

CORRECTION

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Correction to: JOINT for large-scale single-cell RNAsequencing analysis via soft-clustering and parallel computing

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Correction to: BMC Genomics 22, 47 (2021)
<https://doi.org/10.1186/s12864-020-07302-6>

Following publication of the original article [1], several errors were identified in the “JOINT algorithm” and the “Imputation algorithm for data visualization” sub-sections, as well as in the Additional files and their captions.

In the “JOINT algorithm” sub-section the first two equations contained errors, which are shown below:

Incorrect

In the JOINT algorithm we consider a general mixture model

$$q_{g,k,0} + \sum_{l=1}^{L-1} q_{g,k,l} \left(\frac{\beta_{g,k,l}}{\beta_{g,k,l} + s_c} \right)^{\alpha_{g,k,l}}$$

where x is observed count number, k is the number of cell-types, π_k is the probability of choosing cell-type k and $f_k(x|\theta_k)$ is the probability of observing x given parameters θ_k in cell-type k . Given x and θ_k , we compute the posterior probability of observed counts x from cell-type k as

$$m_{g,k,l} = \begin{cases} \frac{\alpha_{g,k,l}}{\beta_{g,k,l}} & l > 0 \\ 0, & l = 0 \end{cases}$$

Correct

The original article can be found online at <https://doi.org/10.1186/s12864-020-07302-6>.

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In the JOINT algorithm we consider a general mixture model

$$p(x) = \sum_{k=0}^{K-1} \pi_k f_{k(x|\theta_k)},$$

where x is observed count number, k is the number of cell-types, π_k is the probability of choosing cell-type k and $f_k(x|\theta_k)$ is the probability of observing x given parameters θ_k in cell-type k . Given x and θ_k , we compute the posterior probability of observed counts x from cell-type k as

$$p(k|x) = \frac{\pi_k f_k(x|\theta_k)}{\sum_{k=0}^{K-1} \pi_k f_k(x|\theta_k)}.$$

In the “Imputation algorithm for data visualization” sub-section the below equation was missing following the sentence “The mean of each component l is $s_c m_{g,k,l}$ where”:

$$m_{g,k,l} = \begin{cases} \frac{\alpha_{g,k,l}}{\beta_{g,k,l}} & l > 0 \\ 0, & l = 0 \end{cases}$$

Finally, it was noted that there were several typographical errors in the Additional file captions in the PDF version of the published articles, which have been corrected.

The original article has been updated.



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Reference

1. Cui T, Wang T. JOINT for large-scale single-cell RNA-sequencing analysis via soft-clustering and parallel computing. *BMC Genomics*. 2021;22:47 <https://doi.org/10.1186/s12864-020-07302-6>.