Yanlin Zhang

Curriculum Vitae

School of Computer Science
McGill University, Montreal, QC, Canada
✉ *yanlin.zhang2@mail.mcgill.ca*

Education

2018–2023 (expected) **PhD (direct entry), Computer Science**, *McGill University*, Montreal.
Advisor: Mathieu Blanchette

2017–2018 **PhD-level study, Quantitative Life Sciences**, *McGill University*, Montreal.
Advisor: Mathieu Blanchette, Simon Gravel

2010–2015 **Bachelor of Science, Computer Science**, *City University of Hong Kong*, Hong Kong.

Research highlights

My current research is funded by the Government of Quebec (*FRQNT-B2X* scholarship in Information Technology and Communications). I have applied advanced data analytics skills in interpreting complex biological data sets (genomics, proteomics, and disease). This includes:

1. I proposed a reference panel enabled data analytics framework for computational 3D genomics – a paradigm shift in 3D genomics study. This achievement is demonstrated by my publication records in prestigious, multidisciplinary venues such as *Nature Communications* (IF=17.6) and *ISMB* (top conference in bioinformatics). In addition, I have several ongoing projects in this direction.
2. I contributed to the fields of population genetics and healthcare by publishing papers in high-impact journals (in biology and medicine) including *Nature Communications*, *Cell Reports* (IF=9.9), and *Cancer Research* (IF=12.7), etc.

Research Interests

My research focuses on developing and applying **computational methods** (i.e., algorithmic and machine learning approaches) for **interpreting complex biological data sets**.
My research goal is to develop and apply new algorithmic and machine learning methods to understand the molecular machinery of the cell.

Publications

Refereed Articles

2023 **Yanlin Zhang** and Mathieu Blanchette. Reference panel guided super-resolution inference of hi-c data. *accepted at* ***ISMB/ECCB-2023*** (acceptance rate=17.9%). 2023.

2022 Zhe Zhang*, **Yanlin Zhang***, Yinan Wang*, Zicheng Zhao*, Melinda Yang, Lin Zhang, Bin Zhou, Bingying Xu, Hongbo Zhang, Teng Chen, et al. The tibetan-yi region is both a corridor and a barrier for human gene flow (**cover article**). ***Cell Reports***, volume 39, page 110720, 2022.

2022 **Yanlin Zhang** and Mathieu Blanchette. Reference panel guided topological structure annotation of hi-c data. ***Nature Communications***, volume 13, page 7426, 2022.

2020 Changfa Wang, Haijing Li, Yu Guo, Jinming Huang, Yan Sun, Jiumeng Min, Jinpeng Wang, Xiaodong Fang, Zicheng Zhao, Shuai Wang, **Yanlin Zhang**, et al. Donkey genomes provide new insights into domestication and selection for coat color. ***Nature communications***, volume 11, page 6014, 2020.

2019 **Yanlin Zhang**, Weiwei Liu, Yu Lin, Yen Kaow Ng, and Shuaicheng Li. Large-scale 3d chromatin reconstruction from chromosomal contacts. ***BMC genomics***, volume 20, pages 129–141, 2019.

2016 Zhenyu Yang, Zhirong Guo, Chuangzhao Qiu, Yinhu Li, Xin Feng, Yanhong Liu, **Yanlin Zhang**, Pengyu Pang, Ping Wang, Qian Zhou, et al. Preliminary analysis showed country-specific gut resistome based on 1267 feces samples. ***Gene***, volume 581, pages 178–182. Elsevier, 2016.

2016 Xiangchun Li, William KK Wu, Rui Xing, Sunny H Wong, Yuexin Liu, Xiaodong Fang, **Yanlin Zhang**, Mengyao Wang, Jiaqian Wang, Lin Li, et al. Distinct subtypes of gastric cancer defined by molecular characterization include novel mutational signatures with prognostic capabilitygenomic analysis of gastric cancer. ***Cancer research***, volume 76, pages 1724–1732, 2016.

2015 **Yanlin Zhang**, Chuan-Yih Yu, Ehwang Song, Shuai Cheng Li, Yehia Mechref, Haixu Tang, and Xiaowen Liu. Identification of glycopeptides with multiple hydroxylysine o-glycosylation sites by tandem mass spectrometry. ***Journal of proteome research***, volume 14, pages 5099–5108, 2015.

Preprints

2023 **Yanlin Zhang**, Rola Dali, and Mathieu Blanchette. Robustad: nonparametric test detects hierarchical topologically associating domains. *GLBIO-2023 Poster; In preparation for submitting to Genome Biology*. 2023.

2023 **Yanlin Zhang**, Christopher Cameron, and Mathieu Blanchette. Posterior inference of hi-c contact frequency through sampling. *Invited contribution to the article collection "Algorithms and Tools for Analyzing Spatial Genome Organization" with Frontiers in Bioinformatics*. 2023.

2023 Chris Drogaris*, **Yanlin Zhang***, Zhang, Elena Nazarova, Roman Sarrazin-Gendron, Yan Cyr, Jacek Majewski, Mathieu Blanchette, and Jérôme Waldispühl. Argv: Simple exploration of 3d genome structures using augmented reality. *Under review at Genome Biology*. 2023.

Conference Presentation

July, 2023 **31st Conference on The Intelligent Systems for Molecular Biology (ISMB) and 21st European Conference on Computational Biology (ECCB)**, *Lyon*.
Reference panel guided super-resolution inference of Hi-C data (Oral)

May, 2023 **15th Great Lakes Bioinformatics (GLBIO) Conference**, *Montreal*.
RobusTAD: nonparametric test detects hierarchical topologically associating domains (Poster)
Exploring 3D Genome with Augmented Reality (Oral)

Research Experience

McGill University, Montreal

Sept,2017 – Now ***Research assistant***.
FRQNT funded doctoral study on computational 3D genome analysis: Collected many published Hi-C data sets and developed a series of computational tools (RefHiC, RobusTAD, and ARGV) that significantly improved Hi-C data analysis by leveraging the created reference panel.

Jan,2018 – April, 2018 ***Research assistant***.
Proposed a probabilistic graphical model for demographic inference and used it to compute the expected joint frequency spectrum with natural selection.

City University of Hong Kong, Hong Kong

Sept,2015 – July, 2017 ***Research assistant***.
Developed a computational tool to infer 3D genome structures from chromatin contact maps. Analyzed large collections of genomes to study population genetics.

Indiana University, Indianapolis.

Sept,2013 – July, 2014 ***Research assistant intern***.
Developed the first computational tool to identify glycopeptides with multiple O-glycosylation sites from LC-MS/MS data.

Teaching Experience

Fall, 2021	**McGill: Computational Biology Methods and Research**, *COMP462/561*. Instructor (∼100 students)
Fall, 2020	**McGill: Computational Biology Methods and Research**, *COMP462/561*. Teaching assistant (∼120 students)
Winter, 2020	**McGill: Applied Machine Learning**, *COMP551*. Head teaching assistant (∼400 students, 11 TAs)
2012	**CityU: Introduction to Computer Programming**, *CS1301*. Teaching assistant (∼50 students)

Scholarships & Awards

2020 – 2024	**FRQNT Doctoral Scholarship**, Quebec
2018 – 2022	**Grad Excellence Award in Computer Science, McGill**, Quebec
2017 – 2018	**Grad Excellence Award in Quantitative Life Sciences, McGill**, Quebec
2016	**Outstanding Academic Papers by Students, CityU**, Hong Kong
2015	**Hong Kong government scholarship**, Hong Kong
2014	**Hong Kong government scholarship**, Hong Kong
2013	**Chan Wing Fui Scholarship, CityU**, Hong Kong
2010-2015	**Dean'se List, College of Science and Engineering, CityU**, Hong Kong
2010-2014	**University Entrance Scholarship, CityU**, Hong Kong

Academic Service

2023	**reviewer**, *ISMB/ECCB 2023*.
2019	**reviewer**, *MLCB 2019*.

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