


CORRECTION

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# Correction to: Use of genomic information to exploit genotype-by-environment interactions for body weight of broiler chicken in bio-secure and production environments

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## Correction to: *Genet Sel Evol* (2019) 51:50

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After publication of this work [1], we noticed that there was an error: the formula to calculate the standard error of the estimated correlation ( $\widehat{\rho}_{f,r}$ ) between  $\hat{u}_{f_i}$  and  $\hat{u}_{r_i}$  in Appendix on page 12 was mistyped. The correct formula for calculation of the standard error should be:

$$SE(\widehat{\rho}_{f,r}) = \sqrt{\frac{1 - \widehat{\rho}_{f,r}^2}{n - 2}}$$

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## Reference

1. Chu TT, Bastiaansen JWM, Berg P, Rome H, Marois D, Henshall J, Jensen J. Use of genomic information to exploit genotype-by-environment interactions for body weight of broiler chicken in bio-secure and production environments. *Genet Sel Evol*. 2019;51:50. <https://doi.org/10.1186/s12711-019-0493-3>.

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