Chang He

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Research interests: Bioinformatics/Systems biology/RNA biology

EDUCATION

Tsinghua University, Beijing   Aug 2022 - Jun 2026 (expected)
Bachelor of Science: Biology, Statistics (minor)   GPA 3.84/4.00

ACADEMIC EXPERIENCE

Establishment of a scRNA-seq dataset reliability assessment system
Advisor: Bin Li   National Institute of Biological Sciences, Beijing   2023.12 - 2024.6

- Built a clustering strategy to annotate cells, describing their typicalities.
- Discovered the system's biological significance in diseases and cell development.
- Integrated and examined "center" cells to improve clustering and annotation performance.

Cell-specific landscape of RNA in different lupus organ involvements and treatment responses
Advisor: Zhi John Lu   Tsinghua University   2024.8 - 2025.2

- Calculated multi-omics features based on novel transcripts, including mRNA, TE RNA, alternative splicing, etc.
- Found biomarkers for SLE diagnosis or prognosis.
- Selected the most involved cell types regarding organ involvement and treatment response based on machine learning.
- Built data portal website to display metadata and basic analytics (dataportal-five.vercel.app).

Development of novel metric of cell-free RNA fragmentation revealing RNA metabolism
Advisor: Zhi John Lu   Tsinghua University   2025.1 - present

- Designed statistical model to calculate a novel metric and enhanced cancer classification.
- Examined the capability of the metric to mitigate batch effect of cell-free RNA datasets.
- Discovered the biological mechanism and tested the metric in both cellular and cell-free data of lupus.

Multi-omics analysis of tRNA dynamics and codon-specific translation in the human brain
Advisor: Tao Pan   University of Chicago   2025.6 - present

- Designed and applied a pipeline for Ribo-seq data analysis from scratch.
- Analysed and compared codon usage bias based on Ribo-seq, proteomics, and bulk mRNA-seq data.
- Bridged codon usage bias with tRNA modification and tRNA charging across life span and Alzheimer's Disease patients.

ACADEMIC PAPERS

- Yilan Bai[*], **Chang He**[*], Yuhuan Tao, Pengfei Bao, and Zhi John Lu. "Leveraging Fragmentation Patterns of cell-free RNA to Mitigate Batch Effects for Cancer Classification." (in manuscript)
  [*] These authors contributed equally to the work.

AWARDS

China High School Biology Olympiad 1st Prize   China Zoological Society & Botanical Society of China
Gold medal   Aug 2021
Best Report Award   Tsinghua University
For excellent reporting in General Biology Fieldwork   Sep 2023
Academic Excellence Scholarship   Tsinghua University
For exceptional academic performance and significant progress   Oct 2023

ACADEMIC PRESENTATION

Journal Club on Lung Cancer Metastasis Signature
X-idea in Current Biology, advised by Qiaoran Xi   May 2023
Journal Club on Nuclear Substructure and RNA Processing
X-idea in Current Biology, advised by Xuerui Yang   Oct 2023
Journal Club on Transposable Elements in Cancer
Biological Research Training (honor), advised by Nian Liu   Jun 2024

Annual Research Report
Biological Research Training (honor), A- grade   Dec 2024

SKILLS

- **Programming:** R; Python; Typescript/Javascript; Bash (Linux); C
- **Software:** Single-cell & bulk RNA-seq analysis; Ribo-seq analysis; IGV; Git
- **Language:** Chinese (native); English (TOEFL 98); Portuguese (intermediate)

REFERENCES

Prof. Qiaoran Xi
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Scholar Profiles: Personal Page — Google Scholar

Prof. Zhi John Lu
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Prof. Tao Pan
Professor, Department of Biochemistry & Molecular Biology, University of Chicago
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