

RUIHAO LI

Curriculum Vitae

Molecular Biology and Genetics
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Career

- 2024–present **Postdoctoral Fellow, Molecular Biology and Genetics, Cornell University, USA.**
Genetic regulatory network inference, Mathematical modeling of biological systems, Genomic and proteomic sequence, Molecular biology, Microbiology, Machine Learning and Deep Learning
- 2017–2023 **PhD, Quantitative and Systems Biology, University of California, Merced, USA.**
Genetic regulatory network inference, Mathematical modeling of biological systems, Genomic and proteomic sequence, Molecular biology, Microbiology, Machine Learning and Deep Learning
- 2016–2017 : **Exchange Student, Integrative Biology, University of California, Berkeley, USA,** Fully funded by studying abroad & international exchange student program for National Excellent Undergraduates, China Scholarship Council.
- 2013–2017 : **Bachelor of Science, General Biology, Huazhong University of Science & Technology (HUST), China.**

Publications

In Progress

- 2023 Mohammad Qasim, **Li, Ruihao**, Morgan Quail, Clarrisa Nobile, and Aaron Hernday. Interplay between chromatin organizing transcription factors and dynamic nucleosomes regulate cell fate decisions and developmental processes in *Candida albicans*. **Preparing for submission**, 2023.

Published Articles

- 2023 **Li, Ruihao**, Jordan C Rozum, Morgan M Quail, Mohammad N Qasim, Suzanne S Sindi, Clarissa J Nobile, Réka Albert, and Aaron D Hernday. Inferring gene regulatory networks using transcriptional profiles as dynamical attractors. ***PLOS Computational Biology***, volume 19(8), page e1010991. Public Library of Science San Francisco, CA USA, 2023.
- 2021 Mingyue Cheng, Zhangyu Cheng, Yiyan Yu, Wangjie Liu, **Li, Ruihao**, Zhenyi Guo, Jiyue Qin, Zhi Zeng, Lin Di, Yufeng Mo, et al. An engineered genetic circuit for lactose intolerance alleviation coupled with gut microbiota recovery. ***BMC biology***, volume 19(1):137. BioMed Central, 2021.
- 2016 Shuyan Tang, Wang Xi, Zhangyu Cheng, Lei Yin, **Li, Ruihao**, Guozhao Wu, Wangjie Liu, Junjie Xu, Shuaiying Xiang, Yanxiao Zheng, et al. A living eukaryotic autocementation kit from surface display of silica binding peptides on *Yarrowia lipolytica*. ***ACS Synthetic Biology***, volume 5(12), pages 1466–1474. ACS Publications, 2016.

Presentations

- 2023 **Li, Ruihao**, Jordan Rozum, Morgan Quail, Mohammad Qasim, Suzanne Sindi, Clarrisa Nobile, Réka Albert, and Hernday Aaron. Inferring gene regulatory networks using transcriptional profiles as dynamical attractors. ***The 22nd International Conference on Systems Biology (Talk)***, 2023.
- 2023 **Li, Ruihao**, Morgan Quail, Mohammad Qasim, Suzanne Sindi, Clarrisa Nobile, and Hernday Aaron. Inferring gene regulatory networks using transcriptional profiles as dynamical attractors and its applications. ***The Math Bio Seminar at University of California, Merced (Talk)***, 2023.

2019 **Li, Ruihao**, Morgan Quail, Mohammad Qasim, Suzanne Sindi, Clarrisa Nobile, and Hernday Aaron. Gene regulatory network reverse engineering using attractor-based evolutionary algorithm. *The Math Bio Seminar at University of California, Merced (Talk)*, 2019.

Research Experience

2024 – present ***Inferring the Entire Gene Regulatory Network in *Saccharomyces cerevisiae*, General purposes: whole network inference, functionality prediction.***

- Infer the regulatory interactions among the sequence-specific transcription factors using the **stable-state transcriptional profiles**, **ChIP-exo data**, and **pre-initiation complex occupancy** as the indicator of gene-specific promoter strengths.
- Expand the network to non-TFs using linear models.
- Simulate the **regulatory reprogramming and dynamics** of transient/intermediate processes such as **heatshock**.

Advisor : **Dr. Franklin Pugh**, Professor, Molecular Biology and Genetics, Cornell University([Personal Web-page](#))

Collaborator : **Dr. William Lai**, Assistant Research Professor, Molecular Biology and Genetics and Computational Biology, Cornell University([Personal Web-page](#))

University of California, Merced

2018 – 2023 ***Inferring the Gene Regulatory Network that Governs the White-opaque Switch in *Candida albicans*, General purposes: fungal pathogenesis, antifungal therapies development.***

- Built an **ODE-based model implemented with logic gates** to simulate the biological processes of transcription, translation, and transcriptional regulation in a casual gene regulatory network.
- Wrote an **evolutionary algorithm** to automatically and iteratively reconstruct the ODEs according to the gene regulatory network structure, solve the ODEs numerically, select the networks whose ODEs can better reproduce the transcriptional profiles as steady states, and mutate the network structure.
- Ran the evolutionary algorithm on a Linux-based high-performance computing cluster and applied **parallel computing** to accelerate the speed of the algorithm.
- Demonstrated a **proof-of-principle** that illustrates how the network structures are linked to their steady states. Tested the performance of the approach on *in-silico* datasets and made **comparisons** against six other leading methods.
- Applied the approach to the **white-opaque switch core circuit** in *Candida albicans* and inferred a network. Made **testable predictions** on the transcriptional profile produced upon genetic perturbation.
- Tested the predictions experimentally with **genome-editing** tools and RNA sequencing and further refined the model.

Advisor : **Dr. Aaron Hernday**, Full Professor, Department of Molecular Cell Biology, University of California, Merced([Personal Web-page](#))

Collaborator : **Dr. Réka Albert**, Distinguished Professor of Physics and Biology, Pennsylvania State University([Personal Web-page](#))

2019 – 2023 ***Identifying the Roles of Chromatin Accessibility in Regulating the White-opaque Switch in *Candida albicans*, General purposes: epigenetic landscape characterization.***

- **Mapped, analyzed, and visualized** the ATAC-seq and MNase-seq data of white and opaque *Candida albicans*.
- Performed **nucleosome occupancy prediction** on *Candida albicans* genome and compare the result against experimental data;
- Performed **intrinsic disorder region prediction** on *Candida albicans* proteome.

Advisor : **Dr. Aaron Hernday**, Full Professor, Department of Molecular Cell Biology, University of California, Merced

- 2018 – 2019 **Identifying Novel Transcription Factors Involved in the White-opaque Switch in *Candida albicans***, *General purposes: transcriptional regulation study, antifungal therapies development.*
- Mapped the RNA-seq data of various TF knock-out mutants and performed **differential expression analysis**.
 - Applied **logistic regression and prion-like amino acid composition scores** to select the potential transcription factors.
 - Knocked out the potential transcription factors and measured the white-opaque switch frequencies.
 - Applied **support vector machine** to classify white and opaque cells with different switching frequencies.

Advisor : **Dr. Aaron Hernday**, *Full Professor, Department of Molecular Cell Biology, University of California, Merced*

Huazhong University of Science & Technology (HUST)

- 2016 – 2018 **Signal filter: A toolkit controlling gene expression based on negative feedback multi-stable state circuits**, *General purposes: lactose intolerance alleviation.*
- Independently responsible for research proposal and **design of the gene circuit**: a negative feedback tri-stable system with the capability of reducing noise and converting pulse signal into a robust and persistent signal.
 - Performed gene circuit analysis followed by mathematical modeling.

Advisor : **Dr. Kang Ning**, *Associate Professor, College of Life Science & Technology, Huazhong University of Science & Technology (HUST)* ([Personal Web-page](#))

- 2015 – 2017 **Innovation in Technology of DNA-based Preservation and Access of Digital Information**, *General purposes: high-density storage of digital information.*
- Translated a poem between binary codes and DNA sequence using **Huffman coding**.
 - Studied the **robustness and fidelity of DNA sequence** subject to changing pH, temperature, shear force, and salt concentration.

Advisor : **Dr. Kang Ning**, *Associate Professor, College of Life Science & Technology, Huazhong University of Science & Technology (HUST)*

Fellowships & Awards

- 2018 **QSB Summer Research Fellowship** of University of California, Merced.
- 2016 **GOLD MEDAL**, INTERNATIONAL GENETICALLY ENGINEERED MACHINE (iGEM) COMPETITION, Boston, Massachusetts, USA.
- 2015 **GOLD MEDAL**, INTERNATIONAL GENETICALLY ENGINEERED MACHINE (iGEM) COMPETITION, Boston, Massachusetts, USA.

General Research Skills

Machine Learning	Regression, Classification, Clustering, Dimensionality reduction, Neural nets, Deep learning, Big data, Graph model, etc..
Programming	Python, R, Matlab, C++, Perl, Shell/Bash, MySQL, HTML, etc..
Wet Lab Techniques	Genome editing technique, Molecular cloning, SDS-PAGE, ELISA, qPCR, etc..

Teaching Assistantship

- Fall, 2017 : **BIO 002L: Molecular Biology Lab.**
- Spring, 2018 – Spring, 2020: **BIO 120L: General Microbiology Lab.**
- Fall, 2020 : **BIO 001: Contemporary Biology.**
- Spring, 2021 : **BIO 140: Genetics.**
- Fall, 2021 : **BIO 001: Contemporary Biology.**

Referees

Dr. Aaron Hernday

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