

Zhana Duren

Center for Human Genetics
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EDUCATION

PhD, Operational Research and Cybernetics
Academy of mathematics and systems science, Chinese Academy of Sciences 2017
Dissertation title: Modelling gene regulatory network
Advisor: Prof. Yong Wang

B.S., Mathematics and applied mathematics
Beihang University, Beijing, China 2012

RESEARCH EXPERIENCE

Visiting PhD student
Department of Statistics, Stanford University 2015 to 2017
Advisor: Prof. Wing Hung Wong

Postdoctoral research fellow
Department of Statistics, Stanford University 2017 to 2020
Postdoctoral supervisor: Prof. Wing Hung Wong

- 1) Built statistical inference models for gene regulatory network from paired gene expression and chromatin accessibility data.
- 2) Built integrative analysis models for single cell genomics data.
- 3) Interpret genetic variants by cellular context specific gene regulatory networks

Assistant professor
Center for Human Genetics, Clemson University 2020 to present

- 1) Developed a computational method for comparison of gene regulatory networks between two conditions using scRNA-seq and scATAC-seq data.
- 2) Developed a dimension reduction method and R package for single cell multiome data measuring gene expression and chromatin accessibility data on the same cell.

PUBLICATIONS

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). (* Co-first)

Zhana Duren*, Wenhui Sophia Lu*, Joseph G Arthur, Preyas Shah, Jingxue Xin, Francesca Meschi, Miranda Lin Li, Corey M Nemec, Yifeng Yin, and Wing Hung Wong.

Sc-compReg enables the comparison of gene regulatory networks between conditions using single-cell data. *Nature Communications* (2021). (* Co-first)

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.

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).

Xiang Zhu, **Zhana Duren**, and Wing Hung Wong. Modeling regulatory network topology improves genome-wide analyses of complex human traits. *Nature Communications* (2021).

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).

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).

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). (* Co-first)

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). (*Co-first)

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): gr-257063. (*Co-first)

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.

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. (* Co-first)

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.

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.

Zhana Duren*, Xi Chen*, Mahdi Zamanighomi*, Wanwen Zeng, Ansuman T. Satpathy, Howard Y. Chang, Yong Wang, and Wing Hung Wong. Integrative analysis of single-cell genomics data by coupled nonnegative matrix factorizations. *Proceedings of the National Academy of Sciences* 115.30 (2018): 7723-7728. (*Co-first)

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.

Zhana Duren, Xi Chen, Rui Jiang, Yong Wang, and Wing Hung Wong. Modeling gene regulation from paired expression and chromatin accessibility data. *Proceedings of the National Academy of Sciences* (2017): 201704553.

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.

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.

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.

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.

Xinxin Wang*, **Zhana Duren***, Chao Zhang, Lin Chen, and Yong Wang. Clinical data analysis reveals three subtypes of gastric cancer[C]//Systems Biology (ISB), 2012 IEEE 6th International Conference on. IEEE, 2012: 315-320. (* Co-first)

PRESENTATIONS

- **Zhana Duren**. “Regulatory analysis of single cell multiome gene expression and chromatin accessibility data with scREG”. Department seminar of Biostatistics and Bioinformatics, Genentech, May 2022, San Francisco, California (Virtual talk).
- **Zhana Duren**. “Comparison of gene regulatory networks between two conditions using single-cell genomics data”. Department seminar of Biostatistics and Bioinformatics, Emory University, Aug. 2021, Atlanta, Georgia.
- **Zhana Duren**, Xi Chen, JIngxue Xin, Yong Wang, and Wing Hung Wong “Time course regulatory analysis based on paired expression and chromatin accessibility data,” Poster presentation at the 17th annual meeting of Center of Excellence in Genomic (CEGS), Nov. 2019. Harvard Medical School, Boston.
- **Zhana Duren**. “DC3: a method for deconvolution and coupled clustering from bulk and single-cell genomics data,” Talk presented at meeting of Center of Excellence in Genomic (CEGS), Feb. 2019, Stanford, California.
- **Zhana Duren**, Wanwen Zeng, Yong Wang, Rui Jinag, Wing Hung Wong. “Simultaneous clustering of single-cell genomics data and deconvolution of bulk chromatin interaction data,” Talk presented at the Cold Spring Harbor Biological Data Science meeting, Nov. 2018, Cold Spring Harbor, New York.
- **Zhana Duren**, Wanwen Zeng, Yong Wang, Rui Jinag, Wing Hung Wong. “Simultaneous clustering of single-cell genomics data and deconvolution of bulk 3D chromatin interaction data,” Poster presented at the 16th annual meeting of Center of Excellence in Genomic (CEGS), Dec. 2018. Chicago, Illinois.
- **Zhana Duren**. “Integrative analysis of single-cell genomics data by coupled nonnegative matrix factorizations,” Talk presented at meeting of Center of Excellence in Genomic (CEGS), Aug. 2018, Stanford, California.
- **Zhana Duren**. “Modelling gene regulatory network from paired gene expression and chromatin accessibility data,” Talk presented at meeting of Center of Excellence in Genomic (CEGS), Oct. 2016, Stanford, California.

TEACHING EXPERIENCE

Regulatory Genomics 2022-present
Clemson University graduate course
GEN8900
every spring

AWARD AND HONORS

National Scholarship, The Ministry of Education of the China 2013
Merit Student, Chinese academy of sciences 2013
Excellent Student Cadre, Chinese academy of sciences 2013
Excellent Undergraduate Thesis, Beihang University 2012
Outstanding Graduates, Beijing Municipal Commission of Education 2012
Guanghua scholarship, Beihang University 2010

SERVICE

Reviewer for academic journals 2014-present
Nature Methods
Nature Communications
Genome Biology
Plos Computational Biology
BMC Bioinformatics
Plos One
PeerJ
IEEE/ACM Transactions on Computational Biology and Bioinformatics
IEEE Transactions on Geoscience and Remote Sensing
IEEE Journal of Selected Topics in Applied Earth Observations and Remote Sensing.

President of the student union
School of mathematics, Beihang University 2010-2011
Institute of applied mathematics, Chinese Academy of Sciences 2014-2015