## CORRECTION Open Access

## Correction: iDESC: identifying differential expression in single-cell RNA sequencing data with multiple subjects

Yunqing Liu<sup>1</sup>, Jiayi Zhao<sup>1</sup>, Taylor S. Adams<sup>2</sup>, Ningya Wang<sup>1</sup>, Jonas C. Schupp<sup>2,3</sup>, Weimiao Wu<sup>1,4</sup>, John E. McDonough<sup>2</sup>, Geoffrey L. Chupp<sup>2</sup>, Naftali Kaminski<sup>2</sup>, Zuoheng Wang<sup>1\*</sup> and Xiting Yan<sup>1,2\*</sup>

The original article can be found online at https://doi.org/10.1186/s12859-023-05432-8.

\*Correspondence: zuoheng.wang@yale.edu; xiting.yan@yale.edu

<sup>3</sup> Department of Respiratory

Correction: BMC Bioinformatics (2023) 24:318

https://doi.org/10.1186/s12859-023-05432-8

Following publication of the original article [1], the authors identified an error in Table 2. The correct table is given below.

The incorrect Table 2 is:

**Table 2** Fisher's exact test and Jaccard index measuring the DE genes overlapping between the two chosen scRNA-seq datasets in macrophage and fibroblast

Method	iDESC	MAST-RE	Muscat-MM	Muscat-PB	subT
Macrophage					
P value	$1 \times 10^{-5}$	1.000	0.269	$1 \times 10^{-5}$	0.085
Jaccard Index	0.137	0.061	0.108	0.055	0.028
Fibroblast					
P value	$4 \times 10^{-21}$	$4 \times 10^{-6}$	$3 \times 10^{-5}$	$2 \times 10^{-7}$	0.011
Jaccard Index	0.077	0.067	0.071	0.035	0.024

The correct Table 2 is:

**Table 2** Fisher's exact test and Jaccard index measuring the DE genes overlapping between the two chosen scRNA-seq datasets in macrophage and fibroblast

Method		iDESC	MAST-RE	Muscat-MM	Muscat-PB	subT
Macrophage	P-value	$1 \times 10^{-5}$	1.000	0.269	$1 \times 10^{-5}$	0.085
	Jaccard Index	0.137	0.061	0.108	0.055	0.028
Fibroblast	P-value	$4 \times 10^{-21}$	$4 \times 10^{-6}$	$3 \times 10^{-5}$	$2 \times 10^{-7}$	0.011
	Jaccard Index	0.077	0.067	0.071	0.035	0.024



© The Author(s) 2023. **Open Access** This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if changes were made. The images or other third party material in this article are included in the article's Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, visit http://creativecommons.org/licenses/by/4.0/. The Creative Commons Public Domain Dedication waiver (http://creativecommons.org/publicdomain/zero/1.0/) applies to the data made available in this article, unless otherwise stated in a credit line to the data.

<sup>&</sup>lt;sup>1</sup> Department of Biostatistics, Yale School of Public Health, New Haven, CT 06520, USA <sup>2</sup> Section of Pulmonary, Critical Care and Sleep Medicine, Yale School of Medicine, New Haven, CT 06520, USA

Medicine, Hannover Medical School and Biomedical Research in End-Stage and Obstructive Lung Disease Hannover, German Center for Lung Research (DZL), Hannover, Germany <sup>4</sup> Meta Platforms, Inc, Cambridge,

<sup>&</sup>lt;sup>4</sup> Meta Platforms, Inc, Cambridge, USA

Liu et al. BMC Bioinformatics (2023) 24:394 Page 2 of 2

Published online: 19 October 2023

## Reference

 Liu Y, et al. iDESC: identifying differential expression in single-cell RNA sequencing data with multiple subjects. BMC Bioinformatics. 2023;24:318. https://doi.org/10.1186/s12859-023-05432-8.

## **Publisher's Note**

Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.