Calculation of Heritability Coefficient Estimation Using Analysis of Variance in Performance Values in Related Individuals

Analysis of the variance of groups of half-sibs by fathers

In one breed, the increase in live weight of bulls, half-sibs on the father's side were monitored at the age of three months. At random, 40 half-sibs by five fathers (equal numbers per subclass ~ fathers – balanced design of the experiment), were selected from this non-inbreed population.

Estimate the heritability coefficient and its standard error by means determination by analyzing the variance of groups of half-sibs.

Dataset:

n	S_1	S_2	S_3	S_4	S_5
1	717	732	603	648	690
2	704	694	731	669	650
3	753	691	737	693	788
4	700	631	678	718	678
5	675	683	747	606	611
6	793	592	763	669	674
7	691	680	687	657	658
8	687	618	618	600	717
$\sum$	5720	5321	5564	5260	5466

Statistical model of one-way analysis of variance:

$$\mathbf{y_{ij} = \mu + a_i + e_{ij}}$$

y_{ij} – performance of the j-th offspring after the i-th sire
μ – general population average
a_i – influence of the i-th father
e_{ij} – other random influences

Pre-calculated sums, square of sums and sum of squares:

Groups	$Y_{i\bullet}$	$Y_{i\bullet}^2$	$Y_{i\bullet}^2/n_i$	$\sum y_{ij}^2$
S_1	5720	32718400	4089800.00	4100638
S_2	5321	28313041	3539130.13	3554379
S_3	5564	30958096	3869762.00	3894 894
S_4	5260	27667600	3458450.00	3469684
S_5	5466	29877156	3734644.50	3753878
$Y_{\bullet\bullet}$	= 27331		18691786.63	**18773473**
$Y_{\bullet\bullet}^2$	= 746983561		$\sum Y_{i\bullet}^2/n_i$	$\sum\sum y_{ij}^2$

$p = 5$ $n = 40$ $n_i = n_0 = 8$

Calculation of the sum of the squares of the deviations from the mean:

- Between groups by sires

$$SS_a = \sum_{i=1}^{p} \frac{Y_{i\bullet}^2}{n_i} - \frac{Y_{\bullet\bullet}^2}{n} = \qquad =$$

- within groups by sire (progeny within sires, residual)

$$SS_e = \sum_{i=1}^{p}\sum_{j=1}^{m_j} y_{ij}^2 - \sum_{i=1}^{p} \frac{Y_{i\bullet}^2}{n_i} = \qquad =$$

- total (not necessary for the calculation of heritability)

$$SS_T = \sum_{i=1}^{p}\sum_{j=1}^{m_j} y_{ij}^2 - \frac{Y_{\bullet\bullet}^2}{n} = \qquad\qquad =$$

Analysis of Variance Table:

Source of variability	SS	df	MS	Composition of MS
Between groups (a)	SS_a	$p - 1 =$		$= \sigma_e^2 + n_0\sigma_g^2$
Within groups (e)	SS_e	$n_0 - p =$		$= \sigma_e^2$
Total (T)	SS_T	$n - 1$		

SS – sum of squares of deviations from the mean; df –degrees of freedom; MS – mean of square (~ variance)

The statistical analysis is followed by genetic analysis, where we calculate the genetic variance according to the fathers from the estimated variances between groups and within groups of related individuals!

The variance component σ_S^2 estimates ¼ of the additive genetic variance. The variance component σ_e^2 estimates the remainder of the genetic variance plus all the environmental variance.

Calculation of the estimate the genetic variations according to fathers σ_g^2:

$$MS_a = \sigma_e^2 + n_0\sigma_g^2 = MS_e + n_0\sigma_g^2$$

$$\sigma_g^2 = \frac{MS_a - MS_e}{n_0} = \qquad\qquad =$$

$$\sigma_e^2 = MS_e$$

$$\sigma_P^2 = \sigma_g^2 + \sigma_e^2 = \qquad\qquad =$$

$$\rho = r_i = \frac{\sigma_g^2}{\sigma_g^2 + \sigma_e^2} = \qquad\qquad =$$

$$h^2 = 4\rho = 4\frac{\sigma_g^2}{\sigma_g^2 + \sigma_e^2} = 4\frac{\sigma_g^2}{\sigma_P^2} = \qquad\qquad =$$

Calculation of estimation of **the standard error** of h^2:

a) as four times the standard error of the intraclass correlation coefficient:

$$se_{h^2} = 4.s_\rho = 4.\sqrt{\frac{2.(1-\rho)^2(1+(n_0-1)\rho)^2}{n_0(n_0-1)(p-1)}} = \qquad\qquad =$$

b) based on its size of weighted number of individuals in a group of half-sibs and the number of groups of half-sibs

$$se_{h^2} = \left(h^2 + \frac{4}{n_0}\right).\sqrt{\frac{2}{p}} = \qquad\qquad =$$

$$h^2 \pm se_{h^2} = \qquad \pm$$

The estimate of the heritability coefficient based on the calculation of the analysis of variance of the half-siblings was .... with its mean error ………… This example is unrepresentative because of the low number of observations of half-siblings. The calculated estimate of the heritability coefficient is unusable because of its high mean estimation error.