Zhijian Li

Broad Institute of MIT and Harvard
415 Main St, Cambridge, MA 02142, USA
Phone: +1-617-251-8024
Email: lizhijia@broadinstitute.org
Web: https://lzj1769.github.io/
Google scholar: https://scholar.google.de/citations?user=xG5HYekAAAAJ&hl=en

---

Position

2023 - present   Postdoc, Broad Institute of MIT and Harvard, USA

Education

2016 - 2022   Ph.D., Computer Science, RWTH Aachen University, Germany
2014 - 2016   M.Sc., Computer Science, Central China Normal University, China
2008 - 2012   B.S., Computer Science and Technology, Jilin University, China

Awards

2022   Outstanding Self-financed Students Abroad, China Scholarship Council
2021   Poster Award of e: Med Meeting on Systems Medicine 2021, Germany
2016   Third Place (Conference Round), ENCODE-DREAM in vivo TFBS Prediction Challenge
2016   Outstanding Master Thesis, Central China Normal University
2015   National Scholarship of China

Presentations

2021   Flash Talk & Poster Presentation, e:Med Meeting on Systems Medicine 2021, Germany
2020   Regular Talk, ECCB 2020
2020   Poster Presentation, ISMB 2020
2019   Poster Presentation, ISMB/ECCB 2019
2018   Poster Presentation, RECOMB 2018

Teaching

2021   Teaching Assistant, Single-cell data analysis, RWTH Aachen University
2020   Teaching Assistant, Introduction to Bioinformatics, RWTH Aachen University
2018   Teaching Assistant, Bioinformatics, RWTH Aachen University

Memberships

2018 -   Member, International Society for Computational Biology (ISCB)

Publications

Co-first authors; * Co-corresponding authors

First/co-first author papers

9. **Z Li**#, Z Patel#, D Song, G Yao, J Li and L Pinello. Benchmarking computational methods to identify spatially variable genes and peaks. ***Nature Methods*** (2023) (Submitted).

8. Z Chen, L Ye, M Zhu, C Xia, J Fan, H Chen, **Z Li***, and S Mou*. Single-cell multi-omics of fibrotic kidneys reveal a deficiency in antioxidation and apoptosis-related gene regulation within the proximal tubule. (2023) (Submitted).

7. **Z Li**#*, C C Kuo#, F Ticconi, M Shaigan, E G Gusmao, M Allhoff, M Manolov, M Zenke, I G Costa*. RGT: a toolbox for the integrative analysis of high throughput regulatory genomics data. ***BMC Bioinformatics*** (2023).

6. **Z Li**, J Nagai, C Kuppe, R Kramann, I G Costa. scMEGA: Single-cell Multiomic Enhancer-based Gene Regulatory Network Inference. ***Bioinformatics Advances*** (2023).

5. C Kuppe#, **Z Li**#, R T Levinson#, P B Mompel#, T Lu, R Flores, M Halder, M Cheng, X Zhang, R K Schneider, R Thadhani, S Hayat, K Lim, I G Costa*, J S Rodriguez*, R Kramann*. Integrative single-cell multi-omics analysis reveals traits associated with early heart failure. (2022) (Submitted).

4. C Kuppe#, R O R Flores#, **Z Li**#, S Hayat, R T Levinson, X Liao, M T Hannani, J Tanevski, F Wünnemann, J S Nagai, M Halder, D Schumacher, S Menzel, G Schäfer, K Hoeft, M Cheng, S Ziegler, X Zhang, F Peisker, N Kaesler, T Saritas, Y Xu, A Kassner, J Gummert, M Morshuis, J Amrute, R J A Veltrop, P Boor, K Klingel, L W Van Laake, A Vink, R M Hoogenboezem, E M J Bindels, L Schurgers, S Sattler, D Schapiro, R K Schneider, K Lavine, H Milting*, I G Costa*, J Saez-Rodriguez* and R Kramann*. Spatial multi-omic map of human myocardial infarction. ***Nature*** (2022).

3. **Z Li**#, C Kuppe#, S Ziegler, M Cheng, N Kabgani, S Menzel, M Zenke, R Kramann*, I G Costa*. Chromatin-accessibility estimation of single-cell ATAC-seq data with scOpen. ***Nature Communications*** (2021).

2. **Z Li**, M H Schulz, T Look, M Begemann, M Zenke, I G Costa. Identification of transcription factor binding sites using ATAC-seq. ***Genome Biology*** (2019).

1. **Z Li**, J Guo, S Yang. Improving the JADE Algorithm by Clustering Successful Parameters. ***International Journal of Wireless and Mobile Computing*** (2016).

Contributed papers

12. J Ryu, S B, T Yu, M Jankowiak, Y Zhou, M Francoeur, Q V Phan, **Z Li**, M Tognon, L Brown, M I. Love, G Lettre, D B. Ascher, C A. Cassa, R I. Sherwood, L Pinello. Joint genotypic and phenotypic outcome modeling improves base editing variant effect quantification. ***Nature Genetics*** (2023). (Under revision)

11. H Xu, **Z Li**, C C Kuo, K Götz, T Look, MAS de Toledo, K Seré, I G Costa and M Zenke. A lncRNA identifies IRF8 enhancer in feedback control of DC development. ***eLife*** (2023).

10. SH Subramanyam, J Hriczko, S Schulz, T Look, T Goodarzi, T Clarner, M Scheld, M Kipp, E Verjans, S Böll, I Costa, **Z Li**, Lin Gan, B Denecke, S Floess, J Huehn, E Schmitt, T Bopp, H Wasmuth, R Vinograd, R Beyaert, B Lambrecht, M Zenke, N Wagner, K Ohl, K Tenbrock. CREB regulates Foxp3+ST-2+ Tregs with enhanced IL-10 production. (2023) (Submitted).

9. E.F Brandt, T.H Wirtz, **Z Li**, M.M Ibrahim, P Fischer, A Beckers, A Flabhove, I.G Costa, R Kramann, E.P.C van der Vorst, C Liedtke, H Sahin, C Trautwein, M.L Berres. CXCR3-expressing macrophages regulate angiogenesis, tumor cell proliferation, and immune evasion in hepatocellular carcinoma. (2022) (Submitted).

8. D Schumacher#, M Cheng#, C Kuppe, E M Bindels, R K Schneider, **Z Li**, I G Costa*, R Kramann*. Single Nucleus ATAC Sequencing Reveals Epigenomic Regulation After Myocardial Infarction. (2022) (Submitted).

7. Y Xu#, C Kuppe#, JP Patón, S Hayat, J Kranz, A T Abdallah, J Nagai, **Z Li**, F Peisker, T Saritas, M Halder, S Menzel, K Hoeft, A Kenter, H Kim, C van Roeyen, M Lehrke, J Moellmann, T Speer, E M Buhl, R Hoogenboezem, P Boor, J Jansen, C Knopp, I Kurth, B Smeets, E Bindels, M Reinders, C Baan, J Gribnau, E Hoorn, J Steffens, T Huber, I G Costa, J Floege, R K Schneider, J Saez-Rodriguez, B S. Freedman* and R Kramann*. Adult human kidney organoids originate from CD24+ cells and represent an advanced model for adult polycystic kidney disease. ***Nature Genetics*** (2022).

6. M Cheng, **Z Li**, I G Costa. MOJITOO: a fast and universal method for integration of multimodal single-cell data. ***Bioinformatics*** (2022).

5. A Philippi#, S Heller#, I G Costa#, V Senée#, M Breunig, **Z Li**, G Kwon, R Russell, A Illing, Q Lin, M Hohwieler, A Degavre, P Zalloua, S Liebau, M Schuster, J Krumm, X Zhang, R Geusz, J.R Benthuysen, A Wang, J Chiou, K Gaulton, H Neubauer, E Simon, T Klein, M Wagner, G Nair, C Besse, C Dandine-Roulland, R Olaso, J Deleuze, B Kuster, M Hebrok, T Seufferlein, M Sander, B.O Boehm, F Oswald, M Nicolino*, C Julier*, A Kleger*. Mutations and variants of ONECUT1 in diabetes. ***Nature Medicine*** (2021).

4. S Heller, **Z Li**, Q Lin, R Geusz, M Breunig, M Hohwieler, X Zhang, G Nair, T Seufferlein, M Hebrok, M Sander, C Julier, A Kleger*, I G Costa*. Transcriptional changes and the role of ONECUT1 in hPSC pancreatic differentiation. ***Communications Biology*** (2021).

3. J Guo, **Z Li**, S Yang. Accelerating differential evolution based on a subset-to-subset survivor selection operator. ***Soft Computing*** (2019).

2. J Guo, W Xie, **Z Li**. Enhancing JADE utilizing distance of best solutions. ***Computer Engineering and Design*** (2018).

1. J Guo, **Z Li**, W Xie, H Wang. Dissipative differential evolution with self-adaptive control parameters. ***IEEE Congress on Evolutionary Computation*** (2015).

Referees

Ivan G. Costa (Ph.D. supervisor)
RWTH Aachen University
Pauwelsstrasse 19, 52074 Aachen, Germany
Email: ivan.costa@rwth-aachen.de
Web: https://costalab.org

Luca Pinello (Postdoc adviser)
MGH & Harvard Medical School/Broad Institute
149 13th Street, 6th floor
Charlestown, MA 02129, USA
Email: lpinello@mgh.harvard.edu
Web: http://main.pinellolab.partners.org