

Wei Li, Ph.D.

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EMPLOYMENT

- 2018- Assistant Professor
Center for Genetic Medicine Research, Children's Research Institute
Children's National Medical Center, Washington, DC 20010
Department of Genomics and Precision Medicine, School of Medicine and Health Sciences
George Washington University, Washington, DC 20010
- 2012-2018 Postdoctoral Fellow
Department of Biostatistics and Computational Biology
Dana-Farber Cancer Institute, Harvard T.H. Chan School of Public Health
Advisor: X. Shirley Liu
- 2011 Research Intern
Bioinformatics Division, Novartis Institutes for Biomedical Research (NIBR), Emeryville, CA

EDUCATION

- 2008-2012 Ph.D. in Computer Science and Engineering, University of California, Riverside
- Dissertation: RNA-Seq Transcriptome Assembly: Sparsity, Bias Correction and Multiple Sample Comparison.
 - Advisor: Tao Jiang
- 2006-2008 Master in Computer Science, Tsinghua University, Beijing, China
- Advisor: Yannan Zhao
- 2002-2006 Bachelor in Computer Science, Tsinghua University, Beijing, China

HONORS AND DISTINCTIONS

- [1] APBC 2015 Best paper award, 2015
- [2] IEEE ICCABS conference Travel Award, 2012
- [3] Graduate Division Fellowship Award, University of California, Riverside, 2008-2009
- [4] Tsinghua University Student Art Group Fellowship, 2005
- [5] Tsinghua University Academic Career Fellowship, 2004
- [6] Director, Tsinghua University Military Band Freshman Division, 2006-2007
- [7] Deputy Director, Tsinghua University Military Band, 2004-2005
- [8] Freshman Excellence Scholarship, Tsinghua University, 2002
- [9] Highest ranking student in Guangdong Province College Entrance Exam (equivalent to SAT College Admission Exam; ranked 1st/~163,000)

PUBLICATIONS

*First/co-first author. #Corresponding/Co-corresponding author.

Selected papers

- [1] Shiyu Zhu*, **Wei Li***, Jingze Liu, Chen-Hao Chen, Qi Liao, Han Xu, Tengfei Xiao, Zhongzheng Cao, Jingyu Peng, Pengfei Yuan, Myles Brown, Xiaole Shirley Liu & Wensheng Wei. CRISPR/Cas9-mediated genomic deletion screening for long non-coding RNAs using paired-gRNAs. *Nature Biotechnology* 2016, 34:1279-1286.
- [2] **Wei Li***, Han Xu*, Tengfei Xiao, Le Cong, Feng Zhang, Jun S. Liu, Myles Brown, X. Shirley Liu.

- MAGeCK enables robust identification of essential genes from genome-scale CRISPR-Cas9 knockout screens. *Genome Biology* 2014, 15:554. **Citation: 87; >24k software downloads**
- [3] **Wei Li***, Johannes Koster*, Tengfei Xiao, Han Xu, Chen-Hao Chen, Jun S. Liu, Myles Brown, Xiaole S. Liu. Quality control, modeling and visualization of genome-wide CRISPR screens using MAGeCK-VISPR. *Genome Biology* 2015, 16:281.
- [4] **Wei Li**, Jianxing Feng, Tao Jiang. IsoLasso: A LASSO Regression Approach to RNA-Seq Based Transcriptome Assembly. *Journal of Computational Biology* 2011, 18(11):1693-1707. Also appear in the Research in Computational Molecular Biology (RECOMB 2011). **Citation: 143**
- [5] **Wei Li** and Tao Jiang. Transcriptome Assembly and Isoform Expression Level Estimation from Biased RNA-Seq Reads. *Bioinformatics* 2012, 28(22):2914-2921. **Citation: 63**
- [6] Jianxing Feng, **Wei Li**, Tao Jiang. Inference of isoforms from short sequence reads. *Journal of Computational Biology* 2011, 18(3):305-321. Also appear in the Research in Computational Molecular Biology (RECOMB 2010). **Citation: 85**
- [7] Masruba Tasnim, Shining Ma, Ei-Wen Yang, Tao Jiang[#] and **Wei Li**[#]. Accurate Inference of Isoforms from Multiple Sample RNA-Seq Data. *BMC Genomics* 2015, 16 (S2):S15. Also appear in 2015 Asian Pacific Bioinformatics Conference (APBC 2015). **APBC 2015 Best Paper Award.**

Submitted manuscripts

- [8] Tengfei Xiao*, **Wei Li***, Xiaoqing Wang, Han Xu, Qiu Wu, Peng Jiang, Jixin Yang, Teng Fei, Chongzhi Zang, Qi Liao, Jonathan Rennhack, Eran Andrechek, Rinath M. Jeselsohn, X. Shirley Liu, Myles Brown. Drivers of Endocrine Resistance and Synthetic Lethal Vulnerabilities in Breast Cancer. Under review in PNAS.
- [9] Teng Fei*, **Wei Li***, Jingyu Amy Peng, Tengfei Xiao, X. Shirley Liu, Myles Brown. Genome-wide Interrogation of Functional Cistrome by CRISPR Screen. Submitted.
- [10] Chen-Hao Chen*, **Wei Li***, Tengfei Xiao, Han Xu, Peng Jiang, Cliff Meyer, Myles Brown, X. Shirley Liu. Integrative design and analysis of CRISPR screens using MAGeCK-NEST. Under revision.
- [11] Alexander Wu, Tengfei Xiao, Teng Fei, Shirley X Liu, **Wei Li**. Reducing False Positives in CRISPR/Cas9 Screens from Copy Number Variations. bioRxiv 247031; <https://doi.org/10.1101/247031>.

Other journal papers and conference proceedings

- [12] Diana Miao, Claire A Margolis, Wenhua Gao, Martin H Voss, **Wei Li**, Dylan J Martini, Craig Norton, Dominick Bossé, Stephanie M Wankowicz, Dana Cullen, Christine Horak, Megan Wind-Rotolo, Adam Tracy, Marios Giannakis, Frank Stephen Hodi, Charles G Drake, Mark W Ball, Mohamad E Allaf, Alexandra Snyder, Matthew D Hellmann, Thai Ho, Robert J Motzer, Sabina Signoretti, William G Kaelin, Toni K Choueiri, Eliezer M Van Allen. Genomic correlates of response to immune checkpoint therapies in clear cell renal cell carcinoma. *Science* 2018: ean5951.
- [13] Rinath Jeselsohn, Johann S Bergholz, Matthew Pun, MacIntosh Cornwell, Weihai Liu, Agostina Nardone, Tengfei Xiao, **Wei Li**, Xintao Qiu, Gilles Buchwalter, Ariel Feiglin, Kayley Abell-Hart, Teng Fei, Prakash Rao, Henry Long, Nicholas Kwiatkowski, Tinghu Zhang, Nathanael Gray, Diane Melchers, Rene Houtman, X Shirley Liu, Ofir Cohen, Nikhil Wagle, Eric P Winer, Jean Zhao, Myles Brown. Allele-Specific Chromatin Recruitment and Therapeutic Vulnerabilities of ESR1 Activating Mutations. *Cancer Cell* 2018; 33 (2) 173-186.
- [14] Qingyi Cao, Jian Ma, Chen-Hao Chen, Han Xu, Zhi Chen[#], **Wei Li**[#], X. Shirley Liu[#]. CRISPR-FOCUS: a web server for designing focused CRISPR screening experiments. *PLoS ONE* 2017; 12(9): e0184281.
- [15] Mulin Jun 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 Chung Sham, Junwen Wang, Jun S. Liu, X. Shirley Liu; Exploring genetic associations with ceRNA regulation in the human genome. *Nucleic Acids Res* 2017; 45 (10) 5653-5665.
- [16] Teng Fei, Yiwen Chen, Tengfei Xiao, **Wei Li**, Laura Cato, Peng Zhang, Maura B. Cotter, Michaela Bowden, Rosina T. Lis, Shuang G. Zhao, Qiu Wu, Felix Y. Feng, Massimo Loda, Housheng Hansen He, X. Shirley Liu, Myles Brown. HNRNPL and its RNA Targets Regulate Prostate Cancer Growth. In press, Proceedings of the National Academy of Sciences (PNAS).

- [17] Wenhua Gao, **Wei Li**, Tengfei Xiao, Shirley Liu, William G. Kaelin, Jr., M.D. Inactivation of the PBRM1 Tumor Suppressor Gene Amplifies the HIF-Response in VHL-/- Clear Cell Renal Carcinoma. *Proceedings of the National Academy of Sciences (PNAS)* 2017, 114(5) 1027-1032.
- [18] Jian Ma, Johannes Köster, Qian Qin, Shengen Hu, **Wei Li**, Chenhao Chen, Qingyi Cao, Jinzeng Wang, Shenglin Mei, Qi Liu, Han Xu, and Xiaole Shirley Liu. CRISPR-DO for genome-wide CRISPR design and optimization. *Bioinformatics* 2016, 32 (21) 3336-3338.
- [19] Shom Goel, Qi Wang, April C. Watt, Sara M. Tolaney, Deborah A. Dillon, **Wei Li**, Susanne Ramm, Adam C. Palmer, Haluk Yuzugullu, Kwok-Kin Wong, X. Shirley Liu, Piotr Sicinski, Eric P. Winer, Ian E. Krop, Jean J. Zhao. Overcoming Therapeutic Resistance in HER2-Positive Breast Cancers With CDK4/6 Inhibitors. *Cancer Cell* 2016, 29(3):255-269.
- [20] Peng Jiang, Hongfang Wang, **Wei Li**, Chongzhi Zang, Bo Li, Yinling Wong, Cliff Meyer, Jun S. Liu, Jon Aster, X. Shirley Liu. Network analysis of gene essentiality in functional genomic screens. *Genome Biology* 2015, 16:239.
- [21] Han Xu, Chen-Hao Chen, **Wei Li**, Cliff Meyer, Tengfei Xiao, Le Cong, Feng Zhang, Jun S. Liu, Myles Brown, X. Shirley Liu. Sequence determinants of improved CRISPR sgRNA design. *Genome Research* 2015, 25(8):1147-57.
- [22] Xuesong Zhao, Tatyana Ponomaryov, Kimberly J. Ornell, Pengcheng Zhou, Sukriti K. Dabral, Ekaterina Pak, **Wei Li**, Scott X. Atwood, Ramon J. Whitson, Anne Lynn S. Chang, Jiang Li, Anthony E. Oro, Jennifer A. Chan, Joseph F. Kelleher, and Rosalind A. Segal. RAS/MAPK activation drives resistance to Smo inhibition, metastasis and tumor evolution in Shh pathway-dependent tumors. *Cancer Research* 2015, 75(17):3623-35.
- [23] Xiaoqi Zheng, Qian Zhao, Hua-Jun Wu, **Wei Li**, et al. MethylPurify: tumor purity deconvolution and differential methylation detection from single tumor DNA methylomes. *Genome Biology* 2014, 15:419.
- [24] Paul M. Ruegger, Elizabeth Bent, **Wei Li**, Daniel R. Jeske, Xinping Cui, Jonathan Braun, Tao Jiang, James Borneman. Improving Oligonucleotide Fingerprinting of rRNA Genes by Implementation of Polony Microarray Technology. *Journal of Microbiological Methods* 2012, 90(3):235-240.
- [25] **Wei Li**, et al. Workshop: Transcriptome assembly and isoform expression level estimation from biased RNA-Seq reads. *IEEE 2nd Computational Advances in Bio and Medical Sciences (ICCABS 2012)*, pp. 1
- [26] **Wei Li**, et al. Workshop: Transcriptome assembly from RNA-Seq data: Objectives, algorithms and challenges. *IEEE 1st Computational Advances in Bio and Medical Sciences (ICCABS 2011)*, pp. 271
- [27] **Wei Li**, Paul Ruegger, James Borneman, Tao Jiang. Polony Identification Using the EM Algorithm Based on a Gaussian Mixture Model. *IEEE International Conference on Bioinformatics and BioEngineering (BIBE 2010)*, 220-225.
- [28] **Wei Li**, et al. SVM feature selection and sample regression for Chinese medicine research. *2008 International Conference on Information and Automation (ICIA 2008)*, pp. 1773.
- [29] **Wei Li**, et al. COX-2 activity prediction in Chinese medicine using neural network based ensemble learning methods. *International Joint Conference on Neural Networks (IJCNN 2008)*, pp. 1853.

PATENTS

- [1] Compositions and Methods for Making and Decoding Paired-Guide RNA Libraries and Uses Thereof. Jingyu Amy Peng, Tengfei Xiao, **Wei Li**, X. Shirley Liu, Myles Brown. Submitted.
- [2] Drivers of Endocrine Resistance and Synthetic Lethal Vulnerabilities in Breast Cancer. Tengfei Xiao, **Wei Li**, X. Shirley Liu, Myles Brown. Submitted.

PRESENTATIONS

- [1] *Genome-wide CRISPR Screens Identified Drivers of Endocrine Resistance and Synthetic Lethal Vulnerabilities in Breast Cancer.*
 - a. In CSH-Asia Conference: Precision Cancer Biology: From Targeted to Immune Therapies conference (Suzhou, China), September 2017 (oral presentation, acceptance rate ~30%);
 - b. In AACR Precision Medicine Series: Opportunities and Challenges of Exploiting Synthetic Lethality in Cancer (San Diego, USA). January 2017 (oral presentation, acceptance rate ~24%);

- c. In Cold Spring Harbor Laboratory symposium: "Genome Engineering: The CRISPR/Cas9 Revolution", August 2016 (oral presentation, acceptance rate 30%).
- [2] *Genome-wide CRISPR Screens: Algorithms and Applications to Cancer Therapy Resistance.*
 - a. In Children's National Medical Center (Washington DC), August 2017;
 - b. In Department of Cell Systems and Anatomy, University of Texas Health San Antonio, May 2017;
 - c. In Department of Molecular and Cellular Biology, University of Arizona, April 2017
 - d. In Department of Electrical and Computer Engineering, University of Illinois Urbana Champaign, March 2017;
 - e. In Department of Biochemistry, McGill University (Montreal, Canada), February 2017
 - f. In Department of Pharmacy, University of Pittsburgh, May 2016.
- [3] *Computational Algorithms for CRISPR Screens and A Study of Breast Cancer Hormone Independence.* Workshop of CRISPR Congress 2016, Boston, MA
- [4] *Quality Control, Modeling and Visualization of Genome-wide CRISPR Screens Using MAGECK-VISPR.*
 - a. In Frontiers in CRISPR Symposium: New Development and Applications of CRISPR-Cas9 for Genome-Editing. Boston, MA, January 2016.
 - b. In Cold Spring Harbor Laboratory symposium: "Genome Engineering: The CRISPR/Cas9 Revolution", September 2015 (oral presentation, acceptance rate 32%).
 - c. In Genomics GetTogether Seminar, Department of Biostatistics and Computational Biology, Dana-Farber Cancer Institute, July 2015.
- [5] *Introduction to CRISPR Screens.* Seminar in Longwood Translational Medicine China Initiative. October 2015.
- [6] *Identification of cell-type specific essential genes using MAGECK-VISPR.* Center for Functional Cancer Epigenetics Scientific Retreat, Dana-Farber Cancer Institute, August 2015.
- [7] *CRISPR MAGECK and Other Tricks.* Cell Circuits and Epigenomics Program Seminar. Broad Institute of Harvard and MIT. June 2015.
- [8] *Computational Analysis of Genome-Scale CRISPR-Cas9 Knockout Screening Experiments.* Center for Functional Cancer Epigenetics Seminar, Dana-Farber Cancer Institute, Mar. 2014.
- [9] *Transcriptome assembly from RNA-Seq data: Objectives, algorithms and challenges.*
 - a. In Computational Biology and Bioinformatics program, Yale University, June 2012;
 - b. In Department of Biostatistics and Computational Biology, Dana-Farber Cancer Institute, June 2012;
 - c. In Department of Stem Cell and Regenerative Biology, Harvard University, May 2012;
 - d. IEEE International Conference on Computational Advances in Bio and Medical Sciences (ICCABS 2011). Orlando, FL. February 2011.
- [10] *Transcriptome Assembly and Isoform Expression Level Estimation from Biased RNA-Seq Reads.* IEEE International Conference on Computational Advances in Bio and Medical Sciences (ICCABS 2012). Las Vegas, NV. March 2012.
- [11] *IsoLasso: A LASSO Regression Approach to RNA-Seq Based Transcriptome Assembly.* 15th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2011). Vancouver, Canada, March 2012.
- [12] *Polony Identification Using the EM Algorithm Based on a Gaussian Mixture Model.* 10th IEEE International Conference on Bioinformatics and Bioengineering (BIBE 2010). Philadelphia, PA, May 2010.
- [13] *COX-2 Activity Prediction in Chinese Medicine Using Neural Network Based Ensemble Learning Methods.* The 2008 International Joint Conference on Neural Networks (IJCNN 2008). Hong Kong, May 2008.

EDUCATIONAL ACHIEVEMENTS

- 2016 Guest lecturer, Harvard University
 - Introduction to Computational Biology and Bioinformatics (STAT115).
- 2011 Teaching Assistant, University of California, Riverside
 - Machine Learning (CS229).

- 2010 Teaching Assistant, University of California, Riverside
- The Theory of Automata and Formal Languages (CS150).
- 2008-2009 Teaching Assistant, Tsinghua University
- Robot Soccer: Theory and Practice

GRANT APPLICATIONS

Submitted applications

- NIH Pathway to Independence award (K99/R00): Modeling Functional Elements using CRISPR Screens. Submitted July 2016. Impact score: 26
- NIH Pathway to Independence award (K99/R00): Computational Characterization of Functional Elements using CRISPR Screens. Submitted Oct. 2015. Impact score: 46
- Department of Defense (DoD) prostate cancer research program (PCRP) and breast cancer research program (BCRP) postdoctoral training award postdoctoral training award, Burroughs Wellcome Fund (BWF) career awards at the scientific interface, Raymond Lavietes Foundation fellowship, Wong family award

Applications that I helped preparing

- DoD PCRP PC140817 (Brown, Myles and Liu, X.S.): PCRP Synergistic Idea Development Award: Mechanism of Hormone Independence and Drug Resistance in Prostate Cancer (funded)
- NIH/NHGRI R01HG008728 (Brown, Myles and Liu, X.S.): Large-scale In Vivo Functional Characterization of the Human Cistrome (funded)
- NIH/NHGRI R01HG008927 (Liu, X.S.): Computational Methods for Genome-wide CRISPR/Cas9 Knockout Screens (funded)

MEMBERSHIPS AND SERVICES

- Vice President, Harvard Medical School Chinese Scholars and Scientists Association (HMS-CSSA, <http://hms-cssa.org>), 2014-2018
 - Organized and hosted Cancer Epigenetics Mini-symposium, Single Cell Genomics Mini-symposium (2015), CRISPR screening Mini-symposium (2015);
 - Organized 2015, 2016 and 2017 Harvard Chinese Life Science Annual Symposium, a whole-day seminar attracting > 500 participants every year;
- Associate Director, Longwood Translational Medicine China Initiative (LTMCI, <http://www.lwtransmed.org/>), 2013-2016
 - Co-founder of the organization to facilitate the increasing collaboration among doctors and scientists from China and US. Organized over 40 seminars in 3 years
- Member of IEEE, ICSB.

PEER-REVIEWS

Journals:

- Cell, Nature Biotechnology, PLoS Computational Biology, Nucleic Acid Research, Bioinformatics, Biostatistics, BMC Bioinformatics, BMC Genomics, BMC Cancer, Epigenetics and Chromatin, PLoS ONE, Journal of Computational Biology.

Conferences:

- ISMB/ECCB (2012/2013/2014), RECOMB (2013/2014), WABI (2011).