

Li Tai Fang, Ph.D.

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Summary:

- Expert bioinformatician with extensive expertise in high-throughput next generation sequencing (NGS)
- Authored/co-authored 20+ peer-reviewed research articles and 2 book chapters in multiple disciplines
- Invited speaker at
 - 2021: MCBIOS & MAQC Joint Annual Meeting (1st place research award, published in Nat Biotechnol)
 - 2019: Genome in a Bottle Workshop, Corporate Workshop at AMP Annual Meeting
 - 2018: AACR Annual Meeting, AMP Reference Materials Forum, NIH Mutation Detection Symposium
 - 2017: SEQC2 Somatic Mutation Workshop (organized & chaired), Roche Cancer Early Detection Panel
 - 2016: Bio-IT World Conference, Roche R&D ExpertFora, Roche DISRUPT Innovation Mixer

Professional Experience:

Endpoint Health, Inc.

Staff Scientist, Bioinformatics

Palo Alto, CA
October, 2020 – Present

- Develop supervised machine learning methods for biomarker discovery in immune diseases

Roche Sequencing Solutions (Bina Technologies Inc. prior to Dec. 2014)

Staff Scientist, Bioinformatics

Senior Scientist, Bioinformatics

Scientist, Bioinformatics

Belmont, CA
March, 2018 – September, 2020
September, 2015 – March, 2018
March, 2014 – August, 2015

- Led SEQC2 working group to establish somatic mutation reference call set for cancer reference samples
- Led the Data Integration Group for the MDIC Somatic Reference Samples project
- Led Bina Team to compete in the ICGC-TCGA DREAM Somatic Mutation Calling Challenge:
 - **placed #1 and #2** in Stage 5 of the INDEL and SNV challenges
- Developed SomaticSeq: the machine learning mutation detection pipeline (paper was Editor's Pick)
- Developed key SNV and CNV algorithms incorporated in the Roche's AVENIO ctDNA RUO product
- Developed algorithm to detect chimeric extrachromosomal circular DNA (eccDNA)
- Completed somatic SV detection feature set as a part of the \$7.5 million post-acquisition milestone
- Designed the workflow for the 1000 TCGA Exome re-analysis project on Cancer Genomics Cloud
- Core member of the Roche Sequencing's Global Career Opportunities and Development Team

Oxbridge Biotech Roundtable – San Francisco Bay Chapter

Events Director, Voluntary (25K worldwide and 2,000 local members)

San Francisco, CA
May, 2013 – May, 2014

- Organized roundtable discussions, workshops, and debates on the 1) Commercial potential of big data in biotech, 2) Academic-industry partnerships, 3) Gene patents, 4) Genetically modified food, 5) Science writing, 6) FDA policy on direct-to-consumer genetics test, and 7) Data reproducibility.
- Wrote background articles for promotional purposes, and build rapport with invited speakers
- Recruited 5 mentors for GSK/Roche/McKinsey-sponsored \$150K OneStart Business Plan Competition

UCSF Department of Surgery

Bioinformatician, Postdoctoral

San Francisco, CA
March, 2011 – February, 2014

- Implemented the very first Next Generation Sequencing analysis pipeline at Thoracic Oncology Lab
- Co-authored 6 papers, and administered a 56-core computing cluster and group website
- Trained lab technicians linux system and bash scripting to operate the tools I created
- Won \$12,500 grant as a team in the "Idea to IPO 2012" bioentrepreneurship course sponsored by Burrill & Co., by building a business plan and pitching it to the venture capitalists (2 teams awarded)

The Hebrew University of Jerusalem

Theoretical Biophysicist, Postdoctoral

Jerusalem, Israel

March, 2010 – September, 2010

- Developed an RNA folding model of successively finding the longest complementary sequences
- Solved a scaling law between RNA's 3D size and its linear length using ideal branched polymer model

Education:

University of California, Los Angeles

Ph.D. Biochemistry

Los Angeles, CA

September, 2003 – March, 2010

Had 5 years of hands-on wet lab biochemistry, plus 2+ years of computational/theoretical experience

- Won the \$1000 Physical Chemistry Research Award as a Biochemistry PhD Student in 2009
- The **only** student in UCLA Biochemistry during my time to publish a **single-authored** research paper
- On my own initiative, developed a combinatorics model to calculate the 5'-to-3' distance of RNA
- Taught 9 classes in Statistical Mechanics, Quantum Mechanics, Thermodynamics, and Biochemistry
- Dissertation: The Physics of DNA, RNA, and RNA-like Polymers
 - ★ Discovered an entropic force involved in the release of virus genome
 - ★ Measured the bending and electrostatic energies of DNA in viruses
 - ★ Contributed to the understanding of energies and physical forces inside viruses, relevant to genetic engineering efforts using viruses as delivery vehicles

University of California, Berkeley

B.A. Molecular and Cell Biology

Berkeley, CA

August, 1999 – May, 2003

- GRE scores: 800 in quantitative; 770 in analytical and logical reasoning (out of 800)
- SAT II scores: 800 in math; 730 in physics

Selected Publications:

- **Fang LT**, Zhu B, Zhao Y, Chen W, Yang Z, Kerrigan L, Langenbach K, de Mars M, Lu C, Idler K, *et al.* Establishing community reference samples, data and call sets for benchmarking cancer mutation detection using whole-genome sequencing. *Nature Biotechnology*. 2021;39(9):1151-1160. (Commentary by FDA acting commissioner Janet Woodcock)
- **Fang LT**. SomaticSeq: an ensemble and machine learning method to detect somatic mutations. *In: Boegel S. (eds) Bioinformatics for Cancer Immunotherapy. Methods in Molecular Biology*. 2020;2120(1):47-70.
- **Fang LT**, Afshar PT, Chhibber A, Mohiyuddin M, Fan Y, Mu JC, Gibeling G, Barr S, Asadi NB, Gerstein MB, *et al.* An ensemble approach to accurately detect somatic mutations using SomaticSeq. *Genome Biology*. 2015;16(1):197. (Editor's Pick)
- **Fang LT**, Lee S, Choi H, Kim HK, Jew G, Kang HC, Chen L, Jablons D, Kim I-J. Comprehensive genomic analyses of a metastatic colon cancer to the lung by whole exome sequencing and gene expression analysis. *International Journal of Oncology*. 2014;44(1):211221.
- **Fang LT**. The end-to-end distance of RNA as a randomly self-paired polymer. *Journal of Theoretical Biology*. 2011;280(1):101107. (Sole Author)
- **Fang LT**, Gelbart WM, Ben-Shaul A. The size of RNA as an ideal branched polymer. *The Journal of Chemical Physics*. 2011;135(15):155105.
- **Fang LT**, Yoffe AM, Gelbart WM, Ben-Shaul A. A sequential folding model predicts length-independent secondary structure properties of long ssRNA. *The Journal of Physical Chemistry B*. 2011;115(12):31933199.