

PUBLISHER CORRECTION

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Publisher Correction: scDesign2: a transparent simulator that generates high-fidelity single-cell gene expression count data with gene correlations captured

Tianyi Sun¹, Dongyuan Song², Wei Vivian Li^{3*} and Jingyi Jessica Li^{1,4,5,6*}

The original article can be found online at <https://doi.org/10.1186/s13059-021-02367-2>.

* Correspondence: li@rutgers.edu; jli@stat.ucla.edu; lijy03@g.ucla.edu

³Department of Biostatistics and Epidemiology, Rutgers School of Public Health, Piscataway, NJ 08854, USA

¹Department of Statistics, University of California, Los Angeles, CA 90095-1554, USA

Full list of author information is available at the end of the article

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Following publication of the original paper [1], it was noticed that a typesetting error occurred.

The HTML version of this article erroneously contained the incorrect version of Table 1. It was also reported that “SSPsimSeq” should be “SPsimSeq” in the 12th row of Table 1. The correct Table 1 is given below.

The original article [1] has been updated.

Author details

¹Department of Statistics, University of California, Los Angeles, CA 90095-1554, USA. ²Interdepartmental Program of Bioinformatics, University of California, Los Angeles, CA 90095-7246, USA. ³Department of Biostatistics and Epidemiology, Rutgers School of Public Health, Piscataway, NJ 08854, USA. ⁴Department of Human Genetics, University of California, Los Angeles, CA 90095-7088, USA. ⁵Department of Computational Medicine, University of California, Los Angeles, CA 90095-1766, USA. ⁶Department of Biostatistics, University of California, Los Angeles, CA 90095-1772, USA.

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1. Sun T, Song D, Li WW, et al. scDesign2: a transparent simulator that generates high-fidelity single-cell gene expression count data with gene correlations captured. *Genome Biol.* 2021;22:163. <https://doi.org/10.1186/s13059-021-02367-2>.

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Table 1 Summary of 16 simulators (including our proposed scDesign2) in six properties

Property	1 protocol adaptive	2 gene preserved	3 gene cor. captured	4 cell num. seq. dep. flexible	5 transparent	6 comp. and sample efficient
Simulator						
dyngen [77]	✓	✗	✗	✓	✓	✓
Lun2 [78]	✓	✓	✗	✓	✓	✓
powsimR [75]	✓	✓	✗	✓	✓	✓
PROSST [68]	✓	✓	✗	✓	✓	✓
scDD [74]	✓	✗	✗	✓	✓	✓
scDesign[35]	✓	✓	✗	✓	✓	✓
scGAN [72]	✓	✓	✓	✓	✗	✗
splat simple[69]	✓	✗	✗	✗	✓	✓
splat [69]	✓	✗	✗	✗	✓	✓
kersplat [69]	✓	✗	✓	✗	✓	✓
SPARSim [71]	✓	✓	✓	✗	✓	✓
SPsimSeq [79]	✓	✓	✓	✓**	✓	✓
SymSim[70]	✓	✗	✗	✗	✓	✓
ZINB-WaVe[39]	✓	✓	✓	✗	✓	✓
SERGIO [76]	✓	✓	✗*	✓	✓	✓
scDesign2	✓	✓	✓	✓	✓	✓

Property 1: protocol adaptiveness

Property 2: gene preservation

Property 3: gene correlation capture

Property 4: flexible cell number and sequencing depth choices

Property 5: transparency

Property 6: computational and sample efficiency

For each simulator and each property, a checkmark, checkcross, or cross means that the simulator satisfies, partially satisfies, or does not satisfy the property, respectively

*SERGIO requires a user-specified gene regulatory network, and it does not capture/estimate gene correlations from a real dataset

**SPsimSeq can vary cell number but not sequencing depth