

Fangfei Li

✉ fangfeili0525@gmail.com

☎ 631 833-7934

📍 Westampton, NJ

🌐 <https://fangfeili05.github.io/>

🐙 <https://github.com/FangfeiLi05/>

🌐 <https://www.linkedin.com/in/fangfeili/>

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

SUMMARY & SKILLS

• **Ph.D. in Computational Biology, Applied Mathematics & Statistics** | 2 yrs postdoc + 2 yrs biotech startup + 3 yrs wet-lab (synthetic barcoding-based *in vivo* yeast lineage tracing, molecular biology) • **Skills:** data analysis & visualization, machine learning (generative learning), bioinformatics, Bayesian optimization, Python (NumPy, Matplotlib, tkinter, Flet), Git, SQL, API, MATLAB, 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
 - XCS236 Deep Generative Models: [Certificate](#)
 - XCS231N Deep Learning for Computer Vision: [Certificate](#)
- DeepLearning.AI (Coursera) – 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 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.
- Developed an optimization algorithm to segment DNA sequences into overlapping fragments that minimize overlap-region scores (e.g., undesirable DNA structural features) under fixed or ranged constraints on fragment count and fragment/overlap length.
- Improved a fitness estimation algorithm and developed a Python pipeline ([FitSeq2](#)), an enhanced version of [Fit-Seq](#).

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).