

CURRICULUM VITAE

Chongzhi Zang, PhD

Assistant Professor
University of Virginia
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Charlottesville, VA 22908, USA
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EDUCATION AND TRAINING

Peking University	B.S., Physics	07/2005
The George Washington University	Ph.D., Physics	09/2010
Harvard University/Dana-Farber Cancer Institute	Postdoctoral training, Computational biology	10/2016

APPOINTMENTS

11/2016 –	University of Virginia School of Medicine <i>Assistant Professor</i> , Center for Public Health Genomics (11/2016–) <i>Assistant Professor</i> , Department of Public Health Sciences (11/2016–) <i>Assistant Professor</i> (secondary), Department of Biochemistry and Molecular Genetics (12/2016–) <i>Assistant Professor</i> (courtesy), Department of Biomedical Engineering (09/2017–) <i>Faculty Member</i> , University of Virginia Cancer Center (03/2017–) <i>Faculty Member</i> , University of Virginia Data Science Institute (03/2017–)
07/2010 – 10/2016	Harvard University/Dana-Farber Cancer Institute <i>Research Fellow</i> , Department of Biostatistics and Computational Biology, Dana-Farber Cancer Institute (07/2010–10/2016) <i>Postdoctoral Fellow</i> , Department of Biostatistics, Harvard T.H. Chan School of Public Health (10/2010–10/2016)
05/2007 – 06/2010	National Institutes of Health <i>Predoctoral Research Assistant</i> , Laboratory of Molecular Immunology, National Heart, Lung, and Blood Institute
09/2005 – 06/2010	The George Washington University <i>Graduate Research Assistant</i> , Department of Physics (09/2006–06/2010) <i>Graduate Teaching Assistant</i> , Department of Physics (09/2005–05/2008)

PUBLICATIONS

Peer-reviewed Journal Articles

Total citations > 7000; H-index = 21 (Google Scholar)

1. Zhenjia Wang, Mete Civelek, Clint L. Miller, Nathan C. Sheffield, Michael J. Guertin, Chongzhi Zang. “BART: a transcription factor prediction tool with query gene sets or epigenomic profiles”, *Bioinformatics*, doi:10.1093/bioinformatics/bty194 (2018).
2. Cynthia C Jose, Lakshmanan Jagannathan, Vinay Singh Tanwar, Xiaoru Zhang, Chongzhi Zang, Suresh Cuddapah. “Nickel exposure induces persistent mesenchymal phenotype in human lung epithelial cells through epigenetic activation of ZEB1”, *Molecular Carcinogenesis* 57, 794–806 (2018).
3. André L. Martins, Ninad M. Walavalkar, Warren D. Anderson, Chongzhi Zang, Michael J. Guertin. “Universal correction of enzymatic sequence bias reveals molecular signatures of protein/DNA interactions”, *Nucleic Acids Research* 46 (2), e9 (2017).
4. Shenglin Mei, Clifford A. Meyer, Rongbin Zheng, Qian Qin, Qiu Wu, Peng Jiang, Bo Li, Xiaohui Shi, Binbin Wang, Jingyu Fan, Celina Shih, Myles Brown, Chongzhi Zang[§]([§] co-corresponding author), X. Shirley Liu[§]. “Cistrome Cancer: a web resource for integrative gene regulation modeling in cancer”, *Cancer Research* 77, e19–e22 (2017).
5. Eric Severson*, Kelly L. Arnett*, Hongfang Wang*, Chongzhi Zang*(^{*} co-first authors), Len Taing, Hudan Liu, Warren S. Pear, X. Shirley Liu, Stephen C. Blacklow, Jon C. Aster. “Genome-wide identification and characterization of Notch transcription complex-binding sequence-paired sites in leukemia cells”, *Science Signaling* 10, 477, eaag1598 (2017).
6. Shenglin Mei, Qian Qin, Qiu Wu, Hanfei Sun, Rongbin Zheng, Chongzhi Zang, Muyuan Zhu, Jiabin Wu, Xiaohui Shi, Len Taing, Tao Liu, Myles Brown, Clifford A. Meyer, X. Shirley Liu. “Cistrome Data Browser: an integrated data portal for ChIP-Seq and chromatin accessibility data in human and mouse”, *Nucleic Acids Research* 45 (D1), D658–D662 (2016).
7. Qian Qin, Shenglin Mei, Qiu Wu, Hanfei Sun, Lewyn Li, Len Taing, Sujun Chen, Fugen Li, Tao Liu, Chongzhi Zang, Han Xu, Yiwen Chen, Clifford A. Meyer, Yong Zhang, Myles Brown, Henry W. Long, X. Shirley Liu. “ChiLin: a comprehensive ChIP-seq and DNase-seq quality control and analysis pipeline”, *BMC Bioinformatics* 17, 404 (2016).
8. Su Wang*, Chongzhi Zang*(^{*} co-first authors), Tengfei Xiao, Jingyu Fan, Shenglin Mei, Qian Qin, Qiu Wu, Xujuan Li, Kexin Xu, Housheng Hansen He, Myles Brown, Clifford A. Meyer, X. Shirley Liu. “Modeling cis-regulation with a compendium of genome-wide

- histone H3K27ac profiles”, *Genome Research* 26, 1417–1429 (2016).
9. Chongzhi Zang*, Annouck Luyten*, Christina Chen, X. Shirley Liu, Ramesh A. Shivdasani. “NF-E2, FLI1 and RUNX1 collaborate at areas of dynamic chromatin to activate transcription in mature mouse megakaryocytes”, *Scientific Reports* 6, 30255 (2016).
 10. Chongzhi Zang*, Tao Wang*, Ke Deng, Bo Li, Sheng’en Hu, Qian Qin, Tengfei Xiao, Shihua Zhang, Clifford A. Meyer, Housheng Hansen He, Myles Brown, Jun S. Liu, Yang Xie, X. Shirley Liu. “High-dimensional genomic data bias correction and data integration using MANCIE”. *Nature Communications* 7, 11305 (2016).
 11. Han Xu*, Kexin Xu*, Housheng H. He, Chongzhi Zang, Chen-Hao Chen, Yiwen Chen, Qian Qin, Su Wang, Chenfei Wang, Sheng’en Hu, Fugen Li, Henry Long, Myles Brown, X. Shirley Liu. “Integrative analysis reveals the transcriptional collaboration between EZH2 and E2F1 in the regulation of cancer-related gene expression”, *Molecular Cancer Research* 14, 163–172 (2015).
 12. Peng Jiang, Hongfang Wang, Wei Li, Chongzhi Zang, Bo Li, Yinling Joey Wong, Clifford A. Meyer, Jun S. Liu, Jon C. Aster, X. Shirley Liu, “Network analysis of gene essentiality in functional genomics experiments”, *Genome Biology* 16, 239 (2015).
 13. Hilary K Finucane, Brendan Bulik-Sullivan, Alexander Gusev, Gosia Trynka, Yakir Reshef, Po-Ru Loh, Verner Anttila, Han Xu, Chongzhi Zang, Kyle Farh, Stephan Ripke, Felix R Day, ReproGen Consortium, Schizophrenia Working Group of the Psychiatric Genomics Consortium, The RACI Consortium, Shaun Purcell, Eli Stahl, Sara Lindstrom, John RB Perry, Yukinori Okada, Soumya Raychaudhuri, Mark Daly, Nick Patterson, Benjamin M Neale, Alkes L Price. “Partitioning heritability by functional annotation using genome-wide association summary statistics”, *Nature Genetics* 47, 1228–1235 (2015).
 14. Hongfang Wang, Chongzhi Zang, X. Shirley Liu, Jon C. Aster. “The role of Notch receptors in transcriptional regulation”, *Journal of Cellular Physiology* 230(5), 982–988 (2015).
 15. Alexander Gusev, S. Hong Lee, Gosia Trynka, Hilary Finucane, Bjarni J Vilhjálmsson, Han Xu, Chongzhi Zang, Stephan Ripke, Brendan Bulik-Sullivan, Eli Stahl, Schizophrenia Working Group of the Psychiatric Genomics Consortium, SWE-SCZ Consortium, Anna K. Kähler, Christina M. Hultman, Shaun M. Purcell, Steven A. McCarroll, Mark Daly, Bogdan Pasaniuc, Patrick F. Sullivan, Benjamin M. Neale, Naomi R. Wray, Soumya Raychaudhuri, Alkes L. Price. “Partitioning heritability of regulatory and cell-type-specific variants across 11 common diseases”, *The American Journal of Human Genetics* 95, 535–552 (2014).
 16. Yumi Yashiro-Ohtani, Hongfang Wang, Chongzhi Zang, Kelly L. Arnett, Will Bailis, Yugong Ho, Birgit Knoechel, Claudia Lanauze, Lumena Louis, Katherine S. Forsyth, Sujun Chen, Yoonjie Chung, Jonathan Schug, Gerd A. Blobel, Stephen A. Liebhaber, Bradley E. Bernstein, Stephen C. Blacklow, X. Shirley Liu, Jon C. Aster, Warren S. Pear. “Long-range enhancer activity determines Myc sensitivity to Notch inhibitors in T cell leukemia”, *Proceedings of the National Academy of Sciences USA* 111(46), E4946–E4953 (2014).
 17. Annouck Luyten*, Chongzhi Zang*(* co-first authors), X. Shirley Liu, Ramesh A.

- Shivdasani. “Active enhancers are delineated *de novo* during hematopoiesis with limited lineage fidelity among specified primary blood cells”, *Genes and Development* 28, 1827–1839 (2014).
18. Alexander Stoeck, Serguei Lejnine, Andrew Truong, Li Pan, Hongfang Wang, Chongzhi Zang, Jing Yuan, Chris Ware, John MacLean, Philip W Garrett-Engle, Michael Kluk, Jason Laskey, Brian B. Haines, Christopher Moskaluk, Leigh Zawel, Stephen Fawell, D. Gary Gilliland, Theresa Zhang, Brandon Kremer, Birgit Knoechel, Bradley E Bernstein, Warren S. Pear, X. Shirley Liu, Jon C Aster, Sriram Sathyanarayanan. “Discovery of biomarkers predictive of GSI response in triple negative breast cancer and adenoid cystic carcinoma”, *Cancer Discovery* 4(10), 1154–1167 (2014).
 19. Xiaoqi Zheng, Qian Zhao, Huajun 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* 15, 419 (2014).
 20. Hongfang Wang*, Chongzhi Zang*(* co-first authors), Len Taing, Kelly Arnett, Yinling Joey Wong, Warren S. Pear, Stephen C. Blacklow, X. Shirley Liu, Jon C. Aster. “NOTCH1-RBPJ complexes drive target gene expression through dynamic interactions with superenhancers”, *Proceedings of the National Academy of Sciences USA* 111, 715–710 (2014).
 21. Housheng Hansen He, Clifford A. Meyer, Sheng'en Shawn Hu, Mei-Wei Chen, Chongzhi Zang, Yin Liu, Prakash K. Rao, Teng Fei, Han Xu, Henry Long, X. Shirley Liu, Myles Brown. “Refined DNase-seq protocol and data analysis reveals intrinsic bias in transcription factor footprint identification”. *Nature Methods* 11, 73–78 (2014).
 22. Su Wang, Hanfei Sun, Jian Ma, Chongzhi Zang, Chenfei Wang, Juan Wang, Qianzi Tang, Clifford A. Meyer, Yong Zhang, X. Shirley Liu. “Targets analysis by integration of transcripome and ChIP-seq data with BETA”. *Nature Protocols* 8, 2502–2515 (2013).
 23. Hong Hao, Douglas S. Kim, Bernward Klocke, Kory R. Johnson, Kairong Cui, Norimoto Gotoh, Chongzhi Zang, Janina Gregorski, Linn Gieser, Weiqun Peng, Yang Fann, Martin Seifert, Keji Zhao, Anand Swaroop. “Transcriptional regulation of rod photoreceptor homeostasis revealed by *in vivo* NRL targetome analysis”. *PLoS Genetics* 8(4), e1002649 (2012).
 24. Jeremy A. Daniel, Margarida A. Santos*, Zhibin Wang*, Chongzhi Zang*(* equal contributions), Mila Jankovic, Anna Gazumyan, Kristopher R. Schwab, Arito Yamane, Darius Filsuf, Young-Wook Cho, Kai Ge, Weiqun Peng, Michel C. Nussenzweig, Rafael Casellas, Gregory R. Dressler, Keji Zhao, André Nussenzweig. “PTIP promotes chromatin changes critical for immunoglobulin switch recombination”. *Science* 329, 917–923 (2010).
 25. Lai Wei, Golnaz Vahedi, Hong-Wei Sun, Wendy T. Watford, Hiroaki Takatori, Haydee L. Ramos, Hayato Takahashi, Jonathan Liang, Gustavo Gutierrez-Cruz, Chongzhi Zang, Weiqun Peng, John J. O'Shea, Yuka Kanno. “Discrete roles of STAT4 and STAT6

transcription factors in tuning epigenetic modifications and transcription during T helper cell differentiation”. *Immunity* 32, 840–851 (2010).

26. Zhibin Wang*, Chongzhi Zang*(* co-first authors), Kairong Cui*, Dustin E. Schones, Artem Barski, Weiqun Peng, Keji Zhao. “Genome-wide mapping of HATs and HDACs reveals distinct functions in active and inactive genes”. *Cell* 138, 1019–1031 (2009). (cited > 900)
27. Chunyuan Jin*, Chongzhi Zang*(* co-first authors), Gang Wei, Kairong Cui, Weiqun Peng, Keji Zhao, Gary Felsenfeld. “H3.3/H2A.Z double variant-containing nucleosomes mark ‘nucleosome-free regions’ of active promoters and other regulatory regions”. *Nature Genetics* 41, 941–945 (2009). (cited > 600)
28. Yasuto Araki, Zhibin Wang, Chongzhi Zang, William H. Wood, Dustin E. Schones, Kairong Cui, Tae-Young Roh, Brad Lhotsky, Robert P. Wersto, Weiqun Peng, Kevin G. Becker, Keji Zhao, Nan-ping Weng. “Genome-wide analysis of histone methylations reveals chromatin state-based regulation of gene transcription and function of memory CD8⁺ T cells”. *Immunity* 30, 912–925 (2009).
29. Chongzhi Zang, Dustin E. Schones, Chen Zeng, Kairong Cui, Keji Zhao, Weiqun Peng. “A clustering approach for identification of enriched domains from histone modification ChIP-Seq data”. *Bioinformatics* 25, 1952–1958 (2009). (cited > 600)
30. Gang Wei, Lai Wei, Jinfang Zhu, Chongzhi Zang, Jane Hu-Li, Zhengju Yao, Kairong Cui, Yuka Kanno, Tae-Young Roh, Wendy Watford, Dustin E. Schones, Weiqun Peng, Hong-wei Sun, William E. Paul, John J. O’Shea, Keji Zhao. “Global mapping of H3K4me3 and H3K27me3 reveals specificity and plasticity in lineage fate determination of differentiating CD4⁺ T cells”. *Immunity* 30, 155–167 (2009). (cited > 900)
31. Kairong Cui*, Chongzhi Zang*(* co-first authors), Tae-Young Roh, Dustin E. Schones, Richard W. Childs, Weiqun Peng, Keji Zhao. “Chromatin signatures in multipotent hematopoietic stem cells indicate the fate of bivalent genes during differentiation”. *Cell Stem Cell* 4, 80–93 (2009). (cited > 500)
32. Zhibin Wang*, Chongzhi Zang*(* co-first authors), Jeffrey A. Rosenfeld*, Dustin E. Schones, Artem Barski, Suresh Cuddapah, Kairong Cui, Tae-Young Roh, Weiqun Peng, Michael Q. Zhang, Keji Zhao. “Combinatorial patterns of histone acetylations and methylations in the human genome”. *Nature Genetics* 40, 897–903 (2008). (cited > 1700)
33. HAO Zuoqiang, ZHANG Jie, YU Jin, ZHANG Zhe, ZHONG Jiayong, ZANG Chongzhi, JIN Zhan, WANG Zhaohua, WEI Zhiyi. “Fluorescence measurement and acoustic diagnostics of plasma channels in air”. *Acta Physica Sinica* 55, 299–303 (2006). (In Chinese)
34. ZANG Chongzhi, ZHANG Jietian, PENG Peizhi. “Experimental study of the relationship between NMR relaxation time and the concentration of solutions”. *Physics Bulletin* 2005 (10), 30–32 (2005). (In Chinese)
35. ZANG Chongzhi, ZHANG Jietian, PENG Peizhi. “Discussion of data processing method for measuring NMR relaxation time”. *Physics Experimentation* 25(5), 45–47 (2005). (In

Chinese)

36. ZANG Chongzhi, PENG Peizhi, ZHANG Jietian, LU Sihua. “Teaching experimentation of MRI”. *Physics Experimentation* 24(8), 3–7 (2004). (In Chinese)

Peer-reviewed Conference Papers

37. Tengfei Xiao, Wei Li, Xiaoqing Wang, Han Xu, Qiu Wu, Peng Jiang, Jixin Yang, Teng Fei, Chongzhi Zang, Qi Liao, Jonathan Rennhack, Eran Andrechek, Nanlin Li, Rinath Jeselsohn, X. Shirley Liu, Myles Brown. “CRISPR screens identified drivers of endocrine resistance and synthetic lethal vulnerabilities in breast cancer”. *Molecular Cancer Therapeutics* 16(10 Supplement), PR06. In: *Proceedings of the AACR Precision Medicine Series: Opportunities and Challenges of Exploiting Synthetic Lethality in Cancer* (2017).
38. Chongzhi Zang*, Tao Wang*, Ke Deng, Bo Li, Sheng'en Hu, Qian Qin, Tengfei Xiao, Shihua Zhang, Clifford A. Meyer, Housheng Hansen He, Myles Brown, Jun S. Liu, Yang Xie, X. Shirley Liu. “High-dimensional genomic data integration and bias correction using MANCIE”. *Cancer Research* 76, B24. *AACR Special Conference: Chromatin and Epigenetics in Cancer* (2015).
39. Hongfang Wang, Yumi Yashiro-Ohtani, Chongzhi Zang, Yinling Joey Wong, Will Bailis, Birgit Knoechel, Bradley Bernstein, Steve Blacklow, X Shirley Liu, Warren S Pear, Jon C Aster. “Alternative Super-Enhancer States Determine MYC Sensitivity to Notch and Brd4 Inhibitors in T Lymphoblastic Leukemia/Lymphoma”. *Blood* 124 (21), *ASH Annual Meeting Abstracts* 863 (2014).
40. Hongfang Wang*, Chongzhi Zang*(* co-first authors), Len Taing, Hoifung Wong, Yumi Yashiro-Ohtani, Stephen Blacklow, Warren S. Pear, X. Shirley Liu, Jon C. Aster. “Genome-wide analysis of NOTCH1, ETS family factors, and RUNX1 binding in human T lymphoblastic leukemia cells reveals distinct regulatory elements”. *Blood* 120 (21), *ASH Annual Meeting Abstracts* 1277 (2012).
41. Hong Hao, Douglas S. Kim, Kory Johnson, Chongzhi Zang, Kairong Cui, Janina Gregorski, Fann Yang, Keji Zhao, Anand Swaroop. “Chip-seq aided elucidation of Nrl-centered transcription regulatory network and implications for retina degeneration”. *Investigative Ophthalmology and Visual Science* 52 (6), 38 (2011).
42. Kalpana Subedi, Yasuto Araki, Supriyo De, William Wood, Alexei Sharov, Chongzhi Zang, Dustin Schones, Brad Lhotsky, Dawood Dudekula, Kevin Becker, Minoru Ko, Weiqun Peng, Keji Zhao, Nan-ping Weng. “Dynamic changes of gene expression in concordance with histone modifications in CD8 T cells after activation”. *The Journal of Immunology* 186, 159.2 (2011).
43. Hong Hao, Douglas S. Kim, Kory Johnson, Chongzhi Zang, Kairong Cui, Janina Gregorski, Fann Yang, Keji Zhao, Anand Swaroop. “Global target analysis of Nrl, the key transcriptional regulator of photoreceptor differentiation and homeostasis”. *Investigative Ophthalmology and Visual Science* 51 (5), 5952 (2010).

44. Chongzhi Zang, Dustin E. Schones, Chen Zeng, Kairong Cui, Keji Zhao, Weiqun Peng. “Genome-wide identification of ChIP-Seq enriched regions based on a statistical model”. In: *Proceedings of the 7th Asia-Pacific Bioinformatics Conference*, edited by Michael Q. Zhang, Michael S. Waterman, Xuegong Zhang. Beijing: Tsinghua University Press, 835 (2009).

SOFTWARE

1. SICER: Spatial-clustering approach for the Identification of ChIP-Enriched Regions, a ChIP-Seq data analysis method and software package. <http://home.gwu.edu/~wpeng/Software.htm>
2. MANCIE: Matrix Analysis and Normalization by Concordant Information Enhancement, a computational method for high-dimensional genomic data integration. <https://cran.r-project.org/web/packages/MANCIE/>
3. MARGE: Model-based Analysis of Regulation of Gene Expression, a comprehensive computational method for inference of cis-regulation of gene expression leveraging public H3K27ac genomic profiles in human or mouse. <http://cistrome.org/MARGE/>
4. BART: Binding Analysis for Regulation of Transcription, a bioinformatics tool for predicting functional transcription factors that bind at genomic cis-regulatory regions to regulate gene expression in the human or mouse genomes, given a query gene set or a ChIP-seq dataset as input. <http://faculty.virginia.edu/zanglab/bart/>

HONORS AND AWARDS

2017–2020	NIH/NCI Transition Career Development Award (K22)
2014	Travel Award, Harvard Program in Quantitative Genomics
2012–2015	Leukemia and Lymphoma Society Fellow Award
2010	Dimitris N. Chorafas Foundation Prize
2009	Parke Prize in Theoretical Physics, The George Washington University
2009	The Best Poster Award, the 7th Asia-Pacific Bioinformatics Conference
2008	Chinese Government Award for Outstanding Self-financed Student Abroad
2008	Student Travel Grant Award, American Physical Society (APS)
2004	2nd Award for Undergraduate Research, School of Physics, Peking University
2001	Freshman Fellowship, Peking University

RESEARCH SUPPORT

Current Research Support

1. NIH/NCI K22 CA204439 PI: Zang 09/01/2017–08/31/2020
Title: Quantitative Modeling for Chromatin Regulation of Gene Expression in Cancer
Role: PI
2. American Cancer Society IRG 81-001-26 PI: Zang 12/18/2017–12/17/2018
Title: Integrative Modeling of Functional Gene Regulation in Colorectal Cancer
Role: PI
3. NFRI MPNST Pre-Clinical Research PI: Zhu 02/01/2018–01/31/2020
Title: Involvement of PRC2 in malignant transformation and metastatic spread of NF1-associated MPNSTs
Role: Co-investigator
4. NIH/NIEHS R01 ES024727 PI: Cuddapah 02/01/2017–06/30/2020
Title: Epigenetic Reprogramming by Nickel through Chromatin Domain Disruption
Role: Co-investigator

Completed Research Support

5. Leukemia & Lymphoma Society Fellowship PI: Zang 07/01/2012–06/30/2015
Title: Computational Studies on Transcriptional Regulation of Notch1 in T-ALL
Role: PI

TEACHING

Spring 2017–	University of Virginia PHS5705: Public Health Genomics	Lecture
05/2016	NIH/NCI Bioinformatics Workshop	Guest Instructor
11/2014	NIH/NCI Bioinformatics Workshop	Guest Instructor
11/2013	Tongji University: Computational Genomics	Guest Lecture
09/2005–05/2008	The George Washington University Physics 001, Physics 002 Astronomy 001, Astronomy 002	Teaching Assistant Lab & Recitation Lab Instructor

INVITED TALKS

1. Department of Pathology, University of Virginia. 12/19/2017
2. Department of Biostatistics, Virginia Commonwealth University. 11/3/2017
3. Center for Quantitative Biology, Peking University. 09/29/2017
4. Institute of Biophysics, Chinese Academy of Sciences. 09/28/2017

5. Beijing Institute for Scientific and Engineering Computing, Beijing University of Technology. 09/27/2017
6. Center for Statistical Science, Tsinghua University. 09/25/2017
7. Department of Physics, Fudan University. 09/23/2017
8. CAS-MPG Partner Institute for Computational Biology, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences. 09/18/2017
9. Department of Biochemistry and Molecular Genetics, University of Virginia. 12/15/2016
10. School of Life Sciences, Peking University. 06/08/2016
11. Workshop on Analysis of ChIP-Seq Data, National Cancer Institute, National Institutes of Health. 05/17/2016
12. Laboratory of Genome Integrity, National Cancer Institute, National Institutes of Health. 04/07/2016
13. Department of Immunobiology, Yale University. 03/11/2016
14. University of Virginia School of Medicine. 02/05/2016
15. The Wistar Institute. 01/29/2016
16. Academy of Mathematics and Systems Science, Chinese Academy of Sciences. 01/07/2016
17. Peking University Third Hospital. 01/05/2016
18. Peking University Medical Center. 01/04/2016
19. University of Illinois College of Medicine, Peoria. 12/17/2015
20. The Stadtman Symposium, National Institutes of Health. 12/10/2015
21. National Heart, Lung, and Blood Institute, National Institutes of Health. 11/20/2015
22. University of Nevada School of Medicine, Reno. 10/06/2015
23. College of Pharmacy, University of Rhode Island. 06/24/2015
24. Uniformed Services University of the Health Sciences. 05/29/2015
25. Department of Electrical & Computer Engineering, University of Nebraska, Lincoln. 02/18/2015
26. National Human Genome Research Institute, National Institutes of Health. 02/04/2015
27. National Cancer Institute, National Institutes of Health. 12/19/2014
28. Cancer epigenetics symposium, Harvard Medical School. 12/14/2014
29. Biophysics Seminar, The George Washington University. 10/02/2014
30. Workshop on big data analysis in biomedical research, Harvard Medical School. 06/24/2014
31. CAS-MPG Partner Institute for Computational Biology, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences. 11/28/2013
32. Institute of Systems Biomedicine, Shanghai Jiao Tong University. 11/26/2013
33. Computational Biology and Bioinformatics Organization, Broad Institute. 10/16/2013
34. Megakaryocyte and Platelet Biology Joint Meeting, Boston Children's Hospital. 09/12/2012
35. Department of Animal and Avian Sciences, College of Agriculture and Natural Resources, University of Maryland, College Park. 09/28/2009

CONTRIBUTED PRESENTATIONS

1. Biophysics of Epigenetic and Chromatin Dynamics Workshop, Higgs Centre for Theoretical Physics, University of Edinburgh. Edinburgh, UK, 04/2018. (*Poster*)
2. American Physical Society (APS) March Meeting. Los Angeles, CA, 03/2018. (*Talk*)
3. Keystone Meeting on Cancer Epigenetics. Breckenridge, CO, 02/2018. (*Poster*)
4. Cold Spring Harbor Asia Meeting on Precision Cancer Biology. Suzhou, China, 09/2017. (*Poster*)
5. Keystone Meeting on Epigenetics and Human Disease. Seattle, WA, 01/2017. (*Poster*)
6. NCI Symposium on Chromosome Biology. Bethesda, MD, 11/2016. (*Poster*)
7. ENCODE Consortium Meeting. San Diego, CA, 06/2016. (*Poster*)
8. AACR Special Conference on Chromatin and Epigenetics in Cancer. Atlanta, GA, 09/2015. (*Poster*)
9. Keystone Meeting on Cancer Epigenetics. Santa Fe, NM, 02/2014. (*Poster*)
10. NCI Symposium on Chromosome Biology. Bethesda, MD, 04/2013. (*Poster*)
11. Cold Spring Harbor Laboratory Meeting on Systems Biology: Global Regulation of Gene Expression. Cold Spring Harbor, NY, 03/2012. (*Poster*)
12. Cold Spring Harbor Laboratory Meeting on Systems Biology: Global Regulation of Gene Expression. Cold Spring Harbor, NY, 03/2010. (*Poster*)
13. The 7th Asia Pacific Bioinformatics Conference. Beijing, China, 01/2009. (*Best Poster Award Winner*)
14. American Physical Society (APS) March Meeting. New Orleans, LA, 03/2008. (*Talk*)

MENTEES AND STUDENTS

Postdoctoral Associates

Zhenjia Wang, PhD (UVA, 01/2017–)
Sheng'en Shawn Hu, PhD (UVA, 11/2017–)

Graduate Students

Wuwei Tan (MS in Statistics, UVA, 03/2017–05/2018)
Yushan Brandon Feng (MS in Statistics, UVA, 05/2018–)

Undergraduate Students

Celina Shih (Johns Hopkins University, 05/2017–07/2017)
Yiren Wang (Peking University, 07/2017–06/2018)
Yayi Feng (UVA, 09/2017–)
Stephany Perez-Rojas (UVA, 01/2018–)
Javier Valcarcel (UVA, 01/2018–)

John Zhang (UVA, 02/2018–)
Yuantao Chen (UVA, 02/2018–)
Jeffrey Yoo (UVA, 02/2018–)
Michael Ferguson (UVA, 02/2018–)
Naifei Pan (UVA, 04/2018–)
Alexander An (UVA, 05/2018–)

Visiting Students/Scholars

Qi Li (PhD Candidate in Statistics, Tsinghua University, 01/2018–02/2018)
Wen Shen (Undergraduate Student, Nanjing University, 02/2018–05/2018)
Rongquan He, MD (PhD Candidate, Guangxi Medical University, 03/2018–)

PhD Committee

Jeffrey Xing (PhD Candidate, Biomedical Engineering, UVA, 01/2017–)

PROFESSIONAL SERVICES

Ad hoc grant reviewer Research Councils UK (RCUK) (2017)
 Netherlands Organisation for Scientific Research (NWO) (2017)

Ad hoc journal reviewer Nature Biotechnology
 Nature Genetics
 Nature Communications
 Genome Research
 Genome Biology
 EMBO Journal
 Nucleic Acids Research
 Cancer Research
 Bioinformatics
 Epigenetics
 PLoS Computational Biology
 BMC Bioinformatics
 BMC Genomics
 Scientific Reports
 Cell Discovery
 PLoS One
 IEEE/ACM Transactions on Computational Biology &
 Bioinformatics
 Computational Statistics and Data Analysis

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