Model for quantitative trait evolution

single trait: $R = h^2 s$

amount of phenotypic change (R), depends on amount of V_A (h^2) and strength of selection (s)

several traits: $\Delta\bar{z} = GP^{-1}s = G\beta$

z is the trait vector ($z_1\ z_2\ z_3 \ldots z_n$)

s is still selection differential ($z - z_s$)

G, **P** are the genotypic and phenotypic variance-covariance matrices

β is the selection gradient

$$s_i = \sum P_{ij}\beta_{ij} = \underbrace{P_{i1}\beta_1}_{\text{direct}} + \underbrace{P_{i2}\beta_2 + P_{i3}\beta_3 + \ldots\ldots + P_{in}\beta_n}_{\text{indirect}}$$

β_1 is the partial regression coefficient

Lande & Arnold 1983 Evolution

An extended derivation, for those who want it:

$$\Delta z = G\, P^{-1}\, s$$

genotypic phenotypic

$$\begin{pmatrix} \Delta z_A \\ \Delta z_B \end{pmatrix} = \begin{pmatrix} \sigma^2{}_A & cov_{AB} \\ cov_{BA} & \sigma^2{}_B \end{pmatrix} \begin{pmatrix} \sigma^2{}_A & cov_{AB} \\ cov_{BA} & \sigma^2{}_B \end{pmatrix}^{-1} \begin{pmatrix} s_A \\ s_B \end{pmatrix}$$

$$P^{-1} = \frac{1}{(\sigma^2{}_A)(\sigma^2{}_B) - (cov_{AB})(cov_{BA})} \begin{pmatrix} \sigma^2{}_B & -\,cov_{AB} \\ -\,cov_{BA} & \sigma^2{}_A \end{pmatrix}$$