Admissible Correlation Estimator of Heritability

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Summary

Admissible estimator of heritability based on intra-class correlation between half-sibs with minimum bias is proposed and illustrated numerically.

Key words : Heritability; Half-sib analysis; Restricted estimator.

Introduction

Half-sib analysis is widely used in the estimation of heritability (h^2) in farm animals. The estimate in this case is obtained from the estimates of components of variance 'among sires' and 'within sires' in the following one way classification model

$$y_{ij} = \mu + s_i + e_{ij} \tag{1}$$

where y_{ij} is the observation on the progeny of the jth dam ($j = 1, 2, \ldots, d$) mated to the ith sire ($i = 1, 2, \ldots, s$), $s_i \sim N(0, \sigma_s^2)$, $e_{ij} \sim N(0, \sigma_w^2)$ and all effects are independent.

If A and B are the observed 'between sires' and 'within sires' components of mean square then an estimate of heritability is

$$h_H^2 = \frac{4(A - B)}{A + (d - 1)B} \tag{2}$$

with approximate sampling variance

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$$V(h_H^2) = \frac{32\,[1 + (d-1)t]^2\,(1-t)^2}{d\,(d-1)\,(s-1)} \tag{3}$$

in which $t = h_H^2/4$

This estimate can assume values outside its permissible limits of $(0,1)$. The aim of this paper is to propose an admissible estimator of heritability based on Federer's [1] approach of obtaining non-negative estimates of variance components.

2. *The Proposed Estimator*

Federer's [1] non-negative variance component estimator of σ_s^2 can be modified suitably by applying exponential correction to both A and B to give an estimator of heritability which always gives values within the admissible range. The modified version of the estimator is

$$\hat{\sigma}_s^2 = \frac{A\,(1 - e^{-\delta_1\,A/B}) - B(1 - e^{-\delta_2\,A/B})}{d} \tag{4}$$

$$\hat{\sigma}_w^2 = B$$

where $\quad \delta_1 = 0$ and $0 < \delta_2 \leq 1 \quad$ when $A \leq \left(1 + \dfrac{d}{3}\right) B \tag{5}$

$$0 < \delta_1 \leq \delta_0 \text{ and } \delta_2 = 0 \quad \text{when } A > \left(1 + \frac{d}{3}\right) B$$

in which

$$\delta_0 = -\frac{B}{A} \log_e \left[1 - \left(1 + \frac{d}{3}\right) \frac{B}{A} \right]$$

Hence using (4) the admissible estimator of heritability based on intra-class correlation between half-sibs becomes

$$h_{HA}^2 = 4 \left[\frac{A\,(1 - e^{-\delta_1\,A/B}) - B(1 - e^{-\delta_2\,A/B})}{A\,(1 - e^{-\delta_1\,A/B}) - B(1 - e^{-\delta_2\,A/B}) + dB} \right] \tag{6}$$

where δ_1 and δ_2 are as defined in (5).

This is a biased estimator and the bias will be minimum when δ_1 or δ_2 as the case may be takes the maximum value in its range (Federer, [1]). Hence, admissible

estimate of heritability with minimum bias is obtained from (6) taking

$$\delta_1 = 0 \text{ and } \delta_2 = 1 \quad \text{when} \quad A \leq (1+d/3)\,B$$

$$\delta_1 = \delta_0 \text{ and } \delta_2 = 0 \quad \text{when} \quad A > (1+d/3)\,B \tag{7}$$

The mean square error of h_{HA}^2 using the 'delta technique', i.e.

$$MSE\,(h_{HA}^2) = \left(\frac{\delta h_{HA}^2}{\delta A}\right)^2 \sigma_A^2 + \left(\frac{\delta h_{HA}^2}{\delta B}\right)^2 \sigma_B^2$$

in which σ_A^2 and σ_B^2 are the variances of A and B and are to be replaced by their unbiased estimators $\dfrac{2A^2}{(s+1)}$ and $\dfrac{2B^2}{[s\,(d-1)+2]}$ respectively (Kempthorne, [2], p. 247) can be shown equal to

$$MSE\,(h_{HA}^2) = \frac{32(N+3)\,d^2A^2B^2\,(1-\delta_2\,e^{-\delta_2 A/B})^2}{[\,A+B(e^{-\delta_2 A/B}-1+d)\,]^4\,(N-s+2)\,(s+1)}$$

$$\text{when} \quad A \leq \left(1+\frac{d}{3}\right)B$$

$$= \frac{32(N+3)\,d^2A^2B^2\,[1-(1-\delta_1\,e^{-\delta_1 A/B})]^2}{[\,A(1-e^{-\delta_1 A/B})+(d-1)\,B\,]^4\,(N-s+2)\,(s+1)}$$

$$\text{when} \quad A > \left(1+\frac{d}{3}\right)B \tag{8}$$

in which N=sd.

The estimator (6) is equally applicable to unbalanced data if we replace d by k where

$$k = \frac{1}{s-1}\left[\,N-\frac{\sum_i n_i^2}{N}\,\right] \text{ and } N = \sum_i n_i$$

in which n_i is the number of progeny from ith sire.

3. Numerical Illustration

Table 1 summarises the estimates of heritability for balanced as well as

unbalanced types of data obtained by using classical (h_H^2) and admissible estimator (h_{HA}^2). The balanced data relates to first 100-day egg production of progeny from 8 sires in poultry (Table 2) while the unbalanced data consists of 100-day egg production from first 14 sires as used by Nigam *et al.* [3].

Table 1. Estimates of heritability by two different methods alongwith their MSE's

Estimator	Balanced data		Unbalanced data	
	Est.	MSE	Est.	MSE
h_H^2	−0.134	0.0065	−0.082	0.0074
h_{HA}^2	0.029	0.0063	0.057	0.0015

Table 2. First 100-day egg production of progeny from 8 sires in poultry

			Sire numbers				
1	2	3	4	5	6	7	8
80	85	92	74	68	82	76	71
80	82	75	89	57	71	73	63
68	67	53	52	81	64	68	62
44	36	76	39	71	84	65	55
64	87	76	71	71	80	71	78
54	79	52	61	69	59	75	67
48	78	47	51	64	76	57	67
87	69	42	85	85	58	86	85
83	60	79	76	83	58	49	75
79	57	72	75	70	60	86	70
75	51	63	67	50	71	75	69
68	62	47	64	50	74	61	63
40	80	89	60	70	75	68	67
38	61	82	48	71	65	67	63
32	80	88	76	68	62	77	55

The proposed estimator (h_{HA}^2) is seen not only to provide estimates within the admissible range but also gives estimates with comparatively low standard errors.

REFERENCES

[1]   Federer, W.T., 1968. Non-negative estimators for components of variance. *Appl. Statist.*, **17**, 171-174.

[2]   Kempthorne, O., 1977. *An Introduction to Genetic Statistics.* Iowa State Univ. Press, Ames. Iowa.

[3]   Nigam, A.K., Srivastava, V.K., Jain, J.P. and Gopalan, R., 1979. A note on estimation of heritability by regression analysis. *Biom. J.*, **21**, 667-673.