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PUBLISHER CORRECTION

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

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

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Correction to: Genome Biol 22, 163 (2021)
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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.

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Reference
1. Sun T, Song D, Li WV, 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.

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