

Ye Zheng

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I am an Assistant Professor at Bioinformatics and Computational Biology Department at the University of Texas MD Anderson Cancer Center and a NIH/NHGRI K99/R00 fellow. My research focuses on developing statistical and computational models to address challenges in genomics and cancer studies.

TRAINING AND EDUCATION

- Sep. 2, 2024 **The University of Texas MD Anderson Cancer Center**, *Bioinformatics and Computational Biology Department*
– Assistant Professor
- Sep. 2, 2024 **The University of Texas MD Anderson Cancer Center**, *Systems Biology Department*
– Affiliated Assistant Professor
- Nov. 1, 2019 **Fred Hutchinson Cancer Center**, *Basic Sciences and Vaccine and Infectious Disease Divisions*
– Sep. 1, Postdoctoral Research Fellow
2024 Mentors: Steven Henikoff, Ph.D.
- Sep. 1, 2014 **University of Wisconsin – Madison**, *Department of Statistics*
– Aug. 26, Ph.D. in Statistics, Minor in Quantitative Biology
2019 Thesis: Statistical Methods Development and Benchmarking for the Analysis of Three-dimensional Chromatin Organization.
Mentor: Sündüz Keleş, Ph.D.
- Sep. 1, 2010 **Renmin University of China**, *School of Statistics*
– June 30, B.E. in Statistics
2014 Honors Thesis: Approximate Bayesian Computation in Estimating the Structure of HIV Transmission Networks in Human Populations.
Mentor: Yang Li, Ph.D.

PROFESSIONAL EXPERIENCE

- Nov. 2019 – **Postdoctoral Research Fellow**, *Seattle, Washington*
- Sep. 2024 Basic Science Division, Fred Hutchinson Cancer Center
Mentors: Steven Henikoff, Ph.D., Raphael Gottardo, Ph.D.
Collaborators and advisors: Cameron Turtle, MBBS, Ph.D., Evan Newell, Ph.D., Manu Setty, Ph.D.
- Integrative modeling of bulk and single-cell transcriptomics, epigenomics and proteomics:**
- Developed FFPE epigenomic landscape processing and analysis pipeline. Proposed customized normalization method for hypertranscription tumor samples.
 - Developed normalization method, ADTnorm, for CITE-seq data to remove the technical batch effect and facilitate data integration across studies.
 - Constructed data processing and analysis pipeline for CUT&RUN and CUT&Tag data and created spike-in free normalization method for multiple sample comparison.
 - Developed statistical models and computational tools for integrative analysis of single-cell 3D genomics, transcriptomics and epigenomics for gene cis-regulatory mechanism discovery.
- Wet lab experimental training:**
- Learned and implemented epigenomic experiments, including FFPE-CUTAC, CUT&Tag, scCUT&Tag, scMulti-Tag, to collect data for multiple ongoing projects in the Henikoff lab.
- Chimeric antigen receptor T (CAR-T) Cell Immunotherapy:**
- Multi-omics integrative analysis to profile the genomic signatures of CAR-T cell therapy products from transcriptomics and epigenomics perspectives using CITE-seq, CUT&RUN and scCUT&Tag data.
 - Constructed tree-based machine learning models to detect genomic features associated with CAR-T cell immunotherapy efficacy and toxicity.
- Statistical consulting for genomics and biomedical studies:**
- Statistical support for single-cell RNA-seq analysis in Hsieh Lab, trajectory analysis in Prlic Lab, and collaborative analysis of cytotoxic HDAC inhibition with Seattle Children's Hospital.

Sep. 2014 – **Research Assistant**, *Madison, Wisconsin*

Oct. 2019 Department of Statistics, Biostatistics and Medical Informatics, University of Wisconsin – Madison
Mentor: Sündüz Keleş, Ph.D.

Three-dimensional chromatin organization:

- Developed biologically motivated hierarchical generative model to leverage reads that map to multiple locations in Hi-C data and investigate the genomic features involving repetitive regions of the genomes.
- Developed a computational tool for simulating realistic three-dimensional proximity ligation data.

Transcriptomics and epigenomics analysis:

- Investigated protein-DNA interactions residing in repetitive regions and integrated multi-mapping reads into Encyclopedia of DNA Elements (ENCODE) ChIP-seq data processing pipeline.
- Leveraged multi-omics analysis, particularly using ATAC-seq and RNA-seq data, to reveal GATA/Heme regulation mechanism in controlling hemoglobin synthesis and erythrocyte development.

Feb. 2014 – **Data Scientist Intern**, *Beijing, China*

June 2014 Data Integration and Analytics Services, IBM Business Analysis

- Developed dynamic text mining model using IBM communication database to infer topic networks.
- Constructed a modified Latent Dirichlet Allocation model to optimize the CPU usage of IBM servers.

June. 2013 – **Research Assistant**, *Ottawa, Canada*

Sep. 2013 Department of Biology, Mathematics and Statistics, University of Ottawa

Mentor: Stéphane Aris-Brosou, Ph.D.

- Investigated Approximate Bayesian Computation (ABC), ABC-Markov Chain Monte Carlo and ABC-Sequential Monte Carlo samplers in estimating the transmission networks of viruses in human populations.

Sep. 2012 – **Exchange Study in Statistics**, *Hong Kong, China*

Jan. 2013 Department of Statistics and Actuarial Science, The University of Hong Kong

PUBLICATIONS

[Google Scholar Link](#) (h-index = 13, > 2100 citations)

* co-first authors, + co-corresponding authors

1. Henikoff S*, **Zheng Y***, Paranal R, Xu Y, Greene J, Henikoff J, Russell Z, Szulzewsky F, Thirimanne H, Kugel S, Holland E, Ahmad K. RNA Polymerase II at histone genes predicts outcome in human cancer. *Science*. ads2169 (2024) <https://www.biorxiv.org/content/10.1101/2024.02.28.582647v4>.
2. Fiorenza S*, **Zheng Y***, Purushe J, Bock T, Sarthy J, Janssens D, Sheih A, Kimble E, Kirchmeier D, Phi T, Gauthier J, Hirayama A, Riddell S, Wu Q, Gottardo R, Maloney D, Yang J, Henikoff S, Turtle C. Histone marks identify novel transcription factors that parse CAR-T subset-of-origin, clinical potential and expansion. *Nature Communications*. (2024) <https://doi.org/10.1038/s41467-024-52503-2>
3. **Zheng Y***, Caron D*, Kim J, Jun S, Tian Y, Florian M, Stuart K, Sims P, Gottardo R. ADTnorm: Robust Integration of Single-cell Protein Measurement across CITE-seq Datasets. *BioRxiv*. Revised for *Nature Communications*. (2024) <https://www.biorxiv.org/content/10.1101/2022.04.29.489989v2>.
4. Henikoff S, **Zheng Y**, Ahmad K. Mitotic errors do not explain aneuploidy in cancer. Under the second round of review of *Trends in Genetics*. (2024)
5. Fiorenza S, Cao Y, **Zheng Y**, Purushe J, Bock T, Kimble E, Janssens D, Kirchmeier D, Hirayama A, Gauthier J, Maloney D, Riddell S, Nguyen-Shaw A, Henikoff S, Yang J, Turtle C. Prediction of Therapeutic Potential of CD19 CAR-T Cells for LBCL By Histone Mark Analyses of Core Epigenetic Programming. *Blood*. (2024) <https://www.sciencedirect.com/science/article/pii/S000649712404775X>.
6. Fiorenza S, **Zheng Y**, Sarthy J, Sheih A, Kimble E, Kirchmeier D, Janssens D, Phi T, Gauthier J, Hirayama A, Wu Q, Gottardo R, Riddell S, Maloney D, Henikoff S, Turtle C. Histone Methylation Mark Analyses Distinguish Carts Manufactured from Distinct Sources and Uncover Novel Transcription Factors Associated with In Vivo Function of Carts after Infusion into DLBCL Patients That Are Not Identified By RNA-Seq. *Blood*. (2023) <https://doi.org/10.1182/blood-2023-188269>.
7. **Zheng Y***, Shen S*, Keles S. Normalization and de-noising of single-cell Hi-C data with BandNorm and scVI-3D. *Genome Biology*. (2022) <https://genomebiology.biomedcentral.com/articles/10.1186/s13059-022-02774-z>.

8. Shen S, **Zheng Y**⁺, Keles S⁺. scGAD: single-cell gene associating domain scores for exploratory analysis of scHi-C data. *Bioinformatics*. (2022) <https://doi.org/10.1093/bioinformatics/btac372>.
9. Germanos AA, Arora S, **Zheng Y**, Goddard ET, Coleman IM, Ku AT, Wilkinson S, Amezcua RA, Zager M, Long A, Yang YC, Bielas J, Gottardo R, Ghajar C, Nelson P, Sowalsky A, Setty M, Hsieh A. Defining cellular population dynamics at single cell resolution during prostate cancer progression. *eLife*. (2022) <https://doi.org/10.1101/2022.03.02.482711>.
10. Chour, T., Hirayama, A., **Zheng, Y.**, Sheih, A., Zhuang, S., Wilson, A., Wu, V., Gottardo, R., Turtle, C., Gardner, R. and Newell, E. Cellular profiling of leukapheresis and infusion products of patients enrolled in CD19 CAR T cell therapy identifies biomarkers associated with clinical outcomes. *Cancer Research*, 82(12_Supplement), pp.3910-3910. (2022) https://aacrjournals.org/cancerres/article/82/12_Supplement/3910/703307
11. Cheng J, Clayton J, Acemel R, **Zheng Y**, Taylor R, Keles S, Harley J, Quail E, Gómez-Skarmeta J and Ulgiati D. Regulatory architecture of the RCA gene cluster captures an intragenic TAD boundary and enhancer elements in B cells. *Frontiers in Immunology, section B Cell Biology*. (2022) <https://doi.org/10.3389/fimmu.2022.901747>.
12. **Zheng Y**, Zhou P, Keleş S. FreeHi-C Spike-in Simulations for Benchmarking Differential Chromatin Interaction Detection. *Methods*. (2021) <https://doi.org/10.1016/j.ymeth.2020.07.001>.
13. Hirayama AV, **Zheng Y**, Dowling MR, Sheih A, Phi TD, Kirchmeier DR, Chucka AW, Gauthier J, Maloney DG, Gottardo R, Turtle CJ. Long-Term Follow-up and Single-Cell Multiomics Characteristics of Infusion Products in Patients with Chronic Lymphocytic Leukemia Treated with CD19 CAR-T Cells. *Blood*. (2021) <https://doi.org/10.1182/blood-2021-151571>.
14. Huang K, Wu Y, Shin J, **Zheng Y**, Siahipirani A, Lin Y, Ni Z, Chen J, You J, Keleş S, Wang D, Roy S, Lu Q. Transcriptome-wide transmission disequilibrium analysis identifies novel risk genes for autism spectrum disorder. *PLOS Genetics*. (2021) <https://doi.org/10.1371/journal.pgen.1009309>.
15. Vitanza N, Biery M, Myers C, Ferguson E, **Zheng Y**, Girard E, Przystal J, Park G, Noll A, Pakiam F, Winter C, Morris S, Sarthy J, Cole B, Leary S, Crane C, Lieberman N, Mueller S, Nazarian J, Gottardo R, Brusniak M, Mhyre A, Olson J, Optimal therapeutic targeting by HDAC inhibition in biopsy-derived treatment-naïve diffuse midline glioma models, *Neuro-Oncology*. (2021) <https://doi.org/10.1093/neuonc/noaa249>.
16. Wu S, Furlan S, Mihalas A, Kaya-Okur H, Feroze H, Emerson S, **Zheng Y**, Carson K, Cimino P, Keene C, Holland E, Sarthy J, Gottardo R, Ahmad K, Henikoff S, Patel A. Single-cell CUTTag analysis of chromatin modifications in differentiation and tumor progression. *Nature Biotechnology*. (2021) <https://doi.org/10.1038/s41587-021-00865-z>.
17. **Zheng Y**, Keleş S. FreeHi-C simulates high-fidelity Hi-C data for benchmarking and data augmentation. *Nature Methods*. (2020) <https://doi.org/10.1038/s41592-019-0624-3>.
18. Liao R*, **Zheng Y***, Liu X, Zhang Y, Seim G, Tanimura N, Wilson G, Hematti P, Coon J, Fan J, Xu J, Keleş S⁺ and Bresnick E⁺. Discovering How Heme Controls Genome Function Through Heme-omics. *Cell Reports*. (2020) <https://doi.org/10.1016/j.celrep.2020.107832>.
19. **Zheng Y**, Ahmad K, Henikoff K. CUTTag Data Processing and Analysis Tutorial. *Protocols.io*. (2020) [dx.doi.org/10.17504/protocols.io.bjk2kkye](https://doi.org/10.17504/protocols.io.bjk2kkye). (17,459 views, 4,355 exports, and 239 questions)
20. The ENCODE Project Consortium, et al. Expanded Encyclopedias of DNA Elements in the Human and Mouse Genomes. *Nature*. (2020) <https://doi.org/10.1038/s41586-020-2493-4>.
21. The ENCODE Project Consortium, Snyder, M.P., Gingeras, T.R., Moore, J.E., Weng, Z., Gerstein, M.B., Ren, B., Hardison, R.C., Stamatoyannopoulos, J.A., Graveley, B.R., Feingold, E.A. and Pazin, M.J. Perspectives on ENCODE. *Nature*. (2020) <https://doi.org/10.1038/s41586-020-2449-8>.
22. **Zheng Y**, Ay F, Keleş S. Generative modeling of multi-mapping reads with mHi-C advances analysis of Hi-C studies. *eLife*. (2019) <https://doi.org/10.7554/eLife.38070>.

23. Soukup AA, **Zheng Y**, Mehta C, Liu P, Hofmann I, Zhou Y, Zhang J, Choi K, Johnson KD, Keles S, Bresnick EH. Single-nucleotide human disease mutation inactivates a blood-regenerative GATA2 enhancer. *Journal of Clinical Investigation*. (2019) <https://doi.org/10.1172/JCI122694>.
24. Tanimura N, Liao R, Wilson GM, Dent MR, Cao M, Burstyn JN, Hematti P, Liu X, Zhang Y, **Zheng Y**, Keles S, Xu J, Coon J, Bresnick E. GATA/Heme Multi-omics Reveals a Trace Metal-dependent Cellular Differentiation Mechanism. *Developmental Cell*. (2018) <https://doi.org/10.1016/j.devcel.2018.07.022>.
25. Zeng X, Li B, Welch R, Rojo C, **Zheng Y**, Dewey CN, Keleş S. Perm-seq: Mapping Protein-DNA Interactions in Segmental Duplication and Highly Repetitive Regions of Genomes with Prior-enhanced Read Mapping. *PLoS Computational Biology*. (2015) <https://doi.org/10.1371/journal.pcbi.1004491>.

Book Chapter

1. Savonen et al. Choosing Genomics Tools. (2023) Chapter 19 CUT&RUN and CUT&Tag.
 - Full author list: https://hutchdatascience.org/Choosing_Genomics_Tools/about-the-authors.html.
 - Online book chapter: https://hutchdatascience.org/Choosing_Genomics_Tools/index.html.
 - The online book chapter was designed for a series of courses for the Informatics Technology for Cancer Research (ITCR) called the Informatics Technology for Cancer Research Education Resource. This material was created by the ITCR Training Network (ITN) which is a collaborative effort of researchers around the United States to support cancer informatics and data science training through resources, technology, and events.

GRANT

1. **Pathway to Independence Award (K99/R00)**. (Aug. 2023 - Aug.2024, \$237,438, for K99 Phase; Sep. 2024 - Aug. 2027, \$747,000, for R00 Phase).
PI: Ye Zheng, Ph.D.
 Title: Bridging the gap: joint modeling of single-cell 1D and 3D genomics.
 Sponsoring agency: NIH/NHGRI
2. **UT System Rising STARs Award**. (Sep. 2024 - Dec. 2025, \$125,000)
PI: Ye Zheng, Ph.D.
 Sponsoring agency: University of Texas
3. **Start-up Funds**. (Sep. 2024 - Aug. 2029, \$1,000,000)
PI: Ye Zheng, Ph.D.
 Sponsoring agency: Office of the Chief Scientific Officer of University of Texas MD Anderson Cancer Center
4. **New Collaborations Pilot Award**. (Oct. 2022 - Oct. 2024, \$100,000, transferred to Dr. Hirayama starting Aug. 2023 due to efforts conflict with K99/R00 award)
Leading PI: Ye Zheng, Ph.D.
 Co-PI: Alexandre Hirayama, M.D.
 Title: A single-cell multimodal atlas of infused CD19 CAR-T cells: computational framework and machine learning modeling of clinical outcomes.
 Sponsoring agency: Fred Hutchinson Cancer Center TDS IRC Media report: [Hutch High Five](#)

PATENTS

1. Henikoff S., Ahmad K., **Zheng Y**. ANALYSIS OF REPLICATION-COUPLED HISTONE. U.S. Provisional Application No. 63/683,342. Starting from Aug. 15, 2024.
2. Zheng F., Wei D., **Zheng Y**. Protected from 15th Nov. 2008 to 15th Nov. 2018. Computer Power Cord. Patent No. ZL 2007 2 0157387.7
3. **Zheng Y.**, Yao S. . Protected from 10th Jan. 2007 to 10th Jan. 2017. Easel. Patent No. ZL 2005 20125184.0

SOFTWARE

1. **ADTnorm**: R package for CITE-seq data normalization and integration of cell surface protein measurement across batches and studies. Available at <https://github.com/yezhengSTAT/ADTnorm>
2. **scGAD**: R package for extracting the three-dimensional chromatin interaction at the unit of genes and facilitate the integration of single-cell 3D genomcis with other single-cell modalities. (Co-developer) Available at <https://ssh82.github.io/BandNorm/articles/scGAD-tutorial.html>
3. **scVI-3D**: Normalization and De-noising of Single-cell Hi-C Data using deep generative modeling using python pipeline. Available at <https://github.com/yezhengSTAT/3DVI>.
4. **BandNorm**: R package for fast band normalization for sing-cell Hi-C data. (Co-developer) Available at <https://github.com/keleslab/BandNorm>.
5. **FreeHiC**: Python pipeline using Fragment Interactions Empirical Estimation method for fast simulation of Hi-C and other 3D proximity ligation sequencing data. Major computing parts are accelerated by C. Available at: <https://github.com/yezhengSTAT/FreeHiC>.
6. **FreeHiC Spike-In**: FreeHi-C python pipeline with a user/data-driven spike-in module to allow a comprehensive comparison of differential chromatin interaction detection methods where the ground truth differential chromatin interactions are known. Available at: <https://github.com/yezhengSTAT/FreeHiC>.
7. **mHi-C**: Python pipeline of multi-mapping strategy for Hi-C data by probabilistically assigning reads originated from repetitive regions. Major computing parts are accelerated by C. Available at: <https://github.com/yezhengSTAT/mHiC>.
8. **permseq**: R package for mapping protein-DNA interactions in highly repetitive regions of the genomes with prior-enhanced read mapping. Available at: <https://github.com/yezhengSTAT/permseq>.
9. **permseqExample**: R package for the permseq package illustration and demo runs. Smaller raw data and demo R scripts are provided for quick runs in order to get to know permseq package. Available at: <https://github.com/yezhengSTAT/permseqExample>.

SCHOLARSHIPS

- March 2023 **SPAC Conference Scholarship Award, \$1500**
Fred Hutchinson Cancer Center, Seattle, USA
- March 2020 **Keystone Symposia Scholarship, \$1200**
Keystone Symposia, Higher-Order Chromatin Architecture in Time and Space, BC, Canada
- Sep. 2017 - **UW-Madison SRGC Conference Presentation Funds, \$1200**
June 2018 University of Wisconsin – Madison, Madison, WI
- Sep. 2011 - **Scholarships for Outstanding Academic Performance, RMB7000**
June 2014 Renmin University of China, Beijing, China
- June 2013 - **Mitacs (Canada) and China Scholarship Council Research Scholarship, \$4500**
Sep. 2013 Mitacs, Canada
- Sep. 2012 - **Fung Scholar Scholarship, HK\$5000**
Jan. 2013 Hong Kong, China

HONORS AND AWARDS

- Nov 2021 **Keystone Spymposia Scholarship for Registration**
Higher-Order Chromatin Architecture in Time and Space, Virtual
- May 2019 **GLBIO Travel Fellowship**
Great Lakes Bioinformatics Conference (GLBIO), Madison, WI
- July 2018 **ASA Statistics in Genomics and Genetics - Distinguished Student Paper Award**
Joint Statistical Meeting, Vancouver, Canada

- Nov. 2017 **Stellar Abstract Award**
2017 Program in Quantitative Genomics Conference, Harvard University, Boston, MA
- June 2017 **Student Travel Award**
14th Graybill Conference on Statistical Genomics and Genetics, Colorado State University – Fort Collins, Fort Collins, CO
- May 2017 **GLBIO Sponsorship Complimentary Registration**
Great Lakes Bioinformatics Conference (GLBIO) 2017, University of Illinois at Chicago, Chicago, IL
- July 2017 **Registration and Travel Scholarships**
Summer Institute in Statistics for Big Data (SISBID), University of Washington, Seattle, WA
- June 2016 **ENCODE Best Lightning Talk – Honorable Mention**
2016 Encyclopedia of DNA Elements (ENCODE) Consortium Meeting, La Jolla, CA
- July 2013 **Ranked 1st in the University Competition; 3rd award in the National Competition**
National Undergraduate Student Computer Science Design and Programming Contest, Beijing, China
- Mar. 2013 **Outstanding Paper Award**
15th Innovation Cup of Academic Paper Competition, Renmin University of China, Beijing, China
- Apr. 2011 **Honorable Mention**
King Base ACM Programming Contest, Renmin University of China, Beijing, China

MENTORING

- Jan. 2025 - **Christopher Ly**, *Ph.D. rotation student from GSBS program of MD Anderson and UTHealth.*
Current Spatial proteomics integration and batch correction.
- Sep. 2024 - **Yiyang Wu**, *Ph.D. student at UTHealth Biostatistics and Data Science Department.*
Current 3D genomics integrative analysis and statistical modeling.
- Sep. 2024 - **Yiyang Niu**, *Master's student at Rice University Statistics Department. Now Research Intern at MD Anderson*
Current Machine learning modeling on single-cell multi-omics to associate genomic features with CAR-T cell immunotherapy clinical outcomes.
- Sep. 2024 - **Zhikang Liu**, *Master's student at Rice University Statistics Department. Now Research Intern at MD Anderson*
Current Statistical and machine learning modeling on single-cell multi-omics in COVID-19 studies.
- July. 2024 - **Zhicheng Luo**, *Summer Research Intern. Now Master's student at Yale University*
Current Proteomics integrative modeling across platform and technologies.
- Feb. 2022 - **Long Nguyen**, *Bioinformatics Analyst I at Fred Hutchinson Cancer Center. Currently Master student at University of Michigan.*
July. 2024 Supervising Long on the single-cell transcriptomics and proteomics integrative analysis for cell atlas construction of CAR-T cell therapy CITE-seq data and association with gene and protein markers with clinical responses.
- June 2020 - **Fanding Zhou**, *VISP student at University of Wisconsin - Madison. Currently Ph.D. student at University of California - Berkeley*
Sep. 2021 Co-mentor with Dr. Sunduz Keles on constructing tree-based statistical models for the false discovery rate control of 3D chromatin organization differential detection.
- June 2019 - **Olivia Rae Steidl**, *Summer Undergraduate Student at University of Wisconsin - Madison.*
Sep. 2019 *Currently Ph.D. student at University of Wisconsin - Madison*
Co-mentor with Dr. Sunduz Keles on investigation of the poly(UG) tails at the end of RNAs and its function in human using eCLIP-seq data.

TEACHING

- Spring 2024 **Guest Lecturer, STAT 423/623 Probability Bioinformatics and Genetics**
Gave lecture to statistics and biostatistics graduate and undergraduate students about statistical analysis in single-cell genomics.
- Fall 2020 **Guest Lecturer, STAT 877 - Statistical Methods for Molecular Biology**
Gave lecture to statistics and biostatistics graduate students about 3D Genomics and Long-range Gene Regulations.
- Winter 2019 **Workshop Lecturer, AMSI BioInfoSummer, University of Sydney, Australia**
Gave a workshop to the faculty and students attending the AMSI BioInfoSummer conference about basic concepts of 3D Genomics and how to do computational data processing and statistical modeling in a practical manner. Led interactive computational group work to process real Hi-C data using Google Box.
- Fall 2019 **Guest Lecturer, STAT 998 - Statistical Consulting**
Lead lectures to discuss real-world consulting problem with statistics graduate students utilizing the traditional and modern statistical tools.
- Summer 2019 **Mentor, Biological Sciences Summer Research Programs**
Mentor summer student regarding quantitative biology research.
- Spring 2019 **Guest Lecturer, STAT 877 - Statistical Methods for Molecular Biology**
Gave lecture to statistics and biostatistics graduate students about 3D Genomics and Long-range Gene Regulations.
- 2017-2018 **Organizer and Instructor, Single-cell Technologies Journal Club**
Gave lectures about single-cell related research topics, such as scRNA-seq, scATAC-seq and scHi-C, to graduate students and post-docs from statistics background, and led paper review discussions.
- 2017-2018 **Organizer and Instructor, Three-dimensional Chromatin Interactions Journal Club**
Gave lectures about 3D chromatin architecture related research topics to graduate students and post-docs from statistics background, and led paper review discussions.
- Fall 2014 **Guest Lecturer for Discussion Sections, STAT301 - Introduction to Statistical Methods**
Led undergraduate students discussions for solving hypothesis testing and statistical estimation problems.

■ JOURNAL REVIEW SERVICE

- Genome Medicine (2)
- Science Advances (2)
- Nature Biotechnology (1)
- Briefings in Bioinformatics (1)
- Scientific Report (5)
- eLife (1)
- Bioinformatics (5)
- PLOS Computational Biology (13)
- BMC Bioinformatics (3)
- Life Science Alliance (2)
- Annals of Applied Statistics (2)
- Computational and Structural Biotechnology (1)

■ PROFESSIONAL SOCIETY MEMBERSHIPS

- American Association for Cancer Research (AACR)
- American Statistical Association (ASA)
- International Biometric Society (ENAR)
- Western North American Region of The International Biometric Society (WNAR)
- Chan Zuckerberg Initiative (CZI)
- American Association of Immunology (AAI)

■ SERVICE

- March 2025 **Retreat Committee**
Joint retreat of Bioinformatics and Computational Biology department and Systems Biology department, MD Anderson Cancer Center, Houston, TX
- Nov. 2024 **Reviewer**
RECOMB 2025 conference paper review.
- August 2024 **Grant Review Committee**
Fred Hutchison Cancer Center TDS IRC Postdoctoral Fellowship and TDS IRC Pilot Award, Seattle, WA
- June - August 2024 **Program Committee**
Regulatory and Systems Genomics Conference with DREAM Challenges (RSGDREAM2024), Madison, WI
- November 2021 **Organizer**
2021 Junior Atlas Builders Program, Virtual
- 2019-2020 **Volunteer for Underdog Pet Rescue**
Volunteered to take care of homeless cats at Underdog Pet Rescue, Madison, WI
- 2017-2019 **Administrator**
Developed and maintained online archive for group discussion, blogs, tutorials and other research resources, Keleş Research Group, University of Wisconsin - Madison, Madison, WI
- 2017-2018 **Organizer and Discussion Lead**
Led weekly Student Literature Review Seminar in computational biology, University of Wisconsin - Madison
- June 2017 **Volunteer for Conference Organization**
Volunteered at the Center for Predictive Computational Phenotyping Third Annual Retreat, Madison, WI
- May 2017 **University Representative to promote UW-Madison Quantitative Biology Initiative**
Volunteered at the Great Lakes Bioinformatics Conference (GLBIO), Chicago, IL
- Oct. 2016 **Volunteer for Conference Organization**
Volunteered at the Wisconsin Science Festival, University of Wisconsin - Madison, Madison, WI