Xin Dong

Ph.D. in Bioinformatics
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EDUCATION

Sep. 2018 – Jul. 2024	**Ph.D. in Bioinformatics** School of Life Sciences and Technology, Tongji University, China Advisors: Dr. Chenfei Wang & Dr. Xiaole Shirley Liu
Sep. 2014 – Jun. 2018	**B.S. in Biotechnology** College of Life Sciences, Shandong Normal University, China

WORK EXPERIENCES

Sep. 2025 – Present	Research Scientist	Sycamore Research Institute of Life Sciences, Shanghai
May 2025 – Sep. 2025	Bioinformatician (part-time)	GV20 Therapeutics LLC
Jul. 2024 – Sep. 2025	Research assistant	School of Life Sciences and Technology, Tongji University

RESEARCH EXPERIENCES

Bioinformatician (part-time), GV20 Therapeutics LLC (May 2025 – Sep. 2025)

- Supported clinical trials; designed and developed a proprietary Trial Master File (TMF) system using Microsoft SharePoint.

Research assistant, School of Life Sciences and Technology, Tongji University (Jul. 2024 - Sep. 2025)

- Developed PyTorch-based deep learning frameworks for predicting transcription factor binding states and regulatory information using single-cell/spatial epigenomics data and sequence information.
- Investigated regulatory mechanisms during murine cardiac development through analysis of single-cell multi-omics data.

Graduate Student, Tongji University (Sep. 2018 – Jul. 2024)

- **Developed and applied computational methods to analyze single-cell and spatial data**
  Advisors: Dr. Chenfei Wang & Dr. Xiaole Shirley Liu
    - I developed SCRIP (**S**ingle-**C**ell **R**egulatory Network **I**nference using ChI**P**-seq and motif) (https://github.com/wanglabtongji/SCRIP), a method that integrates scATAC-seq and a large collection of bulk TR (Transcription Regulator) ChIP-seq to infer single-cell TR activity and targets. The method outperformed other motif-based approaches in assessing TR binding activity. Applying SCRIP to various biological systems shows its utility in lineage tracing, cell-type clustering, and inferring cell-type-specific GRNs. With the advances of single-cell multiomics techniques, we updated it to SCRIPro (https://github.com/wanglabtongji/SCRIPro), which suits both single-cell and spatial multiomics data.
    - We developed TISCH (**T**umor **I**mmune **S**ingle **C**ell **H**ub; http://tisch.compbio.cn) and TISCH2, a large curated resource that integrates the single-cell transcriptome profiles of about 6 million cells from 190 high-quality tumor datasets across 50 cancer types. TISCH allows systematic comparison of gene expression across multiple datasets at the single-cell or cluster level for various cell types, patients, tissue origins, treatment and response groups, and cancer types, aiming to characterize the immune system heterogeneity in cancers and inform immunotherapy.
- **Large-scale genomic data mining and integration analysis**
  Advisors: Dr. Xiaole Shirley Liu & Dr. Clifford Meyer
    - To download the raw sequencing data of the chromatin occupancy experiments from the NCBI's GEO database and extract the metadata, we created a parser. The parser annotated and labeled the experiment

type, tissue type, cell population, and other details of the experiments using the keywords-match strategy.

- We developed CHIPS (**CH**romatin enr**I**chment **P**roce**S**sor) (https://github.com/liulab-dfci/CHIPS), a pipeline that processes the epigenome data to readable results with a single command line. It integrates states-of-the-art tools for cistrome NGS data and chooses the appropriate analysis parameters. It uses the Snakemake framework, which makes it easy to deploy on cloud or cluster servers.
- We developed and maintained the Cistrome Data Browser (http://cistrome.org/db/#/), which hosts many public cistrome sequence datasets. It offers a user-friendly interface to access the data quality and the results of downstream analysis.

Undergraduate Student, Shandong Normal University (2014-2018)

- **Rapid establishment of H7N9 dominant lineage by intragenic recombination in HA segment**
  Undergraduate Dissertation Research; Advisor: Dr. Chengqiang He
- **Screening of newcastle disease virus heat-resistant vaccine by homologous recombination**
  Undergraduate Innovation Program (Presided); Advisor: Dr. Chengqiang He
- **The origin, adaptive evolution and population dynamics of infectious Chicken Anemia Virus in China**
  Undergraduate Innovation Program (Involved); Advisor: Dr. Chengqiang He
- **Diversity of fish in Nansi Lake**
  Undergraduate Innovation Program (Involved); Advisors: Dr. Rongshu Fu & Dr. Mingsheng Miao

SKILLS

- **Bioinformatics**: Single-cell/spatial RNA/ATAC-seq analysis; Epigenome data analysis (ChIP-seq, ATAC-seq, etc.); Machine learning (PyTorch, scikit-learn)
- **Programming**: Python; R; Shell; JavaScript; MySQL
- **Tools & Frameworks**: Git; Django; Vue.js
- **Cloud & HPC:** Snakemake; AWS/GCP computation
- **Server operation and maintenance**: Ubuntu; CentOS / Rocky Linux

PUBLICATIONS

Asterisk (*) denotes the Co-first Authors and Hashtag (#) denotes the Corresponding Authors.

- Chang, Z.*, Xu, Y.*, **Dong, X.***, Gao, Y. & Wang, C.# Single-cell and spatial multiomic inference of gene regulatory networks using SCRIPro. *Bioinformatics* 40, btae466 (2024).
- Sun, F.*, Li, H.*, Sun, D.*, Fu, S.*, Gu, L.*, Shao, X.*, Wang, Q.*, **Dong, X.***, Duan, B.*, Xing, F.*, Wu, J.*, Xiao, M.#, Zhao, F.#, Han, J.-D. J.#, Liu, Q.#, Fan, X.#, Li, C.#, Wang, C.# & Shi, T.# Single-cell omics: experimental workflow, data analyses and applications. *SCIENCE CHINA Life Sciences* (2024).
- Ren, P.*, Shi, X.*, Yu, Z., **Dong, X.**, Ding, X., Wang, J., Sun, L., Yan, Y., Hu, J., Zhang, P., Chen, Q., Zhang, J., Li, T. & Wang, C.# Single-cell assignment using multiple-adversarial domain adaptation network with large-scale references. *Cell Reports Methods*, 3, 100577 (2023).
- Han, Y.*, Wang, Y.*, **Dong, X.***, Sun, D., Liu, Z., Yue, J., Wang, H., Li, T.# & Wang, C.# TISCH2: expanded datasets and new tools for single-cell transcriptome analyses of the tumor microenvironment. *Nucleic Acids Research*, 51, D1029-D1037 (2022).
- Shi, X.*, Yu, Z.*, Ren, P., **Dong, X.**, Ding, X., Song, J., Zhang, J., Li, T.# & Wang, C.# HUSCH: an integrated single-cell transcriptome atlas for human tissue gene expression visualization and analyses. *Nucleic Acids Research*, 51, D1425-D1431 (2022).
- **Dong, X.***, Tang, K.*, Xu, Y., Wei, H., Han, T. & Wang, C. # Single-cell gene regulation network inference by large-scale data integration. *Nucleic Acids Research*, 50, e126 (2022).
- Xu, R.*, Li, S.*, Wu, Q.*, Li, C.*, Jiang, M.*, Guo, L., Chen, M., Yang, L., **Dong, X.**, Wang, H., Wang, C.#, Liu, X.#, Ou, X.# & Gao, S.# Stage-specific H3K9me3 occupancy ensures retrotransposon silencing in human pre-implantation embryos. *Cell Stem Cell*, 29, 1051-1066.e8 (2022).

- Sun, D.*, Wang, J.*, Han, Y.*, **Dong, X.**, Ge, J., Zheng, R., Shi, X., Wang, B., Li, Z., Ren, P., Sun, L., Yan, Y., Zhang, P., Zhang, F.#, Li, T.# & Wang, C.# TISCH: a comprehensive web resource enabling interactive single-cell transcriptome visualization of tumor microenvironment. *Nucleic Acids Research*, 49, D1420-D1430 (2021).
- Zheng, R.*, **Dong, X.***, Wan, C., Shi, X., Zhang, X.# & Meyer, C.A.# Cistrome Data Browser and Toolkit: analyzing human and mouse genomic data using compendia of ChIP-seq and chromatin accessibility data. *Quantitative Biology*, 8, 267-276 (2020).
- Chen, C.-H., Zheng, R., Tokheim, C., **Dong, X.**, Fan, J., Wan, C., Tang, Q., Brown, M., Liu, J.S., Meyer, C.A. # & Liu, X.S.# Determinants of transcription factor regulatory range. *Nature Communications*, 11, 2472 (2020).
- Li, S.*, Wan, C.*, Zheng, R., Fan, J., **Dong, X.**, Meyer, C.A.# & Liu, X.S.# Cistrome-GO: a web server for functional enrichment analysis of transcription factor ChIP-seq peaks. *Nucleic Acids Research*, 47, W206–W211 (2019).

CONFERENCES

2024 Poster Speaking, Human Cell Atlas Asia 2024, Hong Kong SAR, China
2024 Poster Speaking (Awarded), The 2nd Bioinformatics Conference of Yangtze River Delta, Shanghai, China
2023 Poster Speaking, Systems biology of gene regulation and genome editing, Cold Spring Harbor Conferences Asia, Suzhou, China
2023 Poster Speaking, The WLA Research Conference on Cells and Genes, Shanghai, China
2023 Poster Speaking, The 11st National Conference on Bioinformatics and Systems Biology, Guangzhou, China
2023 Poster Speaking, Human Cell Atlas Asia 2021 Meeting, online
2021 Poster Speaking, The 10th National Conference on Bioinformatics and Systems Biology, Chengdu, China
2019 Attendee, 14th International Bioinformatics Workshop, Beijing, China

TEACHING

Teaching assistant, Summer Deep Learning Course, School of Life Sciences and Technology, Tongji University (2023, Shanghai)

Teaching assistant, Summer Bioinformatics Course, School of Life Sciences and Technology, Tongji University (2020-2022, Shanghai)

Teaching assistant, Dragon Star Course, The 14th International Bioinformatics Workshop (2019, Beijing)

AWARDS AND DISTINCTIONS

2024 Outstanding Graduates Awards of Shanghai, Shanghai Municipal Education Commission
2023 The 17th Academic Pioneer (Top 0.05%), Tongji University
2023 National Scholarship (Top 0.2%), Ministry of Education of the People's Republic of China
2022 Outstanding Student Leader, Tongji University
2019 Outstanding Graduate Student Scholarship, Tongji University
2018 Outstanding Undergraduate Thesis for Bachelor's Degree, Shandong Normal University
2017 Outstanding Graduates Awards of Shandong, Human Resources and Social Security Department of Shandong Province
2017 The First Prize of the 15th Challenge Cup Competition in Shandong, Shandong Association for Science & Technology
2017 Outstanding Student Leader of Shandong, Shandong Provincial Education Department
2016 The Grand Prize of Shandong College Students' Biochemistry Experiment Skills Competition, Shandong Association of Science & Technology