

# Author Correction: The shaky foundations of simulating single-cell RNA sequencing data

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**AUTHOR CORRECTION**

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# Author Correction: The shaky foundations of simulating single-cell RNA sequencing data

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The original article can be found online at <https://doi.org/10.1186/s13059-023-02904-1>.

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Following publication of the original article [1], it was pointed out that the legend to Table 1 did not match the content of the table.



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The incorrect Table 1 is as follows:

**Table 1** Overview of scRNA-seq simulators compared in this study. Methods are ordered alphabetically and annotated according to their (in)ability to accommodate multiple batches and/or clusters, support for parallelization (parameter estimation and data simulation, respectively), software availability, and publication year. The right-most column catalogues neutral benchmark studies where each simulator was used. (✓)=yes, ✗=no, (✓)=yes, but based on user input parameters, i.e., no support for parameter estimation, \*requires random splitting of cells into two groups, †/‡=internal/prior resampling from empirical parameter distribution, ◦=no separate estimation step)

	Batches	Clusters	Type(s)	Cell #	Parallelization	Availability	Year	Model
BASICS [37]	✓	✗	b	✗	✓✗	<a href="#">R/Bioc</a>	2015	NB
ESCO [38]	✓	✓	n,b,k	✓	✓✓	<a href="#">R/GitHub</a>	2020	Gamma-Poisson
hierarchicell [39]	✓	✗	n,b	✓	✗✗	<a href="#">R/GitHub</a>	2021	NB
muscat [40]	✓	✓	n,b,k	(✓)†	✗✗	<a href="#">R/Bioc</a>	2020	NB
POWSC [41]	✗	✓	n,k	(✓)†	✗✗	<a href="#">R/Bioc</a>	2020	zero-inflated, log-normal Poisson mixture
powsimR [42]	✗	(✓)	n*	(✓)†	✓✓	<a href="#">R/GitHub</a>	2017	NB
scDD [43]	✗	✗	n*	✓	✓✓	<a href="#">R/Bioc</a>	2016	Bayesian NB mixture model
scDesign [44]	✗	(✓)	n	✓	◦✓	<a href="#">R/GitHub</a>	2019	Gamma-Normal mixture model
scDesign2 [45]	✗	✓	n,k	✓	✓✗	<a href="#">R/GitHub</a>	2020	(zero-inflated) Poisson or NB + Gaussian copula for gene-gene correlations
SCRIP [46]	✓	✓	n,b,k	✓	✗✗	<a href="#">R/GitHub</a>	2020	(Beta-)Gamma-Poisson
SPARSim [47]	✓	✗	n,b	(✓)‡	✗✗	<a href="#">R/GitLab</a>	2020	Gamma-multivariate hypergeometric
splatter [15] (Splat model)	(✓)	(✓)	n	✓	✗✗	<a href="#">R/Bioc</a>	2017	Gamma-Poisson
SPsimSeq [16]	✓	✗	n,b	✓	◦✗	<a href="#">R/Bioc</a>	2020	log-linear model-based density estimation + Gaussian copula for gene-gene correlations
SymSim [48]	✓	✗	n,b	✓	✗✗	<a href="#">R/GitHub</a>	2019	kinetic model using MCMC
ZINB-WaVE [49]	✓	✓	n,b,k	✗	✗✗	<a href="#">R/Bioc</a>	2018	zero-inflated NB
zingeR [50]	✗	✗	n	(✓)†‡	✗✗	<a href="#">R/GitHub</a>	2017	zero-inflated NB

The corrected Table 1 is as follows:

**Table 1** Overview of scRNA-seq simulators compared in this study. Methods are ordered alphabetically and annotated according to their (in)ability to accommodate multiple batches and/or clusters, support for parallelization (parameter estimation and data simulation, respectively), software availability, and publication year. ‘Type(s)’ column specifies which type of simulations can be produced (n: “singular” references: single batch or cluster; b: multiple batches; k: multiple clusters). ‘Cell #’ refers to whether the number of cells can be varied. Symbols: ✓ = yes, ✗ = no, (✓) = yes, but based on user input parameters, i.e., no support for parameter estimation, \*requires random splitting of cells into two groups, †/‡ = internal/prior resampling from empirical parameter distribution, ◦ = no separate estimation step)

	Batches	Clusters	Type(s)	Cell #	Parallelization	Availability	Year	Model
BASICS [37]	✓	✗	b	✗	✓✗	<a href="#">R/Bioc</a>	2015	NB
ESCO [38]	✓	✓	n,b,k	✓	✓✓	<a href="#">R/GitHub</a>	2020	Gamma-Poisson
hierarchicell [39]	✓	✗	n,b	✓	✗✗	<a href="#">R/GitHub</a>	2021	NB
muscat [40]	✓	✓	n,b,k	(✓)†	✗✗	<a href="#">R/Bioc</a>	2020	NB
POWSC [41]	✗	✓	n,k	(✓)†	✗✗	<a href="#">R/Bioc</a>	2020	zero-inflated, log-normal Poisson mixture
powsimR [42]	✗	(✓)	n*	(✓)†	✓✓	<a href="#">R/GitHub</a>	2017	NB
scDD [43]	✗	✗	n*	✓	✓✓	<a href="#">R/Bioc</a>	2016	Bayesian NB mixture model
scDesign [44]	✗	(✓)	n	✓	◦✓	<a href="#">R/GitHub</a>	2019	Gamma-Normal mixture model
scDesign2 [45]	✗	✓	n,k	✓	✓✗	<a href="#">R/GitHub</a>	2020	(zero-inflated) Poisson or NB + Gaussian copula for gene–gene correlations
SCRIP [46]	✓	✓	n,b,k	✓	✗✗	<a href="#">R/GitHub</a>	2020	(Beta-)Gamma-Poisson
SPARSim [47]	✓	✗	n,b	(✓)‡	✗✗	<a href="#">R/GitLab</a>	2020	Gamma-multivariate hypergeometric
splatter [15] (Splat model)	(✓)	(✓)	n	✓	✗✗	<a href="#">R/Bioc</a>	2017	Gamma-Poisson
SPsimSeq [16]	✓	✗	n,b	✓	◦✗	<a href="#">R/Bioc</a>	2020	log-linear model-based density estimation + Gaussian copula for gene–gene correlations
SymSim [48]	✓	✗	n,b	✓	✗✗	<a href="#">R/GitHub</a>	2019	kinetic model using MCMC
ZINB-WaVE [49]	✓	✓	n,b,k	✗	✗✗	<a href="#">R/Bioc</a>	2018	zero-inflated NB
zingeR [50]	✗	✗	n	(✓)†‡	✗✗	<a href="#">R/GitHub</a>	2017	zero-inflated NB

The linked citations and the hyperlinks to the availability of data (in table 1) can be found in the original article. The original article [1] has been corrected.

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#### Reference

1. Crowell HL, Morillo Leonardo SX, Sonesson C, et al. The shaky foundations of simulating single-cell RNA sequencing data. *Genome Biol.* 2023;24:62. <https://doi.org/10.1186/s13059-023-02904-1>.