

SHORT BIO

I obtained my B.Sc. degree in Medicine at Peking University (PKU, 2012), China and PhD degree in Bioinformatics in PhD at Peking University (PKU, 2012), supervised by Prof. Qinghua Cui. My doctoral researches focus on bioinformatics analysis about non-coding RNAs and diseases.

In 2020 I was offered a post doctoral position position at the State Key Laboratory of Lunar and Planetary Sciences of Macao University of Science and Technology in Macao (China) under the supervision of Prof. Kang Zhang. I have been researching multiple aspects of bioinformatics especially metabolomics. My research interest was modeling and understanding mechanisms of complex diseases using multi-omic technologies and artificial intelligence.

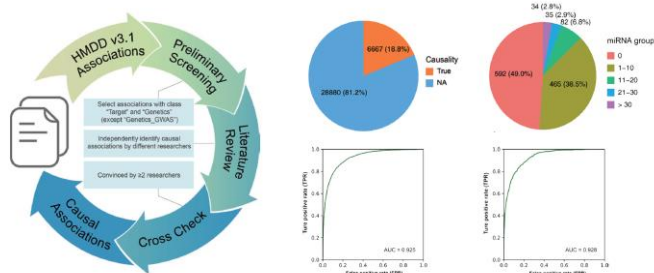
Post Doctoral

Yuanxu Gao



PhD: Bioinformatics – Peking University (China)

B.Sc.: Basic Medical Science – Peking University (China)



Predict the Causal miRNAs for Diseases (Gao et al., 2019, Front. Genet.)

KEY PUBLICATIONS (selected)

- Zhang, K., Liu, X., Xu, J., Yuan, J., Cai, W., Chen, T., Wang, K., **Gao, Y.**, Nie, S., Xu, X., Qin, X., Su, Y., Xu, W., Olvera, A., Xue, K., Li, Z., Zhang, M., Zeng, X., Zhang, C. L., ... Wang, G. (2021). Deep-learning models for the detection and incidence prediction of chronic kidney disease and type 2 diabetes from retinal fundus images. *Nature Biomedical Engineering*, 5(6), 533–545. <https://doi.org/10.1038/s41551-021-00745-6>
- Jia, K., **Gao, Y.**, Shi, J., Zhou, Y., Zhou, Y., & Cui, Q. (2020). Annotation and curation of the causality information in LncRNADisease. *Database: The Journal of Biological Databases and Curation*, 2020. <https://doi.org/10.1093/database/baz150>
- Gao, Y.**, Yang, W., Jin, L., Xue, L., Yang, J., & Cui, Q. (2020). Profiling and bioinformatic analysis reveal differential microRNA expression in the left and right kidneys in normal mice. *FEBS Letters*, 594(4), 636–645. <https://doi.org/10.1002/1873-3468.13644>
- Huang, Z., Shi, J., **Gao, Y.**, Cui, C., Zhang, S., Li, J., Zhou, Y., & Cui, Q. (2019). HMDD v3.0: A database for experimentally supported human microRNA-disease associations. *Nucleic Acids Research*, 47(D1), D1013–D1017. <https://doi.org/10.1093/nar/gky1010>
- Huang, Z., Liu, L., **Gao, Y.**, Shi, J., Cui, Q., Li, J., & Zhou, Y. (2019). Benchmark of computational methods for predicting microRNA-disease associations. *Genome Biology*, 20(1), 202. <https://doi.org/10.1186/s13059-019-1811-3>
- Gao, Y.**, Jia, K., ... Cui, Q. (2019). A Computational Model to Predict the Causal miRNAs for Diseases. *Frontiers in Genetics*, 10, 935. <https://doi.org/10.3389/fgene.2019.00935>

PROFESSIONAL EXPERIENCE

Ongoing – 2020 – Macau University of Science and Technology (MUST), State Key Laboratory of Lunar and Planetary Sciences- Space Science Institute, Macau SAR, China. Supervisor: Prof. Kang Zhang – Post Doctoral