

CORRECTION

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Correction to: scBFA: modeling detection patterns to mitigate technical noise in large-scale single-cell genomics data

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Correction to: *Genome Biol*
<https://doi.org/10.1186/s13059-019-1806-0>

Following publication of the original article [1], the following two errors were found in formulae:

1) In the method section titled “**Benchmarking dimensionality reduction methods for scRNA-seq**”, the brackets should be removed from inside the square roots. The correct equation is shown below:

$$MCC = \frac{TP * TN - FP * FN}{(\sqrt{TP + FP}) * (\sqrt{TP + FN}) * (\sqrt{TN + FP}) * (\sqrt{TN + FN})}$$

2) In the method section titled “**Batch effect correction**”, the position of superscript in the subscript are incorrect. The correct equation is shown below.

$$M_{\text{sub}(i',j)} \sim P \left(g^{-1} \left(\mathbf{x}_{\text{sub}(i')}^T \boldsymbol{\beta}_j + \mathbf{z}_{\text{sub}(i')}^T \mathbf{a}_j + u_{\text{sub}(i')} + v_j \right) \right)$$

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Reference

1. Li, Quon. scBFA: modeling detection patterns to mitigate technical noise in large-scale single-cell genomics data. *Genome Biol.* 2019;20:193 <https://doi.org/10.1186/s13059-019-1806-0>.

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