Fangfei Li

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Authorized to work in the U.S. (no sponsorship required now or in the future)

SUMMARY & SKILLS

• **Ph.D. in Computational Biology** | 2 yrs postdoc + 2 yrs biotech startup + 3 yrs wet-lab (synthetic barcoded yeast construction and barcoding-based *in vivo* lineage tracing, NGS library preparation, molecular biology) • **Skills**: bioinformatics, NGS data analysis & visualization, deep learning, Python (`NumPy`, `Matplotlib`, `tkinter`, `Flet`), Git, SQL, API, Computational modeling & algorithm development, • Strong analytical thinker; detail-oriented, organized, and goal-driven.

INDUSTRIAL & ACADEMIC EXPERIENCE

AI Training with Certificates — 9/2025–current

Online

- Stanford Artificial Intelligence Professional Program (Certificate)
- DeepLearning.AI Deep Learning Specialization (Certificate)

Computational Biology Staff Scientist — 11/2023–8/2025

BacStitch DNA, South San Francisco, CA

- Developed an automated end-to-end DNA assembly workflow (Python, web/GUI) that scores sequences, designs optimal overlapping blocks, checks synthesizability via supplier APIs, and generates automated high-throughput experimental plans.
- Built a Python tool for optimal DNA block design that segments sequences into overlapping blocks with minimal structural features in overlaps, under customizable constraints on block count, block/overlap length, and specific regions forced as blocks/overlaps.
- Created Python visualization tools to (i) plot BLAST results and structural scores (*Example*), (ii) generate *.ab1* files encoding structural scores as ATGC traces at single-nucleotide resolution, and (iii) produce publication-quality figures for publications and internal use.

Postdoctoral Research Fellow — 4/2021–10/2023

Sherlock Lab at Department of Genetics, Stanford University, CA

- Developed a bioinformatics pipeline to process raw NGS reads, perform quality control and barcode extraction, and generate barcode count tables for downstream analysis.
- Improved a fitness estimation algorithm and developed a Python pipeline (*FitSeq2*), an enhanced version of *Fit-Seq*.
- Developed a Bayesian optimization algorithm and a Python pipeline (*FitMut2*) to identify genome-wide adaptive lineages from fitness phenotypes (without WGS) in experimental evolution and estimate mutation fitness effects and occurrence times.

Graduate Researcher — 8/2014–12/2020

Laufer Center for Physical and Quantitative Biology, Stony Brook University, NY

- Developed a fitness estimation tool (*Fit-Seq*) that can estimate unbiased fitness for complex cell pools, using a maximum likelihood algorithm.

- Designed and conducted *in vivo* bar-seq experimental yeast evolution (*yeast genetics, cloning, barcoded library construction, lineage-traced evolution, and NGS prep*). Performed computational analysis (*NGS processing, mathematical modeling for inferring evolutionary parameters from lineage dynamics, and evolutionary simulations for validation*) to explore the epistasis of adaptive mutations in yeast evolution.

EDUCATION

Ph.D., Computational Biology, Applied Mathematics and Statistics — **8/2013–12/2020**
Stony Brook University, Stony Brook, NY

M.S., Systems Theory — **9/2010–7/2013**
University of Chinese Academy of Sciences, Beijing, China

B.S., Mathematics and Applied Mathematics — **9/2006–7/2010**
Beijing Normal University, Beijing, China

PRESENTATIONS

Fitness Estimation of Pooled Amplicon Sequencing Studies (Plenary Talk) — **8/2018**
Yeast Genetics Meeting, Stanford CA

PUBLICATIONS

[1] T Matsui, P-H Hung, H Mei, X Liu, **F Li**, J Collins, W Li, D Miller, N Wilson, E Toro, G J Taghon, G Sherlock, S Levy. High-throughput DNA engineering by mating bacteria. *Preprint* (2024).

[2] **F Li**, A Mahadevan, G Sherlock. An improved algorithm for inferring mutational parameters from Bar-seq evolution experiments. *BMC Genomics* 24, 246 (2023).

[3] **F Li***, J Tarkington*, G Sherlock. Fit-Seq-2.0: an improved software for high throughput fitness measurements using pooled competition assays. *Journal of Molecular Evolution* 91, 334–344 (2023).

[4] G Avecilla, J N Chuong, **F Li**, G Sherlock, D Gresham, Y Ram. Neural networks enable efficient and accurate simulation-based inference of evolutionary parameters from adaptation dynamics. *PLoS Biology* 20, e3001633 (2022).

[5] Z Liu, D Miller, **F Li**, X Liu, S Levy. A large accessory protein interactome is rewired across environments. *eLife* 9, e62365 (2020).

[6] X Liu, Z Liu, A K Dziulko, **F Li**, D Miller, R D Morabito, D Francois, S Levy. iSeq 2.0: a modular and interchangeable toolkit for interaction screening in yeast. *Cell Systems* 8, 338–344 (2019).

[7] **F Li**, M L Salit, S Levy. Unbiased fitness estimation of pooled barcode or amplicon sequencing studies. *Cell Systems* 7, 521–525 (2018).

[8] I Frumkin, D Schirman, A Rotman, **F Li**, L Zahavi, E Mordret, O Asraf, S Wu, S Levy, Y Pilpel. Gene architectures that minimize cost of gene expression. *Molecular Cell* 65, 142–153 (2017).

[9] Y Chen, W Xiong, **F Li**. Convergence of infinite products of stochastic matrices: a graphical decomposition criterion. *IEEE Transactions on Automatic Control* 61, 3599–3605 (2016).

[10] Y Chen, **F Li**, B Hou, S Tan, H Zhu. Convergence analysis of discrete-time consensus algorithm with both self and transmission delays. *Journal of the Franklin Institute* 353, 2467–2481 (2016).

[11] **F Li**, Y Chen, J Lü, D Hill. Cluster consensus of Boolean multi-agent systems. *2013 9th Asian Control Conference (ASCC)* (2013).

[12] Y Chen, W Yu, **F Li**, S Feng. Synchronization of complex networks with impulsive control and disconnected topology. *IEEE Transactions on Circuits and Systems II: Express Briefs* 60, 292–296 (2013).