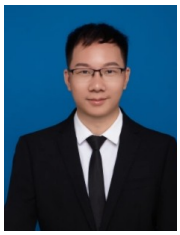
Li Chen 陈力



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Computational Biology / Statistical Genetics

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Profile

Biomedical researcher with more than ten years of experience in computational biology, specializing in statistical genetics and AI methods and dedicated to advancing early-stage drug discovery by combining single-cell foundation models with multi-omics genetics. Research starts from human genetic data and seeks genetically supported drug targets for complex diseases, currently focusing on brain disorders. Received a PhD from Humboldt-Universität zu Berlin, was a postdoctoral researcher in Prof. Jian Yang's group at Westlake University, and is now Research Assistant Professor at the School of Engineering, Westlake University. Representative first- and co-first-author papers appear in *Nature Communications* and *The American Journal of Human Genetics*.

- **Genetics-driven target discovery:** Proficient in GWAS, eQTL mapping, colocalization, SMR and related methods for integrative multi-omics analysis. Prioritizes candidate disease genes and non-coding RNA targets for complex diseases, mainly brain disorders, starting from human genetic evidence and taking cellular-context-dependent genetic effects into account (*The American Journal of Human Genetics*, 2026; *Nature Communications*, 2026).
- **AI-enabled single-cell and spatial omics analysis:** Co-developed STARNet, a framework for inferring gene regulatory networks from spatial multi-omics data, and THItoGene, a deep learning method that predicts spatial transcriptomics from histology images.
- **Toward drug development:** Participant in the National Key R&D Program of China project "Innovation and Application of Multi-omics and AI Technologies in Disease Target Discovery and Drug Discovery" and the NSFC Major Program subproject "Optimization and Efficacy Evaluation of Mirror-Image Nucleic Acid Aptamers". Next goal: to advance target discovery and the design and optimization of nucleic acid drugs through a closed loop between computation and experiment.

Education

Ph.D. in Bioinformatics — Sep 2016 – Apr 2021
Institute of Biology, Humboldt-Universität zu Berlin, Germany
Supervisor: Prof. Kerstin Kaufmann

M.S. in Bioinformatics — Sep 2013 – Mar 2016
Institute of Bioinformatics, College of Agriculture and Biotechnology, Zhejiang University
Supervisor: Prof. Longjiang Fan

B.S. in Facility Agricultural Science and Engineering — Sep 2009 – Jun 2013
College of Horticulture and Forestry Sciences, Huazhong Agricultural University

Work Experience

Research Assistant Professor · School of Engineering, Westlake University — Aug 2024 – present
Supervisor: Prof. Jianyang Zeng | Focus: AI-driven method development for single-cell and spatial omics analysis

Postdoctoral Researcher · School of Life Sciences, Westlake University — Aug 2021 – Jul 2024
Supervisor: Prof. Jian Yang | Focus: integrative multi-omics analysis and statistical-genetics method development

Research Projects

National Key R&D Program of China: Innovation and Application of Multi-omics and AI Technologies in Disease Target Discovery and Drug Discovery

Project No. SQ2025YFC3400197 | Jan 2026 – Dec 2028 | Role: Participant

National Science and Technology Major Project: Pathways and Mechanisms by Which the Host Senses and Regulates Tumor Evolution

Project No. 2024ZD0525100 | Feb 2025 – Jan 2029 | Role: Participant

NSFC Major Program (subproject): Optimization and Efficacy Evaluation of Mirror-Image Nucleic Acid Aptamers

Part of the Major Program "Synthesis and Applications of Mirror-Image Biomacromolecules" (Subproject 4)
Project No. T2596084 | Jan 2026 – Dec 2030 | Role: Key participant

Publications

Li Chen in bold; [#] co-first author; [*] corresponding author; ★ representative publication; years and volume / issue numbers follow the final published versions.

First / Co-first Author Publications

[1] Yuran Jia[#], **Li Chen**[#], Liyang Song, Tianyi Zheng, Jian Yang, Yadong Wang, Tianyi Zhao. Mapping genetic regulation of gene expression to cellular contexts identifies long non-coding RNAs associated with brain disorders. *Nature Communications*, 2026, 17: 10314. ★ **Representative**

Interaction-eQTL mapping with deconvolution-derived cell-type proportions in 2,443 cortical transcriptomes identifies 3,763 lncRNAs with cellular-context-dependent genetic effects; about two-thirds of 118 lncRNA–trait colocalizations are detectable only once cellular context is modeled.

[2] **Li Chen**, Yazhou Guo, Junren Hou, Wen Yang, Ting Qi, Jian Yang. Genetic control of non-coding RNAs in the human brain and their implications for complex traits. *American Journal of Human Genetics*, 2026, 113(1): 149–167. ★ **Representative**

An eQTL atlas of lncRNAs and circRNAs from 2,865 human cortex samples shows that their genetic regulation is largely independent of nearby protein-coding genes, and nominates lncRNAs for 72 GWAS signals with no colocalizing protein-coding eQTL or splicing QTL.

[3] **Li Chen**[*], Qian-Hao Zhu. The evolutionary landscape and expression pattern of plant lincRNAs. *RNA Biology*, 2022, 19(1): 1190–1207.

lincRNAs identified across 26 plant species, including six non-flowering plants, and compared by sequence and synteny across lineages; conserved lincRNAs are enriched for histone-modification and transcription-factor-binding signals, suggesting biological function.

[4] **Li Chen**, Enhui Shen, Yunlei Zhao, Hongmei Wang, Iain Wilson, Qian-Hao Zhu. The conservation of long intergenic non-coding RNAs and their response to *Verticillium dahliae* infection in cotton. *International Journal of Molecular Sciences*, 2022, 23(15): 8594.

lincRNAs in two cultivated allotetraploid cottons and their diploid progenitors: responsiveness to Verticillium dahliae infection increases with conservation, and candidate lincRNAs that may be involved in disease response were identified.

[5] **Li Chen**, Qian-Hao Zhu, Kerstin Kaufmann. Long non-coding RNAs in plants: emerging modulators of gene activity in development and stress responses. *Planta*, 2020, 252: 92. Review

Reviews how plant lncRNAs act in development and stress responses through epigenetic, transcriptional, post-transcriptional and translational mechanisms, and proposes an experimental framework for their functional characterization.

[6] **Li Chen**, Yongyi Yu, Xinchen Zhang, Chen Liu, Chuyu Ye, Longjiang Fan. PcircRNA_finder: a software for circRNA prediction in plants. *Bioinformatics*, 2016, 32(22): 3528–3529. ★ **Representative**

circRNA prediction designed for plant genomes that integrates back-splice candidates from five aligners and filters them by splicing signals; more sensitive than find_circ and CIRCexplorer on simulated and real Arabidopsis and rice data.

[7] Chu-Yu Ye[#], **Li Chen**[#], Chen Liu, Qian-Hao Zhu, Longjiang Fan. Widespread noncoding circular RNAs in plants. *New Phytologist*, 2015, 208(1): 88–95. ★ **Representative**

An early genome-wide survey of plant circRNAs (12,037 in rice, 6,012 in Arabidopsis) that compares them with animal circRNAs; for example, introns flanking plant circRNAs carry fewer repeats and reverse-complementary sequences.

Co-authored Publications

[8] Lei Hu, Shichen Zhang, Xuting Zhang, …, **Li Chen**, …, Jianyang Zeng. STARNet enables spatially resolved inference of gene regulatory networks from spatial multi-omics data. *bioRxiv*, 2025. doi: 10.1101/2025.08.21.671434 Preprint

[9] Yuxin Yi, Wenjie Xu, Pengcheng Mi, Siliang Ye, **Li Chen**, Neal M. Alto, Zixu Liu. Deubiquitinase-dependent transcriptional silencing controls inflammation. *Cell Research*, 2025, 35(9): 675–686.

[10] Yuran Jia, Junliang Liu, **Li Chen**, Tianyi Zhao, Yadong Wang. THItoGene: a deep learning method for predicting spatial transcriptomics from histological images. *Briefings in Bioinformatics*, 2024, 25(1): bbad464.

[11] Longbiao Guo, Jie Qiu, Chuyu Ye, …, **Li Chen**, …, Longjiang Fan. *Echinochloa crus-galli* genome analysis provides insight into its adaptation and invasiveness as a weed. *Nature Communications*, 2017, 8: 1031.

[12] Enhui Shen, Jun Zou, Falk Hubertus Behrens, **Li Chen**, …, Longjiang Fan. Identification, evolution, and expression partitioning of miRNAs in allopolyploid *Brassica napus*. *Journal of Experimental Botany*, 2015, 66(22): 7241–7253.

[13] Chu-Yu Ye, Zhangxiang Lin, Gengmi Li, …, **Li Chen**, …, Longjiang Fan. *Echinochloa* chloroplast genomes: insights into the evolution and taxonomic identification of two weedy species. *PLoS ONE*, 2014, 9(11): e113657.

[14] Jie Qiu, Jinwen Zhu, Fei Fu, …, **Li Chen**, …, Longjiang Fan. Genome re-sequencing suggested a weedy rice origin from domesticated *indica-japonica* hybridization: a case study from southern China. *Planta*, 2014, 240(6): 1353–1363.

Software & Data Resources

- **PcircRNA_finder** GitHub · Manual
  First author · *Bioinformatics*, 2016
  circRNA identification software for plants: collects back-splice sites from five aligners, annotates them with plant gene structures and filters them by U2/U12 splice signals and pseudo-reference re-mapping.
- **Brain non-coding RNA eQTL atlas** Download · Online query · Code
  First author · *The American Journal of Human Genetics*, 2026
  eQTL summary statistics (SMR format) for lncRNAs and circRNAs from 2,865 human cortex samples, ready for SMR, colocalization and related analyses; available for download and online query.
- **Brain-ieQTL Atlas** Browse · Code
  Co-first author · *Nature Communications*, 2026
  Summary statistics of cellular-context interaction eQTLs (ieQTLs) for protein-coding genes and lncRNAs in the human brain, with transcriptome annotation; available to browse and download.

Skills

Statistical genetics	Functional interpretation of GWAS signals; eQTL and cellular-context interaction eQTL mapping (tensorQTL, PEER); colocalization (COLOC), SMR, mashr and heritability enrichment analysis
Omics data analysis	Large-scale RNA-seq data processing; lncRNA / circRNA identification and annotation; single-cell and spatial omics data analysis
AI methods	Deep learning and graph neural networks (co-developed THItoGene, STARNet)
Programming & computing	Python, R, Perl, Shell; Linux high-performance computing

Honors & Awards

2019	Poster/Talk Award, Giens Meeting, France
2015–2016	National Scholarship for Graduate Students, Ministry of Education of China
2015–2016	Outstanding Graduate and Merit Student, Zhejiang University
2015–2016	Graduate Honor Award, Zhejiang University
2013	Outstanding Graduate, Huazhong Agricultural University