

Selection on Multiple Traits

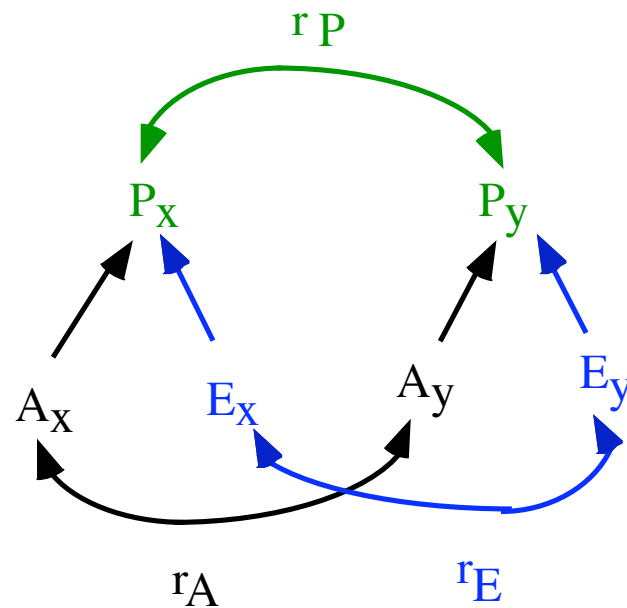
Bruce Walsh lecture notes
Uppsala EQG 2012 course
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Detailed reading: Chapter 30

Genetic vs. Phenotypic correlations

- Within an individual, trait values can be positively or negatively correlated,
 - height and weight -- positively correlated
 - Weight and lifespan -- negatively correlated
- Such phenotypic correlations can be directly measured,
 - r_p denotes the phenotypic correlation
- Phenotypic correlations arise because genetic and/or environmental values within an individual are correlated.

The phenotypic values between traits x and y within an individual are correlated



Correlations between the breeding values of x and y within the individual can generate a phenotypic correlation

Likewise, the environmental values for the two traits within the individual could also be correlated

Genetic & Environmental Correlations

- r_A = correlation in breeding values (the genetic correlation) can arise from
 - pleiotropic effects of loci on both traits
 - linkage disequilibrium, which decays over time
- r_E = correlation in environmental values
 - includes non-additive genetic effects (e.g., D, I)
 - arises from exposure of the two traits to the same individual environment

The relative contributions of genetic and environmental correlations to the phenotypic correlation

$$r_P = r_A h_X h_Y + r_E \sqrt{(1 - h_x^2)(1 - h_Y^2)}$$

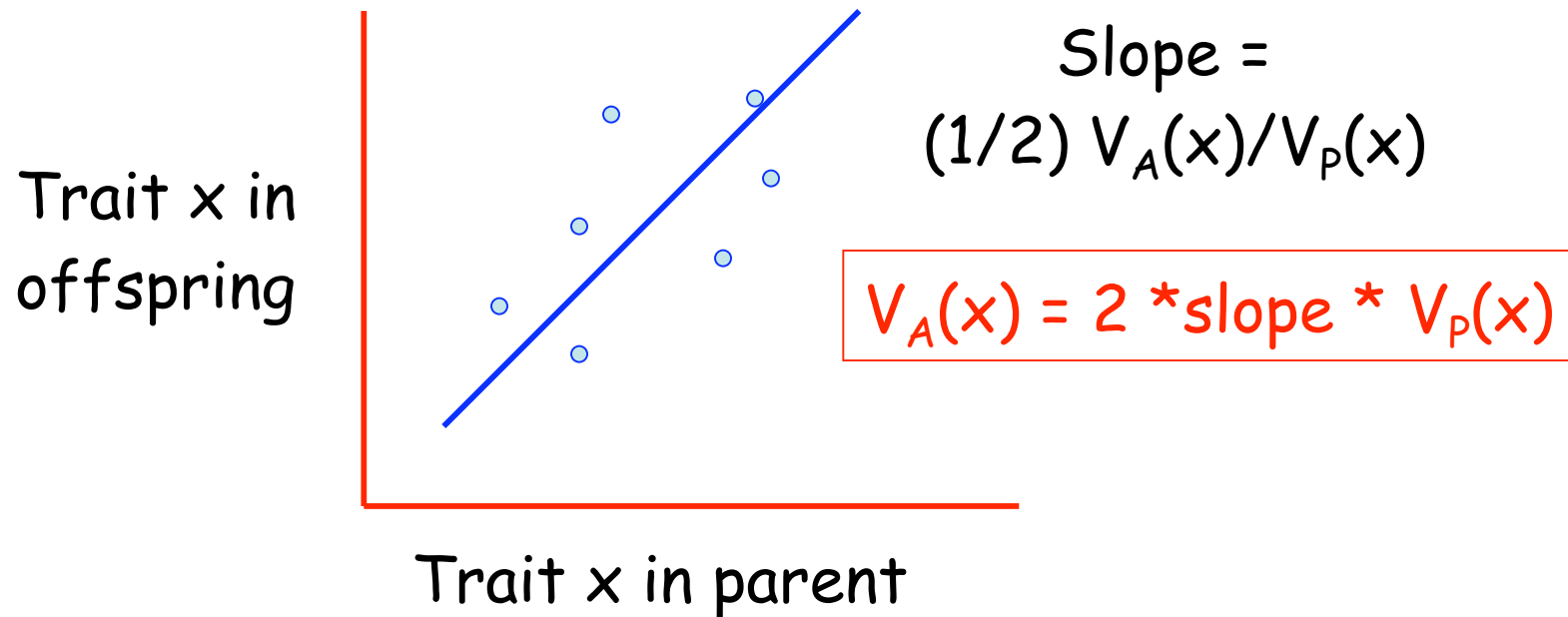
If heritability values are high for both traits, then the correlation in breeding values dominates the phenotypic correlation

If heritability values in EITHER trait are low, then the correlation in environmental values dominates the phenotypic correlation

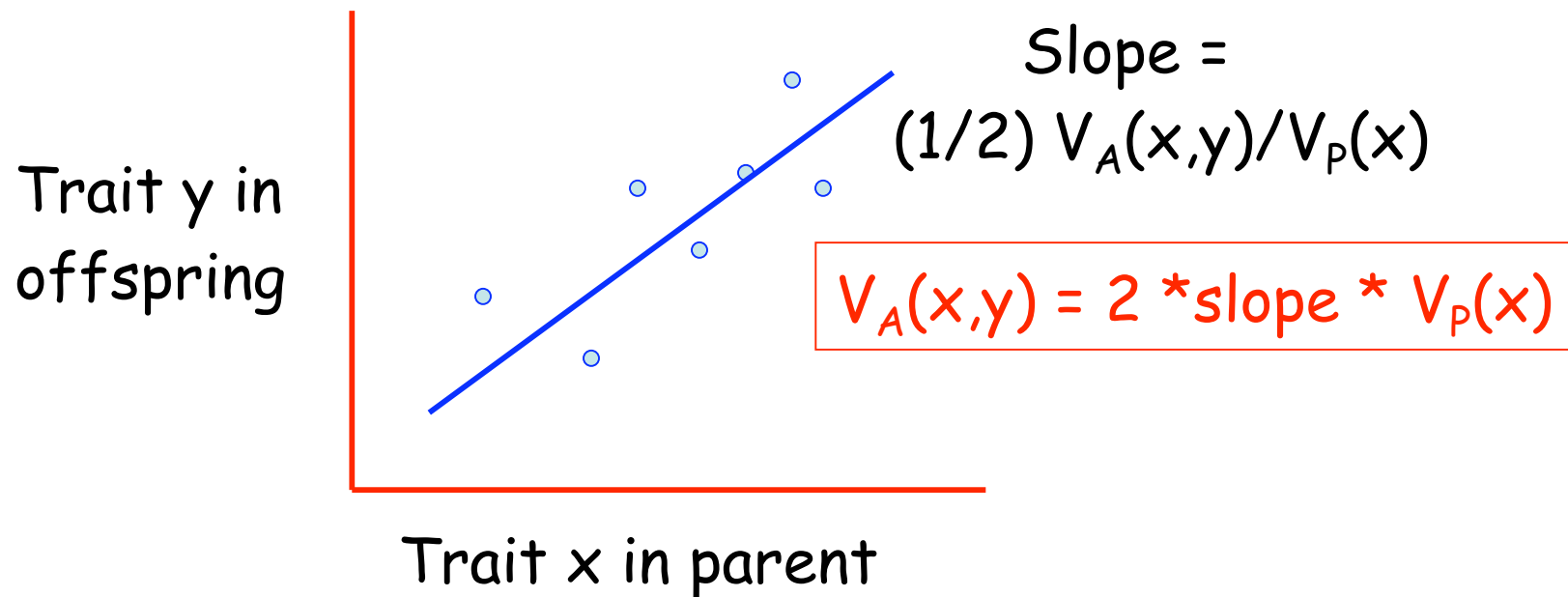
In practice, phenotypic and genetic correlations often have the same sign and are of similar magnitude, but this is not always the case

Estimating Genetic Correlations

Recall that we estimated V_A from the regression of trait x in the parent on trait x in the offspring,



Similarly, we can estimate $V_A(x,y)$, the covariance in the breeding values for traits x and y , by the regression of trait x in the parent and trait y in the offspring



Thus, one estimator of $V_A(x,y)$ is

$$V_A(x,y) = \frac{2 * b_{y|x} * V_P(x) + 2 * b_{x|y} * V_P(y)}{2}$$

$$V_A(x,y) = b_{y|x} V_P(x) + b_{x|y} V_P(y)$$

Put another way,

$$\text{Cov}(x_O, y_P) = \text{Cov}(y_O, x_P) = (1/2) \text{Cov}(A_x, A_y)$$

$$\text{Cov}(x_O, x_P) = (1/2) V_A(x) = (1/2) \text{Cov}(A_x, A_x)$$

$$\text{Cov}(y_O, y_P) = (1/2) V_A(y) = (1/2) \text{Cov}(A_y, A_y)$$

Likewise, for half-sibs,

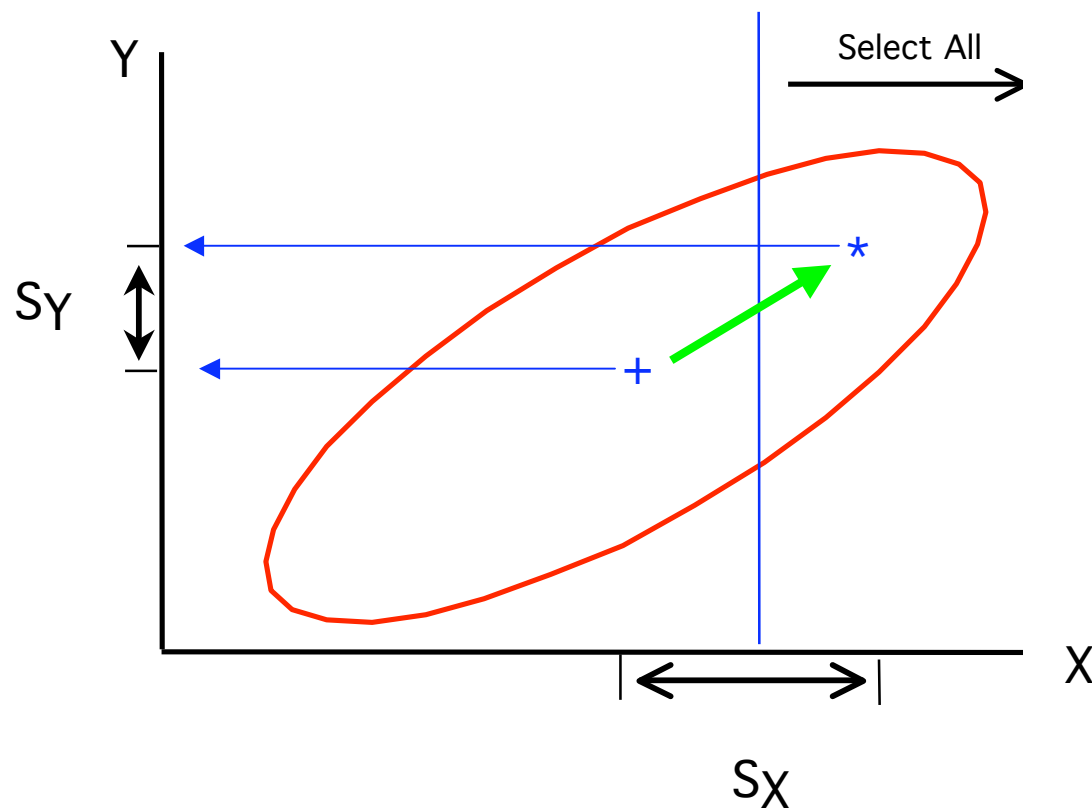
$$\text{Cov}(x_{HS}, y_{HS}) = (1/4) \text{Cov}(A_x, A_y)$$

$$\text{Cov}(x_{HS}, x_{HS}) = (1/4) \text{Cov}(A_x, A_x) = (1/4) V_A(x)$$

$$\text{Cov}(y_{HS}, y_{HS}) = (1/4) \text{Cov}(A_y, A_y) = (1/4) V_A(y)$$

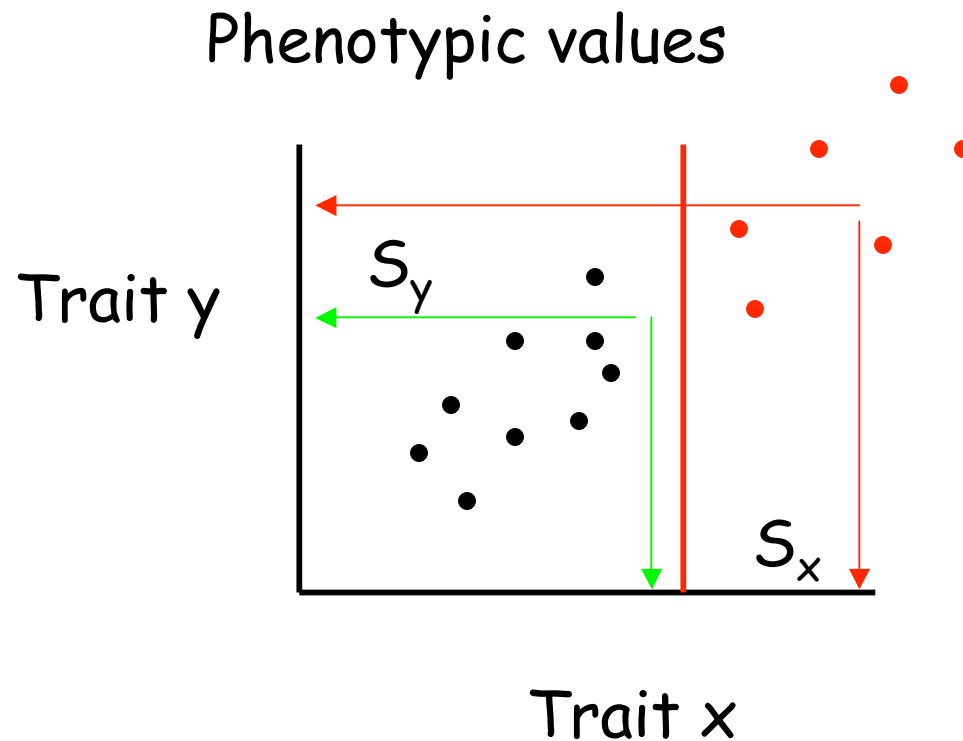
Correlated Response to Selection

Direct selection of a character can cause a within-generation change in the mean of a phenotypically correlated character.



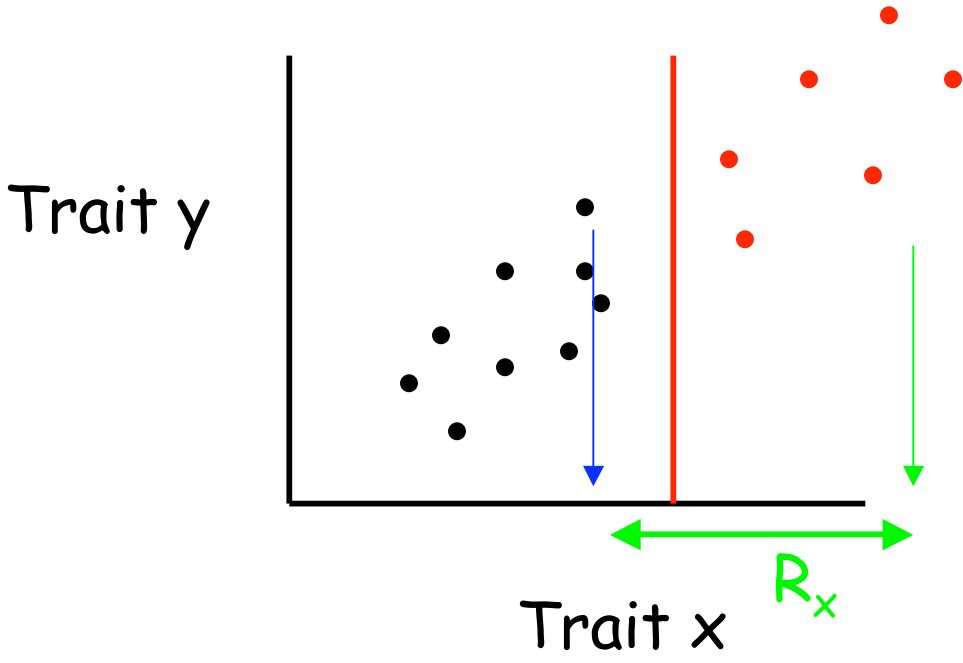
Direct selection on x also changes the mean of y

Phenotypic correlations induce **within-generation changes**

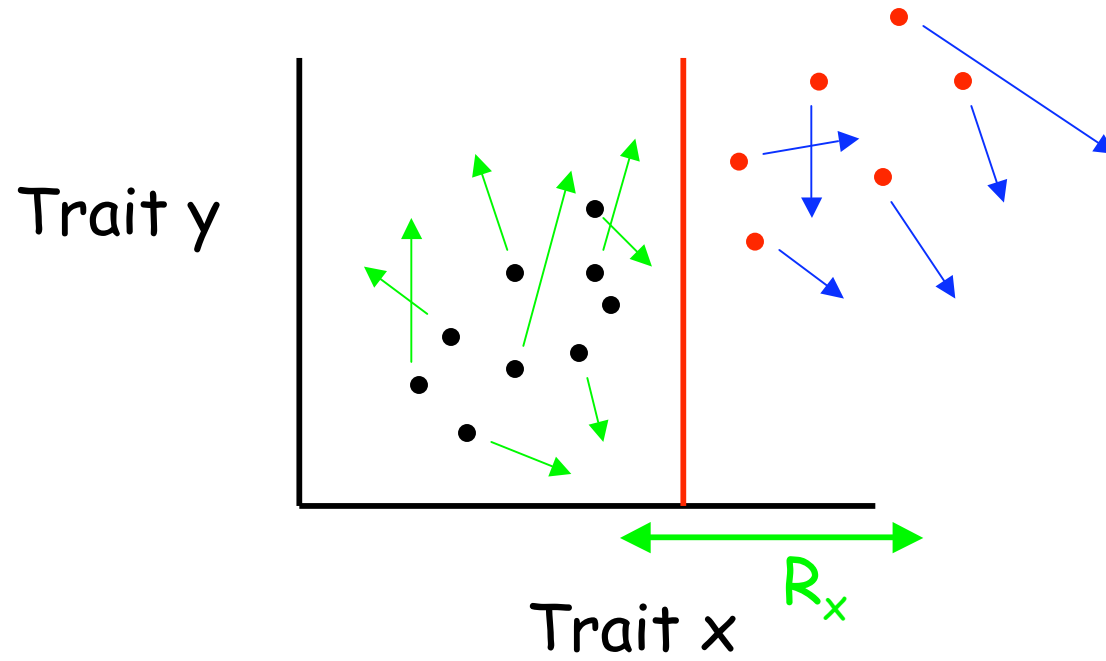


For there to be a **between-generation change**, the **breeding values must be correlated**. Such a change is called a **correlated response to selection**

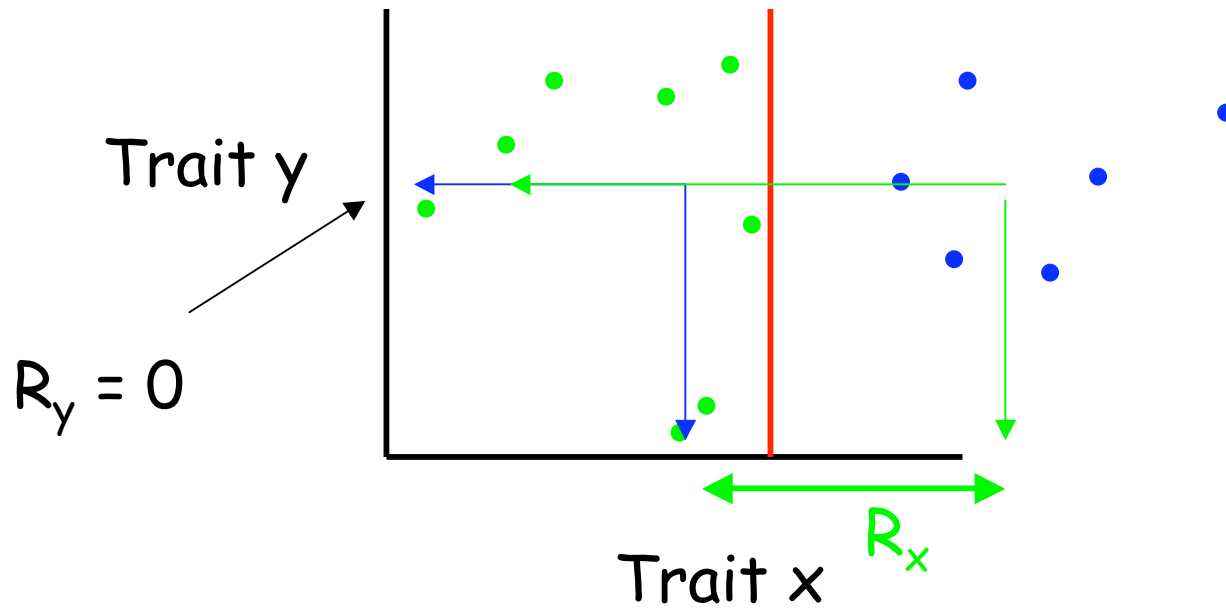
Phenotypic values



Breeding values



Breeding values



Predicting the correlated response

The change in character y in response to selection on x is the regression of the breeding value of y on the breeding value of x ,

where

$$A_y = b_{Ay|Ax} A_x$$
$$b_{Ay|Ax} = \frac{\text{Cov}(A_x, A_y)}{\text{Var}(A_x)} = r_A \frac{\sigma(A_y)}{\sigma(A_x)}$$

If R_x denotes the direct response to selection on x , CR_y denotes the correlated response in y , with

$$CR_y = b_{Ay|Ax} R_x$$

We can rewrite $CR_y = b_{Ay|Ax} R_x$ as follows

First, note that $R_x = h_x^2 S_x = i_x h_x \sigma_A(x)$

Since $b_{Ay|Ax} = r_A \sigma_A(x) / \sigma_A(y)$,

We have $CR_y = b_{Ay|Ax} R_x = r_A \sigma_A(y) h_x i_x$

Substituting $\sigma_A(y) = h_y \sigma_p(y)$ gives our final result:

$$CR_y = i_x h_x h_y r_A \sigma_p(y)$$

Noting that we can also express the direct response as

$$R_x = i_x h_x^2 \sigma_p(x)$$

shows that $h_x h_y r_A$ in the corrected response plays the same role as h_x^2 does in the direct response. As a result,

$h_x h_y r_A$ is often called the **co-heritability**

Estimating the Genetic Correlation from Selection Response

Suppose we have two experiments:

Direct selection on x , record R_x, CR_y

Direct selection on y , record R_y, CR_x

Simple algebra shows that

$$r_A^2 = \frac{CR_x CR_y}{R_x R_y}$$

This is the **realized genetic correlation**, akin to the realized heritability, $h^2 = R/S$

Direct vs. Indirect Response

We can change the mean of x via a direct response R_x or an indirect response CR_x due to selection on y

$$\frac{CR_x}{R_x} = \frac{i_Y r_A \sigma_{AX} h_Y}{i_X h_X \sigma_{AX}} = \frac{i_Y r_A h_Y}{i_X h_X}$$

Hence, indirect selection gives a large response when

$$i_Y r_A h_Y > i_X h_X$$

- Character y has a greater heritability than x , and the genetic correlation between x and y is high. This could occur if x is difficult to measure with precision but y is not.
- The selection intensity is much greater for y than x . This would be true if y were measurable in both sexes but x measurable in only one sex.

The Multivariate Breeders' Equation

Suppose we are interested in the vector R of responses when selection occurs on n correlated traits

Let S be the vector of selection differentials.

In the univariate case, the relationship between R and S was the Breeders' Equation, $R = h^2 S$

What is the multivariate version of this?

To obtain this, recall some facts from the MVN:

Suppose the vector \mathbf{x} follows a MVN distribution.

$$\mathbf{x} = \begin{pmatrix} \mathbf{x}_1 \\ \mathbf{x}_2 \end{pmatrix}$$

$$\boldsymbol{\mu} = \begin{pmatrix} \boldsymbol{\mu}_1 \\ \boldsymbol{\mu}_2 \end{pmatrix} \quad \text{and} \quad \mathbf{V} = \begin{pmatrix} \mathbf{V}_{\mathbf{x}_1\mathbf{x}_1} & \mathbf{V}_{\mathbf{x}_1\mathbf{x}_2} \\ \mathbf{V}_{\mathbf{x}_1\mathbf{x}_2}^T & \mathbf{V}_{\mathbf{x}_2\mathbf{x}_2} \end{pmatrix}$$

The conditional mean of the subvector \mathbf{x}_1 given \mathbf{x}_2 is

$$\boldsymbol{\mu}_{\mathbf{x}_1|\mathbf{x}_2} = \boldsymbol{\mu}_1 + \mathbf{V}_{\mathbf{x}_1\mathbf{x}_2} \mathbf{V}_{\mathbf{x}_2\mathbf{x}_2}^{-1} (\mathbf{x}_2 - \boldsymbol{\mu}_2)$$

Which has associated covariance matrix

$$\mathbf{V}_{\mathbf{x}_1|\mathbf{x}_2} = \mathbf{V}_{\mathbf{x}_1\mathbf{x}_1} - \mathbf{V}_{\mathbf{x}_1\mathbf{x}_2} \mathbf{V}_{\mathbf{x}_2\mathbf{x}_2}^{-1} \mathbf{V}_{\mathbf{x}_1\mathbf{x}_2}^T$$

The conditional distribution of x_1 given x_2 is also MVN

In particular, the regression of x_1 on x_2 is given by

$$\mathbf{x}_1 = \boldsymbol{\mu}_1 + \mathbf{V}_{\mathbf{x}_1\mathbf{x}_2} \mathbf{V}_{\mathbf{x}_2\mathbf{x}_2}^{-1} (\mathbf{x}_2 - \boldsymbol{\mu}_2) + \mathbf{e}$$

Where the vector of residual errors is MVN, with

$$\mathbf{e} \sim \text{MVN}_m(\mathbf{0}, \mathbf{V}_{\mathbf{x}_1|\mathbf{x}_2})$$

Suppose $\mathbf{z} = \mathbf{g} + \mathbf{e}$, where both \mathbf{g} and \mathbf{e} are MVN.
In this case, \mathbf{z} is also MVN

The covariance matrix between \mathbf{g} and \mathbf{z} is

$$\sigma(\mathbf{g}, \mathbf{z}) = \sigma(\mathbf{g}, \mathbf{g} + \mathbf{e}) = \sigma(\mathbf{g}, \mathbf{g}) = \mathbf{G}$$

Hence,

$$\begin{pmatrix} \mathbf{g} \\ \mathbf{z} \end{pmatrix} \sim \text{MVN} \left(\begin{pmatrix} \boldsymbol{\mu} \\ \boldsymbol{\mu} \end{pmatrix}, \begin{pmatrix} \mathbf{G} & \mathbf{G} \\ \mathbf{G} & \mathbf{P} \end{pmatrix} \right)$$

From the previous MVN results, the regression of the vector of breeding values \mathbf{g} on the vector of phenotypic values \mathbf{z} is

$$\mathbf{g} - \boldsymbol{\mu} = \mathbf{G}\mathbf{P}^{-1}(\mathbf{z} - \boldsymbol{\mu}) + \mathbf{e}$$

$$\mathbf{g} - \boldsymbol{\mu} = \mathbf{GP}^{-1}(\mathbf{z} - \boldsymbol{\mu}) + \mathbf{e}$$

Since the offspring mean equals the mean breeding value of the parents, applying the above regression averaged over the selected parents gives the response

$$\begin{aligned}\Delta \boldsymbol{\mu} &= E[\mathbf{GP}^{-1}(\mathbf{z} - \boldsymbol{\mu}) + \mathbf{e}] \\ &= \mathbf{GP}^{-1}E[(\mathbf{z} - \boldsymbol{\mu})] + E(\mathbf{e}) \\ &= \mathbf{GP}^{-1}\mathbf{S}\end{aligned}$$

The multivariate breeders' equation

$$R = G P^{-1} S$$

$$R = h^2 S = (V_A / V_P) S$$

Natural parallels
with univariate
breeders equation

$P^{-1} S = \beta$ is called the **selection gradient**
and measures the amount of direct selection
on a character

The gradient version of the breeders' Equation is

$$R = G \beta$$

Often called the **Lande Equation**

Sources of within-generation change in the mean

Since $\beta = P^{-1} S$, $S = P \beta$,

Within-generation
change in trait j

$$S_j = \sigma^2(P_j) \beta_j + \sum_{i \neq j} \sigma(P_j, P_i) \beta_i$$

Change in mean
from **direct**
selection on trait j

Change in mean from
phenotypically
correlated characters
under direct selection

$$S_j = \sigma^2(P_j) \beta_j + \sum_{i \neq j} \sigma(P_j, P_i) \beta_i$$

Between-generation
change in trait j

$$R_j = \sigma^2(A_j) \beta_j + \sum_{i \neq j} \sigma(A_j, A_i) \beta_i$$

Response from **direct**
selection on trait j

Indirect response from
genetically correlated characters
under direct selection

Realized Selection Gradients

Suppose we observe a difference in the vector of means for two populations, $\mathbf{R} = \mu_1 - \mu_2$.

If we are willing to assume they both have a common \mathbf{G} matrix that has remained constant over time, then we can estimate the nature and amount of selection generating this difference by

$$\beta = \mathbf{G}^{-1} \mathbf{R}$$

Example: You are looking at nose length (z_1) and head size (z_2) in two populations of mice. The mainland population has $\mu_1 = 20$ and $\mu_2 = 30$, while on an island, $\mu_1 = 10$ and $\mu_2 = 35$.

Here

$$\mathbf{R} = \begin{pmatrix} 20 & -10 \\ 30 & -35 \end{pmatrix} = \begin{pmatrix} 10 \\ -5 \end{pmatrix}$$

Suppose the variance-covariance matrix has been stable and equal in both populations, with

$$\mathbf{G} = \begin{pmatrix} 20 & -10 \\ -10 & 40 \end{pmatrix}$$

The amount of selection on both traits to obtain this response is

$$\boldsymbol{\beta} = \begin{pmatrix} 20 & -10 \\ -10 & 40 \end{pmatrix}^{-1} \begin{pmatrix} 10 \\ -5 \end{pmatrix} = \begin{pmatrix} 0.5 \\ 0 \end{pmatrix}$$

Evolutionary Constraints Imposed by Genetic Correlations

While β is the directional optimally favored by selection, the actual response is dragged off this direction, with $R = G \beta$.

Example: Suppose

$$\mathbf{S} = \begin{pmatrix} 10 \\ -10 \end{pmatrix}, \quad \mathbf{P} = \begin{pmatrix} 20 & -10 \\ -10 & 40 \end{pmatrix}, \quad \mathbf{G} = \begin{pmatrix} 20 & 5 \\ 5 & 10 \end{pmatrix}$$

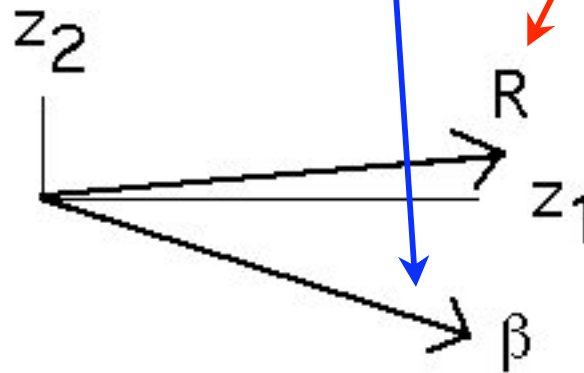
What is the true nature of selection on the two traits?

$$\beta = \mathbf{P}^{-1} \mathbf{S} = \mathbf{P}^{-1} \begin{pmatrix} 10 \\ -10 \end{pmatrix} = \begin{pmatrix} 0.43 \\ -0.14 \end{pmatrix}$$

What does the actual response look like?

$$\mathbf{R} = \mathbf{G}\boldsymbol{\beta} = \begin{pmatrix} 20 & 5 \\ 5 & 10 \end{pmatrix} \begin{pmatrix} 0.43 \\ -0.14 \end{pmatrix} = \begin{pmatrix} 7.86 \\ 0.71 \end{pmatrix}$$

Direction favored
by selection



Direction of
response

Time for a short diversion: The Geometry of a matrix

A vector is a geometric object, leading from the origin to a specific point in n-space.

Hence, a vector has a **length** and a **direction**.

We can thus change a vector by both rotation and scaling

The length (or **norm**) of a vector \mathbf{x} is denoted by **$\|\mathbf{x}\|$**

$$\|\mathbf{x}\| = \sqrt{x_1^2 + x_2^2 + \cdots + x_n^2} = \sqrt{\mathbf{x}^T \mathbf{x}}$$

The (**Euclidean**) distance between two vectors \mathbf{x} and \mathbf{y} (of the same dimension) is

$$\|\mathbf{x}-\mathbf{y}\|^2 = \sum_{i=1}^n (x_i - y_i)^2 = (\mathbf{x}-\mathbf{y})^T (\mathbf{x}-\mathbf{y}) = (\mathbf{y}-\mathbf{x})^T (\mathbf{y}-\mathbf{x})$$

The angle θ between two vectors provides a measure for how they differ.

If two vectors satisfy $\mathbf{x} = a\mathbf{y}$ (for a constant a), then they point in the same direction, i.e., $\theta = 0$ (Note that $a < 0$ simply reflects the vector about the origin)

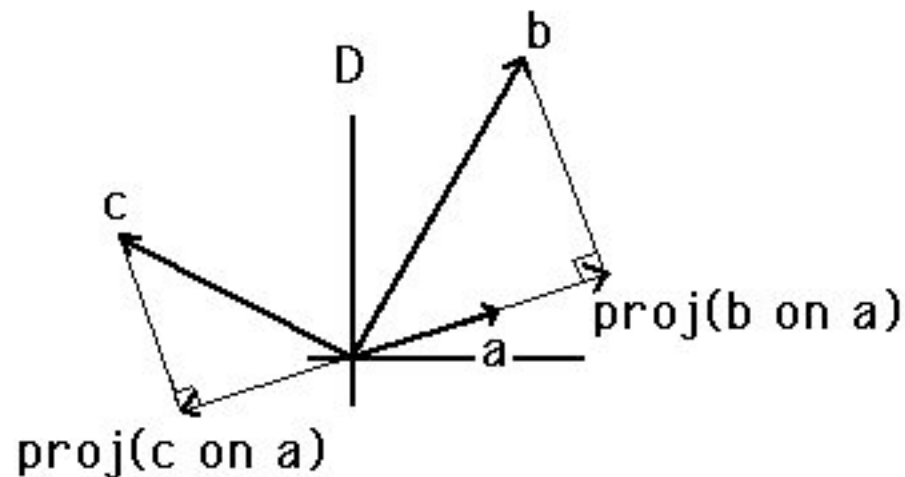
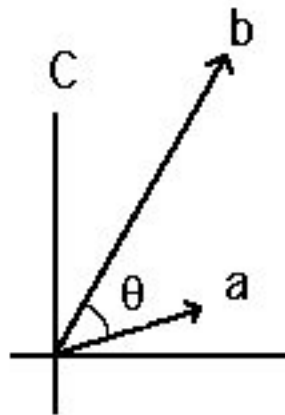
Vectors at right angles to each other, $\theta = 90^\circ$ or 270° are said to be **orthogonal**. If they have unit length as well, they are further said to be **orthonormal**.

The angle θ between two vectors is given by

$$\cos(\mu) = \frac{\mathbf{x}^T \mathbf{y}}{\|\mathbf{x}\| \|\mathbf{y}\|} = \frac{\mathbf{y}^T \mathbf{x}}{\|\mathbf{x}\| \|\mathbf{y}\|}$$

Thus, the vectors \mathbf{x} and \mathbf{y} are orthogonal **if and only if** $\mathbf{x}^T \mathbf{y} = 0$

The angle between two vectors ignores their lengths. A second way to compare vectors is the **projection** of one vector onto another



This projection is given by

Projection in the same direction as y

$$\text{Proj}(\mathbf{x} \text{ on } \mathbf{y}) = \frac{\mathbf{x}^T \mathbf{y}}{\mathbf{y}^T \mathbf{y}} \mathbf{y} = \frac{\mathbf{x}^T \mathbf{y}}{\|\mathbf{y}\|^2} \mathbf{y} = \left(\cos(\mu) \frac{\|\mathbf{x}\|}{\|\mathbf{y}\|} \right) \mathbf{y}$$

fraction of length of x that projects onto y

Note if x and y are orthogonal, then the projection is a vector of length zero.

At the other extreme, if x and y point in the same direction, the projection of x on y recovers x .

If we have a set y_1, \dots, y_n of mutually orthogonal n dimensional vectors, then any n dimensional vector x can be written as

$$\mathbf{x} = \sum_{i=1}^n \text{Proj}(\mathbf{x} \text{ on } \mathbf{y}_i)$$

Matrices Describe Vector transformations

Matrix multiplication results in a **rotation** and a **scaling** of a vector

The action of multiplying a vector x by a matrix A generates a new vector $y = Ax$, that has different dimension from x unless A is square.

Thus A describes a **transformation** of the original coordinate system of x into a new coordinate system.

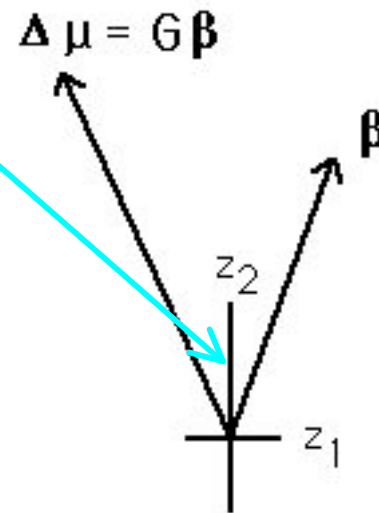
Example: Consider the following G and β :

$$\mathbf{G} = \begin{pmatrix} 4 & -2 \\ -2 & 2 \end{pmatrix} \quad \beta = \begin{pmatrix} 1 \\ 3 \end{pmatrix}, \quad \mathbf{R} = \mathbf{G}\beta = \begin{pmatrix} -2 \\ 4 \end{pmatrix}$$

The resulting angle between \mathbf{R} and β is given by

$$\cos \mu = \frac{\beta^T \mathbf{R}}{\|\mathbf{R}\| \|\beta\|} = \frac{1}{\sqrt{2}}$$

For an angle of $\theta = 45^\circ$



Eigenvalues and Eigenvectors

The **eigenvalues** and their associated **eigenvectors** fully describe the geometry of a matrix.

Eigenvalues describe how the original coordinate axes are **scaled** in the new coordinate systems

Eigenvectors describe how the original coordinate axes are **rotated** in the new coordinate systems

For a square matrix A , any vector y that satisfies $Ay = \lambda y$ for some scalar λ is said to be an eigenvector of A and λ its associated eigenvalue.

Note that if y is an eigenvector, then so is a^*y for any scalar a , as $Ay = \lambda y$.

Because of this, we typically take eigenvectors to be scaled to have unit length (their norm = 1)

An eigenvalue λ of A satisfies the equation $\det(A - \lambda I) = 0$, where \det = determinant

For an n -dimensional square matrix, this yields an n -degree polynomial in λ and hence up to n unique roots.

Two nice features:

$\det(A) = \prod_i \lambda_i$. The determinant is the product of the eigenvalues

$\text{trace}(A) = \sum_i \lambda_i$. The **trace** (sum of the diagonal elements) is the sum of the eigenvalues

Note that $\det(A) = 0$ if and only if at least one eigenvalue = 0

For symmetric matrices (such as covariance matrices) the resulting n eigenvectors are mutually orthogonal, and we can factor A into its **spectral decomposition**,

$$\mathbf{A} = \lambda_1 \mathbf{e}_1 \mathbf{e}_1^T + \lambda_2 \mathbf{e}_2 \mathbf{e}_2^T + \cdots + \lambda_n \mathbf{e}_n \mathbf{e}_n^T$$

Hence, we can write the product of any vector \mathbf{x} and A as

$$\begin{aligned} \mathbf{A}\mathbf{x} &= \lambda_1 \mathbf{e}_1 \mathbf{e}_1^T \mathbf{x} + \lambda_2 \mathbf{e}_2 \mathbf{e}_2^T \mathbf{x} + \cdots + \lambda_n \mathbf{e}_n \mathbf{e}_n^T \mathbf{x} \\ &= \lambda_1 \text{Proj}(\mathbf{x} \text{ on } \mathbf{e}_1) + \lambda_2 \text{Proj}(\mathbf{x} \text{ on } \mathbf{e}_2) + \cdots + \lambda_n \text{Proj}(\mathbf{x} \text{ on } \mathbf{e}_n) \end{aligned}$$

Example: Let's reconsider a previous G matrix

$$\begin{aligned} |\mathbf{G} - \lambda\mathbf{I}| &= \left| \begin{pmatrix} 4 - \lambda & -2 \\ -2 & 2 - \lambda \end{pmatrix} \right| \\ &= (4 - \lambda)(2 - \lambda) - (-2)^2 = \lambda^2 - 6\lambda + 4 = 0 \end{aligned}$$

The solutions are

$$\lambda_1 = 3 + \sqrt{5} \simeq 5.236 \quad \lambda_2 = 3 - \sqrt{5} \simeq 0.764$$

The corresponding eigenvectors become

$$\mathbf{e}_1 \simeq \begin{pmatrix} -0.851 \\ 0.526 \end{pmatrix} \quad \mathbf{e}_2 \simeq \begin{pmatrix} 0.526 \\ 0.851 \end{pmatrix}$$

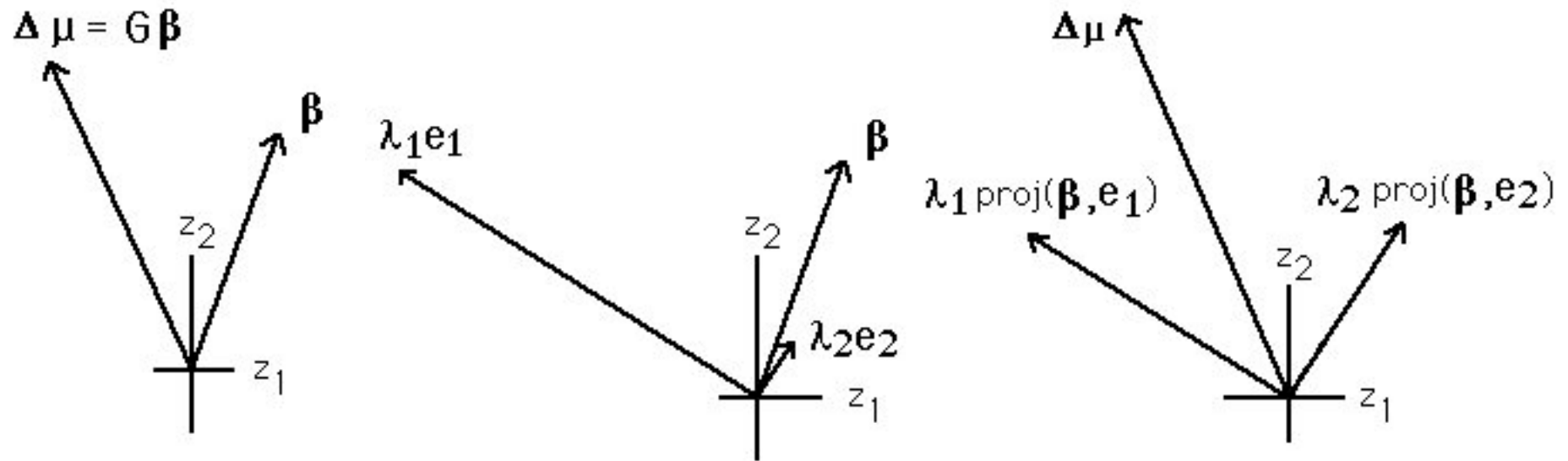
Consider the vector of selection gradients from this example.

$$\cos(\mu|\mathbf{e}_1, \boldsymbol{\beta}) \simeq \frac{0.727}{\sqrt{10}} \simeq 0.201 \quad \text{and} \quad \cos(\mu|\mathbf{e}_2, \boldsymbol{\beta}) \simeq \frac{3.079}{\sqrt{10}} \simeq 0.974$$

Hence, $\boldsymbol{\beta}$ is 78.4° from \mathbf{e}_1 and 13.2° from \mathbf{e}_2 .

The projection of $\boldsymbol{\beta}$ onto these two eigenvectors is

$$\lambda_1 \text{Proj}(\boldsymbol{\beta} \text{ on } \mathbf{e}_1) \simeq \begin{pmatrix} -3.236 \\ 2 \end{pmatrix}, \quad \lambda_2 \text{Proj}(\boldsymbol{\beta} \text{ on } \mathbf{e}_2) \simeq \begin{pmatrix} 1.236 \\ 2 \end{pmatrix}$$



Even though β points in a direction very close of e_2 , because most of the variation is accounted for by e_1 , its projection in this dimension yields a much longer vector. The sum of these two projections yields the selection response R .

Quantifying Multivariate Constraints to Response

Is there genetic variation in the direction of selection?

Consider the following \mathbf{G} and $\boldsymbol{\beta}$:

$$\mathbf{G} = \begin{pmatrix} 10 & 20 \\ 20 & 40 \end{pmatrix}, \quad \boldsymbol{\beta} = \begin{pmatrix} 2 \\ -1 \end{pmatrix}$$

Taken one trait at a time, we might expect $R_i = G_{ii}\beta_i$

Giving $R_1 = 20$, $R_2 = -40$.

What is the actual response?

$$\mathbf{R} = \mathbf{G}\boldsymbol{\beta} = \begin{pmatrix} 0 \\ 0 \end{pmatrix}$$

Real world data: Blows et al. (2004) cuticular hydrocarbons (CHC) in *Drosophila serata*

8 CHCs measured, with the first two eigenvectors of the resulting G matrix accounting for 78% of total variance

These two eigenvectors, along with β are as follows:

$$\mathbf{e}_1 = \begin{pmatrix} 0.232 \\ 0.132 \\ 0.255 \\ 0.536 \\ 0.449 \\ 0.363 \\ 0.430 \\ 0.239 \end{pmatrix}, \quad \mathbf{e}_2 = \begin{pmatrix} 0.319 \\ 0.182 \\ 0.213 \\ -0.436 \\ 0.642 \\ -0.362 \\ -0.014 \\ -0.293 \end{pmatrix}, \quad \beta = \begin{pmatrix} -0.099 \\ -0.055 \\ 0.133 \\ -0.186 \\ -0.133 \\ 0.779 \\ 0.306 \\ -0.465 \end{pmatrix}$$

The angle between \mathbf{e}_1 and β is

$$\cos(\mu) = \frac{\mathbf{e}_1^T \beta}{\|\mathbf{e}_1\| \|\beta\|} = \frac{\mathbf{e}_1^T \beta}{\sqrt{\mathbf{e}_1^T \mathbf{e}_1} \sqrt{\beta^T \beta}} = \frac{0.147496}{\sqrt{0.99896 \cdot 0.999502}} = 0.1476$$

or $\theta = 81.5$ degrees. The $\mathbf{e}_2 - \beta$ angle is 99.65 degrees

Schluter's g_{\max} , Genetic lines of least resistance

The notion of multivariate constraints to response dates back to Dickerson (1955)

It surprisingly took over 40 years to describe the potential geometry of these constraints.

Schluter (1996) defined his **genetic line of least resistance**, g_{\max} , as the first **principal component** (PC) of G (the eigenvector associated with the leading eigenvalue)

Schluter (in a small set of vertebrate morphological data) looked at the angle θ between g_{\max} , and the vector of population divergence

For this small (but diverse) data set, Schluter observed some consistent patterns.

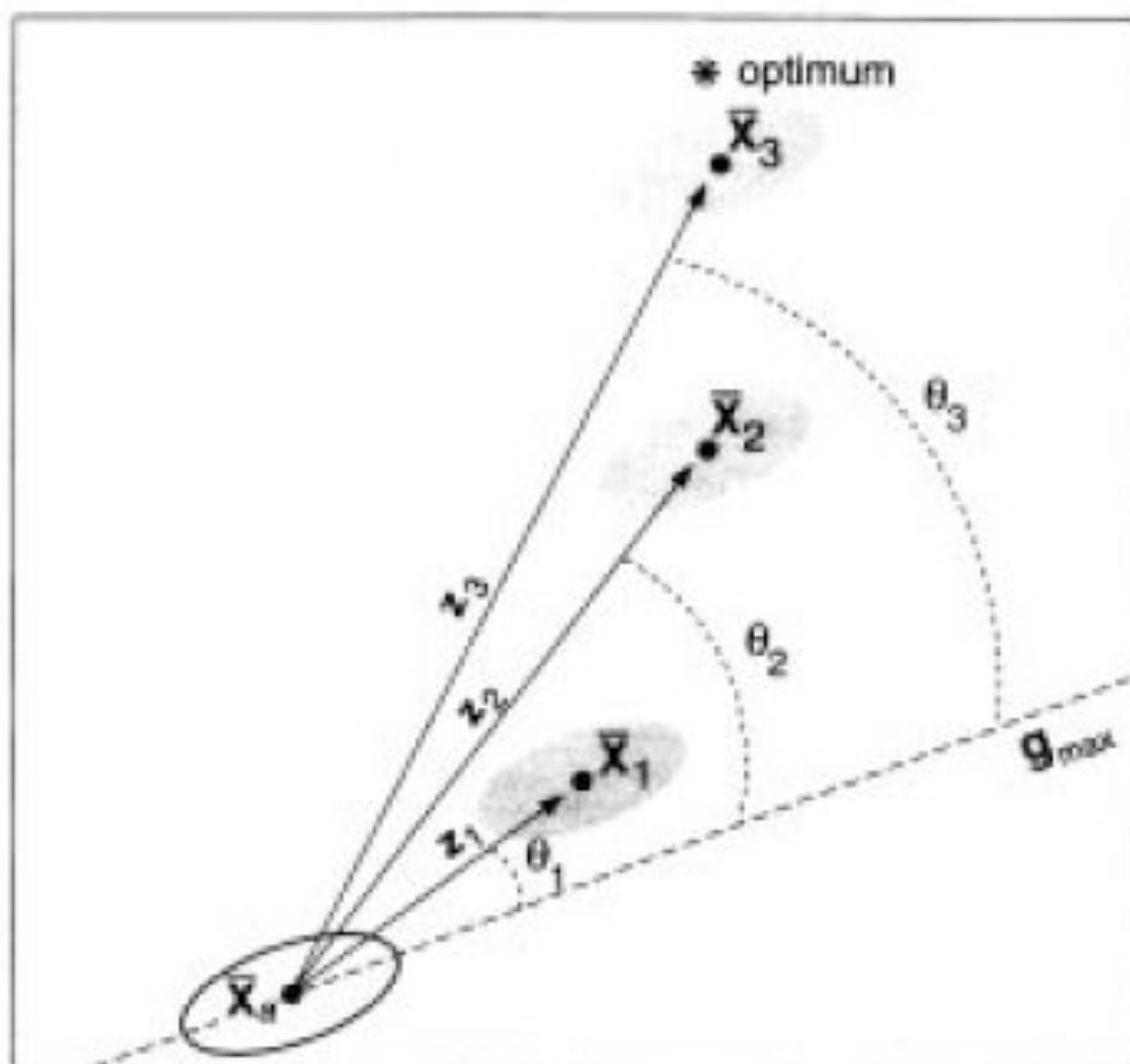
- The smallest values of θ occurred between the most recently diverged species
- The greater the value of θ , the smaller the total amount of divergence.
- The effect of g_{\max} on the absolute amount of divergence showed no tendency to weaken with time (the maximal divergence in the data set was 4MY).

Hence, it appears that populations tend to evolve along the lines of least genetic resistance

Such lines may constrain selection.

However, such lines also have maximal drift variance

Trait 2



Trait 1

McGuigan et al. (2005): Support and counterexamples

Looked at two species of Australian rainbow fish.



Both species have pops. differentially adapted to lake vs. stream hydrodynamic environments.

Divergence between species, as well as divergence between replicate population of the same species in the same hydrodynamic environments followed g_{\max} .

However, same species populations in different hydrodynamic environments were at directions quite removed from g_{\max} , as well as the other major eigenvectors of G .

Hence, between-species and within species divergence in the same hydrodynamic environments consistent with drift.

Within-species adaptation to different hydrodynamic environments occurred against a gradient of little variation

Blow's Matrix Subspace Projection Approach

Schluter's approach only considers the leading eigenvector. How do we treat the case where a few eigenvectors account for most of the variation in G ?

Recall that $\lambda_k / \sum_i \lambda_i = \lambda_k / \text{trace}(G)$ is the fraction of variation accounted for by the k -th eigenvector

A common problem when G contains a number of traits is that it is **ill-conditioned**, with $\lambda_{\max} \gg \lambda_{\min}$. In such cases estimates of the smallest eigenvalues are nearly zero, or even negative do to sampling error

Nearly zero or even negative eigenvalues suggest that there is very little variation in certain dimensions.

Indeed, it is often the case that just a few eigenvalues of G account for the vast majority of variation

Blows et al. (2004) have suggested a **matrix subspace projection** to consider case where just a few eigenvectors of G explain most of the variation. Consider the first k eigenvalues, and use these to define a matrix A

$$\mathbf{A} = (\mathbf{e}_1, \mathbf{e}_2, \dots, \mathbf{e}_k)$$

The projection matrix for this space is defined by

$$\mathbf{P}_{roj} = \mathbf{A} (\mathbf{A}^T \mathbf{A})^{-1} \mathbf{A}^T$$

In particular, the projection vector \mathbf{p} of the selection gradient onto this subspace of G is given by

$$\mathbf{p} = \mathbf{P}_{roj} \boldsymbol{\beta} = \mathbf{A} (\mathbf{A}^T \mathbf{A})^{-1} \mathbf{A}^T \boldsymbol{\beta}$$

Example: Reconsider Blow's CHC data

First two eigenvectors account for 78% of the total variation in G .
The A matrix and resulting projection of β onto this space are

$$\mathbf{A} = (\mathbf{e}_1, \mathbf{e}_2) = \begin{pmatrix} 0.232 & 0.319 \\ 0.132 & 0.182 \\ 0.255 & 0.213 \\ 0.536 & -0.436 \\ 0.449 & 0.642 \\ 0.363 & -0.362 \\ 0.430 & -0.014 \\ 0.239 & -0.293 \end{pmatrix} \quad \mathbf{p} = \mathbf{P}_{roj} \boldsymbol{\beta} = \begin{pmatrix} -0.0192 \\ -0.0110 \\ 0.0019 \\ 0.1522 \\ -0.0413 \\ 0.1142 \\ 0.0658 \\ 0.0844 \end{pmatrix}$$

The angle θ between \mathbf{b} and its projection onto this subspace is just

$$\mu = \cos^{-1} \left(\frac{\mathbf{p}^T \boldsymbol{\beta}}{\sqrt{\mathbf{p}^T \mathbf{p}} \sqrt{\boldsymbol{\beta}^T \boldsymbol{\beta}}} \right) = \cos^{-1} (0.223) = 77.1^\circ$$