions.
- Nemo can model adaptation to many climatic conditions via selection on many traits.



Practice: basic models for validation

① Mutation-drift model in one WF pop:

- Re-use previous simulation file for a single WF pop without selection.
- Replace the `ntr1` trait parameter with those for the `quant` trait.

continuous quanti trait

```
quanti_traits          1
quanti_loci            100
quanti_allele_model    continuous
quanti_mutation_rate   1e-5
quanti_mutation_variance 0.1    #HoC setting  $V_m=200*1e-5*0.1=2e-4$ 
quanti_recombination_rate 1e-3
quanti_init_model      0
stat                   adlt.quanti
```

- Make multiple replicates and check that `stat adlt.q1.Va` equilibrates around the neutral expectation of $V_A = 2V_mN_e$.

Practice: basic models for validation

② Mutation-selection-drift model in one WF pop:

- Add selection parameters to the previous simulation:

add parameters of the Gaussian model

```
breed_selection      1  #with standard parameters for a WF pop
...
selection_trait      quant
selection_model      gaussian
selection_trait_dimension 1  # selection on a single trait
selection_local_optima 0  # optimum trait value on the patch
selection_variance    10  #this is w^2; 10=rather strong selection
```

- Make multiple replicates and check that `stat.adlt.q1.Va` equilibrates around the HoC expectation of $V_A = 2V_mN_e/(1 + N_e\sigma_a^2/V_S)$, where V_S is given by `selection_variance`, and σ_a^2 by `quantumutation_variance`.

Exercise 1: local adaptation with migration on a gradient

① Build a lattice model with gradual variation of local conditions

- Create a 10x10 lattice with patch of size = 100, range = 1, border = absorbing, rate = 0.001.
- Local optimum trait value increases gradually from left to right, column-wise.
- Initialize the trait so that patches start at their optimum (`quanti_init` LCE).

dispersal matrix:

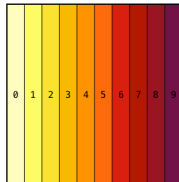
1	2	3	4	5	6	7	8	9	10
11	12	13	14	15	16	17	18	19	20
21		23							30
31			34						40
41				45					50
51					56				60
61						67			70
71							78		80
81								89	90
91	92	93	94	95	96	97	98	99	100

local optima: $\{\{0\}\{1\}\{2\}\{3\}\{4\}\{5\}\{6\}\{7\}\{8\}\{9\}\}$

0	1	2	3	4	5	6	7	8	9
---	---	---	---	---	---	---	---	---	---



0	1	2	3	4	5	6	7	8	9
---	---	---	---	---	---	---	---	---	---



same with `quanti_init_trait_values`

- Set $V_S = 10$ in all patches.

Exercise 1: local adaptation with migration on a gradient

① Monitor the demography and local adaptation

- Run 5000 generations.
- Population model in non-WF (demographic stochasticity). Specify `mean_fecundity` ≥ 3 .
- Record patch sizes, mean trait and fitness values within patches, *after* selection but *before* dispersal. Adjust the life cycle accordingly.
- Record patch state every 100 generations. Record within patch size, mean fitness and trait values, V_A and global `quant` stats.
- Show how population density, mean fitness and trait values (=local adaptation) vary with the `dispersal_rate = 0.001 ... 0.1` across the whole range. Plot spatial variation of those stats.

Exercise 2: persistence on a shifting gradient

② Implement a constant shift of the gradient over time

- Use parameter `selection_rate_environmental_change` .
- Do a burn-in of 5000 generations before starting the shift for 5000 more generations.
- Monitor population density and persistence across the range. Do all population persists? How does persistence depend on the rate of change, the migration rate and the additive variance?

Exercise 3: range expansion on a gradient

And the genetics of adaptation

③ Create a model of range expansion on the grid

- Run 10000 generations.
- Run a burn-in of 5000 generation in the first habitat with $\theta = 0$. The other habitats are empty.

⇒ use a temporal argument to change patch sizes @generation 5000

Initialize $K = 100$ in the first column and $K = 0$ otherwise

```
generations      10000
patch_capacity    (@g0 {{rep(q(c(100,rep(0,9))))}}, @g5000 100)
```

- Model di-allelic loci on a genetic map:

quant trait

```
quanti_trait      1
quanti_loci       100
quanti_mutation_rate 1e-4
quanti_allele_model diallelic_HC
quanti_allele_value 0.1
quanti_random_genetic_map {{rep(10,5)}} #5 chromosomes 10cM each
quanti_genetic_map_resolution 0.1 #min rec rate = 1e-3
quanti_init_model 2 # "polarized" loci, mean trait=0
```


Exercise 3: range expansion on a gradient

And the genetics of adaptation (continued)

- Save the allele frequencies at the end of the simulation for further analyses.

quant trait output

```
quanti_dir          quanti    #relative to the root directory of the simulation
quanti_freq_output            #for di-allelic loci, frequency of the larger allele
quanti_freq_logtime 10000     #only at the last generation
```

- Monitor expansion and local adaptation across the range.
- Find loci which show a cline in allele frequency across habitats.

