Erratum to “Improving accuracy of genomic predictions within and between dairy cattle breeds with imputed high-density single nucleotide polymorphism panels” (J. Dairy Sci. 95:4114–4129)

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An error appeared in the equation and description of the log likelihood of the method BayesR beginning on page 4119. The corrected version is as follows:

The likelihood that SNP i is in distribution k is

$$\text{LogL}(i, k) = -0.5 \log |\mathbf{V}| - \frac{0.5 (\mathbf{y}^*{}' \mathbf{y}^* - \mathbf{y}^* \mathbf{Z}^* u_k^*)}{\sigma_e^2} + \log(p r_k),$$

where $\mathbf{y}^*$ is the vector of phenotypes corrected for all marker effects other than marker i , the overall mean, and the polygenic effects; u_k^* is the mean of the posterior distribution of the SNP effect when assumed to be in the k th distribution; $\mathbf{Z}^*$ is a column vector containing the SNP genotypes of all animals for SNP i ; $\mathbf{V}$ is the variance-covariance structure of a reduced model in-

cluding only the effect of the respective SNP and a residual effect; and $\log |\mathbf{V}|$ was calculated as

$$n \log(\sigma_e^2) + \log \left(\frac{\sigma_k^2 \mathbf{Z}^*{}' \mathbf{Z}^*}{\sigma_e^2} + 1 \right),$$

where $\mathbf{Z}^*$ contains only the information for the current SNP effect.

The authors regret the error.

REFERENCES

- Erbe, M., B. J. Hayes, L. K. Matukumalli, S. Goswami, P. J. Bowman, C. M. Reich, B. A. Mason, and M. E. Goddard. 2012. Improving accuracy of genomic predictions within and between dairy cattle breeds with imputed high-density single nucleotide polymorphism panels. J. Dairy Sci. 95(7):4114–4129.