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  
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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:

\[
MCC = \frac{TP \cdot TN - FP \cdot FN}{\sqrt{TP + FP}} \cdot \frac{\sqrt{TP + FN}}{(\sqrt{TN + FP}) \cdot (\sqrt{TN + FN})}
\]

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

\[
M_{sub(i,j)} \sim P \left( \mathbf{g}^{-1} \left( \mathbf{x}_{sub(i)}^T \mathbf{B}_j + \mathbf{z}_{sub(i)}^T \mathbf{a}_j + u_{sub(i)} + \nu_j \right) \right)
\]

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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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