

AUTHOR CORRECTION

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Author Correction: scINSIGHT for interpreting single-cell gene expression from biologically heterogeneous data

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The original article can be found online at <https://doi.org/10.1186/s13059-022-02649-3>.

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Correction to: *Genome Biol* 23, 82 (2022)

<https://doi.org/10.1186/s13059-022-02649-3>

Following publication of the original article [1], the authors identified a missing reference and citation in the last paragraph of the section “The scINSIGHT model”. The last two sentences of this paragraph should read:

These limitations are resolved by scINSIGHT to better jointly analyze single-cell samples from different biological conditions. In addition, scINSIGHT is different from the CSMF method [2], which learns common and specific patterns among J datasets from J conditions.

The original article [1] has been corrected.

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Published online: 21 April 2022

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2. Zhang L, Zhang S. Learning common and specific patterns from data of multiple interrelated biological scenarios with matrix factorization. *Nucleic Acids Res.* 2019;47(13):6606–17.

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