



# Correction to: Bayesian high-dimensional covariate selection in non-linear mixed-effects models using the SAEM algorithm

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## Correction to: *Statistics and Computing* (2024) 34:53

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In this article, subsection section C.4 should have been removed, and Equation 5 has to be read correctly as given in this Correction.

Incorrect (have to be removed).

C.4 Table of results of the application on real data.

Table 4 summarises for each chromosome, the number of covariates, the number of heading QTLs, the number of major flowering genes present in that chromosome, and the number of SNPs selected by SAEMVS.

Incorrect symbol in Equation 5.

Symbol “ $\eta$ ” is not correct.

$$\pi(\tilde{\beta}_{\ell'm} | \tilde{\delta}_{\ell'm}) = \mathcal{N}(0, \Sigma_{\beta|\delta}) \quad (5)$$

$$\text{with } \Sigma_{\beta|\delta} = \left(1 - \tilde{\delta}_{\ell'm}\right) v_0 + \tilde{\delta}_{\ell'm} (\mathbb{K}_{\ell'>1} v_1 + \mathbb{K}_{\ell'=1} \sigma_\mu^2)$$

Correct symbol in Equation 5.

The symbol “ $\eta$ ” should read as “ $\mathbb{1}$ ”.

The original publication has been corrected.

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