

LI TAI FANG, PH.D. (U.S. CITIZEN)

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SUMMARY OF ACCOMPLISHMENTS:

- Expert bioinformaticist with extensive experience in cancer informatics and project management
- Leading the somatic SNV/indel analysis team for FDA's SEQC2 Somatic Mutation Working Group
- Steering Committee Member of the Massive Analysis and Quality Control Society (MAQC)
- Authored/co-authored 16 peer-reviewed research articles across multiple disciplines
- Completed The Leadership Edge's From The Laboratory To Leadership program
- Speaker at 2017 Roche Sequencing Early Cancer Detection Panel, 2017 FDA SEQC2 Somatic Mutation Workshop, 2016 Roche R&D ExpertFora, 2016 Roche DISRUPT Innovation Mixer, 2016 Bio-IT World Conference, and 2014 California Alumni Healthcare Career Panel

PROFESSIONAL EXPERIENCE:

Bina Technologies (acquired by Roche in 12/2014)

Sr. Bioinformatics Scientist
Bioinformatics Scientist

Belmont, CA
September, 2015 – Present
March, 2014 – August, 2015

- Lead developer of SomaticSeq: the machine learning cancer analysis pipeline (paper is editor's pick)
- Led Bina team's participation in the ICGC-TCGA DREAM Somatic Mutation Calling Challenge:
 - placed #1 and #2 in Stage 5 of the INDEL and SNV challenges
- Developed key SNV and CNV algorithms incorporated in the Roche's AVENIO ctDNA RUO product
- Completed the SV detection feature sets as a part of the \$7.5 million post-acquisition milestone payment
- Designed the workflow for the 1000 TCGA Exome re-analysis project on Cancer Genomics Cloud
- Manage data analysis collaboration projects with internal research groups and external customers
- Write white papers, official blogs, peer-reviewed articles, and give live online seminars and talks
- Advocate meticulous documentation practices in the informatics teams using internal wikispaces

UCSF Medical Center

Bioinformaticist, Postdoctoral

San Francisco, CA
March, 2011 – Present

- Implemented the very first Next Generation Sequencing analysis pipeline at Thoracic Oncology Lab
- Created internal data analysis software for Gene Expression and Next Generation Sequencing
- Co-authored 5 papers, managed a 56-core computing cluster, group website *kimlab.surgery.ucsf.edu*
- Represented and spoke for UCSF Applied Genomics Lab at the 2012 Stanford Lung Cancer Symposium
- Trained lab technicians Linux commands, Bash scripting, computer algorithms, and 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)

Oxbridge Biotech Roundtable – Bay Chapter

Events Director (25K+ members worldwide, including 2,000 local)

San Francisco Bay Area, CA
May, 2013 – June, 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 DTC Genetics Test, and 7. Data Reproducibility.
- Wrote background articles for marketing purposes, and build rapport with invited speakers
- Recruited mentors for GSK/Roche/McKinsey-sponsored \$150K OneStart Business Plan Competition

SCIMALS, West Coast Team

Investment Analyst

San Francisco, CA
June, 2013 – Present

- Completed a Next Generation Sequencing & Genomic Medicine market analysis project for the venture arm of a hospital network, by leading a team of 5 scientists across different geographical locations

- Prepared project proposals and progress reports, and attended conference calls with venture firms

Vicaya Energy

Policy & Data Researcher

Los Angeles, CA

September, 2010 – March, 2011

- Consulted a start-up solar energy company on scientific and science policy issues

The Hebrew University of Jerusalem

Theoretical Biophysicist, Postdoctoral

Jerusalem, Israel

March, 2010 – September, 2010

- Developed and implemented a mathematical model of RNA in 6 months, and published the results
- Discovered and formulated a scaling relationship between RNA's 3D size and its linear length

EDUCATION:

University of California, Los Angeles

Ph.D. Biochemistry

Los Angeles, CA

September, 2003 – March, 2010

Conducted both experimental and theoretical research on viruses and their genetic materials.

- Won the Departmental Physical Chemistry Research Award as a Biochemistry Graduate Student
- Thesis Advisors: Professors William M. Gelbart and Charles M. Knobler
- Taught 9 classes in Statistical Mechanics, Quantum Mechanics, Thermodynamics, and Biochemistry
- Dissertation Title: The Physics of DNA, RNA, and RNA-like Polymers
 - ★ On my own initiative, developed a mathematical model to calculate the 5' to 3' distance of RNA
 - ★ Discovered an additional 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 (out of 800)
- SAT scores: 800 in math; 730 in physics

PEER-REVIEWED PUBLICATIONS:

- Pedro Mendez, **Li Tai Fang**, David Jablons, and Il-Jin Kim. Systematic Comparison of Two Whole-Genome Amplification Methods for Targeted Next-Generation Sequencing Using Frozen and FFPE Normal and Cancer Tissues. *Scientific Reports*, 7:4055. (2017)
- Bayo Lau, Marghoob Mohiyuddin, John C. Mu, **Li Tai Fang**, Narges Bani Asadi, Carolina Dallett, and Hugo Y.K. Lam. LongISLND: In silico Sequencing of Lengthy and Noisy Datatypes. *Bioinformatics*, 32(24):3829-3832. (2016)
- Hio Chung Kang, Hong Kwan Kim, Sharon Lee, Pedro Mendez, James Kim, Gavitt Woodard, Jun-Hee Yoon, Kuang-Yu Jen, **Li Tai Fang**, Kirk Jones, David Jablons, and Il-Jin Kim. Whole Exome and Targeted Deep Sequencing Identify Genome-wide Allelic Loss and Frequent SETDB1 Mutations in Malignant Pleural Mesotheliomas. *Oncotarget*, 7(7):8321-8331. (2016)
- Li Tai Fang**, Pegah Tootoonchi Afshar, Aparna Chhibber, Marghoob Mohiyuddin, Yu Fan, John C. Mu, Greg Gibeling, Sharon Barr, Narges Bani Asadi, Mark B. Gerstein, Daniel C. Koboldt, Wenyi Wang, Wing H. Wong, and Hugo Y.K. Lam. An Ensemble Approach to Accurately Detect Somatic Mutations Using SomaticSeq. *Genome Biology*, 16(1):197. (2015) ** Editor's Pick **
- Li Tai Fang**, Sharon Lee, Helen Choi, Hong Kwan Kim, Gregory Jew, Hio Chung Kang, Lin Chen, David Jablons, and Il-Jin Kim. Comprehensive Genomic Analyses of a Metastatic Colon Cancer to the Lung by Whole Exome Sequencing and Gene Expression Analysis. *International Journal of Oncology*, 44(1): 211-221. (2014)

11. Shulin Zhang, Yi-Lin Yang, Yucheng Wang, Bin You, Yuyuan Dai, Geraldine Chan, David Hsieh, Il-Jin Kim, **Li Tai Fang**, Alfred Au, Hubert J. Stoppler, Zhidong Xu, David M. Jablons, and Liang You. CK2 α , Over-expressed in Human Malignant Pleural Mesothelioma, Regulates the Hedgehog Signaling Pathway in Mesothelioma Cells. *Journal of Experimental & Clinical Cancer Research*, 33:93. (2014)
10. Yi-Lin Yang, Ming-Szu Hung, Yang Wang, Jian Ni, Jian-Hua Mao, David Hsieh, Alfred Au, Atul Kumar, David Quigley, **Li Tai Fang**, Che-Chung Yeh, Zhidong Xu, David M. Jablons, and Liang You. Lung Tumorigenesis in a Conditional Cul4A Transgenic Mouse Model. *The Journal of Pathology*, 233(2): 113-123. (2014)
9. Genevieve Bosco-Clement, Fang Zhang, Zhao Chen, Hai-Meng Zhou, Hui Li, Iwao Mikami, Tomomi Hirata, Adam Yagui-Beltran, Natalie Lui, Hanh T. Do, Tiffany Cheng, Hsin-Hui Tseng, Helen Choi, **Li Tai Fang**, Il-Jin Kim, Dongsheng Yue, Changli Wang, Qingfeng Zheng, Naoaki Fujii, Michael Mann, David Jablons, and Biao He. Targeting Gli Transcription Activation by Small Molecule Suppresses Tumor Growth. *Oncogene*, 33(16):2087-2097. (2013)
8. Michael Mulvihill, Yong-Won Kwon, Sharon Lee, **Li Tai Fang**, Helen Choi, Roshni Ray, Hio Chung Kang, Jian-Hua Mao, David Jablons, and Il-Jin Kim. Gremlin is Overexpressed in Lung Adenocarcinoma and Increases Cell Growth and Proliferation in Normal Lung Cells. *PLoS ONE*, 7(8): e42264. (2012)
7. James Wan Soo Kim, Sharon Lee, Natalie Lui, Helen Choi, Michael Mulvihill, **Li Tai Fang**, Hio Chung Kang, Yong-Won Kwon, David Jablons, and Il-Jin Kim. A Somatic TSHR Mutation in a Patient with Lung Adenocarcinoma with Bronchioloalveolar Carcinoma, Coronary Artery Disease and Severe Chronic Obstructive Pulmonary Disease. *Oncology Reports*, 28(4): 1225-1230. (2012)
6. **Li Tai Fang**, William M. Gelbart, and Avinoam Ben-Shaul. The Size of RNA as an Ideal Branched Polymer. *Journal of Chemical Physics*, 135(15): 155105. (2011)
5. **Li Tai Fang**. The End-to-End Distance of RNA as a Randomly Self-Paired Polymer. *Journal of Theoretical Biology*, 280(1): 101-107. (2011)
4. **Li Tai Fang**, Aron M. Yoffe, William M. Gelbart, and Avinoam Ben-Shaul. A Sequential Folding Model Predicts Length-Independent Secondary Structure Properties of Long ssRNA. *Journal of Physical Chemistry B*, 115(12): 3193-3199. (2011)
3. Xiangyun Qiu, Donald C. Rau, V. Adrian Parsegian, **Li Tai Fang**, Charles M. Knobler, and William M. Gelbart. Salt-Dependent DNA-DNA Spacings in Intact Bacteriophage λ Reflect Relative Importance of DNA Self-Repulsion and Bending Energies. *Physical Review Letters*, 106(2): 028102. (2011)
2. Peter Prinsen, **Li Tai Fang**, Aron M. Yoffe, Charles M. Knobler, and William M. Gelbart. The Force Acting on a Polymer Partially Confined in a Tube. *Journal of Physical Chemistry B*, 113(12): 3873-3879, (2009)
1. Alex Evilevitch, **Li Tai Fang**, Aron M. Yoffe, Martin Castelnovo, Donald C. Rau, V. Adrian Parsegian, William M. Gelbart, and Charles M. Knobler. Effects of Salt Concentrations and Bending Energy on the Extent of Ejection of Phage Genomes. *Biophysical Journal*, 94(3): 1110-20, (2008)

CONFERENCE PRESENTATIONS:

10. OnkoInsight: an End-to-End Cancer Informatics Pipeline to Generate Insights from Large Sequencing Datasets. *AACR Annual Meeting. Washington DC. 2017*
9. SomaticSeq: an Ensemble Approach to Accurately Detect Somatic Mutations. *Oral Presentation for OncoSeq ExpertFora. Roche Diagnostics R&D Fair. Burlingame, CA. 2016*
8. An Ensemble Approach with Machine Learning to Detect Cancer Variants. *Oral Presentation for Clinical Genomics and Cancer Informatics. Bio-IT World Conference & Expo. Boston, MA. 2016*
7. A Comprehensive SomaticSeq Workflow to Prioritize Biologically Relevant Somatic Mutations in Cancer. *American Society of Human Genetics. Baltimore, MD. 2015*
6. SomaticSeq: A Machine Learning Approach to Accurately Detect Somatic Mutations. *The Clinical Genome Conference. San Francisco, CA. 2015*
5. An Ensemble Approach to Accurately Detect Somatic Mutations via Adaptive Boosting. *AACR Annual Meeting. Philadelphia, PA. Late-Breaking Abstract, 2015*

4. Applying Logistic Regression to Combine Multiple Somatic Mutation Call Sets for Increased Overall Prediction Accuracy. *RECOMB/ISCB Conference. San Diego, CA. 2014*
3. An Accurate and Integrative Computational Approach for Cancer Eeome Studies. *American Society of Human Genetics. San Diego, CA. 2014*
2. Addressing the Data Deluge: Accurate, Scalable, and Easy-to-Use NGS Data Analysis. *Beyond the Genome: Cancer Genomes, Harvard Medical School, MA. 2014*
1. Integrative Genomics Approaches for Personalized Medicine in Lung Cancer. *Oral Presentation. Lung Cancer Symposium. Stanford University, CA. 2012*

NON PEER-REVIEWED PUBLICATIONS:

8. SomaticSeq: An ensemble and machine learning approach to accurately detect somatic mutations. *Live Webinar, (12/2/2015)*
7. Bina's official blogs: <http://blog.bina.com/read/author/li-tai-fang>
6. Bina Cancer White Paper. *Released in 2014 during ASHG Conference*
5. This House Believes the FDA Should Deregulate Direct-to-Consumer Genetic Testing. *Oxbridge Biotech Roundtable, (4/7/2014)*
4. Genetically Modified Organisms: What's on your plate? *Oxbridge Biotech Roundtable, (12/2/2013)*
3. This House Believes Genes Should Be Patented. *Oxbridge Biotech Roundtable, (10/7/2013)*
2. Marriage of Convenience? How Academic-Pharma Partnerships are Fueling Drug Discovery. *Oxbridge Biotech Roundtable, (8/12/2013)*
1. Student Groups Holding Networking Event – Come Join Us at Mission Bay on February 28. *Synapse, The UCSF Student Newspaper, (2/23/2012)*