

Effect of Master Sample on the Estimate of Standard Error of Heritability by Parent-offspring Regression Method

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SUMMARY

The bootstrap estimates of standard error of heritability are found invariant to master sample which is used to obtain its estimate. The standard error of heritability decreased considerably with increase in sample size. It was also found that the bias in bootstrap estimates of heritability are negligible. The optimum size of sample for obtaining the accurate estimate of standard error is around 1000 and the optimum number of bootstrap replications required to obtain a stable estimate of standard error is around 200. The percentile confidence intervals are found to be either shorter or approximately equal to the standard normal confidence intervals. The former stabilizes in about 800-1000 bootstrap replications.

Key words : Heritability, Bootstrap technique, Simulation.

1. Introduction

The regression of offspring on parent is commonly used method by animal breeders for estimation of heritability, an important genetic parameter. This method assumes the normality of data and the estimates obtained from such data which do not fulfill the normality assumption are likely to be inaccurate and imprecise. Under such situations, it is desirable to use analytical methods. One such analytical method, which is highly computer oriented is the bootstrap technique given by Efron [1]. The main advantage of this technique is that it needs no prior assumption about the distribution of the observations as well as the estimator. Keeping in view the importance of this technique, the present investigation is conducted for studying the effect of master sample on bootstrap estimates of standard error of heritability and optimum sample size. The optimum number of bootstrap replication are also obtained for getting an accurate and stable estimate of standard error of heritability.

2. Material and Methods

2.1 Regression of Offspring on Parent

In the present investigation, the heritability is estimated as the regression of the offspring on one of the parent, that is

$$b_{op} = \frac{\Sigma yz}{\Sigma y^2}$$

$$\hat{h}_{op}^2 = 2b_{op}$$

with sampling variance as $4V(b_{op})$ and

$$V(b_{op}) = \frac{\Sigma z^2 - b_{op} \Sigma yz}{(N-2)\Sigma y^2}$$

in which y denote the performance record on parent and z on the offspring, both y and z being measured from their respective means, and N is the number of paired observations.

The important simulation model for regression or correlation as given by Ronningen [2] has been used for generating data sets for different parametric values.

3. Results and Discussion

As per the methodology described in the previous section, using simulation programmes, the data was generated to study the statistical properties of the heritability by regression of offspring on parent. The data for 200, 500, 1000 and 1500 pairs of offspring and parent were generated from the population with heritability values 0.1, 0.25 and 0.5. Different master samples were selected and analyzed to obtain the estimates of the heritability along with their standard error. These samples were further used to obtain the bootstrap estimates of bias and standard error. From Table 1 we observed that the estimate of standard error are invariant to change in master sample and the optimum number of bootstrap replication required for estimation of standard error from population having heritability value 0.1 lies between 100-200. The optimum number of bootstrap replication required to get stable estimate of standard error decreases as the sample size increases above 500. The 100 bootstrap replications are sufficient for obtaining the stable estimate of standard error of heritability except for the sample size 200-500 for which at least 200 bootstrap replications are required. It is also observed that if the number of bootstrap replications is increased then the

Table 1. Bootstrap estimates of mean , bias, standard error of heritability by parent offspring regression method

Sample Size	Bootstrap Replication	Population $h^2 = 0.1$			
		Master Sample		Bootstrap	
		Estimate	S.E.	Estimate (Bias)	S.E.
200	100	0.107	0.147	0.115 (0.008)	0.144
	200	0.102	0.146	0.117 (0.015)	0.140
	400	0.101	0.141	0.097 (-0.004)	0.131
	800	0.087	0.136	0.088 (0.001)	0.129
500	100	0.169	0.091	0.151 (-0.018)	0.091
	200	0.151	0.094	0.149 (-0.002)	0.090
	400	0.106	0.089	0.107 (0.001)	0.087
	800	0.106	0.089	0.106 (0.000)	0.083
1000	100	0.119	0.065	0.107 (-0.012)	0.064
	200	0.099	0.063	0.098 (-0.001)	0.063
	400	0.097	0.061	0.096 (-0.001)	0.058
	800	0.097	0.061	0.095 (-0.002)	0.057
Population $h^2 = 0.25$					
200	100	0.286	0.138	0.267 (-0.019)	0.129
	200	0.256	0.131	0.282 (0.026)	0.123
	400	0.249	0.124	0.243 (-0.006)	0.116
	800	0.249	0.124	0.247 (-0.002)	0.114
500	100	0.268	0.094	0.273 (0.005)	0.093
	200	0.220	0.095	0.231 (0.011)	0.092
	400	0.237	0.095	0.234 (-0.003)	0.090
	800	0.270	0.086	0.273 (0.003)	0.081
1000	100	0.283	0.065	0.283 (0.000)	0.063
	200	0.271	0.063	0.270 (-0.001)	0.062
	400	0.273	0.061	0.273 (0.000)	0.061
	800	0.273	0.061	0.271 (-0.002)	0.061
Population $h^2 = 0.5$					
200	100	0.495	0.144	0.485 (-0.010)	0.137
	200	0.548	0.135	0.545 (-0.003)	0.135
	400	0.426	0.129	0.433 (0.007)	0.129
	800	0.513	0.138	0.510 (-0.003)	0.127
500	100	0.517	0.090	0.523 (0.006)	0.087
	200	0.489	0.089	0.495 (0.006)	0.083
	400	0.511	0.086	0.507 (-0.004)	0.083
	800	0.499	0.083	0.495 (-0.004)	0.078
1000	100	0.457	0.060	0.454 (-0.003)	0.060
	200	0.457	0.060	0.460 (0.003)	0.059
	400	0.481	0.062	0.480 (-0.001)	0.057
	800	0.450	0.059	0.451 (0.001)	0.057

estimate of standard error will decrease for all the sample sizes. The estimates of heritability obtained by bootstrap method are slightly biased and the bias is almost negligible. As per expectation, it is observed that the estimates of standard error by traditional method are influenced by sample size. The optimum sample size for obtaining the stable and accurate standard error of heritability from populations with heritability value 0.1 is approximately one thousand. The similar trend is observed for other parametric values of heritability.

Table 2. Confidence intervals of heritability for optimum sample size (1000)

h^2	Normal Confidence Interval			Percentile Confidence Interval		
	Lower Limit	Upper Limit	Length	Lower Limit	Upper Limit	Length
0.10	-0.024	0.217	0.240	-0.024	0.207	0.231
0.25	0.154	0.392	0.238	0.147	0.387	0.240
0.50	0.334	0.567	0.233	0.341	0.559	0.218

The result clearly shows that the bootstrap method can not only be used to estimate standard error and confidence interval of heritability but can also be exploited for estimating heritability. The percentile and normalized confidence intervals of different heritability values viz., 0.1 0.25 and 0.5 for optimum sample size with bootstrap replication 1000 each were also obtained (Table 2). The estimates of confidence interval by percentile method are either shorter or approximately same as standard normal intervals. The bootstrap estimates of confidence interval stabilize in about 800-1000 bootstrap replications. These results were found consistent with results obtained by Wahi *et al.* [3].

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