

# Xin Dong

Ph.D. in Bioinformatics

Department of Bioinformatics, School of Life Sciences and Technology

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## EDUCATION

**Sep. 2020 – Jul. 2024**

**Ph.D. in Bioinformatics**

School of Life Sciences and Technology, Tongji University, China

Advisors: Dr. Chenfei Wang & Dr. Xiaole Shirley Liu

**Sep. 2018 – Aug. 2020**

**M.S. Student in Bioinformatics**

School of Life Sciences and Technology, Tongji University, China

Advisors: Dr. Xiaole Shirley Liu & Dr. Xiaoyan Zhang & Dr. Zhiping Weng

**Sep. 2014 – Jun. 2018**

**B.S. in Biotechnology**

College of Life Sciences, Shandong Normal University, China

## RESEARCH EXPERIENCE

Graduate Student, Tongji University (2018-2024)

- **Developed and applied computational methods to analyze single-cell and spatial data**

Advisors: Dr. Chenfei Wang & Dr. Xiaole Shirley Liu

- To search and screen single-cell transcriptome and chromatin accessibility datasets from the GEO of NCBI, I developed a parser that can automatically obtain the metadata and download the raw data. This provides the foundation for our subsequent works.
- We developed SCRIP (Single-Cell Regulatory Network Inference using ChIP-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. Our method outperformed other motif-based approaches in assessing TR binding activity. It also enabled us to identify TR target genes and construct GRNs (Gene Regulation Networks) at the single-cell level using a regulatory potential model. We applied SCRIP to various biological systems and showed its utility in lineage tracing, cell-type clustering, and inferring cell-type-specific GRNs.
- We developed TISCH (Tumor Immune Single Cell Hub; <http://tisch.comp-genomics.org>) 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 even cancer types. TISCH aims to address the computational challenges of using the massive published datasets to inform immunotherapy and to characterize the immune system heterogeneity in cancers.

- **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 (CHromatin enrichment ProceSsor) (<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.
- I investigated the reads-keeping strategy of ATAC-seq that captures the chromatin accessibility of the genome. I discovered that using only the fragments with less than 150 bp length can yield more peaks from ATAC-seq. I implemented this strategy in the CHIPS pipeline.
- We used unsupervised clustering to identify the low-quality dataset and examine the characteristics of high-quality and low-quality data for broad signal histone modifications, such as H3K27me3, which are challenging to assess the quality of the experiment.

#### 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:** High-throughput sequence data analysis; Single-cell data analysis; Epigenome data analysis; Machine Learning and statistic modeling; Deep learning
- **Programming:** Python; R; shell; JavaScript; MySQL
- **High performance computing:** Snakemake pipeline development; Cloud computation; Cluster computation
- **User interface development:** Django; Vue.js; Bootstrap
- **Code version control system:** git
- **Server management:** Ubuntu; CentOS / Rocky Linux
- **Experiment skills:** Cell culture; PCR; Gel electrophoresis

## **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 (Awarded), The 2<sup>nd</sup> 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 11<sup>st</sup> National Conference on Bioinformatics and Systems Biology, Guangzhou, China
- 2023 Poster Speaking, Human Cell Atlas Asia 2021 Meeting, Online
- 2021 Poster Speaking, The 10<sup>th</sup> National Conference on Bioinformatics and Systems Biology, Chengdu, China
- 2019 Attendance, 14<sup>th</sup> International Bioinformatics Workshop, Beijing, China

## TEACHING

- 2023 Teaching assistant, Summer Deep Learning Course, School of Life Sciences and Technology, Tongji University, Shanghai, China
- 2022 Teaching assistant, Summer Bioinformatics Course 2022, School of Life Sciences and Technology, Tongji University, Shanghai, China
- 2021 Teaching assistant, Summer Bioinformatics Course 2021, School of Life Sciences and Technology, Tongji University, Shanghai, China
- 2020 Teaching assistant, Summer Bioinformatics Course 2020, School of Life Sciences and Technology, Tongji University, Shanghai, China
- 2019 Teaching assistant, Dragon Star Course, The 14<sup>th</sup> International Bioinformatics Workshop, Beijing, China

## AWARDS AND DISTINCTIONS

- 2024 Outstanding Graduates of Shanghai, Shanghai Municipal Education Commission
- 2023 The 17<sup>th</sup> Academic Pioneer, Tongji University
- 2023 National Scholarship, Ministry of Education of the People's Republic of China
- 2022 Outstanding Student Leader, Tongji University
- 2022 Social Activities Scholarship, Tongji University
- 2019 Outstanding Graduate Student Scholarship, Tongji University
- 2018 Outstanding Undergraduate Thesis for Bachelor's Degree, Shandong Normal University
- 2017 Outstanding Graduates of Shandong, Human Resources and Social Security Department of Shandong Province

- 2017 The First Prize of the 15<sup>th</sup> Challenge Cup Competition in Shandong, Shandong Association for Science and 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

## LEADERSHIP AND PUBLIC SERVICE

- 2023**                    **Director, Chairman of Organizing Committee**  
Graduation party of School of Life Sciences and Technology, Tongji University
- 2022**                    **Volunteer of PCR Test for COVID-19**  
Liferiver Bio-Tech Corp., Shanghai, China
- 2020**                    **Census Taker**  
7<sup>th</sup> Census of China
- 2016 – 2017**          **Vice-president, Chairman of Executive Committee**  
Students' Union, Shandong Normal University
- 2015 – 2016**          **Head of Literatures and Arts Department**  
Students' Union, Shandong Normal University
- 2016**                    **Chairman of Organizing Committee**  
30<sup>th</sup> Top Ten Campus Singers Competition of Shandong Normal University
- 2015**                    **Chairman of Organizing Committee**  
Golden Microphone Host Competition of Shandong Normal University
- 2015 – 2016**          **Committee Member of Network Department**  
Students' Union, School of Life Sciences, Shandong Normal University
- 2014 – 2015**          **Member of Rights and Interests Department**  
Students' Union, Shandong Normal University