

Dongyuan Song

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EDUCATION

University of California, Los Angeles (UCLA) 09/2019 - present
Ph.D. candidate in *Bioinformatics*, Interdepartmental Ph.D. Program Los Angeles, CA
Advisor: Dr. Jingyi Jessica Li

Harvard University 09/2022 - 09/2023
Visiting Ph.D. student, Department of Statistics Boston, MA

Harvard T.H. Chan School of Public Health 09/2017 - 05/2019
M.S. in *Computational Biology*, Department of Biostatistics Boston, MA
Thesis: Normalization methods for Universal Protein Binding Microarray (PBM) data analysis
Advisor: Dr. Rafael Irizarry

Fudan University 09/2013 - 06/2017
B.S. in *Biological Science*, School of Life Sciences Shanghai, China

RESEARCH INTERESTS

My research focuses on improving the interpretability in analyzing single-cell and spatial genomics. Major research topics include:

- Generative models of high-dimensional single-cell and spatial multi-omics data
- Double-dipping agnostic post-clustering differential expression (DE) analysis via synthetic null data generation and p -value-free false discovery rate (FDR) control
- Hypothesis testing of DE by accounting for uncertainty in inferred variables
- Feature selection and cell subsampling of large-scale single-cell data

PUBLICATIONS

author* equal contribution author co-corresponding author

Peer reviewed

1. Guanao Yan, **Dongyuan Song**, and Jingyi Jessica Li. scReadSim: a single-cell RNA-seq and ATAC-seq read simulator. *Nature Communications*, 14(1):7482, 2023
2. **Dongyuan Song**, Qingyang Wang, Guanao Yan, Tianyang Liu, Tianyi Sun, and Jingyi Jessica Li. scDesign3 generates realistic in silico data for multimodal single-cell and spatial omics. *Nature Biotechnology*, 2023
3. Elvis Han Cui*, **Dongyuan Song***, Weng Kee Wong, and Jingyi Jessica Li. Single-cell generalized trend model (scGTM): a flexible and interpretable model of gene expression trend along cell pseudotime. *Bioinformatics*, 38(16):3927–3934, 2022

4. **Dongyuan Song***, Nan Miles Xi*, Jingyi Jessica Li, and Lin Wang. scSampler: fast diversity-preserving subsampling of large-scale single-cell transcriptomic data. *Bioinformatics*, 38(11):3126–3127, 2022
5. Tianyi Sun, **Dongyuan Song**, Wei Vivian Li, and Jingyi Jessica Li. Simulating single-cell gene expression count data with preserved gene correlations by scDesign2. *Journal of Computational Biology*, 29(1):23–26, 2022
6. Ruochen Jiang, Tianyi Sun, **Dongyuan Song**, and Jingyi Jessica Li. Statistics or biology: the zero-inflation controversy about scRNA-seq data. *Genome biology*, 23(31), 2022
7. **Dongyuan Song***, Kexin Li*, Zachary Hemminger, Roy Wollman, and Jingyi Jessica Li. scPNMF: sparse gene encoding of single cells to facilitate gene selection for targeted gene profiling. *Bioinformatics*, 37(Supplement_1):i358–i366, 2021
8. Xinzhou Ge, Yiling Elaine Chen, **Dongyuan Song**, MeiLu McDermott, Kyla Woysner, Antigoni Manousopoulou, Ning Wang, Wei Li, Leo D Wang, and Jingyi Jessica Li. Clipper: p-value-free FDR control on high-throughput data from two conditions. *Genome biology*, 22(288), 2021
9. Tianyi Sun, **Dongyuan Song**, Wei Vivian Li, and Jingyi Jessica Li. scDesign2: a transparent simulator that generates high-fidelity single-cell gene expression count data with gene correlations captured. *Genome biology*, 22(163), 2021
10. **Dongyuan Song** and Jingyi Jessica Li. PseudotimeDE: inference of differential gene expression along cell pseudotime with well-calibrated p-values from single-cell RNA sequencing data. *Genome biology*, 22(124), 2021
11. Elizabeth Christina Miller, Kenji T Hayashi, **Dongyuan Song**, and John J Wiens. Explaining the ocean’s richest biodiversity hotspot and global patterns of fish diversity. *Proceedings of the Royal Society B*, 285(1888):20181314, 2018
12. **Dongyuan Song***, Zhe Wang*, Zhuo-Jun Song, Cheng-Chuan Zhou, Peng-Hao Xu, Jie Yang, Ji Yang, and Bao-Rong Lu. Increased novel single nucleotide polymorphisms in weedy rice populations associated with the change of farming styles: Implications in adaptive mutation and evolution. *Journal of Systematics and Evolution*, 55(2):149–157, 2017

Under review

13. **Dongyuan Song***, Kexin Li*, Xinzhou Ge, and Jingyi Jessica Li. ClusterDE: a post-clustering differential expression (DE) method robust to false-positive inflation caused by double dipping. *bioRxiv*, 2023
14. Zhijian Li, Zain Patel, **Dongyuan Song**, Jingyi Jessica Li Guanao Yan, and Luca Pinello. Benchmarking the efficacy and scalability of computational methods for the identification of spatially variable genes and peaks. *Under review at Nature Methods*, 2023
15. Qingyang Wang, Zhiqian Zhai, **Dongyuan Song**, and Jingyi Jessica Li. Review of computational methods for estimating cell potency from single-cell rna-seq data, with a detailed analysis of discrepancies between method description and code implementation. *Under review at Nature Communications*, 2023
16. Kian Hong Kock, Patrick K Kimes, Stephen S Gisselbrecht, Sachi Inukai, Sabrina K Phanor, James L Anderson, Gayatri L Ramakrishnan, Colin H Lipper, **Dongyuan Song**, Jesse V Kur-

land, Julia M Rogers, Raehoon Jeong, Stephen C Blacklow, Rafael A Irizarry, and Martha L Bulyk. DNA binding analysis of rare variants in homeodomains reveals novel homeodomain specificity-determining residues. *Under review at Nature Communications*, 2023

17. Bicna Song, Dingyu Liu, Weiwei Dai, Natalie McMyn, Qingyang Wang, Dapeng Yang, Adam Krejci, Anatoly Vasilyev, Nicole Untermoser, Anke Loregger, et al. Decoding heterogenous single-cell perturbation responses. *Submitted to Nature Cell Biology*, 2023

AWARDS

Dissertation Year Fellowship (\$38,000), UCLA	2023
James P. Taylor Foundation + CSHL Biology of Genomes Scholarship (\$1,600)	2023
Summer Mentored Research Fellowship (\$6,000), UCLA	2021
QCBio Retreat Best Poster Award, UCLA	2021
Outstanding Graduate Student (Top 5%), Fudan University	2017
National Life Science Innovation Competition First Prize, China	2017
Member of National Top Talent Undergraduate Training Program, Fudan University	2017
DuPont First-class Scholarship (Top 3%), Fudan University	2016
First-Class Scholarship Awarded by the NTTUTP (Top 10%), Fudan University	2016

TEACHING

Undergraduate level

STATS 100B <i>Introduction to Mathematical Statistics</i> : Teaching Assistant	Winter 2022
STATS 19 <i>Fiat Lux Seminar</i> : Guest Lecturer	Winter 2021

Graduate level

STATS M254 <i>Statistical Methods in Computational Biology</i> : Teaching Assistant	Winter 2022
STATS 205 <i>Hierarchical Linear Models</i> : Teaching Assistant	Fall 2021

PRESENTATIONS

Invited talks

1. Eastern North American Region of International Biometric Society (ENAR 2024) 03/2024
scDesign3 generates realistic in silico data for multimodal single-cell and spatial omics
2. CMSE department seminar at Michigan State University 10/2023
Improving statistical rigor in single-cell and spatial omics
3. BU-Tsinghua-Keio Workshop 2023: Probability and Statistics 06/2023
In silico data generation and statistical model inference for single-cell and spatial omics
4. Chan Zuckerberg Initiative (CZI) Single-Cell Monthly Webinar 11/2022
Fast diversity-preserving subsampling of large-scale single-cell transcriptomic data
5. 26th Conference on Intelligent Systems for Molecular Biology 07/2021
and the 20th European Conference on Computational Biology (ISMB/ECCB 2021)
scPNMF: sparse gene encoding of single cells to facilitate gene selection for targeted gene profiling

Seminar talks

6. UCLA Institute for Quantitative and Computational Biosciences (QCBio) 03/2023
ClusterDE: a post-clustering differentially expressed (DE) gene identification method robust to false-positive inflation caused by double-dipping
7. STAT 300, Department of Statistics, Harvard University 11/2022
scDesign3: an all-in-one statistical framework that generates realistic single-cell omics data and infers cell heterogeneity structure
8. UCLA Institute for QCBio 01/2022
scDesign3: an all-in-one statistical framework that generates realistic single-cell omics data and infers cell heterogeneity structure
9. UCLA Institute for QCBio 10/2020
PseudotimeDE: inference of differential gene expression along cell pseudotime with valid p-values from single-cell RNA sequencing data

Poster presentations

10. Biology of Genomes Meeting, Cold Spring Harbor Laboratory (CSHL) 05/2023
A unified framework of realistic in silico data generation and statistical model inference for single-cell and spatial omics
11. UCLA Jonsson Comprehensive Cancer Center Annual Retreat 05/2022
PseudotimeDE: inference of differential gene expression along cell pseudotime with well-calibrated p-values from single-cell RNA sequencing data
12. Human Cell Atlas (HCA) General Meeting 06/2021
scPNMF: sparse gene encoding of single cells to facilitate gene selection for targeted gene profiling
13. Biology of Genomes Meeting, Cold Spring Harbor Laboratory (CSHL) 05/2021
PseudotimeDE: inference of differential gene expression along cell pseudotime with well-calibrated p-values from single-cell RNA sequencing data

MENTORING

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| Shiyu Ma, Undergraduate student at UCLA | 02/2022-05/2023 |
| <i>Construction of cell-type hierarchy by machine learning on scRNA-seq data</i> | |
| Lehan Zou, Undergraduate student at UCLA | 05/2022-12/2022 |
| <i>Development of scGTM R package</i> | |
| Tianyang Liu, Master of Applied Statistics at UCLA | 02/2021-04/2022 |
| <i>Differential expression test along cell pseudotime by quantile non-parametric additive models</i> | |
| Huy Nguyen, Undergraduate student at UCLA | 02/2021-03/2022 |
| <i>Differential expression test along cell pseudotime by quantile non-parametric additive models</i> | |

PROFESSIONAL SERVICE**Reviewer for Scientific Journals** (# papers in parentheses):

Annals of Applied Statistics (1), Nature Communications (1), Cell Systems (1), Bioinformatics (2), Journal of Computational Biology (1), Scientific Reports (1), STAR Protocols (1),

IEEE/ACM Transactions on Computational Biology and Bioinformatics (1), Frontiers in Molecular Biosciences (1)

PROFESSIONAL AFFILIATIONS

International Society for Computational Biology (ISCB)	2021-2023
American Statistical Association (ASA)	2022-2023

SOFTWARE PACKAGES

1. **ClusterDE**: a post-clustering DE method for controlling FDR regardless of clustering quality.
R package: <https://github.com/SONGDONGYUAN1994/ClusterDE>
2. **PseudotimeDE**: a DE method that accounts for the uncertainty in pseudotime inference.
R package: <https://github.com/SONGDONGYUAN1994/PseudotimeDE>
3. **scDesign3**: a realistic simulator for multimodal single-cell and spatial omics.
R package: <https://github.com/SONGDONGYUAN1994/scDesign3>
4. **scPNMF**: a dimensionality reduction method to facilitate gene selection
R package: <https://github.com/JSB-UCLA/scPNMF>
5. **scsampler**: diversity-preserving subsampling of large-scale single-cell transcriptomic data
Python package: <https://github.com/SONGDONGYUAN1994/scsampler>

SKILLS

Computer Languages	R, Python, shell script
Tools	Git/GitHub, L ^A T _E X