

—More detail, click link: [Linkedin](#), [GitHub](#) and [ORCID](#)

Xiang Li, Ph.D.

Contact Information

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EDUCATION

Ph.D., George Washington University, Biophysics, 09/2016 ~ 05/2021
[Thesis Summary](#) Study of Transcriptional and Post-transcriptional Regulation in Immune Systems
 B.S., Huazhong University of Science & Technology, Applied Physics 09/2011 ~ 07/2015

SKILLS

AWS Certified Cloud Practitioner 12/2022
[Certificate](#)., DeepLearning.AI, Neural Networks and Deep Learning 04/2021

Program, Software Skills and Database:

- Advanced: Linux Admin, Shell Script, *Python*(data mining→visual→ML), NGS Tools,
- Intermediate: PyPi, Nextflow, AWS S3 & EC2, flask, boto3, Fortran, Gitlab, Github, SGE, \LaTeX
- Basic : Snakemake, Docker, Web and Server Support(Nginx), MATLAB, C/C++, Java, R
- Bio Database : 4DN, NCBI, GEO, ENCODE, HapMap, 1000 Genomes, GIAB, genomAD, dbSNP

Work Experiences

[GentiBio](#) , Bioinformatics Scientist II

Boston MA, 2022 ~ Present

- Build a full-stack web application (on aws) for automation. Similar to [CRISPResso2 Web](#)
 An automated data processing system
 Integrates web application(frontend) and complex analysis workflows (backend).
 Do the heavy analysis with just a few clicks and received results in email link.
- Bioinformatics-Lead in building Cellular Profiling Platform:
 Deploy GentiBio internal chatGPT & Automation pipeline through AWS
 Deploy AWS VC-backed startup package and build Bioinformatics Infrastructure.
 Write analysis tools (python R) and pipeline (bash, Nextflow Docker)
 Adopt bulk/scRNAseq analysis pipeline and downstream analysis
- Build every computational components for GENTI122 IND package (Safety assessment for Gene Editing Product).
 On/Off-Target analysis protocol: in-Silico \Rightarrow *GUIDESeq* \Rightarrow *rhAMPSeq*.
 Troubleshooting on every technical detail (Sequencing QC)
 Analysis tools benchmark (CRISPResso2, Crispector, CRISPRpic, CRISPAItRations)

Department of Physics, [GWU](#)

Washington, DC, 2017 ~ 2023

Ph.D Researcher, (Supervisor: [Prof. W. Peng](#) , Collaborator: [Prof. H. Xue](#))

- [Nature Com](#): Develop analysis framework (python-base for data representation, visualization and ML)
- Integration of Multi-omics: scRNAseq(10X), RNAseq and DNase_seq, ATAC_seq, ChIPseq, Cut&Run, HiC, MiCroC, HiChIP and etc.
- Chromatin structure and function: Develop a tool ([HiChHub](#), which solved the problem on identifying a mixed range of altered genome structure(from looping to larger than TAD). This tool outperforms similar software in HiC data analysis with a significantly increase in the computational efficiency.
- [Nucleic Acids Research](#): mRNA stability Mathematical Modeling and data analysis.
- Study regulatory roles of Tcf1/Lef1 in CD8⁺ T cells in immunue response. ([JEM](#), 2019, 2018)
- Impact upon deficiency of miRNA-34b/c during somatic reprogramming progress.

- Organize Journal Club and give presentation once per month.
- HPC management. (Linux Admin, data storage & sharing & backup, computation dependencies setup, jupyter notebook & Rstudio server and on-call for tech emergency.
- Build analysis pipeline, dependencies and visualization tools on a cloud platform. (AWS, Linux ssh).

[Sana Biotechnology Scientist](#), Computational Biology

Seattle WA, 2021 ~ 2022

- Tech support for biologists with data in Cell therapy development.
- Assay Development for Cell Characterization 1. Amplicon Seq, from primer design, through pipeline development (Nextflow) and into the automation process. 2. Develop and maintain production level code in python. 3. Provide variants calling pipeline with robustness testing on reaching the limit of detection. 4. Combine databases (gnomeAD, dbSNP) for variants Annotation.

Team Lead, NLP Course Project

George Washington University

Washington, DC, 2019

- Natural language processing, use different models for user profiling task in given posts from twitter.
- Write model to implement different language models, Hidden Markov model and bayesian classifier.

Joint Leader of Student Innovation Group (Adviser: B. Yu)

Qiming College of Huazhong University of Science & Technology

Boston, Summer and Fall 2014

- Built a team for 2014 [BIOMOD, Harvard](#), Cambridge, Massachusetts.
- Invested nano-scale transportation system based with magnetic control device.
- Conducted the final presentation on behalf of our team.
- For more detail, please visit our website: [BIOMOD 2014: HUST](#)

Teaching

- Graduate TA. General Physics (with: [X. Qiu](#) / [G. Younes](#) / [S. Guiriec](#)) 09/2016 ~ 05/2018
- Instructor. Astrophysics (with: [Kalvir Dhuga](#)) 01/2019 ~ 05/2019

Consultant

- Computational Workflow Development for [Verily Life Sciences](#) 2023 ~ Present

HONORS AND AWARDS

- The Parke Prize, awarded for excellence in theoretical biophysics
- [Visiting Scholar](#) (Host: Chairman Emeritus of CME Group [Leo Melamed](#))
- Scholarship in Department of Biostatistics, University of Washington, \$1,950
- Second Prize of Poster in 3rd International Ocean Sciences Summer School. \$800
- Project Awards: Silver; International Biomolecular Design Competition 2014, [BIOMOD, Harvard](#)
- Fellowship \$12000 total, Undergraduate Fellowship from College of Life Science & Technology,

Publications & Patents & Presentations

- [HiCHub: A Network-Based Approach to Identify Domains of Differential Interactions from 3D Genome Data](#) [Xiang Li](#)[†], ..., Hai-Hui Xue, Weiqun Peng., bioRxiv (TBD)
- [Lysine methyltransferase Kmt2d regulates naive CD8+ T cell activation-induced survival](#) Jaekwan Kim, T.N., ..., Xiang Li, ..., Nan-ping Weng., Frontiers in Immunology (2023)
- [Tcf1 CTCF cooperativity shapes genomic architecture to promote CD8+ T cell homeostasis](#) Q. S[†], ..., [Xiang Li](#), ..., Hai-Hui Xue., Nature Immunology (2022)
- [Tcf1 and Lef1 maintain CD8+ T cell identity by organizing genomic architecture](#) Q. S[†], [Xiang Li](#)[†], ..., Hai-Hui Xue., Nature Communications (2021)

- **Selected Oral Presentation**, 2021 Network Biology, Cold Spring Harbour Laboratory [Network analysis reveal the critical role of TCF1/LEF1](#), Speaker: **Xiang Li**
- [Sepsis leads to lasting changes in phenotype and function of memory CD8 T cells](#) Isaac J. Jensen[†], **Xiang Li**[†],..., Weiqun Peng and Vladimir P. Badovinac., 2021 eLife
- [Arid1a-Plagl1-Hh signaling is indispensable for differentiation-associated cell cycle arrest of tooth root progenitors](#) Yang Chai, ..., **Li Xiang**, Xinquan Jiang. Cell Reports (2021).
- [Transcriptome-wide stability analysis uncovers LARP4-mediated NFB1 mRNA stabilization during T cell activation.](#) Tian Y.[†], Zeng Z.[†], **Li Xiang**[†], ..., Peng W. and Zhu J. Nucleic Acids Research (2020).
- [Integrated analysis of carbon dioxide and oxygen concentrations as a quality control of ocean float data](#) Yingxu Wu, D. Bakker, E. Achterberg, ..., **Xiang Li**, ... Communications Earth Environment, Accepted. (Mar, 2022)
- [Tcf1 and Lef1 transcription factors are required for the immunosuppressive function of regulatory T cells](#) Xing S., Gai K., **Li Xiang**,..., Peng W. and Xue H., J Exp Med (2019).
- [Tle corepressors are differentially partitioned to instruct CD8+ T cell lineage choice and identity](#) Xing S., ..., **Xiang Li**,..., Peng W. and Xue H., J Exp Med (2018).