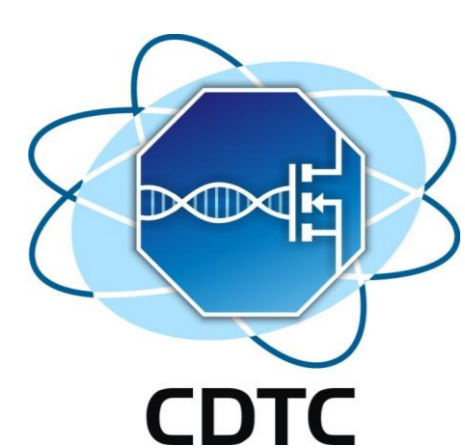




# Correlations among molecular breeding values estimated by different Bayesian methods

Rezende, F.M.<sup>1</sup>; Ferraz, J.B.S.<sup>2</sup>; Eler, J.P.<sup>2</sup>; Meirelles, F.V.<sup>2</sup>; Ibañez-Escriche, N.<sup>3</sup>

<sup>1</sup>Federal University of Uberlandia, Campus Patos de Minas, MG, Brazil, [frezende@ingeb.ufu.br](mailto:frezende@ingeb.ufu.br)  
<sup>2</sup>NAP-GMABT, College of Animal Science and Food Engineering, University of Sao Paulo, Pirassununga, SP, Brazil <sup>3</sup>IRTA-Cataluña, Genetic and Animal Breeding, Lleida, Cataluña, Spain



## Objectives

To compare differences among estimates of molecular breeding values obtained from six different methodologies: Bayesian multiple regression, Bayesian ridge regression, Bayes A, Bayes B, Bayes C $\pi$  and Bayesian Lasso.

## Material and Methods

**Data:** 3,160 animals belonging to a Nelore beef cattle selection program, measured for post-weaning gain, scrotal circumference and muscle score were genotyped for a panel, that considered, after quality control, 106 SNP markers.

**Statistical analyses:** Allele substitution effects were estimated by Bayesian multiple regression (BMR), Bayesian ridge regression (BRR), Bayes A (BA), Bayes B (BB), Bayes C $\pi$  (BC $\pi$ ) and Bayesian Lasso (LASSO) and molecular breeding values were calculated by adding the estimates for all markers. Pearson's correlation coefficient and Spearman's rank correlation were used to measure the strength of the association of the molecular breeding values estimated.

## Results

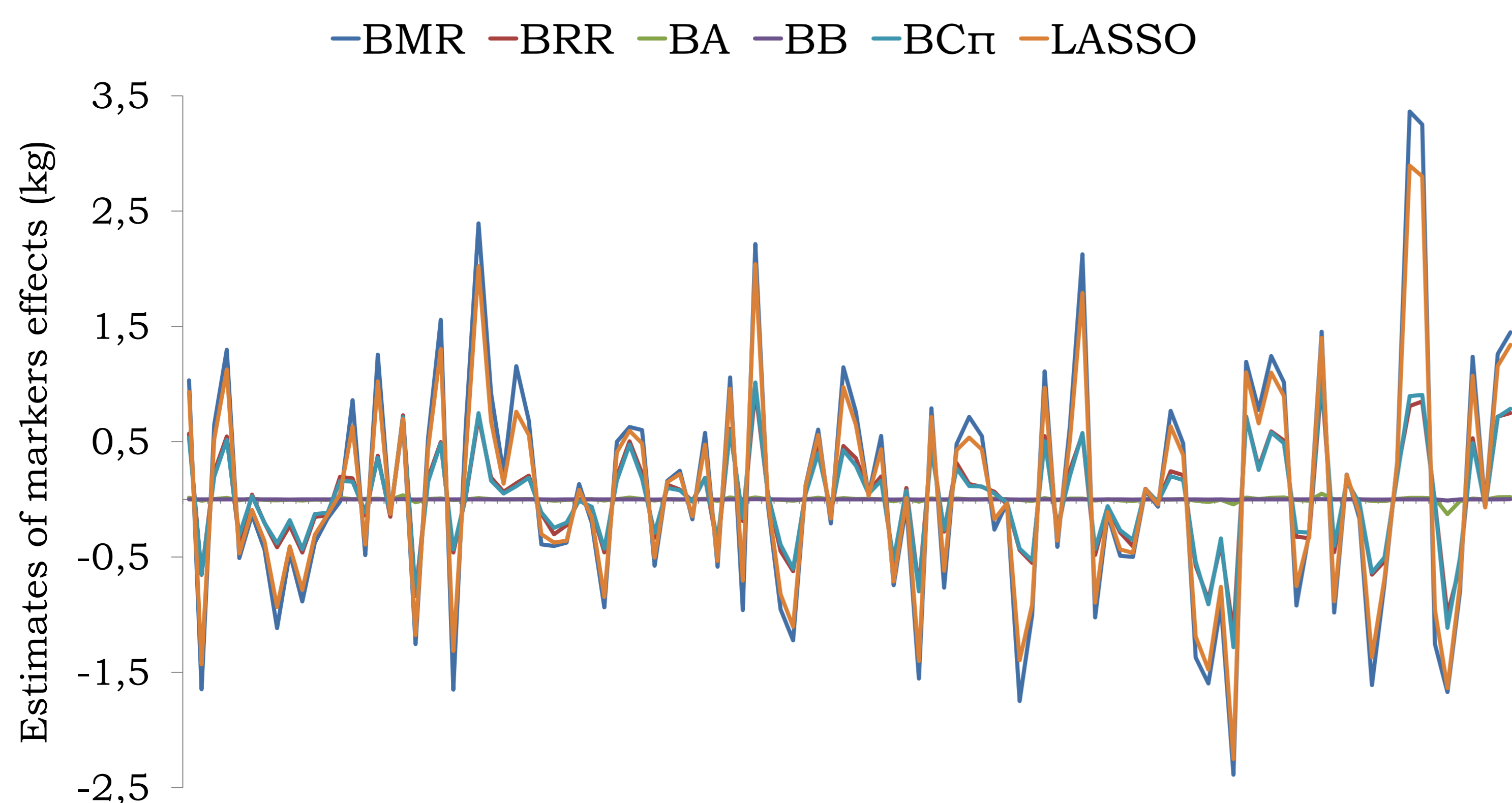


Figure 1. Allele substitution effects estimated by Bayesian multiple regression (BMR), Bayesian ridge regression (BRR), Bayes A (BA), Bayes B (BB), Bayes C $\pi$  (BC $\pi$ ) and Bayesian Lasso (LASSO) for post-weaning gain.

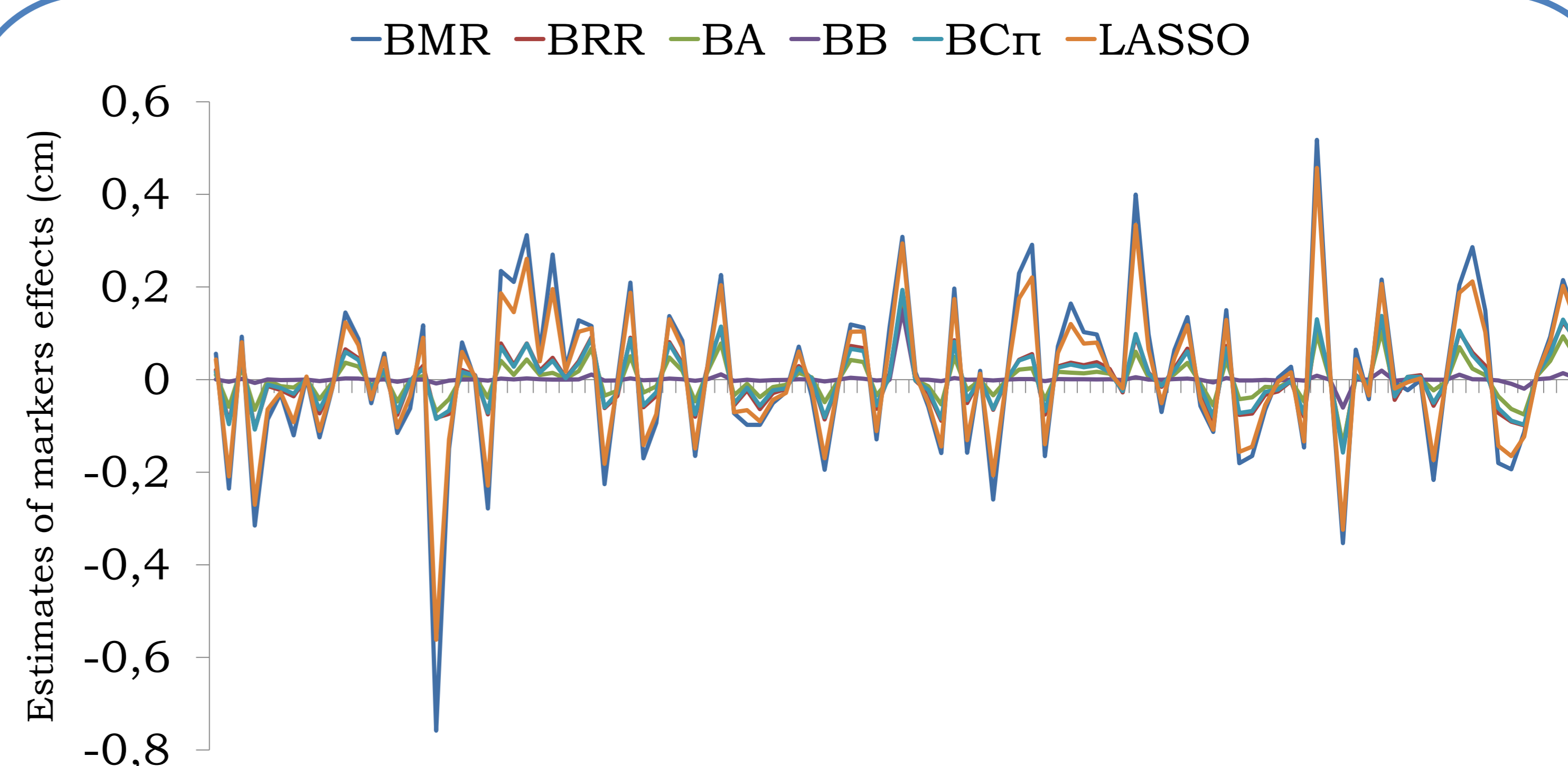


Figure 2. Allele substitution effects estimated by Bayesian multiple regression (BMR), Bayesian ridge regression (BRR), Bayes A (BA), Bayes B (BB), Bayes C $\pi$  (BC $\pi$ ) and Bayesian Lasso (LASSO) for scrotal circumference.

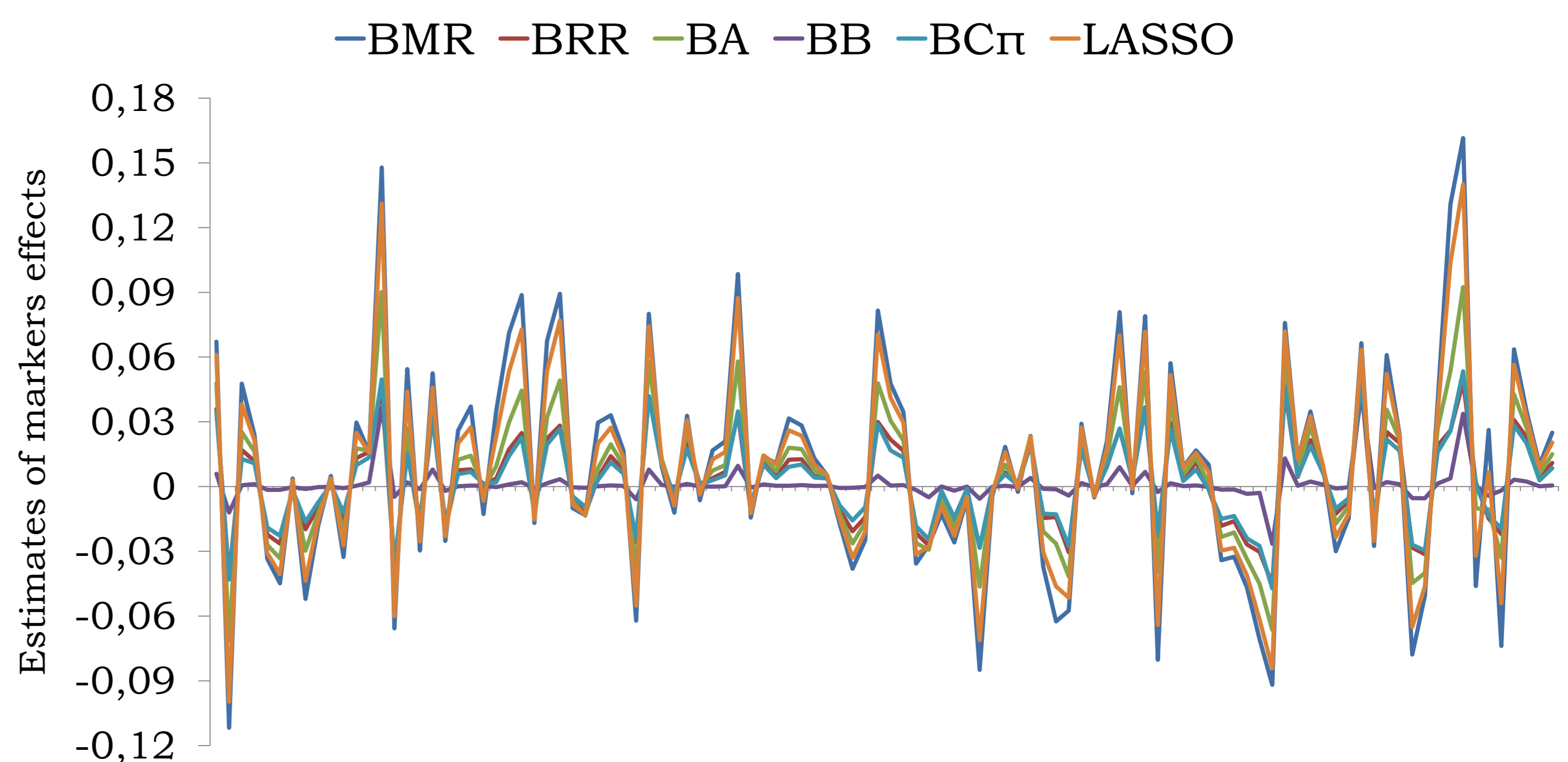


Figure 3. Allele substitution effects estimated by Bayesian multiple regression (BMR), Bayesian ridge regression (BRR), Bayes A (BA), Bayes B (BB), Bayes C $\pi$  (BC $\pi$ ) and Bayesian Lasso (LASSO) for muscle score.

Table 1. Pearson (above diagonal) and Spearman (below diagonal) correlations among molecular breeding values estimated by Bayesian multiple regression (BMR), Bayesian ridge regression (BRR), Bayes A (BA), Bayes B (BB), Bayes C $\pi$  (BC $\pi$ ) and Bayesian Lasso (LASSO).

POST-WEANING GAIN						
Método	BMR	BRR	BA	BB	BC $\pi$	LASSO
BMR		0.95	0.75	0.68	0.95	1.00
BRR	0.95		0.87	0.79	1.00	0.97
BA	0.75	0.87		0.97	0.88	0.77
BB	0.69	0.80	0.96		0.81	0.71
BC $\pi$	0.95	1.00	0.88	0.81		0.97
LASSO	1.00	0.97	0.77	0.72	0.96	
SCROTAL CIRCUMFERENCE						
BMR		0.94	0.88	0.50	0.93	1.00
BRR	0.93		0.97	0.59	1.00	0.96
BA	0.88	0.97		0.75	0.98	0.91
BB	0.51	0.61	0.76		0.63	0.53
BC $\pi$	0.93	1.00	0.98	0.64		0.96
LASSO	1.00	0.95	0.91	0.54	0.95	
MUSCLE SCORE						
BMR		0.95	0.98	0.69	0.95	1.00
BRR	0.95		0.99	0.73	1.00	0.97
BA	0.98	0.99		0.74	0.99	0.99
BB	0.69	0.72	0.74		0.77	0.71
BC $\pi$	0.95	1.00	0.99	0.77		0.97
LASSO	1.00	0.97	0.99	0.71	0.97	

## Conclusion

Differences observed on markers effects estimates were due the shrinkage process applied by each analyzed method. Under this study, estimates of molecular breeding value were almost equivalent when using BMR, BRR, BC $\pi$  and LASSO.