

Corrigendum for de los Campos *et al. GENETICS* 182 (1) 375-385.

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CORRIGENDUM

In the article by G. DE LOS CAMPOS, H. NAYA, D. GIANOLA, J. CROSSA, A. LEGARRA, E. MANFREDI, K. WEIGEL, and J. M. COTES (*GENETICS* 182: 375-385) entitled “Predicting Quantitative Traits With Regression Models for Dense Molecular Markers and Pedigree”, File S1 of the supporting information contains a mistake in the fully conditional density of the residual variance. This mistake has been corrected in the new version of File S1 that is available online at <http://www.genetics.org/content/182/1/375/suppl/DC1>. Importantly, the R-program used for analysis in the article, which is provided in File S2 (BRL.rda), as well as the BLR program of R (<http://cran.r-project.org/web/packages/BLR/index.html>) do not suffer from that mistake.

We thank Professors Rohan Fernando and Rob Tempelman for pointing out the mistake in File S1.

Corrected text now shown on page 5SI (first 3 lines):

$$\begin{aligned}
 p(\sigma_\varepsilon^2 | else) &\propto \left[\prod_{i=1}^n N(y_i | \mu + \mathbf{x}'_{ri} \boldsymbol{\beta}_r + \mathbf{x}'_{li} \boldsymbol{\beta}_l + u_i, \sigma_\varepsilon^2) \right] \left[\prod_{j=1}^p N(\beta_{lj} | 0, \sigma_\varepsilon^2 \tau_j^2) \right] \chi^{-2}(\sigma_\varepsilon^2 | S_\varepsilon, df_\varepsilon) \\
 &\propto \left[\prod_{i=1}^n N(\varepsilon_i | \sigma_\varepsilon^2) \right] \left[\prod_{j=1}^p N(\tilde{\beta}_{lj} | 0, \sigma_\varepsilon^2) \right] \chi^{-2}(\sigma_\varepsilon^2 | S_\varepsilon, df_\varepsilon) \\
 &= \chi^{-2}(\sigma_\varepsilon^2 | S = S_\varepsilon + \boldsymbol{\varepsilon}' \boldsymbol{\varepsilon} + \tilde{\boldsymbol{\beta}}' \tilde{\boldsymbol{\beta}}, df = df_\varepsilon + n + p)
 \end{aligned}
 \tag{14}$$

where $\boldsymbol{\varepsilon} = (\varepsilon_1, \dots, \varepsilon_n) = \mathbf{y} - \mathbf{1}\mu - \mathbf{X}_r \boldsymbol{\beta}_r - \mathbf{X}_l \boldsymbol{\beta}_l - \mathbf{u}$, $\tilde{\beta}_{lj} = \left(\frac{\beta_{lj}}{\tau_j} \right)$ and $\tilde{\boldsymbol{\beta}} = (\tilde{\beta}_{l1}, \dots, \tilde{\beta}_{lp})$