SKLplanet Academic Staff Resume

Name: Yuanxu Gao
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Academic Qualification

Ph.D. in Bioinformatics, Peking University (Beijing, China)
Bachelor in Basic Medical Science, Peking University (Beijing, China)

Research Area

Dr Gao gained considerable expertise on bioinformatics and have a broad research interests. His doctoral research focused on profiling associations between non-coding RNA and huamn disease. During PhD study time, he developed a series of tools to predict and analyse miRNA and disease association. His research area now is non-coding RNA, metabolomics and medical artificial intelligence. He is particularly interested in dessecting metabolic status of organisms under different conditions especially extremely environment and space.

Working Experience

2021-persent: PostDoc fellow of Astrobiology Group- 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

Certification, Awards and Membership

Beijing Graduate with Distinction (2020)
Peking University Graduate with Distinction (2020)

Academic Publication

1. 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

2. 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

3. **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

4. 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

5. 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

6. **Gao, Y.**, Jia, K., Shi, J., Zhou, Y., & 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