

Ye Zheng

EDUCATION AND TRAINING

2019 – **Fred Hutchinson Cancer Center**, *Vaccine and Infectious Disease and Basic Sciences Division*

present Postdoctoral Research Fellow

Single-cell Transcriptomics, Epigenomics, Proteomics Modeling and CAR-T Cell Immunotherapy Analysis

Mentors: Raphael Gottardo, Ph.D., Steven Henikoff, Ph.D.

Collaborators and advisors: Cameron Turtle, Ph.D., Evan Newell, Ph.D.

2014 – 2019 **University of Wisconsin – Madison**, *Department of Statistics*

Ph.D. in Statistics, Minor in Quantitative Biology

Thesis: Statistical Methods Development and Benchmarking for the Analysis of Three-dimensional Chromatin Organization.

Mentor: Sündüz Keleş, Ph.D.

2010 – 2014 **Renmin University of China**, *School of Statistics*

B.E. in Statistics

Honors Thesis: Approximate Bayesian Computation in Estimating the Structure of HIV Transmission Networks in Human Populations.

Mentor: Yang Li, Ph.D.

2012 – 2013 **The University of Hong Kong**, *Department of Statistics and Actuarial Science*

Exchange Study in Statistics

PUBLICATIONS

Three-dimensional Chromatin Organization and Long-range Gene Regulation

1. **Zheng Y***, Shen S*, Keles S. Normalization and De-noising of Single-cell Hi-C Data with BandNorm and scVI-3D. *bioRxiv*. Under the second round of review by *Genome Biology*. (2022). <https://doi.org/10.1101/2021.03.10.434870>. (*: co-first authors)
2. 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/10.1101/2020.02.16.941070>.
3. **Zheng Y**, Zhou P, Keleş S. FreeHi-C Spike-in Simulations for Benchmarking Differential Chromatin Interaction Detection. *Methods*. (2021) DOI:10.1016/j.ymeth.2020.07.001.
4. 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) DOI:<https://doi.org/10.1101/835678>.
5. **Zheng Y**, Keleş S. FreeHi-C simulates high-fidelity Hi-C data for benchmarking and data augmentation. *Nature Methods* (2020) DOI:10.1038/s41592-019-0624-3.
6. 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>.
7. 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). 583(7818), 693-698. <https://doi.org/10.1038/s41586-020-2449-8>.
8. **Zheng Y**, Ay F, Keleş S. Generative modeling of multi-mapping reads with mHi-C advances analysis of Hi-C studies. *eLife*. (2019) DOI:10.7554/eLife.38070.

Integrative Modeling of Single-cell and Bulk-cell Transcriptomics, Epigenomics, and Proteomics

9. **Zheng Y**, Seong-Hwan J, Tian Y, Florian M, Gottardo R. Robust Normalization and Integration of Single-cell Protein Expression across CITE-seq Datasets. *BioRxiv*. (2022) <https://doi.org/10.1101/2022.04.29.489989>.
10. 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/10.1101/2021.10.22>. (⁺: co-corresponding authors)
11. 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): 1-6. <https://doi.org/10.1038/s41587-021-00865-z>.
12. **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). (15,266 views, 4,355 exports, and 194 questions)
13. 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) Oct 20;11(10):e1004491 <https://doi.org/10.1371/journal.pcbi.1004491>.

Statistical Modeling and Computational Analysis of Immunological and Immunotherapeutic Studies

14. Fiorenza S*, **Zheng Y***, Sarthy J, Sheih AS, Wu Q, Hirayama AV, Kimble EL, Kirchmeier D, Gottardo R, Henikoff S, Turtle CJ. High-throughput, high sensitivity mapping of human T cell and CAR-T cell epigenomic landscapes underscores the role of H3K27me3 in subset differences and therapeutic outcomes. Manuscript in preparation. (* Co-first author)
15. Germanos AA, Arora S, **Zheng Y**, Goddard ET, Coleman IM, Ku AT, Wilkinson S, Amezquita 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. *BioRxiv* (2022). <https://doi.org/10.1101/2022.03.02.482711>. Under review for eLife.
16. 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 Nov 23;138:1749. <https://doi.org/10.1182/blood-2021-151571>.
17. 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>.
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), 31(13), 107832. <https://doi.org/10.1016/j.celrep.2020.107832>. (*co-first authors, ⁺co-corresponding authors)
19. 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) DOI:10.1172/JCI122694.
20. Tanimura N, Liao R, Wilson GM, Dent MR, Cao M, Burstyn JN, Hematti P, Liu X, Zhang Y, **Zheng Y**, Keleş S, Xu J, Coon J, Bresnick E. GATA/Heme Multi-omics Reveals a Trace Metal-dependent Cellular Differentiation Mechanism. *Developmental Cell*. (2018) Sep 10;46(5):581-94. <https://doi.org/10.1016/j.devcel.2018.07.022>.

PROFESSIONAL EXPERIENCE

2019 – **Postdoctoral Research Fellow**, *Seattle*, Washington

Present Vaccine and Infectious Disease Division, Fred Hutchinson Cancer Center

Mentors: Raphael Gottardo, Ph.D., Steven Henikoff, Ph.D.

Collaborators and advisors: Cameron Turtle, Ph.D., Evan Newell, Ph.D.

Statistical modeling of single-cell transcriptomics, epigenomics and proteomics:

- Developed normalization method for CITE-seq data to remove technical batch effect to facilitate comparison and integration across studies.
- Constructed data processing and analysis pipeline for bulk and single cell 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.

CAR-T Cell Immunotherapy:

- Multi-omics integrative analysis to construct cell atlas of chimeric antigen receptor T (CAR-T) cells therapy products using single-cell transcriptomics, epigenomics and proteomics data using CITE-seq, scRNA-seq and scCUT&Tag technologies.
- Construct statistical models to detect genomic marker signatures associated with CAR-T cell immunotherapy efficacy and toxicity.

Statistical consulting for genomics and biomedical studies:

- Statistical support for RNA-seq and single-cell RNA-seq analysis in the Hsieh Vitanza Labs.
- Quantitatively evaluation to decipher the transcriptional changes shared by cytotoxic HDAC inhibition in collaboration with Dr. Nicholas Vitanza and Dr. James Olson from Seattle Children's Hospital.

2014 – 2019 **Research Assistant**, *Madison*, Wisconsin

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 fast simulation of 3D proximity ligation sequencing data.
- Formulated detection of differential 3D genome interactions as a hierarchical testing problem and studied its operating characteristics in terms of false discovery rate control and detection power.

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.
- Investigated the impact of single nucleotide mutation in the Ets motif of GATA2 enhancer on its function to control hematopoiesis through a comprehensive transcriptomic differential analysis.
- Integrated epigenomics data to infer across species lifting-over position.

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.

GRANT APPLICATION EXPERIENCES

1. K99/R00 NIH Pathway to Independence Award. (2021 February. Impact score is 31 and application is pending for NHGRI Council Review).

PI: Ye Zheng.

Title: Bridging the gap: joint modeling of single-cell 1D and 3D genomics.

2. Fred Hutch TDS IRC New Collaborations Pilot Award (2022 July. Pending review)

PI: Ye Zheng, Alexandre Hirayama.

Title: A single-cell multimodal atlas of infused CD19 CAR-T cells: computational framework and machine learning modeling of clinical outcomes

3. Innovation in Cancer Informatics Grant. (2022 March. Not funded)
PI: Ye Zheng, Alexandre Hirayama.
Title: Cell atlas construction and clinical modeling of infused CD19 CAR-T cells
4. Chan Zuckerberg Initiative - Single-Cell Biology Data Insights Funding Opportunity. (2021 Nov. Not funded).
PI: Ye Zheng.
Title: Integrative analysis of single-cell 3D genomics, transcriptomics, and epigenomics
5. Immunotherapy Integrated Research Center Postdoctoral Fellowship Award. (2020 Nov. Not funded.)
PI: Ye Zheng.
Title: Chimeric antigen receptor-T cell therapy multi-omics platform for standardized and automatic quality check, quantitative analysis and clinical inference
6. Contributed to preliminary analysis for the R21 application (HG009744) funded by NIH/NHGRI in 2017.

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 genomics 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 single-cell Hi-C data. (Co-developer) Available at <https://github.com/keleslab/BandNorm>.
5. **FreeHiC**: Python pipeline using **F**ragment Interactions **E**mpirical **E**stimation 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 **m**ulti-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>.

Journal Reviewer

Genome Medicine, Science Advances, PLOS Computational Biology, BMC Bioinformatics, Life Science Alliance, Annals of Applied Statistics

PATENTS

1. 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
2. **Zheng Y.**, Yao S. . Protected from 10th Jan. 2007 to 10th Jan. 2017. Easel. Patent No. ZL 2005 20125184.0

SCHOLARSHIPS

- 2020 **Keystone Symposia Scholarship, \$1200**
Keystone Symposia, Higher-Order Chromatin Architecture in Time and Space, BC, Canada
- 2017-2018 **UW-Madison SRGC Conference Presentation Funds, \$1200**
University of Wisconsin – Madison, Madison, WI
- 2011-2014 **Scholarships for Outstanding Academic Performance, RMB7000**
Renmin University of China, Beijing, China
- 2013 **Mitacs (Canada) and China Scholarship Council Research Scholarship, \$4500**
Mitacs, Canada
- 2012 **Fung Scholar Scholarship, HK\$5000**
Hong Kong, China

HONORS AND AWARDS

- Nov 2021 **Keystone Symposia 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

PROFESSIONAL SOCIETY MEMBERSHIPS

- o American Statistical Association (ASA)
- o International Biometric Society (ENAR)
- o International Society for Computational Biology (ISCB)
- o Chan Zuckerberg Initiative (CZI)

INTERNATIONAL AND NATIONAL PRESENTATIONS

- June 2022 **Chan Zuckerberg Initiative Single-Cell Biology Next Generation Researcher Symposium**
Contributed talk, Virtual
- June 2022 **Chan Zuckerberg Initiative Single-cell Webinar**
Invited talk, Virtual
- May 2022 **Chan Zuckerberg Initiative - Assembling Tissue References Workshop**
Invited talk, Santa Rosa, CA, USA
- May 2022 **Cold Spring Harbor Laboratory - Genome Organization and Nuclear Function**
Contributed poster, Virtual
- March 2022 **Bioinformatics Seminar Series by the Sydney Precision Bioinformatics Alliance at the University of Sydney**
Invited talk, Virtual
- November 2021 **Keystone Symposia: Higher-Order Chromatin Architecture in Time and Space**
Contributed poster, Virtual
- April 2021 **CSHL Probabilistic Modeling in Genomics**
Contributed poster, Virtual
- November 2020 **CZI Seed Networks Annual 2020 Meeting**
Lightening talk and invited poster, Virtual
- December 2019 **AMSI BioInfoSummer 2019**
Invited talk and invited workshop, Sydney, Australia
- May 2019 **Great Lakes Bioinformatics Conference (GLBIO)**
Contributed talk, Madison, WI, USA
- July – Aug. 2018 **Joint Statistical Meeting (JSM)**
Contributed talk, Vancouver, Canada
- July 2018 **26th Conference on Intelligent Systems for Molecular Biology (ISMB)**
Two contributed talks, Chicago, IL, USA
- Mar. 2018 **International Biometric Society Eastern North American Region Annual Meeting**
Contributed talk, Atlanta, GA, USA
- Dec. 2017 **10th International Conference of the ERCIM WG (CMStatistics)**
Invited talk, University of London, London, UK
- Nov. 2017 **Program in Quantitative Genomics Conference**
Contributed poster, Harvard University, Boston, MA, USA
- June 2017 **14th Graybill Conference on Statistical Genomics and Genetics**
Contributed poster, Colorado State University–Fort Collins, Fort Collins, CO, USA
- May 2017 **Great Lakes Bioinformatics Conference (GLBIO)**
Contributed poster, University of Illinois at Chicago, Chicago, IL, USA
- July – Aug. 2016 **Joint Statistical Meeting (JSM)**
Contributed talk, Chicago, IL, USA
- June 2016 **Encyclopedia of DNA Elements (ENCODE) Consortium Meeting**
Invited lightening talk and poster, La Jolla, CA, USA

LOCAL PRESENTATIONS

- June 2021 **Biostatistics Post-Doc Meeting**
Invited talk, Seattle, WA
- April 2020 **Computational Biology Graduates and Postdoctoral Researchers Meeting**
Invited talk, Seattle, WA

- Oct. 2018 **3rd Annual Epigenetics Symposium**
Contributed poster, Madison, WI
- May 2018 **Center for Predictive Computational Phenotyping Fourth Annual Retreat**
Invited talk, Madison, WI
- Oct. 2017 **16th Computation and Informatics in Biology and Medicine Training Program**
Contributed poster, Madison, WI
- June 2017 **Center for Predictive Computational Phenotyping Third Annual Retreat**
Contributed poster, Madison, WI
- Nov. 2016 **Gene Expression, Chromatin and Transcription Mechanisms Research Club**
Invited talk, Madison, WI
- Oct. 2016 **15th Computation and Informatics in Biology and Medicine Training Program**
Contributed poster, Madison, WI
- June 2016 **Center for Predictive Computational Phenotyping Second Annual Retreat**
Contributed poster, Madison, WI
- Oct. 2015 **14th Computation and Informatics in Biology and Medicine Training Program**
Contributed poster, Madison, WI
- June 2015 **Center for Predictive Computational Phenotyping First Annual Retreat**
Contributed poster, Madison, WI
- June 2015 **NSF Conference Statistics for Complex Systems**
Contributed poster, Madison, WI
- May 2015 **12th Annual Genomic Sciences Program Retreat**
Contributed poster, Madison, WI

MENTORING

- Feb. 2022 - **Long Nguyen**, *Bioinformatics Analyst I at Fred Hutchinson Cancer Center*
Present 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 - **Siqi Shen**, *Ph.D. Candidate at University of Wisconsin - Madison*
Present Co-mentor with Dr. Sunduz Keles on single-cell 3D chromatin organization normalization and integrative analysis with single-cell transcriptomics and epigenomics.
- June 2020 - **Fanding Zhou**, *VISP student at University of Wisconsin - Madison*, Currently Ph.D. student at
Sep. 2021 University of California - Berkeley
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

- 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.
- 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.

SERVICE

- November 2021 **Organizer**
2021 Junior Atlas Builders Program, Virtual
- 2020-Now **Organizer and Discussion Lead**
Weekly Literature Review Seminar, VIDD, Fred Hutchinson Cancer Research Center
- 2019-2020 **Volunteer for Underdog Pet Rescue**
Volunteer to take care of homeless cats at Underdog Pet Rescue, Madison, WI
- 2017-Now **Administrator**
Develop and maintain 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**
Weekly Student Literature Review Seminar, Department of Biostatistics, University of Wisconsin - Madison
- June 2017 **Volunteer for Conference Organization**
Center for Predictive Computational Phenotyping Third Annual Retreat, Madison, WI
- May 2017 **University Representative to promote Quantitative Biology Initiative (QBI) at UW-Madison**
Great Lakes Bioinformatics Conference (GLBIO), Chicago, IL
- Oct. 2016 **Volunteer**
Wisconsin Science Festival, University of Wisconsin - Madison, Madison, WI

COMPUTING SKILLS

- Daily: Shell, Python, R, C, Cython, Docker, Conda, Grid/Distributed computing systems (HTCondor), Slurm, Git, Markdown, L^AT_EX
- Proficient: Pandas, Numpy, dplyr, Julia, R package construction, SAS Certified Base Programmer, Matlab
- Experienced: JAVA, Eviews, JMP, SPSS, MySQL

References

Raphael Gottardo, Professor, Postdoctoral Supervisor
Professor of Biomedical Science, University of Lausanne, Switzerland
Director of Biomedical Data Sciences, University Hospital of Lausanne, Switzerland
Affiliated Investigator, Fred Hutchinson Cancer Center, USA
Raphael.Gottardo@chuv.ch

Steven Henikoff, Professor, Postdoctoral Supervisor
Howard Hughes Medical Institute Investigator, USA
Basic Sciences Division, Fred Hutchinson Cancer Center, USA
Affiliate Faculty, Genome Sciences, University of Washington, USA

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Sündüz Keleş, Professor, Ph.D. Supervisor
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Cameron Turtle, Professor, Postdoctoral Advisor and Collaborator
Anderson Family Endowed Chair for Immunotherapy, Fred Hutchinson Cancer Center, USA
Clinical Research Division, Fred Hutchinson Cancer Center, USA
University of Washington School of Medicine, USA
Attending Physician, Seattle Cancer Care Alliance, USA
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Evan Newell, Associate Professor, Postdoctoral Advisor and Collaborator
Vaccine and Infectious Disease Division, Fred Hutchinson Cancer Center, USA
Public Health Sciences Division, Fred Hutchinson Cancer Center, USA
Herbold Computational Biology Program, Fred Hutchinson Cancer Center, USA
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