Lecture 15. Truncation selection. Resemblance between relatives.

5.3 Truncation selection

Artificial selection aiming at a certain phenotypic value
use a truncation point T for parent selection
so that the offspring of selected parents have
phenotypic distribution with a desired bias

To estimate heritability compare phenotypic mean values
μ = parent mean before selection
μ_s = mean for selected parents
μ' = mean for the offspring of selected parents

$$\boxed{R/S = \text{realized heritability}}$$

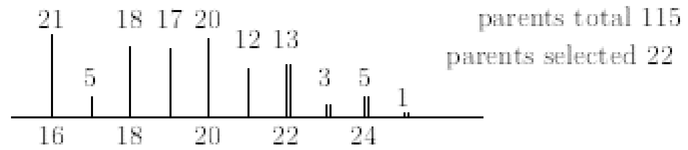
$S = \mu_s - \mu$ selection differential
$R = \mu' - \mu$ response to selection

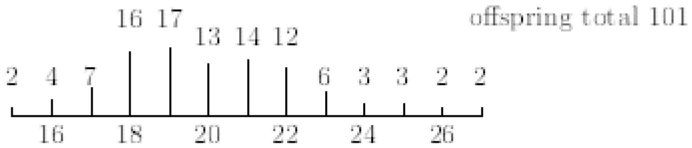
$$\boxed{\text{Prediction equation: } R = Sh^2 \text{ irrespective of } T}$$

Ex 7: seed weight

Fig 9.6, p. 409: edible beans of the genus *Phaseolus*
P = weight of seed in mg, truncation point $T = 650$
$\mu = 403.5$, $\mu_s = 691.7$, $\mu' = 609.1$, $\frac{R}{S} = \frac{205.6}{288.2} = 71.3\%$

Ex 8: drosophila bristles





Truncation selection with T=22
verify that $\mu = 19.304$, $\mu_s = 22.727$, $\mu' = 20.149$
realized heritability $h^2 = \frac{\mu' - \mu}{\mu_s - \mu} = \frac{0.845}{3.423} = 0.247$

Repeated truncation selection

Selection program over n generations with
new truncation points changing in certain direction
$\mu_0 \xrightarrow{T_0} \mu_{s0} \xrightarrow{h^2} \mu_1 \xrightarrow{T_1} \mu_{s1} \xrightarrow{h^2} \ldots \mu_{n-1} \xrightarrow{T_{n-1}} \mu_{s(n-1)} \xrightarrow{h^2} \mu_n$
$S_0 = \mu_{s0} - \mu_0$, $R_0 = \mu_1 - \mu_0$, $R_0 = S_0 h^2$
$S_1 = \mu_{s1} - \mu_1$, $R_1 = \mu_2 - \mu_1$, $R_1 = S_1 h^2, \ldots$

Total response to selection assuming constant h^2

$\mu_n - \mu_0 = R_0 + R_1 + \ldots + R_{n-1} = (S_0 + \ldots + S_{n-1})h^2$

cumulative selection differential $C_n = S_0 + \ldots + S_{n-1}$

Ex 9: body weight in mice

Fig 9.19, p. 445

body weight in mice plotted against C_t

linearity supports the assumption of constant h^2

which is usally true for at least ten first generations

Ex 10: oil content in corn

Fig 9.4, p. 407: selection for high oil content in corn seeds

over 76 generations, $\mu_0 = 4.8\%$, $\mu_{76} = 18.8\%$

Given that C_t increased by 1.1% per generation

estimate $h^2 = \frac{18.8-4.8}{1.1\times 76} = 0.168$

5.4 Resemblance between relatives

Another characterisation of h^2 via comparison of

P_o = male offspring's phenotypic values

P_f = father's phenotypic values

Regression line

$P_o = \mu_o + b(P_f - \mu_f)$ with the slope $b = \frac{\mathrm{Cov}(P_o, P_f)}{\mathrm{Var}(P_f)}$

Diallelic model neglecting the environmental component

$\mathrm{Cov}(P_o, P_f) = \mathrm{E}(P_o \cdot P_f) - \mu^2 = pq\alpha^2 = \frac{1}{2}\sigma_a^2$

$b = \frac{\sigma_a^2}{2\sigma_p^2} = \frac{h^2}{2}$

joint distribution	$O = a$	$O = d$	$O = -a$	total
$P = a$, A_1A_1	p^3	p^2q	0	p^2
$P = d$, A_1A_2	p^2q	pq	pq^2	$2pq$
$P = -a$, A_2A_2	0	pq^2	q^3	q^2
total	p^2	$2pq$	q^2	1

Offspring and midparent value

$P_h = \frac{1}{2}(P_m + P_f)$

$\mathrm{Cov}(P_o, P_h) = \frac{1}{2}\sigma_a^2$, $\mathrm{Var}(P_h) = \frac{1}{2}\sigma_p^2$, $b = h^2$

Observed heritabilities

Fig 9.17-18, p. 438-9: animal and plant h^2, human H^2

low heritabilities of fitness related traits

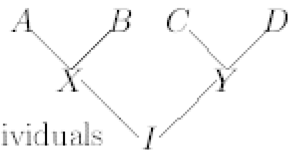
General covariance and slope

Table 9.7 p. 436: covariances between close relatives

$$\boxed{\mathrm{Cov}(X, Y) = r\sigma_a^2 + u\sigma_d^2} \quad \boxed{b = (r - u)h^2 + uH^2}$$

$r = 2F_{XY}$

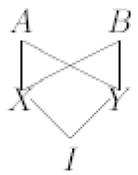
$u = F_{AC}F_{BD} + F_{AD}F_{BC}$



Coefficient of coancestry for two individuals

$$\boxed{F_{XY} = F_I = \mathrm{P(IBD\ genes\ of\ hypothetical\ offspring\ } I)}$$

Ex 13: full siblings



Two genes in I are IBD if they both come

1. from the same grandparent
2. from the same chromosome of that grandparent

$F_{XY} = 0.5 \cdot 0.5 = 0.25$

$r = 2 \cdot 0.25 = 0.5$

$u = F_{AA}F_{BB} + F_{AB}F_{BA} = 0.5 \cdot 0.5 + 0 \cdot 0 = 0.25$

Covariance and slope

$\mathrm{Cov}(X, Y) = \frac{\sigma_a^2}{2} + \frac{\sigma_d^2}{4}$, $b = \frac{h^2}{4} + \frac{H^2}{4}$

Literature:

1. D.L.Hartl, A.G.Clarc. Principle of population genetics. Sinauer Associates, 2007.
2. R.Nielson, M. Statkin. An introduction to population genetics: theory and applications, Sinauer Associates. 2013.