Shuang Li

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EDUCATION:

2010-2017	**New York University (NYU), New York, NY**
	Ph.D. in Biology
2006-2010	**Nanjing Agricultural University (NAU), Nanjing, China**
	B.S. in Life Science

RESEARCH EXPERIENCE:

Department of Pharmacology, University of North Carolina at Chapel Hill

<u>Bioinformatics Scientist</u>, J. Mauro Calabrese Lab, 05/2023-Present

- Functional inference of long non-coding RNA (lncRNA) based on sequence features

- Molecular mechanism of lncRNA function through RNA-binding proteins

Department of Pharmacology, University of North Carolina at Chapel Hill

<u>Postdoctoral Associate</u>, Henrik Dohlman & Timothy Elston Lab, 05/2018-04/2023

- Multi-omics analysis of glucose signaling pathway in *Saccharomyces cerevisiae*

- Evolutionary conservation of sequence motifs at sites of protein modification

Department of Biology, New York University

<u>Postdoctoral Associate</u>, Mark Siegal Lab, 06/2017-04/2018

- Regulation of single cell growth by intracellular pH in *Saccharomyces cerevisiae*

<u>Ph.D. student,</u> Mark Siegal Lab, 01/2011-05/2017

- Thesis project: RAS/cAMP/PKA/MSN2/4 pathway regulates non-genetic heterogeneity in growth rate and stress tolerance in *Saccharomyces cerevisiae*

- Platform: Robust colony recognition for high-throughput growth analysis from suboptimal low-magnification brightfield micrographs

Department of Life Science, Nanjing Agricultural University, China

<u>Undergraduate student</u>, Sheng Qiang Lab, 03/2007-06/2010

- National Undergraduate Innovation Research Program (No. GJ0719): Mutagenesis of *Curvularia eragrostidis* for an improved bioherbicide

CERTIFICATES:

- Sequence Models; Structuring Machine Learning Projects and Improving Deep Neural Networks of Deep Learning Specialization, by Andrew Ng, DeepLearnig.AI, Coursera, 10/2022

- [The Advanced SQL Server Masterclass For Data Analysis](#), by Travis Cuzick, Udemy, 07/2022
- [Basic Image Classification with TensorFlow](#), by Amit Yadav, Coursera, 06/2020
- [Machine Learning](#), by Andrew Ng, Stanford, Coursera, 05/2020
- [Statistical Inference and Modeling for High-throughput Experiments](#) and [High-Dimensional Data Analysis](#) by Rafael Irizarry, HarvardX, edX, 09/2016

RESEARCH SKILLS:

Data Analysis
- High-dimensional data exploration, analysis and visualization (R)
- Linear mixed-effects modeling (R)
- Fluorescence and Bright-field Image analysis (Matlab, Python)
- RNA-seq and LC-MS data processing and analysis (Linux, Python, R)
- Multi-omics data integration and Pathway analysis (R)
- High-performance computing workload managing (Slurm)
- Shiny Web App development and deployment (R)
- Relational database management and data analysis (mySQL and SQL Server)
- Machine Learning, Deep Learning, Transformer (Python, Keras, TensorFlow)
- Package development and Dockernization (Python, Linux, Docker)

Microscopy and Imaging
- Fluorescence Time-lapse microscopy

Molecular Biology
- RNA-seq library preparation
- Complex plasmid construction
- Yeast and bacteria transformation

WEB APP DEVELOPMENT:

[CoSMoS.c.](#) – Conserved Sequence Motif in Saccharomyces cerevisiae that calculates conservation score on amino acid level based on 1011 wild and domesticated yeast isolates. **Featured links** under Protein - Post-translational Modifications for all non-intron containing ORFs on *Saccharomyces* **Genome Database ([SGD](#))**.

[PaperDater](#) – Keyword, Journal and Author PubMed search results analysis and alluvial plotting, serving as a digital matchmaker for manuscripts and journals.

PACKAGE DEVELOPMENT:

[seekr](#) – sequence evaluation from k-mer representation that quantifies k-mer based similarity as a powerful complement to BLAST-like linear alignment algorithms. When the sequences being compared functions through spatial arrangements of related sequence motifs and evolves rapidly, their similarities might not be detectable by traditional methods of linear sequence alignment, but could be successfully quantified through their k-mer profile.

[hmseekr](#) – hidden Markov model seekr that identifies regional and whole-transcript

similarities in k-mer content of a query sequence among an interested area of sequence that otherwise lacks linear sequence similarities.

PUBLICATIONS:

- **Li S**, Dohlman HG   Evolutionary conservation of sequence motifs at sites of protein modification. *Journal of Biological Chemistry* (2023)

- **Li S**, Li Y, Rushing BR, Harris SE, McRitchie SL, Dominguez D, Sumner SJ, Dohlman HG Multi-Omics Analysis of Multiple Glucose-Sensing Receptor Systems in Yeast. *Biomolecules* (2022) **Editor's Choice**

- **Li S**, Li Y, Rushing BR, Harris SE, McRitchie SL, Jones JC, Dominguez D, Sumner SJ, Dohlman HG   Multi-omics analysis of glucose-mediated signaling by a moonlighting Gβ protein Asc1/RACK1. *PLoS genetics* (2021)

- Plavskin Y*, **Li S***, Jung H, Sartori FMO, Buzby C, Müller H, Ziv N, Levy SF, Siegal ML Robust colony recognition for high-throughput growth analysis from suboptimal low-magnification brightfield micrographs. *bioRxiv* (2021) (* these authors contributed equally to this work)

- Rangarajan N, Kapoor I, **Li S**, Drossopoulos P, White KK, Madden VJ, Dohlman HG Potassium starvation induces autophagy in yeast. *Journal of Biological Chemistry* (2020)

- Geiler-Samerotte KA, **Li S**, Lazaris C, Taylor A, Ziv N, Ramjeawan C, Paaby AB, Siegal ML   Extent and context dependence of pleiotropy revealed by high-throughput single-cell phenotyping. *PLoS biology* (2020)

- **Li S**, Giardina DM, Siegal ML   Control of nongenetic heterogeneity in growth rate and stress tolerance of Saccharomyces cerevisiae by cyclic AMP-regulated transcription factors. *PLoS genetics* (2018)

- Bauer CR, **Li S**, Siegal ML   Essential gene disruptions reveal complex relationships between phenotypic robustness, pleiotropy, and fitness. *Molecular Systems Biology* (2015)

- Geiler-Samerotte KA, Bauer CR, **Li S**, Ziv N, Gresham D, Siegal ML   The details in the distributions: why and how to study phenotypic variability. *Current Opinion in Biotechnology* (2013)

PRESENTATION & POSTERS:

2016/07   **Platform Talk; The Allied Genetics Conference, Genetics Society of America**
Non-genetic heterogeneity in yeast growth rate and stress resistance

2016/01   Poster; **New York Symposium on the Quantitative Biology of the Cell**
Non-genetic heterogeneity in yeast growth rate and stress resistance

2014/07   Poster; **The Yeast Genetics Meeting, Genetics Society of America**
Non-genetic heterogeneity in yeast growth rate and stress resistance

2013/06   Poster; **Gordon Conferences: Biological Mechanisms in Evolution Genetics**

TEACHING EXPERIENCE:

2011 & 2014 Fall Instructor; Molecular and Cell Biology I, NYU

2012 & 2014 Spring Instructor; Principles of Biology II, NYU

2012 Fall Instructor; Principles of Biology I, NYU

2011 Spring Lab Instructor; Principles of Biology II, NYU

OUTREACH ACTIVITIES:

2013 & 2016 Workshop Instructor, Johns Hopkins University

  Center for Talented Youth Family Academic Program

2013 Speaker, Oregon State University

  International Student Exchange Program

HONORS & AWARDS:

2016 Dean's Dissertation Fellowship, Graduate School of Arts and Science, NYU

2011 Kopac Teaching Award, Department of Biology, NYU