Stanford

Xiangqi Bai

Postdoctoral Scholar, Oncology

Bio

BIO

My research is focused on computational and systems biology. My primary research interest lies in developing new computational algorithms and statistical methods for the analysis of complex data in biological systems, especially related to the large-scale single-cell RNA sequencing data. The specific topics I have examined include:

1. Integration of single-cell multi-omics datasets for tumor

2. Statistical test of cell developmental trajectories

3. Visualization and reconstruction of single-cell RNA sequencing data

4. Computational analysis of the bifurcating event revealed by dynamical network biomarker methods

HONORS AND AWARDS

- China Scholarship of State Scholarship Fund, China Scholarship Council (2019)

- Chinese Academy of Sciences President Awards, Chinese Academy of Sciences Academy of Mathematics and Systems Science (2019)

- Jiaqing Zhong Excellent Paper Award, Chinese Society of Probability and Statistics (2019)

- National Scholarship for Doctoral Students, Chinese Academy of Sciences (2019)

- Travel Grants, The 20th International Conference on Systems Biology (2019)

- Merit Student of University of Chinese Academy of Sciences, Chinese Academy of Sciences (2015)

- Third-class Comprehensive scholarship, Sichuan University (2014)

- Second-class Individual scholarship, Sichhuan University (2011)

- Cyrus Tang Scholarship, Sichuan University (2010)

PROFESSIONAL EDUCATION

- Ph.D, Academy of Mathematics and Systems Sciences, Chinese Academy of Science , System Science (2021)

- B.S., Sichuan University , Statistics (2015)

- B.S., Sichuan University , Economics (2015)

LINKS

- Github: https://github.com/XQBai

Publications

PUBLICATIONS

- **Unsupervised topological alignment for single-cell multi-omics integration**
  Cao, K., Bai, X., Hong, Y., Wan, L.
  OXFORD UNIV PRESS.2020: 48-56

- **A Branch Point on Differentiation Trajectory is the Bifurcating Event Revealed by Dynamical Network Biomarker Analysis of Single-Cell Data** *IEEE-ACM TRANSACTIONS ON COMPUTATIONAL BIOLOGY AND BIOINFORMATICS*
  Chen, Z., Bai, X., Ma, L., Wang, X., Liu, X., Liu, Y., Chen, L., Wan, L.
  2020; 17 (2): 366-375

- **Joint Inference of Clonal Structure using Single-cell Genome and Transcriptome Sequencing Data**
  Bai, X., Duren, Z., Wan, L., Xia, L.
  In progress.
  2020

- **Statistical test of structured continuous trees based on discordance matrix** *BIOINFORMATICS*
  Bai, X., Ma, L., Wan, L.
  2019; 35 (23): 4962-4970

- **DensityPath: an algorithm to visualize and reconstruct cell state-transition path on density landscape for single-cell RNA sequencing data** *BIOINFORMATICS*
  Chen, Z., An, S., Bai, X., Gong, F., Ma, L., Wan, L.
  2019; 35 (15): 2593-2601

PRESENTATIONS

- Joint Inference of Clonal Structure using Single-cell DNA-Seq and RNA-Seq data - The 28th Conference on Intelligent Systems for Molecular Biology (ISMB) (7/1/2020 - 7/1/2020)

- Statistical test of structured continuous trees based on discordance matrix - The 20th International Conference on Systems Biology (ICSB) (November 2019 - November 2019)

- Statistical testing of the continuous tree structure based on the spiked matrix model with application to single-cell lineage reconstruction - The 11th Chinese Society of Probability and Statistics National Congress (October 2018 - October 2018)

- Statistical testing of the binary tree structure based on the spiked matrix model - The 16th Annual Conference of China Society for Industrial and Applied Mathematics (September 2018 - September 2018)

- A branch point on differentiation trajectory is the bifurcating event revealed by dynamical network biomarker analysis of single-cell data - The 11th International Conference on Computational Systems Biology (8/2017 - 8/2017)