

## Shawn Li, Ph.D.

### INTERESTS

Equity Research for Biotech  
"visiting student" at Georgetown, department of economics.

### EDUCATION

Ph.D., George Washington University, Biophysics (**Honor: Parke Prize**), 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, (**Honor**) 09/2011 ~ 07/2015

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### 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, S3 & EC2, flask, dash, boto3, Fortran, Gitlab, Github, SGE,  $\LaTeX$
- Basic: Snakemake, Docker, Web and Server Support(Nginx), MATLAB, C/C++, Java, R
- DB: genomAD, 4DN, NCBI, GEO, ENCODE, HapMap, 1000 Genomes, GIAB, dbSNP

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### Work Experiences

[GentiBio](#), Senior Scientist, Bioinformatics Lead in a small team

Boston MA, 2022 ~ Present

- Research Collaboration: Study Mouse IgA Model Using scRNAseq & scATACseq from kidney biopsies from IgAN (15w, 21w, 52w) and Mock
- Implement AlphaFold2 & AlphaMissense for CAR design, IBD model.
- Build SNP-aware (gnomAD v4.0) insilico Off-target analysis for Cas9 editing
- Build a full-stack web app (aws) for automation. Similar to [CRISPResso2 Web](#)  
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, CRISPRatRations)

Internship (Collaborator: [Dr. Z. Jin](#))

International Monetary Fund

Washington, DC, Aug 2018 ~ Dec, 2018

- Modeling Study of Currency Exchange Rate on economic datasets.
- Implementing Recurrent Neural Network(RNN) with Long-Short-Term-Memory unit.

**Sana Biotechnology Scientist**, Computational Biology  
Seattle WA, 2021 ~ 2022

- Work as IC in corporate team, focusing on computational pipelines (nextflow) development.
- iPSC Master Cell Bank, Cell Characterization & Safety Assessment

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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 (**HiCHub**, 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<sup>+</sup> 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).

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**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**

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## 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
- Computational Workflow Development for Insights Driven Research (IDR) one time

## Reviewer

- Machine Learning for Genomics **MLGenX** 2024
- Phenomics Youth Editorial Board 2023 ~ Present
- Society of Artificial Intelligence Research **SAIR** 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**<sup>†</sup>, ..., 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<sup>†</sup>, ..., **Xiang Li**,..., Hai-Hui Xue., Nature Immunology (2022)
- [Tcf1 and Lef1 maintain CD8+ T cell identity by organizing genomic architecture](#) Q. S<sup>†</sup>, **Xiang Li**<sup>†</sup>,..., 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<sup>†</sup>, **Xiang Li**<sup>†</sup>,..., 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.<sup>†</sup>, Zeng Z.<sup>†</sup>, **Li Xiang**<sup>†</sup>, ..., 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).

## Work extensively used HiCHub

- [Tcf1 CTCF cooperativity shapes genomic architecture to promote CD8+ T cell homeostasis](#) Nature Immunology (2022)
- [CTCF mediates CD8+ effector differentiation through dynamic redistribution and genomic reorganization](#) JEM (2023)