ZHANA DUREN, PhD

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RESEARCH FOCUS

Computational regulatory genomics; mechanistic and element-resolved gene regulatory network inference; single-cell and spatial multiomics; integration of heterogeneous and incomplete genomic measurements. Research program centered on learning regulatory mechanisms from information-rich genomic data and transferring that knowledge to biological contexts where regulatory measurements are incomplete or unavailable.

EDUCATION

PhD, Operational Research and Cybernetics, Academy of Mathematics and Systems Science, Chinese Academy of Sciences — **July 2017**

Dissertation: *Modelling gene regulatory network* | Advisor: Prof. Yong Wang

B.S., Mathematics and Applied Mathematics, Beihang University — 2012

ACADEMIC APPOINTMENTS AND TRAINING

Associate Professor, Indiana University School of Medicine | 2024–present
Department of Medical and Molecular Genetics; Center for Computational Biology and Bioinformatics

Assistant Professor, Clemson University | 2020–2024
Department of Genetics and Biochemistry; Center for Human Genetics.

Postdoctoral Research Fellow, Stanford University | 2017–2020
Department of Statistics; supervisor: Prof. Wing Hung Wong

Visiting PhD Student, Stanford University | 2015–2017
Department of Statistics; advisor: Prof. Wing Hung Wong

SELECTED KEY PUBLICATIONS IN BIOINFORMATICS / COMPUTATIONAL BIOLOGY

*Selected to highlight the development of mechanistic regulatory modeling, regulatory-informed multimodal integration, and the independent research trajectory. * co-first authors; # co-corresponding authors.*

1. Qiuyue Yuan and Zhana Duren. Inferring gene regulatory networks from single cell multiome data using atlas-scale external data. Nature Biotechnology (2024).

   LINGER — independent PI work; context-specific, element-resolved GRN inference using atlas-scale external regulatory information.

2. Lixin Ren, Ishita Debnath and Zhana Duren. Reference Regulatory Element-Guided Gene Expression Analysis for Mechanistic Inference of Gene Regulatory Networks. bioRxiv preprint (2026). Under Review.

   Independent PI work; element-resolved GRN inference from gene expression and reference regulatory-element information without requiring sample-specific ATAC-seq.

3. Ishita Debnath and Zhana Duren. Inference of spatial chromatin accessibility via integration of spatial transcriptomics and single-cell multi-omics data. Nature Communications (2026).

   ISON — independent PI work; infers spatial chromatin accessibility and reconstructs spatially resolved GRNs.

4. Fnu Naqing, Qiuyue Yuan, and Zhana Duren. Benchmarking component choices for unpaired single cell RNA and epigenomic integration. Genome Biology (2026).

   UnPairBench — independent PI work; systematic component-level benchmarking of unpaired RNA–epigenomic integration.

5. Qiuyue Yuan and Zhana Duren. Integration of single-cell multi-omics data by regression analysis on unpaired observations. Genome Biology (2022).

   UnpairReg — independent PI work; regression-based integration of unpaired RNA and chromatin-accessibility observations.

6. Zhana Duren*#, Fengge Chang*, Fnu Naqing, Jingxue Xin, Qiao Liu, and Wing Hung Wong#. Regulatory analysis of single cell multiome gene expression and chromatin accessibility data with scREG. Genome Biology (2022).

   scREG — developed after establishment of the independent lab; regulatory-informed dimensionality reduction using cis-regulatory potential.

7. Zhana Duren*, Wenhui Sophia Lu*, Joseph G. Arthur, et al., and Wing Hung Wong. Sc-compReg enables the comparison of gene regulatory networks between conditions using single-cell data. Nature Communications (2021).

   Comparative analysis of regulatory network rewiring between biological conditions.

8. Zhana Duren*, Xi Chen*, Jingxue Xin, Yong Wang, and Wing Hung Wong. Time course regulatory analysis based on paired expression and chromatin accessibility data. Genome Research (2020).

   TimeReg — dynamic regulatory modeling across temporal cellular transitions.

9. Zhana Duren*, Xi Chen*, Mahdi Zamanighomi*, et al., Yong Wang, and Wing Hung Wong. Integrative analysis of single-cell genomics data by coupled nonnegative matrix factorizations. PNAS (2018).

   CoupledNMF — integrative analysis of heterogeneous single-cell genomic measurements through coupled latent structure.

10. Zhana Duren, Xi Chen, Rui Jiang, Yong Wang, and Wing Hung Wong. Modeling gene regulation from paired expression and chromatin accessibility data. PNAS (2017).

    PECA — foundational mechanistic framework connecting TFs, cis-regulatory elements, and target genes.

INDEPENDENT RESEARCH TRAJECTORY

Duren established his independent research program as an Assistant Professor at Clemson University in 2020 and moved to Indiana University School of Medicine in 2024. As an independent PI, he has continued and substantially expanded his methodological foundations through scREG, UnpairReg, LINGER, ISON, UnPairBench, and REGA, extending the program toward single-cell multiomics, transferable regulatory knowledge, spatial GRN, and broadly applicable element-resolved GRNs.

RESEARCH SUPPORT

NIGMS/NIH Maximizing Investigators' Research Award (MIRA), R35 GM150513 — PI | 2023–2028 | $1,787,572
Statistical methods for interpretation of genetic variants by gene regulatory networks

NIDA/NIH R21 DA060503 — PI | 2024–2026 | $419,375
Statistical methods for gene regulatory analysis of substance use disorder

COBRE in Human Genetics, P20 GM139769 — Research Project Leader | 2022–2023 | $260,295/year
Four-year project; role ended upon transition from Clemson

COBRE in Human Genetics, P20 GM139769 — Pilot Project Leader | 2022 | $114,375/year
Pilot project

AWARDS AND HONORS

- Maximizing Investigators' Research Award (MIRA), NIGMS/NIH, 2023.
- National Graduate Scholarship, Ministry of Education of China, 2013.
- Outstanding Graduate of Beijing, 2012 (the top 2% of undergraduates across universities in Beijing).

SELECTED INVITED PRESENTATIONS

- International Conference on Intelligent Biology and Medicine (ICIBM), 2026 — "How to Align Unpaired Single-Cell Omics: Benchmarks, Practical Guidelines, and Impacts on Gene Regulatory Modeling."
- University of Nevada, Las Vegas, Department of Mathematical Sciences Statistics Seminar, 2025 — "Integrating Multi-Omics Data for Gene Regulatory Network Inference."
- University of Chicago, Program in Computational Biology Seminar, 2025 — "Integrated Multi-Omics for Gene Regulatory Networks Analysis."
- Pennsylvania State University, Biostatistics Seminar, 2025 — "Integrative analysis of single cell and spatial multi-omics data."

- International Conference on Intelligent Biology and Medicine (ICIBM), 2025 — “Spatial Resolved Gene Regulatory Networks Analysis.”
- ICSA-China, 2025 — “Spatial Resolved Gene Regulatory Networks Analysis.”
- BIRS Spatial Omics Workshop, 2025 — “Integrated Spatial Omics Network from spatial transcriptomics and single cell multiome data.”
- Conference on Statistics in Genomics and Genetics (STATGEN), 2025 — “Modeling of Epigenomics and Spatial Transcriptomics for Spatial Resolved Gene Regulatory Networks Analysis.”
- Boston Children’s Hospital, Data Science Seminar, 2025 — “Integrative analysis of single cell multi-omics data.”
- Cincinnati Children’s Hospital, Biomedical Informatics Seminar, 2025 — “Spatial resolved gene regulatory analysis.”
- McGill University, Biostatistics Seminar, 2025 — “Integrative analysis of single cell multi-omics data.”
- University of Georgia, Institute of Bioinformatics Seminar, 2024 — “Computational system biology approaches for context dependent Gene Regulatory Networks.”
- International Conference on Intelligent Biology and Medicine (ICIBM), 2024 — “Gene regulatory network analysis from single cell multi-omics data.”
- 7th International Conference on Econometrics and Statistics (EcoSta), 2024 — “Gene regulatory network analysis from single cell multi-omics data.”
- International Conference on Intelligent Systems for Molecular Biology (ISMB), 2024 — “Gene regulatory network analysis from single cell multi-omics data.”
- ICSA Applied Statistics Symposium, 2024 — “Gene regulatory network analysis from single cell multi-omics data.”
- NIDA Genetics and Epigenetics Cross-Cutting Research Meeting, 2024 — “Inferring gene regulatory networks from single cell multiome data using atlas-scale external data.”
- 20th Annual Meeting of the MidSouth Computational Biology and Bioinformatics Society, 2024 — “Inferring gene regulatory networks from single cell multiome data using atlas-scale external data.”
- Washington University in St. Louis, Department of Genetics Seminar, 2023 — “Gene regulatory network analysis from single cell multi-omics data.”
- BIRS Single-Cell Plus: Data Science Challenges in Single-Cell Research, 2023 — “Modelling gene regulation via integrative analysis of single cell multi-omics data.”
- University of Sydney, Sydney Precision Data Science Centre Bioinformatics Seminar, 2023 — “Continuous lifelong learning for modeling of gene regulation from single cell multiome data by leveraging atlas-scale external data.”
- Genentech, Computational Biology Seminar, 2022 — “Regulatory analysis of single cell multiome gene expression and chromatin accessibility data with scREG.”
- Emory University, Department of Biostatistics and Bioinformatics Seminar, 2021 — “Comparison of gene regulatory networks between two conditions using single-cell genomics data.”

SELECTED PROFESSIONAL SERVICE

- Editorial Board Member, Genome Biology, 2023–present.
- Co-Chair Track Leader (Single-cell Omics Track), ASA Conference on Statistics in Genomics and Genetics (STATGEN), 2027.
- Program Committee Member, International Conference on Intelligent Systems for Molecular Biology (ISMB), 2026.
- 2026 — Organizer and Co-Chair, “Advanced Computational Methods in Single-cell and Spatial Omics,” MidSouth Computational Biology and Bioinformatics Society (MCBIOS) Annual Meeting.
- 2026 — Organizer and Co-Chair, “Machine Learning Advances in Single-cell Omics,” MidSouth Computational Biology and Bioinformatics Society (MCBIOS) Annual Meeting.

- 2024 — Organizer and Co-Chair, “Computational Methods for Single Cell Multi-Omics Data,” MidSouth Computational Biology and Bioinformatics Society (MCBIOS) Annual Meeting.
- 2024 — Organizer and Co-Chair, “Computational Methods for Single Cell and Spatial Omics Data,” MidSouth Computational Biology and Bioinformatics Society (MCBIOS) Annual Meeting.
- 2024 — Organizer and Chair, “Computational Methods for Single Cell/Spatial Multi-Omics Data,” International Conference on Intelligent Biology and Medicine (ICIBM).
- NIH peer review: BCTB Special Emphasis Panel (2025); MGG Special Emphasis Panel (2026); MGG Fellowships Panel (2026); MGG Special Emphasis Panel (2025); GCAT study section (2025); NIDA Special Emphasis Panel (2024); DISAM/dGTEx Special Emphasis Panel (2024); MBBC-G study section (2023); BDMA study section (2022).
- Selected journal review: Cell, Nature Methods, Nature Genetics, Nature Machine Intelligence, Nature Reviews Genetics, Nature Communications, Genome Research, Nucleic Acids Research, PLOS Computational Biology.

MENTORING AND TEACHING

- Major advisor of graduate students at Clemson University (2020–2024) and Indiana University (2024–present); supervisor of postdoctoral fellows at Clemson and Indiana University.
- Trainee placement & honors: Former postdoctoral fellow Qiuyue Yuan is now an independent PI at Southern University of Science and Technology; former PhD student Fnu Naqing is a postdoctoral fellow at Emory University; current trainees Fengge Chang and Lixin Ren received ISMB 2026 Travel Awards.
- Instructor, Regulatory Genomics (GEN 8900), Clemson University graduate course, 2022–2024.
- Instructor, Single Cell and Spatial Omics (G888), Indiana University graduate course, 2025-present.

ADDITIONAL PUBLICATIONS

Complete publication list from the June 2026 CV, excluding the selected key publications above where duplication would be unnecessary.

1. Nicholas C. Green, Hongyu Gao, Xiaona Chu, Qiuyue Yuan, Patrick McGuire, Dongbing Lai, Guanglong Jiang, Xiaoling Xuei, Jill L. Reiter, Julia Stevens, Greg T. Sutherland, Alison M. Goate, Zhiping P. Pang, Paul A. Slesinger, Ronald P. Hart, Jay A. Tischfield, Arpana Agrawal, Yue Wang, Zhana Duren, Howard J. Edenberg and Yunlong Liu. Integrated single-cell multiomic profiling of caudate nucleus suggests key mechanisms in alcohol use disorder. Nature Communications (2025).
2. Monica Bodogai, Bongsoo Park, Fatima-Zohra Braikia, Fnu Naqing, Konda Kumaraswami, Chen Chen, Emeline Ragonnaud, Sharon Stack, Steffen Ormanns, Michael Günther, Hellen Ishikawa-Ankerhold, Supriyo De, Luigi Ferrucci, Ranjan Sen, Zhana Duren, Isabel Beerman and Arya Biragyn. A distinct population of CD8+ T cells expressing CD39 and CD73 accumulates with age and supports cancer progression. Nature Aging (2025).
3. Tomasz Włodarczyk, Aaron Lun, Diana Wu, Minyi Shi, Xiaofen Ye, Shreya Menon, Shushan Toneyan, Kerstin Seidel, Liang Wang, Jenille Tan, Shang-Yang Chen, Timothy Keyes, Aleksander Chlebowski, Adrian Waddell, Wei Zhou, Yangmeng Wang, Qiuyue Yuan, Yu Guo, Liang-Fu Chen, Bence Daniel, Antonina Hafner, Meng He, Alejandro Chibly, Yuxin Liang, Zhana Duren, Ciara Metcalfe, Marc Hafner, Christian W Siebel, M Ryan Corces, Robert Yauch, Shiqi Xie, Xiaosai Yao. Epiregulon: Single-cell transcription factor activity inference to predict drug response and drivers of cell states. Nature Communications (2025).
4. Zhanying Feng, Xi Chen, Zhana Duren, Jingxue Xin, Hao Miao, Qiuyue Yuan, Yong Wang, and Wing Hung Wong. Modeling combinatorial regulation from single-cell multi-omics provides regulatory units underpinning cell type landscape using cRegulon. Genome Biology (2025).
5. Xiangqi Bai, Zhana Duren, Lin Wan, and Li C Xia. Joint inference of clonal structure using single-cell genome and transcriptome sequencing data. NAR Genomics and Bioinformatics 6.1 (2024): lqae017.
6. Zhanying Feng, Zhana Duren, Jingxue Xin, Qiuyue Yuan, Yaoxi He, Bing Su, Wing Hung Wong, and Yong Wang. Heritability enrichment in context-specific regulatory networks improves phenotype-relevant tissue identification. Elife 11 (2022): e82535.
7. Zhanying Feng, Xianwen Ren, Zhana Duren, and Yong Wang. Human genetic variants associated with COVID-19 severity are enriched in immune and epithelium regulatory networks. Phenomics (2022), 1-15.
8. David G. Gennert, Rachel C. Lynn, Jeffrey M. Granja, Evan W. Weber, Maxwell R. Mumbach, Yang Zhao, Zhana Duren, Elena Sotillo, William J. Greenleaf, Wing H. Wong, Ansuman T. Satpathy, Crystal L. Mackall, and Howard Y. Chang. Dynamic chromatin regulatory landscape of human CAR T cell exhaustion. Proceedings of the National Academy of Sciences 118, no. 30 (2021): e2104758118.
9. Meng Zou, Zhana Duren, Qiuyue Yuan, Henry Li, Andrew Paul Hutchins, Wing Hung Wong, and Yong Wang. MIMIC: an optimization method to identify cell type-specific marker panel for cell sorting. Briefings in bioinformatics (2021).
10. Xiang Zhu, Zhana Duren, and Wing Hung Wong. Modeling regulatory network topology improves genome-wide analyses of complex human traits. Nature Communications (2021).
11. Zhanying Feng, Zhana Duren, Ziyi Xiong, Sijia Wang, Fan Liu, Wing Hung Wong, and Yong Wang. hReg-CNCC reconstructs a regulatory network in human cranial neural crest cells and annotates variants in a developmental context. Communications biology (2021).

12. Lixin Ren, Caixia Gao, Zhana Duren, and Yong Wang. GuidingNet: revealing transcriptional cofactor and predicting binding for DNA methyltransferase by network regularization. Briefings in Bioinformatics (2020).
13. Jingxue Xin*, Hui Zhang*, Yaoxi He*, Zhana Duren*, Chaoying Cui*, Lang Chen, Xin Luo, Dong-Sheng Yan, Chaoyu Zhang, Xiang Zhu, Qiuyue Yuan, Xuebing Qi, Ouzhuluobu, Wing Hung Wong, Yong Wang, and Bing Su. Chromatin accessibility landscape and regulatory network of high-altitude hypoxia adaptation. Nature Communications (2020).
14. Wenran Li*, Zhana Duren*, Rui Jiang, and Wing Hung Wong. A method for scoring the cell-type specific impacts of non-coding variants in personal genomics. Proceedings of the National Academy of Sciences (2020).
15. Xianglong Zhang, David Hong, Shining Ma, Thomas Ward, Marcus Ho, Reenal Pattni, Zhana Duren, Atanas Stankov, Sharon Bade Shrestha, Joachim Hallmayer, Wing Hung Wong, Allan L. Reiss, and Alexander E. Urban. Integrated functional genomic analyses of Klinefelter and Turner syndromes reveal global network effects of altered X chromosome dosage. Proceedings of the National Academy of Sciences 117, no. 9 (2020): 4864-4873.
16. Wanwen Zeng*, Xi Chen*, Zhana Duren*, Yong Wang, Rui Jiang, and Wing Hung Wong. DC3 is a method for deconvolution and coupled clustering from bulk and single-cell genomics data. Nature Communications, 10.1 (2019): 1-11.
17. Zhana Duren, Yaling Wang, Jiguang Wang, Xing-Ming Zhao, Le Lv, Xiaobo Li, Jingdong Liu, Xin-Guang Zhu, Luonan Chen & Yong Wang. Hierarchical graphical model reveals HFR1 bridging circadian rhythm and flower development in Arabidopsis thaliana. NPJ systems biology and applications 5.1 (2019): 1-11.
18. Lingjie Li, Yong Wang, Jessica L.Torkelson, Gautam Shankar, Jillian M.Pattison, Hanson H.Zhen, Fengqin Fang, Zhana Duren, JingxueXin, Sadhana Gaddam, Sandra P.Melo, Samantha N.Piekos, Jiang Li, Eric J.Liaw, Lang Chen, Rui Li, Marius Wernig, Wing H. Wong, Howard Y. Chang, Anthony E. Oro. TFAP2C-and p63-Dependent Networks Sequentially Rearrange Chromatin Landscapes to Drive Human Epidermal Lineage Commitment. Cell stem cell 24.2 (2019): 271-284.
19. Mahdi Zamanighomi, Zhixiang Lin, Timothy Daley, Xi Chen, Zhana Duren, Alicia Schep, William J. Greenleaf, Wing Hung Wong. Unsupervised clustering and epigenetic classification of single cells. Nature Communications, 9.1 (2018): 2410.
20. Zhana Duren, and Yong Wang. A systematic method to identify modulation of transcriptional regulation via chromatin activity reveals regulatory network during mESC differentiation [J]. Scientific reports, 2016, 6.
21. Zhenwei Shi, Wei Tang, Zhana Duren, Zhiguo Jiang. Subspace matching pursuit for sparse unmixing of hyperspectral data[J]. IEEE Transactions on Geoscience and Remote Sensing, 2014, 52(6): 3256-3274.
22. Wei Tang, Zhenwei Shi, and Zhana Duren. Sparse hyperspectral unmixing using an approximate L 0 norm[J]. Optik-International Journal for Light and Electron Optics, 2014, 125(1): 31-38.
23. Zhana Duren, Yong Wang, Shigeru Saito, and Katsuhisa Horimoto. Inferring gene regulatory network for cell reprogramming[C]//Control Conference (CCC), 2012 31st Chinese. IEEE, 2012: 7437-7442.
24. Xinxin Wang*, Zhana Duren*, Chao Zhang, Lin Chen, and Yong Wang. Clinical data analysis reveals three subytpes of gastric cancer[C]//Systems Biology (ISB), 2012 IEEE 6th International Conference on. IEEE, 2012: 315-320.