

Chi Zhang

Assistant Professor

Center for Computational Biology and Bioinformatics

Department of Medical and Molecular Genetics

Indiana University, School of Medicine

*Adjunct in Department of Electrical and Computer
Engineering, Purdue University*

410 W. 10th St., Suite 5000 (Room 5021),

Indianapolis, IN, 46202

Phone: 317-278-9625, Email: czhang87@iu.edu

Web Page: <https://medicine.iu.edu/departments/genetics/faculty/27057/zhang-chi/>

Lab page: <https://zcslab.github.io/>

RESEARCH INTERESTS

- Development of cutting-edge statistical modeling method and machine learning method for large scale data analysis and integration.
- Low rank and local low rank representation of large matrix
- Knowledge graph and its application in biomedical data study
- Computational modeling of cancer and inflammatory disease microenvironment
- Develop statistical deconvolution method to predict the alterations of immune and stroma cells in tissue-based omics data.
- Single cell RNA-Seq data modeling, gene co-regulation analysis and applications in tissue gene expression
- Enhanced biological inference and interpretation from single cell multi-omics data.
-

EDUCATION

Ph.D. Bioinformatics with a secondary master's degree in statistics

Advisor: Dr. Ying Xu.

The University of Georgia, Athens, GA (2010.9-2015.11)

Thesis: Identification of the key micro-environmental alterations, genomic alterations and their associations in cancer initiation and progression

B.S. Bachelor of Science in Mathematics and Applied Mathematics

Peking University, Beijing, China (2006.9-2010.7)

WORKING EXPERIENCE:

2016.8-now Assistant Professor

Center for Computational Biology and Bioinformatics

Department of Medical and Molecular Genetics

Indiana University, School of Medicine

2017.09-now Adjunct Assistant Professor

Department of Electrical and Computer Engineering,
Purdue University

2016.01-08 Postdoc Fellow, the University of Georgia

2015-2016 Co-advisor of Undergraduate Research Thesis (BCMB 4990H)
Computational Systems Biology Laboratory,
The University of Georgia, Athens, GA

2014-2016 Instructor of Undergraduate Research Course (BIOL/BCMB 4960/4970)
Computational Systems Biology Laboratory,
The University of Georgia, Athens, GA

2010-2016 Graduate Research Assistant Advisor: Dr. Ying Xu
Computational Systems Biology Laboratory,
The University of Georgia, Athens, GA

2008-2010 Undergraduate Research Assistant Advisor: Dr. Hong Qu
Center of Bioinformatics (CBI), School of Life Sciences
Peking University Beijing, China,

AWARDS:

1. Outstanding investigator award
SCBA, Indiana US Nov 2019
2. Showalter Trust Young Investigator Award
Showalter foundation and Indiana CTSI Aug 2017
3. Graduate student excellence-in-research award. (One recipient in Life Sciences, five recipients in the whole school every year)
The University of Georgia. Feb 2016
4. Best poster award in the “Big data challenge in life sciences”
Atlanta, GA, US Oct 2015
5. Graduate school travel funding for talk “Cancer is not a bad luck disease” in JSM2015
The University of Georgia. Aug 2015
6. Best student publication award at Institute of Bioinformatics.
The University of Georgia. Mar 2015
7. Innovative and Interdisciplinary Research Grant.
The University of Georgia May 2013
8. Outstanding Graduate with honor.
Peking University Jul 2010

PUBLICATIONS (*corresponding author, +first author):

1. Changlin Wan, Wennan Chang, Tong Zhao, Mengya Li, Sha Cao, **Chi Zhang***. MEBF: a fast and efficient Boolean matrix factorization method. 2020. Proceedings of thirty fourth AAAI conference on Artificial Intelligence. (AAAI 2020) <https://doi.org/10.1609/aaai.v34i04.6072>
2. Changlin Wan, Wennan Chang, Tong Zhao, Sha Cao, **Chi Zhang***. Denoising individual bias for a fairer binary submatrix detection. 2020. The Conference on Information and Knowledge Management (CIKM 2020), Doi: 10.1145/3340531.3412156
3. Changlin Wan, Wennan Chang, Tong Zhao, Sha Cao, **Chi Zhang***. Geometric All-Way Boolean Tensor Decomposition, 2020, Conference on Neural Information Processing Systems. (NeurIPS 2020), arXiv:2007.15821
4. Yuanzhang Fang, Lifei Wang, Changlin Wan, Yifan Sun, Kevin Van der Jeught, Zhuolong Zhou, Tianhan Dong, Ka Man So, Tao Yu, Yujing Li, Haniyeh Eyvani, Austyn Colter, Edward Dong, Sha Cao, Jin Wang, Bryan P Schneider, George Sandusky, Yunlong Liu, **Chi Zhang***, Xiongbin Lu, Xinna Zhang. MAL2 drives immune evasion in breast cancer by suppressing tumor antigen presentation, 2020. The Journal of Clinical Investigation. <https://doi.org/10.1172/JCI140837>.
5. Norah Alghamdi, Wennan Chang, Pengtao Dang, Xiaoyu Lu, Changlin Wan, Zhi Huang, Jiashi Wang, Melissa Fishel, Sha Cao, **Chi Zhang***. scFEA: A graph neural network model to estimate cell-wise metabolic flux using single cell RNA-seq data. Genome Research 2020. doi: <https://doi.org/10.1101/2020.09.23.310656>
6. Zhigang Cai, **Chi Zhang**, Jonathan J Kotzin, Adam Williams, Jorge Henao-Mejia, Reuben Kapur. Role of lncRNA Morrbid in PTPN11(Shp2)E76K-driven juvenile myelomonocytic leukemia. Blood Advances, 2020. <https://doi.org/10.1182/bloodadvances.2020002123>
7. Wennan Chang, Changlin Wan, Yong Zang, **Chi Zhang***, Sha Cao*. Supervised clustering of high dimensional data using regularized mixture modeling, Briefings in Bioinformatics 2020. arXiv:2007.09720
8. Xiaoyu Lu, Szu-Wei Tu, Wennan Chang, Changlin Wan, Jiashi Wang, Yong Zang, Baskar Ramdas, Reuben Kapur, Xiongbin Lu, Sha Cao, **Chi Zhang***. SSMD: A semi-supervised approach for a robust cell type identification and deconvolution of mouse transcriptomics data. Briefings in Bioinformatics 2020.
9. Wennan Chang, Xinyu Zhou, Yong Zang, **Chi Zhang***, Sha Cao*. A New Algorithm using Component-wise Adaptive Trimming for Robust Mixture Regression. arXiv:2005.11599
10. Wennan Chang, Changlin Wan, Chun Yu, Weixin Yao, **Chi Zhang***, Sha Cao. RobMixReg: an R package for robust, flexible and high dimensional mixture regression. BioRxiv 2020. doi: <https://doi.org/10.1101/2020.08.02.233460>

11. Daniela Pucciarelli, Steven P Angus, Benjamin Huang, **Chi Zhang**, Hiroki J Nakaoka, Ganesh Krishnamurthi, Sourav Bandyopadhyay, D Wade Clapp, Kevin Shannon, Gary L Johnson, Jean L Nakamura. Nfl mutant tumors undergo transcriptome and kinome re-modeling after inhibition of either mTOR or MEK. *Molecular Cancer Therapeutics* 2020. DOI: 10.1158/1535-7163.MCT-19-1017
12. Yifei Zhang, Sha Cao, **Chi Zhang**, Yong Zang. A Bayesian Adaptive Phase I/II Clinical Trial Design with Late-onset Competing Risk Outcomes. *Biometrics* (2020). <https://doi.org/10.1111/biom.13347>
13. Kirstin B VanderWall, Kang-Chieh Huang, Yanling Pan, Sailee S Lavekar, Clarisse M Fligor, Anna R Allsop, Kelly A Lentsch, Pengtao Dang, **Chi Zhang**, Henry C Tseng, Theodore R Cummins, Jason S Meyer. Retinal Ganglion Cells With a Glaucoma OPTN (E50K) Mutation Exhibit Neurodegenerative Phenotypes when Derived from Three-Dimensional Retinal Organoids. *Stem Cell Reports* 2020. <https://doi.org/10.1016/j.stemcr.2020.05.009>
14. Zhigang Cai, Fabiola Aguilera, Baskar Ramdas, Swapna Vidhur Daulatabad, Rajneesh Srivastava, Jonathan J Kotzin, Martin Carroll, Gerald Wertheim, Adam Williams, Sarath Chandra Janga, **Chi Zhang**, Jorge Henao-Mejia, Reuben Kapur. Targeting Bim via a lncRNA Morrbid Regulates the Survival of Preleukemic and Leukemic Cells. *Cell reports* 2020. <https://doi.org/10.1016/j.celrep.2020.107816>
15. Julie A Mund, Su-Jung Park, Abbi E Smith, Yongzheng He, Li Jiang, Eric Hawley, Michelle J Roberson, Dana K Mitchell, Mohannad Abu-Sultanah, Jin Yuan, Waylan K Bessler, George Sandusky, Shi Chen, **Chi Zhang**, Steven D Rhodes, D Wade Clapp. Genetic disruption of the small GTPase RAC1 prevents plexiform neurofibroma formation in mice with neurofibromatosis type 1. *Journal of Biological Chemistry*. 2020. doi: 10.1074/jbc.RA119.010981
16. Jian Chen, Yun Tan, Fenghuan Sun, Likun Hou, **Chi Zhang**, Tao Ge, Huansha Yu, Chunxiao Wu, Yuming Zhu, Liang Duan, Liang Wu, Nan Song, Liping Zhang, Wei Zhang, Di Wang, Chang Chen, Chunyan Wu, Gening Jiang, Peng Zhang. Single-cell transcriptome and antigen-immunoglobulin analysis reveals the diversity of B cells in non-small cell lung cancer. *Genome Biology* 2020. <https://doi.org/10.1186/s13059-020-02064-6>
17. Zhi Huang, Travis S Johnson, Zhi Han, Bryan Helm, Sha Cao, **Chi Zhang**, Paul Salama, Maher Rizkalla, Christina Y Yu, Jun Cheng, Shunian Xiang, Xiaohui Zhan, Jie Zhang, Kun Huang. Deep learning-based cancer survival prognosis from RNA-seq data: approaches and evaluations. *BMC medical genomics* 2020. <https://doi.org/10.1186/s12920-020-0686-1>
18. Kevin Van der Jeught, Yifan Sun, Yuanzhang Fang, Zhuolong Zhou, Hua Jiang, Tao Yu, Jinfeng Yang, Malgorzata M Kamocka, Ka Man So, Yujing Li, Haniyeh Eyvani, George E Sandusky, Michael Frieden, Harald Braun, Rudi Beyaert, Xiaoming He,

- Xinna Zhang, **Chi Zhang**, Sophie Paczesny, Xiongbin Lu. ST2 as checkpoint target for colorectal cancer immunotherapy. *JCI Insight*. DOI: 10.1172/jci.insight.136073
19. Yuanzhang Fang, Lifei Wang, Changlin Wan, Yifan Sun, Kevin Van der Jeught, Zhuolong Zhou, Tianhan Dong, Kaman So1, Tao Yu1, Yujing Li, Yunlong Liu, **Chi Zhang***, Xiongbin Lu*, Xinna Zhang*. Mal2 drives immune evasion by reducing antigen presentation on tumor cells. (2020) *Journal of Clinical Investigation*.
 20. Andrea M Gross, Pamela L Wolters, Eva Dombi, Andrea Baldwin, Patricia Whitcomb, Michael J Fisher, Brian Weiss, AeRang Kim, Miriam Bornhorst, Amish C Shah, Staci Martin, Marie C Roderick, Dominique C Pichard, Amanda Carbonell, Scott M Paul, Janet Therrien, Oxana Kapustina, Kara Heisey, D Wade Clapp, **Chi Zhang**, Cody J Peer, William D Figg, Malcolm Smith, John Glod, Jaishri O Blakeley, Seth M Steinberg, David J Venzon, L Austin Doyle, Brigitte C Widemann. Selumetinib in children with inoperable plexiform neurofibromas. *New England Journal of Medicine* (2020). DOI: 10.1056/NEJMoa1912735
 21. Yan Guo, Xia Ning, Ewy Mathé, Kai Wang, Lang Li, **Chi Zhang**, Zhongming Zhao. Innovating Computational Biology and Intelligent Medicine: ICIBM 2019 Special Issue. *Gene* 2020. <https://doi.org/10.3390/genes11040437>
 22. **Chi Zhang***, Ewy Mathé, Xia Ning, Zhongming Zhao, Kai Wang, Lang Li, Yan Guo. The International Conference on Intelligent Biology and Medicine 2019 (ICIBM 2019): computational methods and applications in medical genomics. *BMC Medical Genomics*. <https://doi.org/10.1186/s12920-020-0678-1>
 23. Anjun Ma, Cankun Wang, Yuzhou Chang, Faith H Brennan, Adam McDermaid, Bingqiang Liu, **Chi Zhang**, Phillip G Popovich, Qin Ma. IRIS3: integrated cell-type-specific regulon inference server from single-cell RNA-Seq. *Nucleic Acids Res*, 2020. doi: 10.1093/nar/gkaa394
 24. Precise targeting of POLR2A for treating triple negative breast cancer with Chr17p loss. Xiongbin Lu, Yujing Li, Yifan Sun, Kevin Van der Jeught, Michael Kulke, Pahl Andreas, Xinna Zhang, Xiaoming He and **Chi Zhang**. *Cancer Research* 2020. DOI: 10.1158/1538-7445.SABCS19-P3-10-19
 25. Z Zhao, Y Dai, **C Zhang**, E Mathé, L Wei, K Wang. The International Conference on Intelligent Biology and Medicine (ICIBM) 2019: bioinformatics methods and applications for human diseases, 2019, *BMC bioinformatics* 20 (24), 1-5. <https://doi.org/10.1186/s12859-019-3272-9>
 26. Changlin Wan, Wennan Chang, Yu Zhang, Fenil Shah, Xiaoyu Lu, Yong Zang, Anru Zhang, Sha Cao, Melissa L Fishel, Qin Ma, **Chi Zhang***, LTMG: a novel statistical modeling of transcriptional expression states in single-cell RNA-Seq data, *Nucleic Acids Research*, Volume 47, Issue 18, 10 October 2019, Page e111, <https://doi.org/10.1093/nar/gkz655>

27. Jin Zhao, Haodi Feng, Daming Zhu, Chi Zhang & Ying Xu. DTA-SiST: de novo transcriptome assembly by using simplified suffix trees. BMC Bioinformatics 2019. <https://doi.org/10.1186/s12859-019-3272-9>
28. Fenil Shah, Olivia Babb, **Chi Zhang**, Silpa Gampala, Emily Zhang, Steven D Rhodes, Andrew R Tee, Brian Calver, Ellie Rad, Verena Staedtke, Karen E Pollok, D Wade Clapp, Mark R Kelley, Melissa L Fishel. Signaling through Ref-1 and STAT3 in soft tissue sarcoma (MPNST) and the effects of perturbing this pathway on tumor cell survival and gene expression. MOLECULAR CANCER THERAPEUTICS, 2019. DOI: 10.1158/1535-7163
29. Juan Xie, Anjun Ma, Yu Zhang, Bingqiang Liu, Sha Cao, Cankun Wang, Jennifer Xu, **Chi Zhang***, Qin Ma*, QUBIC2: a novel and robust biclustering algorithm for analyses and interpretation of large-scale RNA-Seq data, Bioinformatics, btz692, <https://doi.org/10.1093/bioinformatics/btz692>
30. Yu Zhang, Changlin Wan, Pengcheng Wang, Wennan Chang, Yan Huo, Jian Chen, Qin Ma, Sha Cao, **Chi Zhang***. M3S: A comprehensive model selection for multi-modal single-cell RNA sequencing data. BMC Bioinformatics (2019), ICIBM2019 special issue. BMC bioinformatics 20 (24), 1-5
31. Hai Lin, Katherine A Hargreaves, Rudong Li, Jill L Reiter, Yue Wang, Matthew Mort, David N Cooper, Yaoqi Zhou, Chi Zhang, Michael T Eadon, M Eileen Dolan, Joseph Ipe, Todd C Skaar, Yunlong Liu. RegSNPs-intron: a computational framework for predicting pathogenic impact of intronic single nucleotide variants. Genome Biology, 2019. <https://doi.org/10.1186/s13059-019-1847-4>
32. Ruchi Pandey, Baskar Ramdas, Changlin Wan, George Sandusky, Morvarid Mohseni, **Chi Zhang**, and Reuben Kapur. SHP2 inhibition reduces leukemogenesis in models of combined genetic and epigenetic mutations. The Journal of Clinical Investigation. 2019 10.1172/JCI130520.
33. Melissa L Fishel, Hanyu Xia, Jack McGeown, David W McIlwain, May Elbanna, Ariel A Craft, Hristos Z Kaimakliotis, George E Sandusky, **Chi Zhang**, Roberto Pili, Mark R Kelley, Travis J Jerde, Antitumor Activity and Mechanistic Characterization of APE1/Ref-1 Inhibitors in Bladder Cancer, Molecular cancer therapeutics, 2019 DOI: 10.1158/1535-7163.MCT-18-1166
34. Menghao Huang, Hyeong Geug Kim, Xiaolin Zhong, Chuanpeng Dong, Brian Zhang, Zhigang Fang, Yang Zhang, Xiaoyu Lu, Romil Saxena, Yunlong Liu, **Chi Zhang**, Suthat Liangpunsakul, X Charlie Dong, Sestrin 3 Protects Against Diet-Induced Nonalcoholic Steatohepatitis in Mice Through Suppression of Transforming Growth Factor beta Signal Transduction, Hepatology. 2019 Jun 19. doi: 10.1002/hep.30820
35. Marta Codrich, Marina Comelli, Matilde Clarissa Malfatti, Catia Mio, Dilara Ayyildiz, **Chi Zhang**, Mark R Kelley, Giovanni Terrosu, Carlo EM Pucillo, Gianluca

- Tell. Inhibition of APE1-endonuclease activity affects cell metabolism in colon cancer cells via a p53-dependent pathway. 2019, DNA repair 82, 102675
36. Sumegha Mitra, Kartikeya Tiwari, Ram Podicheti, Taruni Pandhiri, Douglas B Rusch, Andrea Bonetto, Chi Zhang, Anirban K Mitra. Transcriptome Profiling Reveals Matrisome Alteration as a Key Feature of Ovarian Cancer Progression. 2019. *Cancers* 11 (10), 1513
 37. Jinyu Yang, Anjun Ma, Adam D Hoppe, Cankun Wang, Yang Li, **Chi Zhang**, Yan Wang, Bingqiang Liu, Qin Ma. Prediction of regulatory motifs from human Chip-sequencing data using a deep learning framework. *Nucleic Acids Research*, Volume 47, Issue 15, 05 September 2019, Pages 7809–7824, <https://doi.org/10.1093/nar/gkz672>
 38. Jing Zhang, Joydeep Ghosh, Safa F Mohamad, **Chi Zhang**, Xinxin Huang, Maegan L Capitano, Andrea M Gunawan, Scott Cooper, Bin Guo, Qingchun Cai, Hal E Broxmeyer, Edward F Srour. CD166 engagement augments mouse and human hematopoietic progenitor function via activation of stemness and cell cycle pathways. *Stem Cells*. 2019 <https://doi.org/10.1002/stem.3053>
 39. Clarisse M. Fligor, Kirstin B. Langer, Akshayalakshmi Sridhar, Yuan Ren, Priya K. Shields, Michael C. Edler, Sarah K. Ohlemacher, Valentin M. Sluch, Donald J. Zack, **Chi Zhang**, Daniel M. Suter & Jason S. Meyer. Three-Dimensional Retinal Organoids Facilitate the Investigation of Retinal Ganglion Cell Development, Organization and Neurite Outgrowth from Human Pluripotent Stem Cells. **Scientific Reports**. (2019) <https://doi.org/10.1038/s41598-018-32871-8>
 40. Yong Zang, Beibei Guo, Yan Han, Sha Cao, **Chi Zhang**. A Bayesian adaptive marker-stratified design for molecularly targeted agents with customized hierarchical modeling. *Statistics in Medicine* 2019. <https://doi.org/10.1002/sim.8159>
 41. Yong Zang, Wing Kam Fung, Sha Cao, Hon Keung Tony Ng, Chi Zhang. Robust tests for gene-environment interaction in case-control and case-only designs. (2018) *Computational Statistics & Data Analysis*. <https://doi.org/10.1016/j.csda.2018.08.014>
 42. Yunhua Liu, Hanchen Xu, Kevin Van der Jeught, Yujing Li, Sheng Liu, Lu Zhang, Yuanzhang Fang, Xinna Zhang, Milan Radovich, Bryan P. Schneider, Xiaoming He, Cheng Huang, Chi Zhang, Jun Wan, Guang Ji, and Xiongbin Lu. Somatic mutation of the cohesin complex subunit confers therapeutic vulnerabilities in cancer. **The Journal of Clinical Investigation**. (2018). <https://doi.org/10.1172/JCI98727>.
 43. Huiyan Sun⁺, Chi Zhang⁺, Sha Cao, Tao Sheng, Ning Dong, Ying Xu. Fenton Reactions Drive Nucleotide and ATP Syntheses in Cancer. **Journal of Molecular Cell Biology**. (2018) DOI: <https://doi.org/10.1093/jmcb/mjy039>.
 44. Chi Zhang, Xiyin Wang, Yanett Anaya, Luca Parodi, Lijun Cheng, Matthew L. Anderson, Shannon M. Hawkins. Distinct Molecular Pathways in Ovarian

- Endometrioid Adenocarcinoma with Concurrent Endometriosis. **International Journal of Cancer**. (2018) . <https://doi.org/10.1002/ijc.31768>
45. Yigang Kwak, Burair Alsaihati, Chi Zhang, Ying Xu, Sha Cao. The interplay of immune components and ECM in oral cancer. (2018). doi: <https://doi.org/10.1101/259622>
 46. Yu Zhang, Sha Cao, Jing Zhao, Qin Ma, Chi Zhang*. MRHCA: A nonparametric statistics-based method for hub and co-expression module identification in large gene co-expression network. **Quantitative Biology** (2017). DOI <https://doi.org/10.1007/s40484-018-0131-z>
 47. Fang Fang, Horacio Cardenas, Hao Huang, Guanglong Jiang, Susan M. Perkins, Chi Zhang, Harold N. Keer, Yunlong Liu, Daniela Matei, Kenneth P. Nephew. Genomic and Epigenomic Signatures of Platinum Re-sensitization in Ovarian Cancer. **Cancer Research** (2017). DOI: 10.1158/0008-5472.CAN-17-1492
 48. Sha Cao, Tao Sheng, Xin Chen, Qin Ma, Chi Zhang*. A probabilistic model-based biclustering method for single-cell transcriptomic data analysis. **BioRxiv** (2017). doi: <https://doi.org/10.1101/181362>
 49. Cao S, Zhu X, Zhang C, Qian H, Schuttler HB, Gong J, Xu Y. Competition between DNA Methylation, Nucleotide Synthesis, and Antioxidation in Cancer versus Normal Tissues. **Cancer Research** (2017);77(15):4185-95. doi: 10.1158/0008-5472.CAN-170262. PubMed PMID: 28611042.
 50. Zhang Y, Xie J, Yang J, Fennell A, Zhang C* and Ma Q*, QUBIC: a Bioconductor package for qualitative biclustering analysis of gene co-expression data. **Bioinformatics** (2016) doi: 10.1093/bioinformatics/btw635
 51. Zhang C, Chao L, Cao S and Xu Y. Elucidation of Drivers of High-Level Production of Lactates throughout a Cancer Development. **Journal of Molecular Cell Biology**. (2015) DOI: 10.1093/jmcb/mjv031
 52. Liu C+, Zhang C+, Su J, Zhang DS, Cao S. Stresses drive a cancer's initiation, progression and metastasis: Critical comments on the book "Cancer Bioinformatics". **Journal of bioinformatics and computational biology**. (2015) DOI: 10.1142/S021972001571002X
 53. Cao S+, Zhang C+, and Xu Y. Somatic Mutations May Not Be the Primary Drivers of Cancer Formation. **International Journal of Cancer**. (2015) DOI: 10.1002/ijc.29639
 54. Yao F+, Zhang C+, Du W, Chao L, Ying Xu. Identification of Gene-expression Signatures and Protein Markers for Breast Cancer Grading and Staging. **Plos One**. (2015) DOI: 10.1371/journal.pone.0138213
 55. Chen X, Ma Q, Rao XL, Tang YH, Zhang C, Wang Y, Lo GY, Mao XZ, Dixon R and Xu Y. Genome-Scale Identification of Cell-Wall Related Genes in Switchgrass

- through Comparative Genomics and Computational Analyses of Transcriptomic Data, **BioEnergy Research**. (2016) DOI:10.1007/s12155-015-9674-2
56. Zhang C, Cao S, Toole B, and Xu Y. (2014) Cancer may be a pathway to cell survival under persistent hypoxia and elevated ROS: A model for solid-cancer initiation and early development. **International Journal of Cancer**: DOI: 10.1002/ijc.28975.
 57. Zhang C, Cao S and Xu Y. (2014) Population Dynamics inside Cancer Biomass Driven by Repeated Hypoxia-Reoxygenation Cycles. **Quantitative Biology**. Doi: 10.1007/s40484-014-0032-8
 58. Cui J, Mao X, Ma Q, Zhou W, Zhang C, et al. (2014) Comprehensive characterization of the genomic alterations in human gastric cancer. **International Journal of Cancer**. DOI: 10.1002/ijc.29352
 59. Xu K, Mao X, Cui J, Zhang C, et al. (2013) Elucidation of How Cancer Cells Avoid Acidosis through Comparative Transcriptomic. **PLOS ONE**. DOI: 10.1371/journal.pone.0071177
 60. Xu K, Mao X, Mehta M, Cui J, Zhang C, et al. (2012) A Comparative Study of GeneExpression Data of Basal Cell Carcinoma and Melanoma Reveals New Insights about the Two Cancers. **PLOS ONE** 7(1): e30750. DOI:10.1371/journal.pone.0030750
 61. Jin Zhao, Haodi Feng, Daming Zhu, Chi Zhang, Ying Xu. IsoTree: De Novo Transcriptome Assembly from RNA-Seq Reads . ISBRA 2017: 71-83
 62. Changlin Wan, Wennan Chang, Tong Zhao, Mengya Li, Sha Cao, **Chi Zhang***. MEBF: a fast and efficient Boolean matrix factorization method. AAAI 2020
 63. Changlin Wan, Wennan Chang, Tong Zhao, Sha Cao, **Chi Zhang***. Denoising individual bias for a fairer binary submatrix detection. The Conference on Information and Knowledge Management. CIKM 2020
- (+ for co-first author, * for corresponding author)

BOOK CHAPTERS:

1. Zhang C+, Sheng T+, Cao S, Issa-Boube S, Tang T, Zhu X, Dong N, Du W, Xu Y. Autophagy in Cancer Cells vs Cancer Tissues: two different stories. [Book] Targeting Autophagy in Cancer Therapy, ed. J. Yang. 2016: Springer.
2. Wang Y, Du W, Liang Y, Chen X, Zhang C, Pang W, Xu Y, PUEPro: A Computational Pipeline for Prediction of Urine Excretory Proteins. [Book] Advanced Data Mining and Applications. (2016) DOI: 10.1007/978-3-319-49586-6_5

CONFERENCE TALKS:

- Dec 2020 Geometric All-Way Boolean Tensor Decomposition, **NeurIPS 2020**, virtual meeting

- Oct 23rd 2020 Denoising individual bias for a fairer binary submatrix detection, **CIKM 2020**, virtual meeting
- Feb 10th 2020 Fast and Efficient Boolean Matrix Factorization by Geometric Segmentation, **AAAI 2020**, New York, NY, USA
- Jun 16th 2018 “LTMG (Left truncated mixture Gaussian) based modeling of transcriptional regulatory heterogeneities in single cell RNA-seq data” in **2018 ISCA Applied Statistics Symposium**, New Brunswick, USA
- Jun 10th 2018 “Single cell RNA-seq data analysis” in **2018 International Conference on Intelligent Biology and Medicine**, Los Angeles, CA, USA
- Aug 11th 2015 “Cancer is not a bad luck disease” in **2015 Joint Statistical Meetings**, Seattle, US
- Jul 10th 2015 “Modelling large biological network and deciphering cancer microenvironmental stresses by multiple data types”, a **joint seminar with ICSB2015** in Jilin University, Changchun, China

CONFERENCE POSTERS:

- Feb 15th 2020 Abstract P3-10-19: Precise targeting of POLR2A for treating triple negative breast cancer with Chr17p loss. **AACR 2020**, virtual meeting
- Nov 4th 2020 A semi-supervised approach for cell phenotypic and functional estimation in tissue microenvironment, **PQG meeting 2019**, Harvard University, Boston, MA, USA
- Jul 1st 2019 A new deconvolution algorithm for accurate assessing immune and stromal cell populations in mouse transcriptomic data, **AACR 2019**, Atlanta, GA, USA
- Jul 1st 2019 A semi-supervised deconvolution method for quantifying the composition and activity of tumor-infiltrating cell types, **AACR 2019**, Atlanta, GA, USA
- Jul 1st 2019 Statistical modeling of transcriptional regulatory states in single-cell RNA-Seq data of tumor and infiltrated immune cells, **AACR 2019**, Atlanta, GA, USA
- Jul 1st 2018 Combination therapy in PDAC involving blockade of the APE1/Ref-1 signaling pathway: An investigation into drug synthetic lethality and anti-neuropathy therapeutic approach, **AACR 2018**. Chicago, IL, USA
- Nov 8th 2017 Construction of cell type specific gene co-regulation signatures based on single cell transcriptomics data. **Cold Spring Harbor Single cell analysis meeting**, Cold Spring Harbor, USA.
- Apr 1st 2017 Abstract 5547: A computational approach to predict tissue level cell cycle regulatory network for normal proliferating and cancer cells. **AACR 2017 Annual meeting**, Washington DC, USA.

- Apr 1st 2017 Abstract 1554: Development of a deconvolution algorithm for tissue-based gene expression data. **AACR 2017 Annual meeting**, Washington DC, USA.
- Apr 1st 2017 Abstract 404: A bi-clustering based computational approach to identify molecular markers for Neoadjuvant chemotherapy outcome prediction in complement to cancer subtype classifications. **AACR 2017 Annual meeting**, Washington DC, USA.
- Apr 1st 2017 Abstract 560: A pan-inflammatory and precancerous disease analysis reveals key biological characteristics in chronic inflammatory diseases with high oncogenic risk. **AACR 2017 Annual meeting**, Washington DC, USA.
- Oct 12th 2014 “Modeling the micro-environmental alterations through cancer progression via integrative analysis of cancer transcriptomic data with multiple omics data types” in the **Big data challenges in Life Sciences**, UGA
- Feb 24th 2014 “Prediction of transcriptional regulatory logic in Clostridium Thermocellum ATCC 27405” in the RNA Symposium hosted by Department of Biochemistry and Molecular Biology, UGA
- Nov 7th-9th 2013 “Flux estimation analysis (FEA) reveals key alterations of metabolic flux in colorectal cancer” in the 9th international conference on Bioinformatics, Georgia tech.
- Jul 22nd-25th 2013 “Prediction of transcriptional regulatory logic in Clostridium Thermocellum ATCC 27405” in the BESC (Bio-energy Science Center) retreat 2013, Chattanooga, TN

INVITED TALKS:

- Sep 18th 2020 Development of a new method to identify gene co-regulation modules in scRNA-seq data. Department of Computer Science, University of Missouri
- Nov 23th 2019 Computational modeling of Cancer Micro-environment via integrating single cell and bulk tissue multi-omics--Quantitative challenges in Cancer Immunology and Immunotherapy. Department of Medical and Molecular Genetics, Indiana University School of Medicine
- Mar 18th 2019 Computational modeling of Cancer Micro-environment via integrating single cell and bulk tissue transcriptomics data – with a focus on local low rank structure. Center for Computational Biology and Bioinformatics, Indiana University School of Medicine
- Mar 12th 2019 Proper extraction and representation of low rank modules in gene expression data studies -- with a focus on cancer micro-environment, University of Wisconsin Madison
- Mar 12th 2019 Proper extraction and representation of low rank modules in gene expression data studies -- with a focus on cancer micro-environment, University of Wisconsin Madison
- Jun 17th 2018 Statistical modeling of single cell RNA-seq data, ICSA2918
- Jun 10th 2018 Single cell RNA-seq data modeling workshop, ICIBM2018

- Feb 24th 2017 “Linking cancer genomics landscape with transcriptomics alterations– a computational approach to predict functional impact caused by individual or collective effect of somatic mutations” Department of Biostatistics, IUPUI.
- Feb 17th 2017 “Bi-clustering based omics data modeling – from commonality to heterogeneity” Department of Electronic Computer Engineering, IUPUI.
- Feb 7th 2017 “Linking cancer genomics landscape with transcriptomics alterations– a computational approach to predict functional impact caused by individual or collective effect of somatic mutations” Department of Statistics, Purdue University.
- Dec 7th 2016 “Computational prediction of cell components in cancer tissue data and their associations with genomic mutations” College of Pharmacy, the University of Texas at Austin.
- Oct 21st 2016 “Development of novel bi-clustering algorithm and its application in single cell RNA-seq data analysis and identification of gain or loss of functions of somatic mutations” Department of BioHealth Informatics, IUPUI.
- Sep 28th 2016 “Computational modeling of cancer micro-environment by using large scale data analysis” Center for Computational Biology and Bioinformatics, IUSM.
- Mar 9th 2016 “Understanding Malignant Transformation from Chronic Inflammation: a data mining approach.” Department of Computational Medicine & Bioinformatics, University of Michigan
- Feb 26th 2016 “Understanding Malignant Transformation from Chronic Inflammation: a data mining approach.” Institute of Bioinformatics, the University of Georgia
- Jan 4th 2016 “Understanding Malignant Transformation from Chronic Inflammation: a data mining approach.” Center for Computational Biology and Bioinformatics. Indiana University, Medical School
- Feb 25th 2016 “Understanding Malignant Transformation from Chronic Inflammation: a data mining approach” in Institute of Bioinformatics, the University of Georgia
- Jan 4th 2016 “Understanding Malignant Transformation from Chronic Inflammation: a data mining approach” in Center for Computational Biology and Bioinformatics, University of Indiana School of Medicine
- Oct 16th 2015 “A pan-inflammatory diseases study reveals key characteristics of the cancer prone diseases and their possible roles in cancer initiation” in Department of Biostatistics and Bioinformatics, Emory University
- Nov 21st 2014 “Identification of dynamic cell populations in cancer biomass” in Department of Biostatistics and Bioinformatics, Emory University
- Nov 14th 2014 “Identification of dynamic cell populations in cancer biomass in response to repeated hypoxia and reoxygenation” in Institute of Bioinformatics, the University of Georgia

Aug 11th 2014 “Cancer may be a pathway to cell survival under persistent hypoxia and elevated ROS –a model of cancer initiation” at Dr. Jun Liu’s lab,
Department of Statistics, Harvard University
Jul 22nd 2014 “Models of cancer development driven by micro-environmental stresses”
at Dr. Zhiping Weng’s lab, University of Massachusetts Medical School
Jun 19th 2013 “Computational modelling of biological networks” in Norman Bethune
University of Medical Science, Changchun, China
Jun 2011 “Introduction of bioinformatics and cancer bioinformatics to
undergraduates” in School of Mathematical Sciences, Peking University,
Beijing, China

ACTIVE FUDNING SUPPORTS:

Project title: Metabolic adaptation in lymphoid malignancies

Source of Support: NIH, 1R01CA244625-01

Total Award Amount: \$2,166,318

Total Award Period: 09/01/2019 – 08/31/2024

Person Months Per Year Committed to the Project: 0.36 Cal mos.

Project title: IUSM Alzheimer's Disease Drug Discovery Center

Source of Support: NIH, 1U54AG065181-01

Total Award Amount: \$35,372,142

Total Award Period: 09/01/2019 – 08/31/2024

Person Months Per Year Committed to the Project: 1.8 Cal mos.

Project title: Osteomacs and megakaryocytes interact to regulate hematopoietic stem cell function

Source of Support: NIH, 1R01DK118782-01A1

Total Award Amount: \$1,585,000

Total Award Period: 09/01/2019 – 08/31/2024

Person Months Per Year Committed to the Project: 0.3 Cal mos.

Project title: Construction of cell type specific gene co-regulation signatures based on single cell transcriptomics data

Source of Support: NIH, 1R01GM131399-02

Total Award Amount: \$304,812

Total Award Period: 02/01/2019-12/31/2023

Person Months Per Year Committed to the Project: 1 Cal mos.

Project title: Transcriptional Factor SOX2, LncRNA HBL1, microRNA1 and PRC2 Epigenetic Complex Compose a Network to Orchestrate Cardiac Differentiation from Human Pluripotent Stem Cells

Source of Support: NIH, 1R01HL147871-01

Total Award Amount: \$154,047

Total Award Period: 07/01/2019-06/30/2023

Person Months Per Year Committed to the Project: 0.6 Cal mos.

Project title: Hyperglycemia mediated myeloproliferative disease

Source of Support: NIH, 5R01HL140961-02

Total Award Amount: \$2,329,868

Total Award Period: 04/01/2019 – 03/31/2023

Person Months Per Year Committed to the Project: 0.45 Cal mos.

Project title: CD166 Regulates Human and Murine Hematopoietic Stem Cell Function and the Hematopoietic Niche

Source of Support: NIH, 1R01DK108342-01A1

Total Award Amount: \$1,771,875

Total Award Period: 02/01/2019-12/31/2023

Person Months Per Year Committed to the Project: 0.3 Cal mos.

Project title: Targeting Novel Pathways in JMML

Source of Support: NIH, 5R01HL146137-02

Total Award Amount: \$1,771,875

Total Award Period: 01/15/2019 – 12/31/2022

Person Months Per Year Committed to the Project: 0.6 Cal mos.

Project title: F-box Ubiquitin ligases destabilize neurofibromin

Source of Support: NIH, 5R01NS104489-02

Total Award Amount: \$1,722,655

Total Award Period: 09/01/2018 – 08/31/2023

Person Months Per Year Committed to the Project: 0.6 Cal mos.

Project title: Developmental and HyperActive Ras Tumor (SPORE)

Source of Support: NIH, 5U54CA196519-05

Total Award Amount: \$11,044,527

Total Award Period: 09/01/2015-08/31/2020

Person Months Per Year Committed to the Project: 1.2 Cal mos.

Project title: Exploiting the Ref-1 node in pancreatic cancer: tailoring new pancreatic cancer therapy using multi-targeted combinations

Source of Support: NIH, 5R01CA167291-08

Total Award Amount: \$2,766,192

Total Award Period: 03/09/2018 – 02/28/2023

Person Months Per Year Committed to the Project: 0.6 Cal mos.

Project title: Controlling Influences of Oxygen Tension and CD26/DPP4 Enzymatic Activity on Regulation of Hematopoietic Stem/Progenitor Cells and Hematopoiesis During Health, Ageing, and Disease

Source of Support: NIH, 5R35HL139599-03

Total Award Amount: \$5,376,728

Total Award Period: 05/01/2018-04/30/2025

Person Months Per Year Committed to the Project: 0.6 Cal mos.

COMPLETED FUDNING SUPPORTS:

Title	Granting Agency	Role	% Effort	Amount	Dates
Comprehensive identification of the functional impacts led by individual and collective effects of gene mutations in acute myeloid leukemia (AML)	Showalter Young Investigator Award, Indiana CTSI	PI	10%	\$50,000	07/01/2017-06/30/2018

TEACHING EXPERIENCES:

Indiana University School of Medicine

GRADUATE

Course #	Short Title	Format	Role	Term	Enrollment
CCBB Online course	Elementary Bioinformatics for Biologists	Online	Instructor	Spring 2020	110
G788	Next Gen Sequencing	3 cr	Co-Instructor	Fall 2019	33 students
G848	Bioinformatics, Genomics, Proteomics, and Systems Biology	2 cr	Lecturer	Spring 2019	30 students

G788	Next Gen Sequencing	3 cr	Co-Instructor	Fall 2018	23 students
G848	Bioinformatics, Genomics, Proteomics, and Systems Biology	2 cr	Lecturer	Spring 2018	23 students
G788	Next Gen Sequencing	3 cr	Lecturer	Fall 2017	25 students

University of Georgia

Lecturer	Cancer bioinformatics (BINF8125), the University of Georgia. 2016 spring: Giving 10-12 lectures (1h15min per class) for the graduate level class through the whole semester.
Instructor	Undergraduate Research Course (BIOL/BCMB 4960/4970L) in Computational Systems Biology Laboratory, the University of Georgia. 2014 spring: Reconstruction of Tp53 network, 7 students. 2014 summer: Identification metastasis associated mutations, 5 students. 2014 fall: Evaluating the possible patient age related bias and biological characteristics in TCGA data, 3 students. 2015 spring: Prediction gain or loss of function of Tp53, 2 students.
Co-advisor	Undergraduate Research Thesis (BCMB 4990H) in Computational Systems Biology Laboratory, the University of Georgia: 2015 fall: The role of autophagy in colon cancer progression, 1 students
Teaching assistant	Dragon star 2015 Cancer System Biology Course in Jilin University, Changchun, China July 2015: Teaching assistant
Teaching assistant	Cancer system biology workshop in Jilin University, Changchun, China Jun 2013: Workshop teaching assistant
Instructor	“Introduction of bioinformatics and cancer bioinformatics to Undergraduates” in summer research workshop for undergraduates in School of Mathematical Sciences, Peking University, Beijing, China Jun 2011: Three lectures to introduce the possible bioinformatics topics

MENTORING EXPERIENCE:

Indiana University, School of Medicine and IUPUI

Individual	Role	Inclusive Dates
Tanner Jacobson	Advisor of research rotation	2016.10 – 2016.12
Wennan Chang	Ph.D advisor	2017.08 – now
Changlin Wan	Ph.D advisor	2017.08 – now
Dr. Yan Han	Advisor to master degree	2017.12 – now

Arafat Aljoufi	Research Advisory Committee	2017.12 – now
Xiaoyu Lu	Ph.D advisor	2018.04 – now
Enze Liu	Research Advisory Committee	2018.05 – now
Brooke Richardson	Research Advisor of summer research internship	2018.05 – 2018.08
Jordan Lyles Holly	Research Advisor of the future scientist program	2018.06 – 2018.08
Kaitlyn Elizabeth Collins	Research Advisory Committee	2018.06 – now
Dr. Yu Zhang	Advisor of the visiting scholar	2018.07 – now
Yan Huo	Advisor of the visiting scholar	2018.08 – now
Siyuan Qi	Advisor of hourly paid master student	2018.10 – now
Pengcheng Wang	Advisor of hourly paid master student	2018.10 – now
Siwei Du	Advisor to master degree	2018.10 – now
Norah Alghamdi	PhD advisor	2018.10 – now
Aida Yazdanparast	Thesis Advisory Committee	2018.11 – now
Xinyu Zhou	Co-advisor of the visiting scholar	2018.11 – now
Pengtao Dang	PhD Advisor	2019.08 – now
Alex White	PhD Co-Advisor	2019.08 – now

University of Georgia

1. Burair Alsaihati (2015-present), Department of Biology, the University of Georgia, Ph.D student
2. Fang Yao (2015-present), Jilin University, Graduate student
3. Samira Issa-Boube (2014-present), Department of Biology, the University of Georgia, Undergraduate student
4. Hanyuan Zhang (2014-present), Jilin University, Graduate student
5. Huiyan Sun (2014-present), Jilin University, Graduate student
6. Tianxiao Tao (2014-2015), Department of Biochemistry and Molecular Biology, the University of Georgia, Undergraduate student
7. Nicholas Allen Major (2014-2015), Department of Biochemistry and Molecular Biology, the University of Georgia, Undergraduate student
8. Samuel Kwak (2014), Department of Biochemistry and Molecular Biology, the University of Georgia, Undergraduate student.
9. Shreenal Hitendra Patel (2014), Department of Biochemistry and Molecular Biology, the University of Georgia, Undergraduate student.
10. Shivani Reddy (2014), Department of Biochemistry and Molecular Biology, the University of Georgia, Undergraduate student.
11. Yuan Tian (2013-2014), Jilin University, Graduate student
12. Peilin Yang (2015-2016), Jilin University, Undergraduate student

13. Yue Wu (2016-present), the University of Georgia, Undergraduate-Graduate student

ACADEMIC SERVICES:

- 2020 Program Committee, KDD
- 2020 Session Chair ENAR, KDD
- 2018-2019 Program Committee Chair, ICIBM (International Conference on Intelligent Biology and Medicine)
- 2016-now Program Committee Member, International Symposium on Bioinformatics Research and Applications
- 2016-now Technical committee member, International Conference on Bioinformatics and Biomedical Technology
- 2016-now Reviewer, Oncotarget (1)
- 2016-now Program Committee Member, The IEEE International Conference on Bioinformatics and Biomedicine (9)
- 2015-now Editorial Board Member, BMC Genomics (5)
- 2012-now Editorial Board Member, PLOS One (14)
- 2014-now Editorial Board Member, IEEE Transactions on Computational Biology and Bioinformatics (6)
- 2014 Reviewer, Mathematical Biosciences (4)
- 2012 Reviewer, International Conference on Intelligent Biology and Medicine (1)
- 2011 Reviewer, International Symposium on Bioinformatics Research and Applications (1)

SYNERGISTIC ACTIVITIES

- [1] Program Committee Chair of International Conference on Intelligent Biology and Medicine. Program Committee member and session chair of ACM SIGKDD, IEEE BIBM, IJCAI, ISGRA, ENAR. Editorial Board Member/Reviewer of the Journals of IEEE Transactions in Computational Biology and Bioinformatics, Bioinformatics, Briefings in Bioinformatics, NeurIPs, Nucleic Acids Research and Genome Biology. Member of the American Association for Cancer Research (AACR). Member of Center for Computational Biology and Bioinformatics, Indiana University School of Medicine (IUSM). Role: Coordinate and oversight experimental design, sequencing, and provide method development and analysis of the single cell RNA-Seq data generated at IUSM and Purdue University.
- [2] Development of a series of novel Boolean data representation algorithm, including the first (i) fairness adjustment, (ii) $O(N)$ Boolean matrix decomposition, and (iii) high-order Boolean tensor decomposition methods. The methods are currently utilized to improve the prediction and recommendation of substitutable and complementary items at Amazon.
- [3] Advising and mentoring eleven graduate research assistants from four departments, i.e., Medical and Molecular Genetics (IUSM), Department of Biostatistics (IUSM), Electronic and Computer Engineering (Purdue University), Department of Bio-health Informatics (IUPUI). Mentored four undergraduate student and five high school students from SEED&STEM “future scientist” project at IUPUI since the summer of 2017. Development of a summer intern program with IUPUI and DePauw University to provide early exposure of computational biology to the undergraduate and high school students.

A total of 4 students took the internship in 2017-2020. A pathway of training undergraduate at IUPUI and DePauw to the Genetic Counseling Master program at Medical and Molecular Genetics Department IUSM was developed, two students have been enrolled to the graduate program.

- [4] Development a new hands-on graduate course (with three faculty members of Medical and Molecular Genetics, IUSM) named “Introduction to Next Generation Sequencing” in 2017-2020. A total of 42, 35 and 37 graduate students from six departments across IUSM, IUPUI, and Purdue University took this course in the fall of 2017, 2018 and 2019. As a result, the students are now incorporating the cutting-edge data analysis methods in their research topics. Development of a new course “Statistical Learning Methods in Bioinformatics” in 2019. Developed a new online course “Elements of Bioinformatics for Biologists” during the COVID-19 quarantine with Peer Leading Lectures provided by high school trainees (achieved more than 100 subscribers and 10,000 watches on YouTube).
- [5] Development of multiple knowledge bases to facilitate the research supported by the precision health initiative (PHI) of Indiana University School of Medicine, including for the TREAT-AD and DHART-SPORE projects. Developed a series of knowledge base and webservers to facilitate the precision health research including the recent epidemiology study of the spreading of COVID-19 at Indiana State. Development of a knowledge base: <https://github.com/zcslab/IRKB> that support the interdisciplinary method development for single cell multi-omics data and K-12 STEM/undergraduate research training.