

# 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*

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## **RESEARCH INTERESTS**

- Development of cutting-edge statistical modeling method and machine learning method for large scale data analysis and integration.
- Computational modeling of cancer initiation and progression, including energy metabolism reprogramming, interactions between cancer cells and microenvironment
- Low rank and local low rank representation of large matrix  
Bi-clustering algorithm development
- Prediction of gain or loss of function of certain mutations and interactive effect of multiple mutations
- Develop statistical deconvolution method to predict the alterations of immune and stroma cells in tissue-based omics data.
- Single cell RNA-Seq data modeling and gene co-regulation analysis

## **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

M.S. Secondary master's degree in Statistics

Advisor: Dr. Ying Xu, Dr. Ping Ma

The University of Georgia, Athens, GA (2015.5-now)

Thesis: Improved sampling method for regression analysis on big data

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,

#### **GRANTS AND AWARDS:**

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

#### **PUBLICATIONS:**

1. Juan Xie, Anjun Ma, Yu Zhang, Bingqiang Liu, Changlin Wang, Sha Cao, Chi Zhang\*, Qin Ma\*. QUBIC2: A novel biclustering algorithm for large-scale bulk RNA-sequencing

- and single-cell RNA-sequencing data analysis. **BioRxiv** (2018) DOI: <https://doi.org/10.1101/409961> (submitted to Nature Method)
2. 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>.
  3. Huiyan Sun<sup>+</sup>, Chi Zhang<sup>+</sup>, 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>.
  4. 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>
  5. 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>
  6. 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
  7. 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>
  8. 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.
  9. 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
  10. Zhang C, Chao L, Cao S and Xu Y. Elucidation of Divers of High-Level Production of Lactates throughout a Cancer Development. **Journal of Molecular Cell Biology**. (2015) DOI: 10.1093/jmcb/mjv031
  11. Liu C<sup>+</sup>, Zhang C<sup>+</sup>, 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
  12. Cao S<sup>+</sup>, Zhang C<sup>+</sup>, and Xu Y. Somatic Mutations May Not Be the Primary Drivers of Cancer Formation. **International Journal of Cancer**. (2015) DOI: 10.1002/ijc.29639

13. Yao F<sup>+</sup>, Zhang C<sup>+</sup>, 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
  14. 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
  15. 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.
  16. 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
  17. 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
  18. 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
  19. 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
- (+ for co-first author, \* for corresponding author)

#### **BOOK CHAPTERS:**

20. Zhang C<sup>+</sup>, Sheng T<sup>+</sup>, 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.
21. 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

#### **MANUSCRIPTS IN PREPARATION:**

1. Changlin Wan, Wennan Chang, Yu Zhang, Fenil Shah, Sha Cao, Melissa Fishel\*, Qin Ma\*, Chi Zhang\*. LTMG (Left truncated mixture Gaussian) based modeling of transcriptional regulatory heterogeneities in single cell RNA-seq data – a perspective from kinetics of mRNA metabolism. (2018) (Under review by Cell Research)
2. Wennan Chang, Changlin Wan, Yu Zhang, Brooke Richardson, Yan Han, Kaman So, Xiongbu Lu, Sha Cao, Chi Zhang\*. ICAD: Inference of cell types and deconvolution—a next generation deconvolution method for transcriptomics data. (2018) (Ready for submitted to Nature Method)

3. Changlin Wan, Wennan Chang, Alsaihati B, Ying Xu, Qin Ma, Sha Cao, Chi Zhang\*. A bi-clustering based method to predict gain or loss of function of somatic mutations. (2018) Ready for submission.

#### **CONFERENCE PAPERS:**

1. Jin Zhao, Haodi Feng, Daming Zhu, Chi Zhang, Ying Xu. IsoTree: De Novo Transcriptome Assembly from RNA-Seq Reads . ISBRA 2017: 71-83

#### **CONFERENCE TALKS:**

- Jun 16<sup>th</sup> 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 10<sup>th</sup> 2018 “Single cell RNA-seq data analysis” in **2018 International Conference on Intelligent Biology and Medicine**, Los Angeles, CA, USA
- Aug 11<sup>th</sup> 2015 “Cancer is not a bad luck disease” in **2015 Joint Statistical Meetings**, Seattle, US
- Jul 10<sup>th</sup> 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 AND ABSTRACTS:**

- Nov 8<sup>th</sup> 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 1<sup>st</sup> 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 1<sup>st</sup> 2017 Abstract 1554: Development of a deconvolution algorithm for tissue-based gene expression data. **AACR 2017 Annual meeting**, Washington DC, USA.
- Apr 1<sup>st</sup> 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 1<sup>st</sup> 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 12<sup>h</sup> 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 24<sup>th</sup> 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 7<sup>th</sup>-9<sup>th</sup> 2013 “Flux estimation analysis (FEA) reveals key alterations of metabolic flux in colorectal cancer” in the **9<sup>th</sup> international conference on Bioinformatics**, Georgia tech.
- Jul 22<sup>nd</sup>-25<sup>th</sup> 2013 “Prediction of transcriptional regulatory logic in *Clostridium Thermocellum* ATCC 27405” in the **BESC (Bio-energy Science Center) retreat** 2013, Chattanooga, TN

#### **INVITED TALKS:**

- Feb 24<sup>th</sup> 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 17<sup>th</sup> 2017 “Bi-clustering based omics data modeling – from commonality to heterogeneity” Department of Electronic Computer Engineering, IUPUI.
- Feb 7<sup>th</sup> 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 7<sup>th</sup> 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 21<sup>st</sup> 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 28<sup>th</sup> 2016 “Computational modeling of cancer micro-environment by using large scale data analysis” Center for Computational Biology and Bioinformatics, IUSM.
- Mar 9<sup>th</sup> 2016 “Understanding Malignant Transformation from Chronic Inflammation: a data mining approach.” Department of Computational Medicine & Bioinformatics, University of Michigan
- Feb 26<sup>th</sup> 2016 “Understanding Malignant Transformation from Chronic Inflammation: a data mining approach.” Institute of Bioinformatics, the University of Georgia

Jan 4 <sup>th</sup> 2016	“Understanding Malignant Transformation from Chronic Inflammation: a data mining approach.” Center for Computational Biology and Bioinformatics. Indiana University, Medical School
Feb 25 <sup>th</sup> 2016	“Understanding Malignant Transformation from Chronic Inflammation: a data mining approach” in Institute of Bioinformatics, the University of Georgia
Jan 4 <sup>th</sup> 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 16 <sup>th</sup> 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 21 <sup>st</sup> 2014	“Identification of dynamic cell populations in cancer biomass” in Department of Biostatistics and Bioinformatics, Emory University
Nov 14 <sup>th</sup> 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 11 <sup>th</sup> 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 22 <sup>nd</sup> 2014	“Models of cancer development driven by micro-environmental stresses” at Dr. Zhiping Weng’s lab, University of Massachusetts Medical School
Jun 19 <sup>th</sup> 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

#### **FUDNING SUPPORTS:**

**R01 GM131399-01, NIGMS, NIH** Zhang, Chi (PI) 09/10/2018-08/31/2022

Construction of cell type specific gene co-regulation signatures based on single cell transcriptomics data.

The major goal of this project is to construct a computational infrastructure to derive cell type specific gene co-regulation signatures that can form reference map of certain cell types by integrating single cell RNA-Seq data with epi-genomics data.

Role: Multiple-PI

**Showalter Young Investigator, IU CTSI** Zhang, Chi (PI) 07/01/2017-06/30/2018

Comprehensive identification of the functional impacts led by individual and collective effects of gene mutations in acute myeloid leukemia (AML)

To develop cutting-edge data integration methods to predict functional impacts and drug treatment

Role: PI

**U54 CA196519-01, NCI** Clapp, Wade (PI) 09/01/2017-08/31/2020

Developmental and hyperactive Ras Tumor (SPORE)

To implement effective targeted molecular therapies for neoplasms and cancers

Role: Co-Investigator

**IU CTSI Pilot**

Liangpunsakul, Suthat (PI) 9/01/2017-8/31/2018

Characterization of molecular signatures that distinguish excessive alcohol drinking from alcoholic liver disease

To discover a biomarker for the risk of alcoholic liver disease among heavy drinkers

Role Co-PI

**TEACHING EXPERIENCES:**

Co-Instructor G788: Next Generation Sequencing, Indiana University School of Medicine & IUPUI

2017 Fall

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**

1. Tanner Jacobson (2016 Fall), rotation Ph.D student (IBMG program)



2. Jing Li (2016-present), Ph.D student with minor in Bioinformatics (minor advisor)
3. Wennan Chang (2017-present), Ph.D student in Electronic and Computer Engineering, Purdue University
4. Changlin Wan (2017-present), Ph.D student in Electronic and Computer Engineering, Purdue University
5. Yan Han (2017-present), Master student in Biostatistics, IUPUI
6. Jiamin Su (2017-present), Perspective Ph.D student in Bioinformatics, IUPUI

#### **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:**

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)