
Curriculum Vitae

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Research Interests

Bioinformatics

- Algorithm design for regulatory landscape reveals based on single cell multi-omics data.
- Transcriptional Unit analysis and Regulon prediction.
- Developing deep learning-based methods for single-cell multi-omics integration.
- Single-cell drug resistance analysis via deep transfer learning

Education

- Ph.D.** Operation research *Sep. 2020 – Present*
[School of Mathematics](#), Shandong University, Jinan, China
Advisor: Prof. [Bingqiang Liu](#)
- M.S.** Operation research *Sep.2018 - Jul. 2020*
[School of Mathematics](#), Shandong University, Jinan, China
Advisor: Prof. [Bingqiang Liu](#)
- B. S.** Mathematics *Sep.2014 - Jul. 2018*
School of Information and Computing Science, Qingdao University of Science and Technology, Qingdao, China

Honor

- 2014-2015 First Class scholarship, Merit-based scholarship, Title of Outstanding students. Qingdao University of Science and Technology.
- 2015-2016 First Class scholarship, Merit-based scholarship, Title of Excellent Youth League Cadre. Qingdao University of Science and Technology.

- 2016-2017 First Prize of Shandong Province, National Mathematical Contest in Modeling for Postgraduates, First Class scholarship, merit-based scholarship, Title of Top 10 League branch secretary, Title of Outstanding students, Qingdao University of Science and Technology.
- 2017-2018 Provincial Excellent Graduate, First Class scholarship, merit-based scholarship.

Publications

(#Co-first author, *Corresponding author)

1. **Xiaoying Wang#**, Bin Yu#*, Cheng Chen, Anjun Ma, Bingqiang Liu, Qin Ma*, Protein-protein interaction sites prediction by ensemble random forests with synthetic minority oversampling technique, *Bioinformatics*, 2019, 35(14): 2395–2402. (SCI, IF 5.481)
2. DESSO-DB: A web database for sequence and shape motif analyses and identification. **Xiaoying Wang#**, Cankun Wang#, Lang Li, Qin Ma, Anjun Ma*, Bingqiang Liu*, *Computational and Structural Biotechnology Journal*, 2022, V20: 3053-3058.
3. Junyi Chen#, **Xiaoying Wang#**, Anjun Ma, Qi-En Wang, Bingqiang Liu, Lang Li, Dong Xu* & Qin Ma*, Deep Transfer Learning of Drug Sensitivity Response by Integrating Bulk and Single-cell RNA-seq data, *Nature Communication*, 2022.
4. Anjun Ma#, **Xiaoying Wang#**, Cankun Wang, Jingxian Li, Tong Xiao, Juexing Wang, Yuzhou Chang, Yang Li, Yutao Liu, Shaopeng Gu, Duolin Wang, Yuexu Jiang, Jinpu Li, Li Su, Zihai Li, Bingqiang Liu*, Dong Xu*, Qin Ma*, Biological network inference from single-cell multi-omics data using heterogeneous graph transformer, *Nature Communication*, 2023.