

Curriculum Vitae
Zhengqing Ouyang, Ph.D.

CONTACT

Department of Biostatistics & Epidemiology
School of Public Health and Health Sciences
University of Massachusetts
Amherst, Massachusetts 01003

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EDUCATION

- 2010 Ph.D., Stanford University, Biology
 Dissertation Title: Integrative modeling for genome-wide regulation of gene
 expression
 Dissertation Advisor: Professor Wing Hung Wong
- 2005 M.S., Peking University, Bioinformatics
- 2002 B.S., Peking University, Theoretical and Applied Mechanics

TRAINING

- 10/2010–12/2012 Postdoctoral Fellow, Stanford University School of Medicine and Howard
 Hughes Medical Institute
 Postdoctoral Advisors: Professors Howard Chang and Michael Snyder

EMPLOYMENT

- 09/2019–present Associate Professor, Department of Biostatistics and Epidemiology, School
 of Public Health and Health Sciences, UMASS Amherst
- 12/2012–08/2019 Assistant Professor, The Jackson Laboratory for Genomic Medicine

FACULTY AFFILIATION

- 04/2014–08/2019 Institute for Systems Genomics, University of Connecticut
- 03/2013–08/2019 Department of Genetics and Genome Sciences, University of Connecticut
- 01/2013–01/2021 Department of Biomedical Engineering, University of Connecticut

HONORS AND AWARDS

- 2019 Travel Award, Pacific Symposium on Biocomputing, International Society for
 Computational Biology

2017	Travel Award, ENAR Workshop for Junior Biostatisticians in Health Research
2016	Informatics Award, Pharmaceutical Research and Manufacturers of America Foundation
2015	Nominee for Pew Scholar Award, The Jackson Laboratory
2015	Travel Award, IMS 17th Meeting of New Researchers in Statistics and Probability
2015	Travel Award, SAMSI Bioinformatics: Transition Workshop
2015	Travel Award, SAMSI Bioinformatics: Statistical and Computational Challenges in Omics Data Integration Workshop
2015	Travel Award, National Institute for Mathematical and Biological Synthesis for Investigative Workshop: Neurobiology of Expertise
2013	Genome Technology Young Investigators of the Year Award, GenomeWeb
2010	Travel Award, 8th Annual Meeting, International Society for Stem Cell Research
2009	California Institute for Regenerative Medicine Scholar, Stanford University
2009	Travel Award, Bio-X, Stanford University
2004	Innovation Award for Graduate Research, Peking University

GRANTS

Since arrival at UMASS

Active

7R35GM124998-04 (Ouyang) NIH/NIGMS RNA Structurome in Post-Transcriptional Regulation Role: PI	09/01/2019–07/31/2022 Total Cost: \$ \$1,052,089
Office of Faculty Development Mutual Mentoring Program (Flaherty) UMASS Amherst Quantitative Life Sciences Community Role: Team Member	06/01/2021–05/30/2022 Total Cost: \$2,950

Completed

5R35GM124998-05S1 (Ouyang) NIH/NIGMS Administrative Supplements for Equipment Purchases for NIGMS Awardees Role: PI	08/01/2020–07/31/2021 Total Cost: \$136,162
NYU Subaward (Scher) National Psoriasis Foundation	07/01/2019–06/31/2020 Subaward Total Cost: \$100,000

Investigating Cellular and Molecular-Based Biomarkers of Disease Progression in Psoriatic Arthritis
Role: Subaward-PI

Flex Grant for Teaching/Faculty Development (Ouyang) 10/18/2019–06/30/2021
UMASS Amherst Total Cost: \$500
Role: PI

2013-2019

1R35 GM124998-01 (Ouyang) 08/15/2017–08/31/2019
NIH/NIGMS Total Cost: \$869,487
RNA Structurome in Post-Transcriptional Regulation
Role: PI

R01 NS091118 (Frankel) 02/01/2015–01/31/2019
NIH/NINDS Subaward Total Cost: \$319,929
RNA Binding Proteins in Complex Neurological Disease
Role: Co-Investigator/Subaward-PI

ISG-ARC (Cong, Graf, Ouyang) 09/01/2013–08/31/2018
JAX/University of Connecticut Subaward Total Cost: \$26,763
Early Life Physiological and Psychosocial Stress Imprints Gut Microbiome in Preterm Infants
Role: Co-PI

R01 CA186714 (Ruan) 04/01/2014–03/31/2017
NIH/NCI Efforts: 10%
Characterization of RNA-Chromatin Interactome by RNA-DNA Ligation and Sequencing
Role: Co-Investigator

Research Starter Grant in Informatics (Ouyang) 01/01/2016–12/31/2016
PhRMA Foundation Total Cost: \$100,000
Decoding *in Vivo* RNA Structural Regulatory Elements in Cancer Transcriptomes
Role: PI

JAX Cancer Center Pilot Project (Wang, Ouyang, Ucar) 01/01/2015–12/31/2015
JAX Competitive Internal Awards Total Cost: \$90,000
Dissection of Genetic and Epigenetic Variations in CRISPR-mediated Genome Editing in Human Cancer Cells
Role: Multi-PI

Joint Pilot Grant (Levantini, Keck, Ouyang) 01/01/2016–12/31/2016
JAX/BIDMC Competitive Internal Awards Efforts only
Evaluation of a novel anti-BMI1 therapy for lung cancer in Patient Derived Xenograft models
Role: Co-PI

PUBLICATIONS

§ Student or postdoc mentee

† Co-first author

* Corresponding/co-corresponding author

Since arrival at UMASS

49. Ayyala D[§], Lin J[§], **Ouyang Z***. Differential RNA methylation using multivariate statistical methods. *Briefings in Bioinformatics*. Accepted, 2021. Doi: 10.1093/bib/bbab309. pp.1-11.
48. Chen Y[§], Zhang Y, Li J, **Ouyang Z***. LISA2: learning complex single cell trajectory and expression trends. *Frontiers in Genetics*. Accepted, 2021 12:681206. doi: 10.3389/fgene.2021.681206. pp.1-13.
47. Zhang Y*, Mao D[§], **Ouyang Z***. Model-based distance embedding with applications to chromosomal conformation biology. *Annals of Applied Statistics*. Accepted, 2021. pp.1-21.
46. Herrera A[†], Cheng A^{†§}, Mimitou EP, Seffens A, George DD, Bar-Natan M, Heguy A, Ruggles KV, Scher JU, Hymes K, Latkowski JA, Odum N, Kadin ME, **Ouyang Z**, Geskin L, Smibert P, Buus TB, Korolov S. Multimodal single-cell analysis of cutaneous T cell lymphoma reveals distinct sub-clonal tissue-dependent signatures. *Blood*. 2021 Jul 7:blood.2020009346. doi: 10.1182/blood.2020009346. Epub ahead of print. pp.1-27.
45. Singh K, Lin J[§], Lecomte N, Mohan P, Gokce A, Sanghvi V, Jiang M, Grbovic-Huezo O, Burčul A, Stark S, Romesser P, Chang Q, Melchor J, Beyer R, Duggan M, Fukase Y, Yang G, Ouerfelli O, Viale A, de Stanchina E, Stamford A, Meinke P, Rättsch G, Leach S, **Ouyang Z**, and Wendel HG. Targeting eIF4A Dependent Translation of KRAS Signaling. *Cancer Research*. 2021 Apr 15;81(8):2002-2014
44. Chen Y[§], Mao D[§], Zhang Y, **Ouyang Z***. Unsupervised gene selection for predicting cell spatial positions in the Drosophila embryo. *F1000Research*. 2021, 9:124. pp.1-9.
43. Wu H[†], Mao D^{†§}, Zhang Y^{†*}, Chi Z, Stitzel M, **Ouyang Z***. A new graph-based clustering method with application to single-cell RNA-seq data from human pancreatic islets. *NAR Genomics and Bioinformatics*. 2021 Jan 12;3(1):lqaa087. pp.1-10.
42. You Q[†], Cheng AY^{†§}, Gu X[†], Harada BT, Yu M, Wu T, Ren B*, **Ouyang Z***, He C*. Direct DNA crosslinking with CAP-C uncovers transcription-dependent chromatin organization at high resolution. *Nature Biotechnology*. 2021 Feb;39(2):225-235. Epub 2020 Aug 24.
41. Zhang Y*, Chen Y[§], **Ouyang Z***. PATH: An interactive web platform for analysis of time-course high-dimensional genomic data. *International Journal of Computational Biology and Drug Design*. 2020 13, Nos. 5/6. pp.529–538.
40. Lin J[§], Chen Y[§], Zhang Y, **Ouyang Z***. Identification and analysis of RNA structural disruptions induced by single nucleotide variants using Riprap and RibosNitchDB. *NAR Genomics and Bioinformatics*. 2020 Aug 14;2(3):lqaa057. pp.1-12.
39. Lin J[§], **Ouyang Z***. Large-scale analysis of the position-dependent binding and regulation of human RNA binding proteins. *Quantitative Biology*, 2020. 2020 June 9;8:119-129.
38. Zhang Y, **Ouyang Z**, Qian WJ, Smith RD, Wong WH, Davis RW. Meta-analysis of peptides to detect protein significance. *Statistics and Its Interface*. 2020. 2020 July 31;13:465-474.
37. Tanevski J, Nguyen T, Truong B, Karaiskos N, Ahsen ME, Zhang X, Shu C, Xu K, Liang X, Hu Y, Pham HV, Li X, Le TD, Tarca AL, Bhatti G, Romero R, Karathanasis N, Loher P, Chen Y[§], **Ouyang Z**, Mao D[§], Zhang Y, Zand M, Ruan J, Hafemeister C, Qiu P, Tran D, Nguyen T, Gabor A, Yu T, Guinney J, Glaab E, Krause R, Banda P, DREAM SCTC Consortium, Stolovitzky G, Rajewsky N, Saez-Rodriguez J and Meyer P. Gene selection for optimal prediction of cell position in tissues from single-cell transcriptomics. *Life Science Alliance*. 2020 Sep 24;3(11):e202000867. pp.1-13.

2013-2019

36. Herrera A, Fredholm S, Cheng A[§], Mimitou E, Seffens A, Bar-Natan M, Sun A, Latkowski J, Willerslew-Olsen A, Buus T, Gluud M, Krejsgaard T, Rusillow A, Woetmann A, Geisler C, Geskin L, **Ouyang Z**, Smibert P, Ødum N, Koralov S. Low SATB1 expression promotes IL-5 and IL-9 expression in Sezary Syndrome. *Journal of Investigative Dermatology*. 2020 Mar;140(3):713- 716.
35. Lin J[§], Zhang Y, Frankel W, **Ouyang Z***. PRAS: predicting functional targets of RNA binding proteins based on CLIP-seq peaks. *PLoS Computational Biology*. 2019;15(8):e1007227. pp.1-17.
34. Singh K, Lin J[§], Zhong Y, Burčul A, Mohan P, Jiang M, Viale A, Cross JR, Sun L, Yong-Gonzalez V, Hendrickson RC, Rättsch G*, **Ouyang Z***, Wendel HG*. c-MYC regulates mRNA translation efficiency and start site selection. *Journal of Experimental Medicine*. 2019;216(7):1509-1524.
33. Mimitou EP, Cheng A[§], Montalbano A, Hao S, Stoeckius M, Legut M, Roush T, Herrera A, Papalexi E, **Ouyang Z**, Satija R, Sanjana NE, Koralov SB, Smibert P. Expanding the CITE-seq tool-kit: Detection of proteins, transcriptomes, clonotypes and CRISPR perturbations with multiplexing, in a single assay. *Nature Methods*. 2019;16(5):409-412.
32. Li C, Menoret A, Farragher C, **Ouyang Z**, Bonin C, Holvoet P, Vella AT, Zhou B Single cell transcriptomics based-MacSpectrum reveals novel macrophage signatures in diseases. *JCI Insight*. 2019;5:126453. pp.1-21.
31. Chen Y[§], Zhang Y, **Ouyang Z***. LISA: Accurate reconstruction of cell trajectory and pseudo-time for massive single cell RNA-seq data. *Pacific Symposium on Biocomputing*. 2019;24:338-349.
30. Gonzalez G, Lu Z, Leaman R, Weissenbacher D, Boland MR, Chen Y, Du J, Fluck J, Greene CS, Holmes J, Kashyap A, Nielsen RL, **Ouyang Z**, Schaaf S, Taroni JN, Tao C, Zhang Y, Liu H. Text Mining and Machine Learning for Precision Medicine. *Pacific Symposium on Biocomputing*. 2019;24:449-454.
29. Zhang Y*, **Ouyang Z***. Joint principal trend analysis for longitudinal high-dimensional data. *Biometrics*. 2018;74(2):430-438.
28. Zhang Y, Linder MH[§], Shojaie A, **Ouyang Z**, Shen R, Baggerly KA, Baladandayuthapani V, Zhao H. Dissecting pathway disturbances using network topology and multi-platform genomics data, *Statistics in Biosciences*. 2018;10(1):86-106.
27. Jiang Z[†], Lin J^{†§}, Dong H, Zheng X, Marjani SL, Duan J, **Ouyang Z***, Chen J*, and Tian XC*. DNA methylomes of bovine gametes and in vivo produced preimplantation embryos. *Biology of Reproduction*. 2018;99(5):949-959.
26. Zhang Y, **Ouyang Z**, Zhao H. A statistical framework for data integration through graphical models with application to cancer genomics, *Annals of Applied Statistics*. 2017;11(1):161-184.
25. Hanley MP, Hahn MA, Li AX, Wu X, Lin J[§], Wang J, Choi AH, **Ouyang Z**, Fong Y, Pfeifer GP, Devers TJ, Rosenberg DW. Genome-wide DNA methylation profiling reveals cancer-associated changes within early colonic neoplasia, *Oncogene*. 2017;36:5035-5044
24. Zou C[§], Zhang Y, **Ouyang Z***. HSA: integrating multi-track Hi-C data for genome-scale reconstruction of 3D chromatin structure, *Genome Biology*. 2016;17:40. pp.1-14.
23. Wan Y, Qu K, **Ouyang Z**, Chang HY. Genome-wide probing of RNA structures In vitro using nucleases and deep sequencing. *Methods in Molecular Biology*. 2016;1361:141-160.

22. Zou C[§], **Ouyang Z**^{*}. Joint modeling of RNase footprint sequencing profiles for genome-wide inference of RNA structure. *Nucleic Acids Research*. 2015;43:9187-9197.
21. Zhang Y, **Ouyang Z**. Predicting quantitative outcomes of patients using longitudinal gene expression. *Sri Lankan Journal of Applied Statistics Special Issue: "Modern Statistical Methodologies in the Cutting Edge of Science"*. 2014;5:117-126.
20. Wan Y, Qu K, Zhang QC, Flynn RA, Manor O, **Ouyang Z**, Zhang J, Spitale RC, Snyder MP, Segal E, Chang HY. Landscape and variation of RNA secondary structure across the human transcriptome. *Nature*. 2014;505:706-709.
19. Hardee J, **Ouyang Z**, Zhang Y, Kundaje A, Lacroute P, Snyder MP. STAT3 targets suggest mechanisms of aggressive tumorigenesis in diffuse large B cell lymphoma. *G3: Genes, Genomes, Genetics*. 2013;3:2173-2185.
18. Wan Y, Qu K, **Ouyang Z**, Chang HY. Genome-wide mapping of RNA structure using nuclease digestion and high throughput sequencing. *Nature Protocols*. 2013;8:849-869.
17. **Ouyang Z**^{*}, Snyder MP, Chang HY^{*}. SeqFold: Genome-scale reconstruction of RNA secondary structure integrating high-throughput sequencing data. *Genome Research*. 2013;23:377-387.
16. Wan Y, Qu K[‡], **Ouyang Z**[‡], Kertesz M, Li J, Tibshirani R, Nutter RC, Segal E, Chang HY. Genome-wide measurement of RNA folding energies. *Molecular Cell*. 2012;48:1-13. [‡]Contributed equally.
15. Gerstein MB, Kundaje A, Hariharan M, Landt SG, Yan KK, Cheng C, Mu XJ, Khurana E, Rozowsky J, Alexander R, Min R, Alves P, Abyzov A, Addleman N, Bhardwaj N, Boyle AP, Cayting P, Charos A, Chen DZ, Cheng Y, Clarke D, Eastman C, Euskirchen G, Fietze S, Fu Y, Gertz J, Grubert F, Harmanci A, Jain P, Kasowski M, Lacroute P, Leng J, Lian J, Monahan H, O'Geen H, **Ouyang Z**, Partridge EC, Patacsil D, Pauli F, Raha D, Ramirez L, Reddy TE, Reed B, Shi M, Slifer T, Wang J, Wu L, Yang X, Yip KY, Zilberman-Schapira G, Batzoglou S, Sidow A, Farnham PJ, Myers RM, Weissman SM, Snyder M. Architecture of the human regulatory network derived from ENCODE data. *Nature*. 2012;489:91-100.
14. ENCODE Project Consortium (including **Ouyang Z**). An integrated encyclopedia of DNA elements in the human genome. *Nature*. 2012; 489:57-74.
13. Heffelfinger C, **Ouyang Z**, Engberg A, Leffell DJ, Hanlon AM, Gordon PB, Zheng W, Zhao H, Snyder MP, Bale AE. Correlation of global microRNA expression with basal cell carcinoma subtype. *G3: Genes, Genomes, Genetics*. 2012;2:279-286.
12. Pan Y, **Ouyang Z**, Wong WH, Baker JC. A new FACS approach isolates hESC derived endoderm using transcription factors. *PLOS One*. 2011;6:e17536. pp.1-9.
11. **Ouyang Z**, Zheng GX, Chang HY. Noncoding RNA landmarks of pluripotency and reprogramming. *Cell Stem Cell*. 2010;7:649-650
10. Lee EY, Ji H, **Ouyang Z**, Zhou B, Ma W, Vokes SA, McMahon AP, Wong WH, Scott MP. Hedgehog pathway-regulated gene networks in cerebellum development and tumorigenesis. *Proc. Natl. Acad. Sci. USA*. 2010;107:9736-9741.
9. **Ouyang Z**, Zhou Q, Wong WH. ChIP-seq of transcription factors predicts absolute and differential gene expression in embryonic stem cells. *Proc. Natl. Acad. Sci. USA*. 2009;106:21521-21526.

8. Xing Y, **Ouyang Z**, Kapur K, Scott MP, Wong WH. Assessing the conservation of mammalian gene expression using high-density Exon Arrays. *Molecular Biology and Evolution*. 2007;24:1283-1285.
7. Kapur K, Xing Y, **Ouyang Z**, Wong WH. Exon arrays provide accurate assessments of gene expression. *Genome Biology*. 2007;8: R82. pp.1-8.
6. Li E, **Ouyang Z**, Deng X, Zhang Y, Chen W. Parallel implementation of SEMPHY-a structural EM algorithm for phylogenetic reconstruction. *Proceedings of the International Conference on Parallel Computing*. 2005;631-638.
5. **Ouyang Z**, Liu JK, She ZS Hierarchical structure analysis describing abnormal base composition of genomes. *Physical Review E*. 2005; 72:041915. pp,1-9.
4. Zhu H, Hu G, **Ouyang Z**, Wang J, She ZS. Accuracy improvement for identifying translation initiation sites in microbial genomes. *Bioinformatics*. 2004;20(18):3308-3317.
3. **Ouyang Z.**, Wang C, She ZS Scaling and hierarchical structures in DNA sequences. *Physical Review Letters*. 2004;93(7):078103. pp.1-4.
2. **Ouyang Z**, Zhu H, Wang J, She ZS. Multivariate entropy distance method for prokaryotic gene identification. *Journal of Bioinformatics and Computational Biology*. 2004;2:353-373.
1. She ZS, Yang Z, **Ouyang Z**, Zhu H, Wang C, Yin J. A preliminary study to the origin and evolution of SARS-CoV. *Acta Scientiarum Naturalium Universitatis Pekinensis*. 2003;39:809-814.

MANUSCRIPTS UNDER REVISION OR SUBMITTED

6. Wu T[†], Cheng A^{†§}, Zhang L, Ouyang Z, He C. KARR-seq reveals 3D RNA-RNA interactions and principles of mRNP organization under normal and stress conditions. *Cell*. Submitted.
5. Singh K[†], Martinez G[†], Lin J^{†§}, Gregory J, Abdelaal R, Kang K, Brennand K, Grünweller A, **Ouyang Z**, Phatnani H, Kielian M, Wendel HG. Transcriptional and translational dynamics of Zika and Dengue virus infection. *Cell Host & Microbe*. Submitted.
4. Cheng A^{†§}, Mao D^{†§}, Zhang Y^{*}, Glaz J, **Ouyang Z**^{*}. Translocation detection from Hi-C data via scan statistics. Under second-round revision.
3. Lin J[§], Chen Y[§], Zhang Y, Lin H, **Ouyang Z**^{*}. Deciphering the role of RNA structure in translation efficiency. *Biometrics*. Under revision.
2. Zhang Y^{*}, **Ouyang Z**^{*}. Joint model-based distance embedding for chromosomal conformation using multi-track Hi-C data. *Journal of the Royal Statistical Society: Series A*. Under review.
1. Liu Q, Zhang Y, **Ouyang Z**. Structural inference of time-varying mixed graphical models. *Stat*. Under review.

MANUSCRIPTS IN PREPARATION

3. Cheng A, **Ouyang Z**^{*}. Joint integration of simultaneous modalities for single-cell application. 2021c. In preparation.

2. Cheng A, **Ouyang Z***. Precise detection of cross-linking induced termination sites reveals structural contexts and motifs of RNA-binding protein recognition. 2021b. In preparation.
1. Cheng A, **Ouyang Z***. Multi-assay modeling of structural probing data stratifies RNA-protein interactions through quantification of ensemble structures. 2021a. In preparation.

DATA RESOURCES AND SOFTWARE

14. LISA2: a new tool for learning complex single cell trajectory and expression trends.
<https://github.com/ouyang-lab/LISA2>
13. DIMER: a new tool for different RNA methylation sequencing data analysis.
<https://github.com/ouyang-lab/DIMER>
12. Datasets of hundreds of generated RNA sequence and structure features for thousands of transcripts with translation efficiency measurement.
<https://github.com/ouyang-lab/translation>
11. PATH: an interactive web platform for analysis of time-course high-dimensional genomic data.
<https://ouyanlab.shinyapps.io/PATH/>
10. RiboSNitchDB: a database for integrative analysis of riboSNitches (single nucleotide variants that disrupt RNA structure).
<https://people.umass.edu/ouyanlab/ribosnitchdb/>
9. Riprap: a tool for identifying single nucleotide variants that disrupt RNA structure.
<https://github.com/ouyang-lab/Riprap>
8. LISA: An interactive web platform for reconstruction of cell trajectory and pseudo-time for massive single cell RNA-seq data.
<https://ouyanlab.shinyapps.io/LISA/>
7. CAPC: a pipeline for Chemical-crosslinking Assisted Proximity Capture (CAP-C) data analysis.
<https://github.com/ouyang-lab/CAPC>
6. PRAS: a tool for RBP functional targets prediction from CLIP-seq peaks.
<https://github.com/ouyang-lab/PRAS>
5. SCTC-Challenge-zho_team: Source code implementation for the method used in the DREAM Single Cell Transcriptomics Challenge
https://github.com/ouyang-lab/SCTC-Challenge-zho_team
4. JPTA: Joint Principal Trend Analysis for multiple longitudinal data.
<http://onlinelibrary.wiley.com/store/10.1111/biom.12751/asset/supinfo/biom12751-sup-0003-SuppDataCode.tar.gz?v=1&s=4715bc1027946de428e55f8cd4e67f23a1ef6af5>
3. HSA: integrating multi-track Hi-C data for genome-scale reconstruction of 3D chromatin structure.
<http://people.umass.edu/ouyanlab/hsa/>
2. FISH datasets used in Zou et al. integrating multi-track Hi-C data for genome-scale reconstruction of 3D chromatin structure [Data set]. Genome Biology. Zenodo.
<http://dx.doi.org/10.5281/zenodo.45513>

1. SeqFold: Genome-scale reconstruction of RNA secondary structure integrating experimental measurements.
<https://people.umass.edu/ouyanglab/seqfold/>

INVITED AND SELECTED TALK

Since arrival at UMASS

36. Joint Statistical Meetings, Virtual, August 2021.
35. International Conference on Intelligent Biology and Medicine (ICIBM 2021), Virtual, August 2021.
34. RECOMB/ISCB Conference on Regulatory & Systems Genomics with DREAM Challenges, Virtual, November 2020.
33. Chapman Lecture and Gene Regulation (Mammal), The Allied Genetics Conference 2020, Genetics Society of America, Virtual, April 2020.
32. 7th Annual RNA Symposium, The RNA Institute, University at Albany, Albany, New York, March 2020. (Cancelled due to COVID-19 pandemic)

2008-2019

31. International Conference on Intelligent Biology and Medicine (ICIBM 2019), Columbus, Ohio, June 2019.
30. Pacific Symposium on Biocomputing, Big Island of Hawaii, January 2019.
29. Joint Data Science and Computational Science Seminar, University of Massachusetts Dartmouth, North Dartmouth, Massachusetts, December 2018.
28. ICSA China Conference with the Focus on Data Science, Qingdao, China, July 2018.
27. School of Life Sciences, Peking University, Beijing, China, July 2018.
26. International Conference on Intelligent Biology and Medicine (ICIBM 2018), Los Angeles, California, June 2018.
25. 32nd New England Statistics Symposium, University of Massachusetts, Amherst, Massachusetts, April 2018.
24. Workshop on 3D Genome Mapping Technology. The Jackson Laboratory for Genomic Medicine, Farmington, Connecticut, November 2017.
23. ICSA Applied Statistics Symposium, Chicago, Illinois, June 2017.
22. Computational Chemistry and Biology Seminar, The Hong Kong University of Science and Technology, Hong Kong, June 2017.
21. Conference on Lifetime Data Science, Storrs, Connecticut, May 2017.
20. 31th New England Statistics Symposium, Storrs, Connecticut, April 2017.

19. 10th ICSA International Conference: Global Growth of Modern Statistics in the 21st Century, Shanghai, China, December 2016.
18. CAS-MPG Partner Institute for Computational Biology, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences, Shanghai, China, December 2016.
17. International Conference on Intelligent Biology and Medicine (ICIBM 2016), Houston, Texas, December 2016.
16. 13th Annual Conference on Frontiers in Applied and Computational Mathematics, Newark, New Jersey, June 2016.
15. Department of Immunology, UConn Health, Farmington, Connecticut, April 2016.
14. ENAR 2016 Spring Meeting, Eastern North American Region International Biometric Society, Austin, Texas, March 2016.
13. Human Genome Meeting 2016, Houston, Texas, March 2016.
12. Statistics Colloquium, Department of Statistics, University of Connecticut, Storrs, Connecticut, January 2016.
11. Statistical Modeling of Epigenomics and Gene Regulation Workshop, Harvard University, Cambridge, Massachusetts, August 2015.
10. 24th ICSA Applied Statistics Symposium and 13th Graybill Conference, Fort Collins, Colorado, June 2015.
9. 29th New England Statistics Symposium, Storrs, Connecticut, April 2015.
8. School of Information Science and Technology, Tsinghua University, Beijing, China, June 2014.
7. International Young Scholars Systems and Synthetic Biology Symposium, Peking University, Beijing, China, June 2014.
6. Departmental Seminar, Department of Pathobiology and Veterinary Science, University of Connecticut, Storrs, Connecticut, February 2014.
5. Statistics Seminar Series, Department of Mathematical Sciences and Center for Applied Mathematics and Statistics, New Jersey Institute of Technology, New Jersey, December 2013.
4. ICSA-ISBS Joint Statistical Conference, Washington, D.C., June 2013.
3. Regulatory Genomics Special Interest Group, 20th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB), Long Beach, California, July 2012.
2. International Workshop on Probability Theory, Statistics and Their Application to Biology, Peking University, Beijing, China, June 2009.
1. Feldman Lab, Stanford University, Stanford, California, May 2008.

CONTRIBUTED TALK

11. Prospective Students Day, Biostatistics and Epidemiology, UMASS, Amherst, Massachusetts, February 2021.
10. Biomedical Engineering Research Symposium, University of Connecticut, Farmington, Connecticut, January 2017.
9. IMS 17th Meeting of New Researchers in Statistics and Probability, Seattle, Washington, August 2015.
8. Institute for Systems Genomics Networking Workshop, University of Connecticut Health Center, Farmington, Connecticut, December 2014.
7. JAX-UCONN/BECAT/UCHC Joint Workshop on Bioinformatics and Computational Biology, University of Connecticut, Storrs, Connecticut, September 2013.
6. BME Research and Career Workshop, Department of Biomedical Engineering, University of Connecticut, Storrs, Connecticut, August 2013.
5. BME Research and Career Workshop, Department of Biomedical Engineering, University of Connecticut, Storrs, Connecticut, January 2013.
4. 12th Annual Symposium, Biomedical Computation at Stanford, Stanford University, Stanford, California, November 2011.
3. CIRM Grantee Meeting, San Francisco, California, March 2010.
2. Institute for Stem Cell Biology and Regenerative Medicine Retreat, Stanford University, Stanford, California, December 2009.
1. Applied Statistics Symposium, International Chinese Statistical Association, San Francisco, California, June 2009.

TEACHING

UMASS Amherst

BIOSTATS 690T	Applied Statistical Genetics Sole Instructor	3 Credits Fall 2021
BIOSTATS 892D	PhD Seminar Sole Instructor	1 Credits Fall 2021
BIOSTATS 743	Analysis of Categorical Data in Public Health Sole Instructor Enrollment: 10 students (4 master's students and 6 Ph.D. students)	3 Credits Spring 2021
HONORS 391AH-16	Genomic Data Science in Health and Disease Sole Instructor Enrollment: 14 students (14 undergraduates)	1 Credits Spring 2021
BIOSTATS 690T	Applied Statistical Genetics Sole Instructor	3 Credits Spring 2020

Enrollment: 13 students (3 undergraduates, 4 master's students, and 6 Ph.D. students)

University of Connecticut

BME 6094	BME Graduate Seminar <i>RNA genomics: A structural and sequencing overview</i> Guest lecturer	2 Credits Fall 2013
BME 6094	BME Graduate Seminar <i>Integrating high-throughput sequencing into RNA secondary structure reconstruction</i> Guest lecturer	2 Credits Spring 2013

Stanford University

BIO 39N	Networks in Biology Teaching Assistant to Professor Sue Rhee	3 Units Spring 2010
BIO 109B/209B	The Human Genome and Disease: Genetic Diversity and Personalized Medicine Teaching Assistant to Professor Renu Heller	3 Units Spring 2008
BIO/STAT 141	Biostatistics Teaching Assistant to Professor Marcus Feldman	3-5 Units Winter 2007

MENTORING

Ph.D. Dissertation Advisor

2015–2020	Anthony Cheng, Genetics and Genome Sciences, University of Connecticut Dissertation title: Examining the interplay among determinants of higher-order nucleic acid structure via integrative analysis Current position: Postdoctoral Fellow, Genome Institute of Singapore
2013-2019	Jianan Lin, Biomedical Engineering/Bioinformatics, University of Connecticut Dissertation title: Deciphering the gene expression control in epigenetic, post-transcriptional and translational regulation Current position: Assistant Computational Scientist, The Jackson Laboratory

Ph.D. Dissertation Committee Member

2020–2021	Yiding Zhang, Biostatistics and Epidemiology, UMASS Amherst
2018–2019	Emaly Piecuch, Genetics and Genome Sciences, UConn Health
2014–2018	Gopinath Rajadinakaran, Genetics and Genome Sciences, UConn Health,

Ph.D. Academic Advisor

2021–present	Siliangyu (Helen) Cheng, Biostatistics and Epidemiology, UMASS Amherst (Research Assistant)
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2021–present	Xinyang Liu, Biostatistics and Epidemiology, UMASS Amherst (Research Assistant)
2020–2021	Diezhang Wu, Biostatistics and Epidemiology, UMASS Amherst
2013–2014	Tianjiadian Feng, Biomedical Engineering/Bioinformatics, University of Connecticut (Research Assistant)

Postdoctoral Advisor

2020–present	Eric Pederson, Biostatistics and Epidemiology, UMASS Amherst
2019–2020	Yang Chen, Biostatistics and Epidemiology, UMASS Amherst Current position: Visiting Fellow, Division of Intramural Research, NIH/NIDDK
2017–2019	Yang Chen, The Jackson Laboratory
2015–2017	Deepak nag Ayyala, The Jackson Laboratory Current position: Assistant Professor, Augusta University
2013–2016	Chenchen Zou, The Jackson Laboratory Current position: Associate Professor, Qingdao University
2014–2015	Yubing Wan, The Jackson Laboratory Current position: Sr. Data Scientist, QuartzBio
2013–2014	Yizhou Li, The Jackson Laboratory Current position: Associate Professor, Sichuan University

Ph.D. Intern Research Supervisor

2017–2019	Disheng Mao, Statistics, University of Connecticut
2017	M. Henry Linder, Statistics, University of Connecticut

M.S. Intern Research Supervisor

2016	Kimberly McLaughlin, Molecular and Cell Biology, University of Connecticut
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Undergraduate Intern Research Supervisor

2015	Wendell Sprague, Middlesex Community College
2015	Celina Hsieh, Brown University
2014	Ran Liu, Johns Hopkins University

Trainee Activities and Achievements

2018-2019	Our team, including my advisees Yang Chen and Disheng Mao, participated in the 2018 DREAM Single Cell Transcriptomics Challenge with more than 400 registered participants worldwide. Our team was invited to participate in the Post Challenge Phase as one of the top 10 teams among 35 teams that submitted the prediction results and source code.
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- 2018 Anthony Cheng, Poster presentation to The Jackson Laboratory Board of Scientific Counselors, Farmington, Connecticut.
- 2018 Jianan Lin, Poster presentation to The Jackson Laboratory Board of Scientific Counselors, Farmington, Connecticut.
- 2017 Deepak nag Ayyala, Attending Probability and Statistics Day, University of Maryland, Baltimore, Maryland.
- 2016 Deepak nag Ayyala, Led journal club meetings for The Jackson Laboratory Summer Student Program.
- 2016 Deepak nag Ayyala, Oral presentation at Genomics Journal Club, The Jackson Laboratory for Genomic Medicine, Farmington, Connecticut.
- 2016 Chenchen Zou, Oral presentation at the 20th Annual International Conference on Research in Computational Molecular Biology (RECOMB), Los Angeles, California.
- 2016 Jianan Lin, Travel Award for attending the 2nd Summer Institute in Statistics for Big Data, University of Washington, Seattle, Washington.
- 2015 Chenchen Zou, Poster presentation at Joint Statistical Meetings, Seattle, Washington.
- 2015 Chenchen Zou, Poster oral presentation at the 29th New England Statistics Symposium, University of Connecticut, Storrs, Connecticut.
- 2015 Jianan Lin, Poster oral presentation at the 29th New England Statistics Symposium, University of Connecticut, Storrs, Connecticut.
- 2015 Jianan Lin, Tied for Second Place of BME, Poster presentation competition, School of Engineering, University of Connecticut, Connecticut.
- 2015 Chenchen Zou, Travel Award to attend the 56th Annual Short Course on Medical and Experimental Mammalian Genetics, The Jackson Laboratory, Bar Harbor, Maine.
- 2015 Jianan Lin, Travel Award to attend the 56th Annual Short Course on Medical and Experimental Mammalian Genetics, The Jackson Laboratory, Bar Harbor, Maine.
- 2015 Chenchen Zou, Oral Presentation at the SAMSI Epigenetics Workshop, Research Triangle Park, North Carolina.

SERVICE TO PROFESSIONAL COMMUNITIES

Grant Review Activities

- 2020 Member, Special Emphasis Panel on 4D Nucleome Organization and Function in Human Health and Disease, Center for Scientific Review, National Institutes of Health
- 2020 Ad hoc Reviewer, Genetic Mechanisms Cluster, National Science Foundation
- 2019 Ad hoc Reviewer, Longitudinal Population Studies Grants, Wellcome Trust, UK

Editorial Activities

- 2018–present Associate Editor, *Frontiers in Genetics*
- 2015–2018 Review Editor, section Bioinformatics and Computational Biology
Frontiers in Genetics, Frontiers in Bioengineering and Biotechnology, and Frontiers in Plant Science
- 2013–present Editorial Board Member, *Journal of Metabolomics and Systems Biology*
- 2011–present Editorial Board Member, *Biomedical Engineering and Computational Biology*

Reviewer for Scientific Journals

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| 37. Annals of Applied Statistics | 19. Journal of Bioinformatics and Computational Biology |
| 36. Bioinformatics | 18. Journal of the American Statistical Association |
| 35. Bioinformatics and Biology Insights | 17. Journal of Theoretical Biology |
| 34. Biomedical Engineering and Computational Biology | 16. Mathematical Biosciences |
| 33. Biometrics | 15. Methods in Molecular Biology |
| 32. BMC Bioinformatics | 14. Nature Protocols |
| 31. BMC Genomics | 13. Nature Communications |
| 30. BMC Supplements | 12. Nature Machine Intelligence |
| 29. Briefings in Bioinformatics | 11. Nature Methods |
| 28. Cancer Informatics | 10. Neural Computing and Applications |
| 27. Circulation: Genomic and Precision Medicine | 9. Nucleic Acids Research |
| 26. Computational Statistics | 8. PLOS Computational Biology |
| 25. Evolutionary Bioinformatics | 7. PLOS One |
| 24. Frontiers in Genetics | 6. Quantitative Biology |
| 23. Genome Biology | 5. RNA |
| 22. Genome Research | 4. Scientific Reports |
| 21. Genomics Proteomics and Bioinformatics | 3. Stat |
| 20. IEEE/ACM Transactions on Computational Biology and Bioinformatics | 2. Statistics and Its Interface |
| | 1. WIREs Systems Biology and Medicine |

International Conference Services

- 2020 Member, Program Committee, International Conference on Intelligent Biology and Medicine (ICIBM 2020), Virtual
- 2016 Member, Program Committee, 25th International Joint Conference on Artificial Intelligence, New York City, New York

Session Organizing and Chairing Activities

- 2021 Chair, Contributed Speed Session, *Recent Advancements in the Analysis of Large-scale GWAS*, Section on Statistics in Genomics and Genetics, Joint Statistical Meetings (Virtual)
- 2019 Organizer, Invited Session *Statistical and Machine Learning Methods for Large-Scale Biomedical Data Analysis*, 33rd New England Statistics Symposium, Hartford, Connecticut
- 2018 Organizer, Invited Session *Statistical Innovations in Big Data Analysis*, 27th ICSA Applied Statistics Symposium, New Brunswick, New Jersey
- 2017 Organizer and Chair, Invited Session *Statistical Innovations in Genomics*, 31th New England Statistics Symposium, Storrs, Connecticut
- 2017 Organizer and Chair, Invited Session *Advances in Statistical Modeling of Correlated Data*, 2017 Conference on Lifetime Data Science, Storrs, Connecticut
- 2016 Chair, Invited Session *Statistical Advances in Bioinformatics and Integrative Genomics*, The 10th ICSA International Conference: Global Growth of Modern Statistics in the 21st Century, Shanghai Jiao Tong University, Shanghai, China
- 2015 Organizer, Invited Session *Innovative Statistical Methods in Genomics and Genetics*, 24th ICSA Applied Statistics Symposium and 13th Graybill Conference, Fort Collins, Colorado

SERVICE TO DEPARTMENT, SCHOOL, AND UNIVERSITY

UMASS Amherst

- 2021-2022 Biostatistics and Epidemiology Member, Health Equity Faculty Search Committee, School of Public Health and Health Sciences
- 2021-2022 Co-Chair, Biostatistics Graduate Admission Committee, Biostatistics and Epidemiology
- 2021-2022 Member, Biostatistics Curriculum Committee, Biostatistics and Epidemiology
- 2021-2022 Member, Biostatistics Doctoral Exam Committee, Biostatistics and Epidemiology
- 2021 Member, Selection Committee for Woolrich Scholarship, Kozma-Littleton Fund, and Darity Scholarship, School of Public Health and Health Sciences
- 2020-2021 Member, Biostatistics Graduate Admission Committee, Biostatistics and Epidemiology
- 2020-2021 Member, Biostatistics Curriculum Committee, Biostatistics and Epidemiology
- 2019-2020 Member, Biostatistics Graduate Admission Committee, Biostatistics and Epidemiology

2019-2020 Member, Development of Biostatistics MS Degree and Recruitment Committee,
Biostatistics and Epidemiology

The Jackson Laboratory

2013-2019 Host, seminar speakers

2013-2018 Reviewer, faculty candidate applications

2018 *Ad hoc* Member, Grant Review Committee for a senior research scientist

2015 Member, Faculty Retreat Committee

2014 Member, Statistical Genomics Faculty Search Committee, Joint with UConn Health

2014 Member, Faculty Retreat Committee

2013 *Ad hoc* Member, Grant Review Committee for a faculty member