

Curriculum Vitae : Peng Jiang

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Homepage: <https://scholar.harvard.edu/pengjiang>

Experience

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| Start on | Earl Stadtman Tenure-track Investigator |
| 07/01/2019 | National Cancer Institute , National Institutes of Health |
| | • Cancer Data Science Laboratory, Center for Cancer Research |
| 09/13/2013 - | Postdoctoral Research Fellow |
| Current | Dana Farber Cancer Institute & |
| | Harvard T.H.Chan School of Public Health |
| | • Mentor: X. Shirley Liu |

Education

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|--------------|---|
| 09/01/2009 - | Ph.D in Computer Science, Princeton University |
| 08/31/2013 | • Advisor: Mona Singh, Hilary Collier |
| | • Thesis: Combinatorial code analysis for understanding biological regulation |
| | • Committee: Mona Singh, Hilary Collier, Olga Troyanskaya |
| | John Storey, Gertrud (Trudi) M. Schupbach |
| 09/01/2007 - | M.A in Computer science, Princeton University |
| 08/31/2009 | • GPA: 4.0/4.0 |
| 09/01/2003 - | B.E in Computer Science, Tsinghua University |
| 07/01/2007 | • Graduated with highest honors. GPA 92.6/100. Rank 1st out of 165. |

Grant

- **K99 Pathway to Independence Award by National Cancer Institute**
Period: 07/10/2018 - 06/31/2019 Grant Number: K99 CA218900-01
Title: Data-driven approaches to identify biomarkers and regulators of cancer drug resistance
- **DFCI-NOVARTIS Drug Discovery Program Award**
Period: 01/01/2018 - 12/31/2020
Title: Targeting of Epigenetic Regulators of T cell Dysfunction for Cancer Immunotherapy

Publications as first author (*co-first author)

- **Peng Jiang***, Shengqing Gu*, Deng Pan*, Jingxin Fu, Ziyi Li, Xia Bu, Bo Li, Jun Liu, Gordon Freeman, Myles Brown, Kai Wucherpfennig, X. Shirley Liu. Signatures of T-cell dysfunction and exclusion predict cancer immunotherapy response. *Nature Medicine* (2018). 24(10):1550-1558. (Selected by Faculty of 1000)
- **Peng Jiang**, Winston Lee, Xujuan Li, Carl Johnson, Jun S. Liu, Myles Brown, Jon C. Aster, X. Shirley Liu. Genome-scale signatures of gene interaction from compound screens predict clinical efficacy of targeted cancer therapies. *Cell Systems* (2018). S2405-4712.
- Deng Pan*, Aya Kobayashi*, **Peng Jiang***, Lucas Ferrari de Andrade, Rong En Tay, Adrienne Luoma, Daphne Tsoucas, Xintao Qiu, Klothilda Lim, Prakash Rao, Henry W. Long, Guo-Cheng Yuan, John Doench, Myles Brown, X. Shirley Liu, Kai W. Wucherpfennig. A Major Chromatin Regulator Determines Resistance of Tumor Cells to T cell Mediated Killing. *Science* (2018). 359(6377):770-775. (Selected by Faculty of 1000)
- **Peng Jiang**, William R. Sellers, X. Shirley Liu. Data-driven approaches to model cancer drug response and resistance. *Annual Review of Biomedical Data Science* (2018) Inaugural volume.

- **Peng Jiang**, Hongfang Wang, Wei Li, Chongzhi Zang, Bo Li, Yinling Wong, Cliff Meyer, Jun S. Liu, Jon C. Aster, X. Shirley Liu. Network analysis of gene essentiality in functional genomics experiments. *Genome Biology* (2015). 16(1):239.
- **Peng Jiang**, Matthew Freedman, Jun Liu, X. Shirley Liu. Inference of transcriptional regulation in cancers. *Proc Natl Acad Sci USA* (2015). 112(25):7731-6.
- **Peng Jiang**, X. Shirley Liu. Big data mining yields novel insights on cancer. *Nature Genetics* (2015). 47(2):103-4
- **Peng Jiang**, Mona Singh. CCAT: Combinatorial Code Analysis Tool for Transcriptional Regulation. *Nucleic Acids Research* (2014). 42(5):2833-47
- **Peng Jiang**, Mona Singh, Hilary Collier. Computational assessment of the cooperativity between RNA binding proteins and microRNAs in transcript decay. *PLoS Computational Biology* (2013). 9(5):e1003075. (Selected by Faculty of 1000)
- **Peng Jiang**, Hilary Collier. Functional Interactions Between microRNAs and RNA Binding Proteins. *MicroRNA* (2012). 1:70-79.
- **Peng Jiang**, Mona Singh. SPICi: a fast clustering algorithm for large biological networks. *Bioinformatics* (2010). 26(8):1105-11.
- Jing Zhang*, Donghoon Lee*, Vineet Dhiman*, **Peng Jiang***, X. Shirley Liu, Kevin White, Mark Gerstein and others. An integrative ENCODE resource for cancer: interpreting non-coding mutations and gene regulation. *Nature* in Revision for ENCODE 3 release.

Publications as co-author

- Xihao Hu, Jian Zhang, Jin Wang, Jingxin Fu, Taiwen Li, Xiaoqi Zheng, Binbin Wang, Shengqing Gu, **Peng Jiang**, Jingyu Fan, Xiaomin Ying, Jing Zhang, Michael C. Carroll, Kai W. Wucherpfennig, Nir Hacohen, Fan Zhang, Peng Zhang, Jun S. Liu, Bo Li, X. Shirley Liu. Landscape of B cell immunity and related immune evasion in human cancers. *Nature Genetics* (2019). 51: 560-567.
- Tengfei Xiao, Wei Li, Xiaoqing Wang, Han Xu, Jixin Yang, Qiu Wu, Ying Huang, Joseph Geradts, **Peng Jiang**, Teng Fei, David Chi, Chongzhi Zang, Qi Liao, Jonathan Rennhack, Eran Andrechek, Nanlin Li, Simone Detre, Mitchell Dowsett, Rinath M. Jeselsohn, X. Shirley Liu, Myles Brown. Estrogen-regulated feedback loop limits the efficacy of estrogen receptor-targeted breast cancer therapy. *Proc Natl Acad Sci USA* (2018). 115(31):7869-7878.
- Chenhao Chen, Tengfei Xiao, Han Xu, **Peng Jiang**, Cliff Meyer, Wei Li, Myles Brown, X. Shirley Liu. Improved design and analysis of CRISPR knockout screens. *Bioinformatics* (2018). 34(23):4095-4101.
- Shenglin Mei , Clifford Meyer, Rongbin Zheng, Qian Qin, Qiu Wu, **Peng Jiang**, Bo Li, Xiaohui Shi, Binbin Wang, Jingyu Fan, Celina Shih, Myles Brown, X. Shirley Liu, Chongzhi Zang. Cistrome Cancer: a web resource for integrative gene regulation modeling in cancer. *Cancer Research* (2017). 77(21):e19-22
- Mulin J. Li, Jian Zhang, Qian Liang, Chenghao Xuan, Jiexing Wu, **Peng Jiang**, Wei Li, Yun Zhu, Panwen Wang, Daniel Fernandez, Yujun Shen, Yiwen Chen, Jean-Pierre A. Kocher, Ying Yu, Pak C. Sham, Junwen Wang, Jun S. Liu, Shirley. Liu. Exploring genetic associations with ceRNA regulation in the human genome. *Nucleic Acids Research* (2017). 45(10):5653-5665
- Bo Li, Eric Severson, Jean-Christophe Pignon, Haoquan Zhao, Taiwen Li, Jesse Novak, **Peng Jiang**, Hui Shen, Jon C. Aster, Scott Rodig, Sabina Signoretti, Jun S. Liu, X. Shirley Liu. Comprehensive analyses of tumor immunity: implications for cancer immunotherapy. *Genome Biology* (2016). 17:174
- Xiaoqi Zheng, Qian Zhao, Hua-Jun Wu, Wei Li, Haiyun Wang, Clifford A Meyer, Qian Alvin Qin, Han Xu, Chongzhi Zang, **Peng Jiang**, Fuqiang Li, Yong Hou, Jianxing He, Jun Wang, Jun Wang, Peng Zhang, Yong Zhang, X. Shirley Liu. MethylPurify: tumor purity deconvolution and differential methylation detection from single tumor DNA methylomes. *Genome Biology* (2014). 15(8):419

- Attilio Pane, **Peng Jiang**, Yanling Zhao, Mona Singh, Trudi Schupbach. The Cutoff protein regulates piRNA cluster expression and piRNA production in the Drosophila germline. *EMBO J* (2011). 30(22):4601-15.

Honors and Awards

- K99 Pathway to Independence Award by National Cancer Institute (2018).
- Scholar-in-Training Award by American Association for Cancer Research (2018).
- Poster Award in Scientific Retreat of Center for Functional Cancer Epigenetics (2015).
- Outstanding Reviewer Award by Elsevier (2015)
- Princeton International Chinese Music Festival Competition (2012).
1st prize. Featured performance in Carnegie Recital Hall.
- Grand Prix US National Taekwondo Tournament (2008).
Bronze medal in Middle weight.
- Summa cum laude, Highest departmental Honors in Computer Science, Tsinghua University (2007).
- Outstanding Chinese Student Award (2005). Sponsored by Hewlett-Packard.

Talks and Posters

- Cold Spring Harbor Asia: Systems Biology of Gene Regulation & Genome Editing (10/09/2018)
Short talk: Data-driven inference of gene regulators
- SAPA Annual Conference: Bridging US & China's Pharmaceutical Industries (10/06/2018)
Invited talk: Big Data Approaches to Model Cancer Therapy Response and Resistance
- Department of Biomedical Informatics, Harvard Medical School (09/18/2018)
Invited talk: Big Data Approaches to Model Cancer Therapy Response and Resistance
- Computational Oncology Seminar, Memorial Sloan Kettering Cancer Center (07/23/2018)
Invited talk: Big Data Approaches to Model Cancer Therapy Response and Resistance
- Cell Circuits & Epigenomics Seminar, Broad Institute (07/02/2018)
Invited talk: Big Data Approaches to Model the Cancer Immunotherapy Response and Resistance
- Immunobiology Seminar, Yale University (06/08/2018)
Invited talk: Big Data Approaches to Model the Cancer Immunotherapy Response and Resistance
- Computational Biology Seminar, Yale University (04/25/2018)
Invited talk: Big-data Approaches to Model Cancer Therapy Response and Resistance
- DahShu virtual journal club (03/30/2018)
Invited talk: Genome-scale signatures of gene interaction from compound screens predict clinical efficacy of targeted cancer therapies
- AACR Conference on Tumor Immunology and Immunotherapy (10/01-03/2017)
Poster: Digital signatures of T cell dysfunction and exclusion predict immunotherapy response
- Center for Computational Biology and Bioinformatics, Indiana University (09/25/2017)
Invited talk: Digital signatures of T cell dysfunction and exclusion predict immunotherapy response
- Annual Retreat at DFCI Postdocs and Graduate Students Association (09/20/2017)
Talk: Digital signatures of T cell dysfunction and exclusion predict immunotherapy response
- Rising Stars in Data Science Symposium, University of Chicago (09/13/2017)
Invited talk: Data driven approaches in modeling cancer drug resistance
- Center for Functional Cancer Epigenetics Scientific Retreat (07/10/2017)
Talk: Digital signatures of T cell dysfunction and exclusion predict immunotherapy response

- The Challenges of Optimising Immuno and Targeted Therapies from Cancer Biology to the Clinic, EACR at Italy (06/24-27/2017)
Poster: Inference of gene signatures in response and resistance to targeted and immunotherapy
- Refining Precision Therapeutics using Exceptional Response and Resistance, National Cancer Institute (05/11-12/2017)
Poster: Reliable inference of gene signatures in response and resistance to targeted and immunotherapy
- Brain Lunch seminar at Dana Farber Cancer Institute (01/13/2017)
Invited Talk: Reliable Inference of genes associated with resistance to targeted cancer therapy
- PQG Working Group Series at Harvard School of Public Health (09/27/2016)
Invited Talk: Inference of genes associated with resistance to targeted cancer therapy
- Department of Computing and Mathematical Sciences, Caltech (01/11/2016)
Invited Talk: Data-Driven Computational Approach to Understand Cancer Progression and Drug Resistance
- H3 BioMedicine Company (12/03/2015)
Invited Talk: Network analysis of gene essentiality in functional genomics experiments
- CMSA Colloquium at Department of Mathematics, Harvard University (11/18/2015)
Invited Talk: Inference of regulatory abnormality in cancers from heterogeneous public data
- AACR-NCI-EORTC International Conference (11/05-09/2015)
Poster: Network analysis of gene essentiality in CRISPR screens
- PQG Working Group Series at Harvard School of Public Health (10/06/2015)
Invited Talk: Inference of regulatory abnormality in cancers from heterogeneous public data
- The 4th EITA Young Investigator Conference at MIT (08/06-07/2015)
Invited Talk: Inference of transcriptional regulation in cancers
- Center for Functional Cancer Epigenetics Scientific Retreat (08/02/2015)
Poster Award: Network analysis of gene essentiality in CRISPR screens
- Informatics Technology for Cancer Research Annual Meeting 2015 (05/27-28/2015)
Talk and Poster: Developing Informatics Technologies to Model Cancer Gene Regulation
- ENCODE Consortium Meeting 2015 (03/14-17/2015)
Talk and Poster: Inference of transcriptional regulation in cancers
- Center for Functional Cancer Epigenetics Scientific Retreat (07/01/2014)
Talk: The transcriptional and post-transcriptional regulation components in cancer gene expression patterns
- Cell Symposia: Regulatory RNAs (10/10-12/2011)
Poster: RNA binding proteins and microRNAs cooperate to affect transcript decay

Teaching Activities

- STAT 316 Big data statistics in genomic and genetic research (2017), Harvard University
lecture 6: Compound screen and integrative genomics
- STAT 115 Introduction to Computational Biology and Bioinformatics (2017), Harvard University.
lecture 9: Feature selection and regression
lecture 12: Targeted therapy, High throughput screening
- IDS.S30 Statistical Modeling and Machine Learning: with applications in biology and medicine (2016), Massachusetts Institute of Technology
lecture 6: Statistical methods in studying resistance to targeted cancer therapy
- STAT 115 Introduction to Computational Biology and Bioinformatics (2016), Harvard University.
lecture 7: Feature selection and regression
lecture 11: Targeted therapy, High throughput screening

- COS 333 Advanced Programming Techniques (2009), Princeton University.
Teaching Assistant
- COS 109 Computers in Our World (2008), Princeton University.
Teaching Assistant

Mentees

- Perry Palmedo, Rotation student from 09/2014 to 12/2014, Harvard University
- Xujuan Li, Master student, 2014 to 2016, Tongji University, Shanghai China
- Xiaohui Shi, Master student, 2014 to 2016, Tongji University, Shanghai China
- Anthony Hou, Undergraduate student, 2016, Harvard University
- Shayna Stein, Rotation student from 08/2017 to 12/2017, Harvard University
- Jingxin Fu, PhD Student, Current, Tongji University, Shanghai China
- Wubin Zhang, PhD student, Current, Tongji University, Shanghai China
- Binbin Wang, PhD student, Current, Tongji University, Shanghai China

Professional Experience

- Member of American Association for Cancer Research
- Member of Postdoctoral and Graduate Student Association of Dana Farber Cancer Institute

Peer Review

Reviewer for PNAS, Nature Genetics, Nature Biotechnology, Genome Research, Cancer Cell, PLOS Computational Biology, PLOS ONE, BMC Bioinformatics, BMC Genomics, Computers in Biology and Medicine, Computational Biology and Chemistry, BioMed Research International, IEEE Transactions on Knowledge and Data Engineering, IEEE/ACM Transactions on Computational Biology and Bioinformatics, Big Data Analytics in Genomics (Springer)