

# Jingyu (Gavin) Li

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## EDUCATION & AWARDS

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### Applied Biology, Chu Kochen Honors College, Zhejiang University

2018.09-2022.07

- GPA: 3.77/4
- Rank: Top 10%
- First Prize of National Mathematics Competition
- Zhejiang University First Class Scholarship
- Zhejiang University Excellence Award of Professional Scholarship
- Outstanding Graduates of Zhejiang University

## RESEARCH EXPERIENCE

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### Babraham Institute, Cambridge, UK

Research Assistant to Professor Wolf Reik

2021.04-present

- Decoded gene regulation in the mouse embryo using single-cell multiomics

Specifically, I built an algorithm, in silico ChIP-seq, to infer gene regulatory networks underlying lineage commitments and conduct in silico transcription factor perturbation experiments. These findings were subsequently validated through knockout experiments.

- Delineated the dynamics of chromatin states characterized by histone modifications during gastrulation

I utilized an innovative technique, scCUT&Tag&RNA-seq, to characterize the histone modifications at the single-cell level. This allowed me to distinguish unique chromatin states defined by multiple histone marks in various lineages and deduce the crucial transcription factors enriched on the identified enhancers.

### Life Sciences Institute of Zhejiang University, Hangzhou, China

Research Intern to Professor Li Shen

2020.09-2021.03

- Developed an R package to perform dropout imputation and dimensionality reduction for scATAC-seq
- Designed a new algorithm to infer the gene regulation modules from scATAC-seq data

### Zhejiang University School of Medicine, Hangzhou, China

Research Intern to Professor Guoji Guo

2019.09-2020.09

- Conducted the scRNA-seq analysis to construct mouse embryonic development landscape
- Applied deep learning to dissect the relationship between gene sequences and lineage specificity

## PUBLICATIONS

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1. Argelaguet, R., Lohoff, T., **Li, J. G.**, Nakhuda, A., Drage, D., Krueger, F., Velten, L., Clark, S. J., & Reik, W. (2022). Decoding gene regulation in the mouse embryo using single-cell multi-omics. bioRxiv. <https://doi.org/10.1101/2022.06.15.496239>
2. Guo, J\*, **Li, J\***, Huang, F., Chen, J., & Shen, L. (2023). scART: Recognizing cell clusters and constructing trajectory from single-cell epigenomic data. bioRxiv. <https://doi.org/10.1101/2023.04.08.536108>
3. Xiao, Y., Wang, J., Li, J., Zhang, P., **Li, J.**, Zhou, Y., Zhou, Q., Chen, M., Sheng, X., Liu, Z., Han, X., & Guo, G. (2023). An analytical framework for decoding cell type-specific genetic variation of gene regulation. Nature Communications, 14(1), Article 1. <https://doi.org/10.1038/s41467-023-39538-7>
4. Li, J., Wang, J., Zhang, P., Wang, R., Mei, Y., Sun, Z., Fei, L., Jiang, M., Ma, L., E, W., Chen, H., Wang, X., Fu, Y., Wu, H., Liu, D., Wang, X., **Li, J.**, Guo, Q., Liao, Y., ... Guo, G. (2022). Deep learning of cross-species single-cell landscapes identifies conserved regulatory programs underlying cell types. Nature Genetics, 54(11), Article 11. <https://doi.org/10.1038/s41588-022-01197-7>
5. Chen, H., Liao, Y., Zhang, G., Sun, Z., Yang, L., Fang, X., Sun, H., Ma, L., Fu, Y., **Li, J.**, Guo, Q., Han, X., & Guo, G. (2021). High-throughput Microwell-seq 2.0 profiles massively multiplexed chemical perturbation. Cell Discovery, 7(1), Article 1. <https://doi.org/10.1038/s41421-021-00333-7>

## SOFTWARE DEVELOPED

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1. **In silico ChIP-seq**: leveraging multi-modal information to perform accurate prediction of transcription factor binding sites  
<https://github.com/Gavin-Lijy/in-silico-ChIP-seq.git>
2. **scART**: Single cell Chromatin Accessibility based cluster Recognition and Trajectory  
<https://github.com/Gavin-Lijy/scART.git>

## ADDITIONAL SKILLS & INTERESTS

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### Math and CS:

I took additional mathematics and computer-related courses beyond the required curriculum, including advanced linear algebra, numerical analysis, and stochastic processes. Furthermore, I acquired proficiency in operating the Linux operating system and gained expertise in commonly used programming languages such as R, Python, and Matlab.

### Drama:

During my college years, I became a member of drama clubs and actively participated in numerous nationwide drama performances.