

Wang Xi

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Educational Background

Johns Hopkins University

Ph.D Candidate, Biomedical Engineering

Research Advisor: Mike Beer, Ph.D

2017 - Present

University of California, Los Angeles

Research Associate, Bioinformatics

Research Advisor: Yi Xing, Ph.D

2016

University of California, Berkeley

Exchange Student, Integrative Biology

2015

Huazhong University of Science and Technology (China)

B.S., Biotechnology

Research Advisor: Kang Ning, Ph.D

2013 - 2017

Peer-Reviewed Publications

Xi, W., & Beer, M. A. (2021). Loop competition and extrusion model predicts CTCF interaction specificity. *Nature Communications*. 12(1): 1-15

Xi, W., Gao, Y., Cheng, Z., Chen, C., Han, M., Yang, P., & Ning, K. (2019). Using QC-Blind for quality control and contamination screening of bacteria DNA sequencing data without reference genome. *Frontiers in Microbiology*, 10, 1560.

Xi, W., & Beer, M. A. (2018). Local epigenomic state cannot discriminate interacting and non-interacting enhancer-promoter pairs with high accuracy. *PLoS Computational Biology*, 14(12), e1006625.

Tang, S.,* **Xi, W.,*** Cheng, Z.,* Yin, L., Li, R., Wu, G., Liu W., Xu J., Xiang S., Zheng Y.& Ge, Q., Ning K., Yan Y., Zhan Y (2016). A Living Eukaryotic Autocementation Kit from Surface Display of Silica Binding Peptides on *Yarrowia lipolytica*. *ACS synthetic biology*, 5(12), 1466-1474.

Research Presentations

Oral presentations:

Encyclopedia of DNA Elements (ENCODE) Consortium Meeting

2021

5th Annual Excellence in Diversity Symposium (Johns Hopkins University, Best Presentation)

2021

Systems Biology: Global Regulation of Gene Expression (Cold Spring Harbor Laboratory)

2020

Cross-Disciplinary Scholars in Science and Technology (UCLA, Best Presentation)

2016

Poster presentations:

Encyclopedia of DNA Elements (ENCODE) Consortium Meeting

2019

Encyclopedia of DNA Elements (ENCODE) Consortium Meeting

2018

Research Experience

Johns Hopkins University MD

2017- Present

Biomedical Engineering PhD program

- Developed mathematical models to predict CTCF interactions based on loop extrusion.
- Validated and developed computational methods to predict enhancer-promoter interactions across cell types.
- Applied gapped-kmer method to detect conserved regulatory elements in mammalian species.

University of California, Los Angeles CA

2016

Bioinformatics Analyst/Research Assistant (CSST Program)

- Participated in the development of CLIP-seq Analysis for Multi-mapped Reads (CLAM), an expectation-maximum-based method for RBP-bound repetitive elements identification.

Key Laboratory of Molecular Biophysics of the Ministry of Education Wuhan, China 2016 - 2017

Bioinformatics Analyst/Research Assistant

- Developed QC-Bind, a pipeline to do quality control on NGS data without reference genome of target species,
- Performed integrative assessments of virus taxonomic profiling approaches with simulated and real datasets

International Genetically Engineered Machine 2015 Boston, MA 2014 - 2015

Team Leader

- Designed and implemented the project “*Euk.cement – A living eukaryotic cell based auto-cementation kit*”.
- Constructed silica-binding protein pathway on plasmid, performed computational simulation on this pathway with ODE and PDE models.

Honors and Awards

Young Investigators’ Day Award – The Bao Gyo Jung Research Award, Johns Hopkins University 2021

CSST Scholarship, University of California, Los Angeles 2016

School Merit Student, Huazhong University of Science and Technology 2016

School Merit Student, Huazhong University of Science and Technology 2015

National Fellowship, Chinese Ministry of Education 2015

IGEM Gold Medal, iGEM 2015 Committee 2015

CSC Scholarship, China Scholarship Council, NO.2015006160153 2015

School Merit Student, Huazhong University of Science and Technology 2014

National Fellowship, Chinese Ministry of Education 2014

Research Techniques/Skills

Machine Learning	proficient with Python ML environment – sklearn, numpy, pandas, pytorch
Statistical Analysis	proficient with R, ggplot2 and Jupyter notebook
Genomic Data	ChIP-seq, ATAC-seq, RNA-seq, Hi-C, ChIA-PET, GWAS, CRISPR screening
Databases	NCBI/GEO, Ensembl, ENCODE, GTEx, ROADMAP, FANTOM

Teaching Experiences

Methods in Nucleic Acid Sequencing Lab, Teaching Assistant & Instructor 2021

Introduction to Data Science for Biomedical Engineering, Teaching Assistant & Instructor 2019