YUELIN YAO

✉ y.yao-38@sms.ed.ac.uk   🐦 @yaoyuelin11   🌐 https://yuelinyao.github.io/

Education

Nov 2020 – **May 2024**	**Ph.D. Computational biology, University of Edinburgh, UK** School of Informatics, IANC: Machine Learning, Computational Neuroscience, Computational Biology. Thesis: *High order expression dependencies finely resolve cell (sub)type and state in single cell data.* Supervisors: Ava Khamseh, Chris Ponting and Luke Boulter
Sep 2019 – Sep 2020	**M.Sc. Bioinformatics, University of Edinburgh, UK** School of Biological Sciences, Graduated with Distinction. Thesis: *Comparative transcriptome in large-scale human and cattle populations.* Supervisors: Lingzhao Fang
Sep 2015 - Jun 2019	**B.Sc. Plant Protection, Zhejiang University, China**. College of Agriculture and Biotechnology, GPA: 3.63/4.0. Thesis: *Functional analysis of genes related to development and reproduction of Nilaparvata lugens*. Supervisors: Yanyuan Bao

Experience

Biomedical AI Lab

Nov 2020 - Ongoing	Developed state-of-the-art pipeline and computational tool for **scRNA-seq** data analysis.
	Estimated **mutational interactions** across pancancer from WGS data.
	Received training in **Causality in Biomedicine Course**, and **Neuromatch Deep Learning Course.**
Jan 2022 - Ongoing	Teaching. Tutor and marker of **Methods for Causal Inference Course.**
	Supervised Bachelor's thesis & MSc dissertations.
Dec 2023	Presented poster at **CSHL Genome Informatics**, New York State, US.
Nov 2022	Presented poster at **CSHL The Biological Data Science conference**, New York State, US.
Jun 2022	Summer School. **Dynamics and Statistics of Cancer Evolution: Applying Mathematics to Experimental and Clinical Data** Summer School in Marseille, France.
May 2021	Presented poster at **CSHL The Biology of Genomes virtual conference.**

Quantitative Genetics Lab

Jan 2020 - Sep 2020	Systematic comparison of **transcriptional landscape & eQTL** of all orthologous genes across major tissues among mammals.
	Integrative analysis of characterised regulatory elements with **large-scale GWAS** to understand shared & divergent genetic architecture underlying complex phenotypes.

Awards and Achievements

2023	**The Scottish Informatics & Computer Science Alliance (SICSA) Research Scholar**
	Chinese Government Award for Outstanding Self-Financed Students Abroad
	The Institute of Genetics and Cancer POGS Event Best Poster
2022	**The Institute of Genetics and Cancer Early Career Award**
	Informatics Graduate School PGR Student Travel and Conference Fund
2020	**School of Informatics PhD Scholarship, University of Edinburgh**

Skills

Coding	■	R, Python, Java, SQL, HTML, Shell, Docker, Git, Nextflow, LaTeX.
Technical Skills	■	Machine learning, Statistical modelling, High-throughput bioinformatics analysis.
Languages	■	Strong reading, writing and speaking competencies for English, Mandarin Chinese.

Publications

1. A. Jansma*, **Y. Yao***, J. Wolfe, *et al.*, "High order expression dependencies finely resolve cryptic states and subtypes in single cell data," *bioRxiv*, pp. 2023–12, 2023.

2. S. H. Waddell*, **Y. Yao***, P. Olaizola, *et al.*, "A TGF-β-ECM-integrin signaling axis drives structural reconfiguration of the bile duct to promote polycystic liver disease," *Science Translational Medicine*, vol. 15, no. 713, eabq5930, 2023.

3. **Y. Yao***, S. Liu*, C. Xia*, *et al.*, "Comparative transcriptome in large-scale human and cattle populations," *Genome Biology*, vol. 23, no. 1, pp. 1–24, 2022.

4. Z. Pan*, **Y. Yao***, H. Yin, *et al.*, "Pig genome functional annotation enhances the biological interpretation of complex traits and human disease," *Nature Communications*, vol. 12, no. 1, p. 5848, 2021.

5. S. Liu, Y. Gao, O. Canela-Xandri, ..., **Y. Yao**, *et al.*, "A multi-tissue atlas of regulatory variants in cattle," *Nature Genetics*, vol. 54, no. 9, pp. 1438–1447, 2022.

6. T. Jinyan, Y. Gao, ..., **Y. Yao**, *et al.*, "A compendium of genetic regulatory effects across pig tissues," *Nature Genetics*, pp. 1–12, 2024.

7. W. Yang, J. Yu, **Y. Yao**, *et al.*, "Comparative immune-relevant transcriptome reveals the evolutionary basis of complex traits," *Iscience*, vol. 25, no. 12, p. 105 572, 2022.

8. D. Guan, Z. Bai, X. Zhu, ..., **Y. Yao**, *et al.*, "The chickengtex pilot analysis: A reference of regulatory variants across 28 chicken tissues," *bioRxiv*, pp. 2023–06, 2023.

9. W. Wang, R.-R. Yang, L.-Y. Peng, L. Zhang, **Y.-L. Yao**, and Y.-Y. Bao, "Proteolytic activity of the proteasome is required for female insect reproduction," *Open Biology*, vol. 11, no. 2, p. 200 251, 2021.

10. S. Mi, Y. Tang, ..., **Y. Yao**, *et al.*, "Protective roles of folic acid in the responses of bovine mammary epithelial cells to different virulent staphylococcus aureus strains," *Biology*, vol. 10, no. 11, p. 1164, 2021.