

# Kevin Z. Lin

University of Washington, Department of Biostatistics

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CV last updated: December 17, 2025

## EDUCATION

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- **Princeton University** Princeton, NJ  
B.S.E. in Operations Research & Financial Engineering 2010 - 2014  
Advisors: Han Liu and Robert Vanderbei  
Certificates in “Statistics and Machine Learning” and “Applications of Computing”
- **Carnegie Mellon University** Pittsburgh, PA  
Ph.D. in Dietrich’s Statistics & Data Science, Masters in Machine Learning 2014 - 2020  
Thesis advisors: Kathryn Roeder and Jing Lei

## EMPLOYMENT

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- **University of Pennsylvania** Philadelphia, PA  
Post-doctoral researcher in Wharton’s Statistics & Data Science 2020 - 2023  
Advisor: Nancy Zhang
- **University of Washington** Seattle, WA  
Assistant professor (tenure-track) in School of Public Health’s Biostatistics 2023 - Present  
Program faculty, UW Computational Molecular Biology 2023 - Present  
Genentech Endowed Professorship, UW Biostatistics 2025 - Present

## HONORS, AWARDS, AND SCHOLARSHIPS

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- **Teaching assistant excellence award recipient** Carnegie Mellon University  
For Course 36-350: “Statistical Computing” in Fall 2017 May 2017
- **Winner of Statistical Excellence for Early-Career Writing** Significance Magazine  
For article “We, the millennials: The statistical significance of political significance” June 2017  
*Competition held jointly with the Young Statisticians Section of Royal Statistical Society*
- **Honorable mention in student paper competition** American Statistical Association  
For paper “Dependency diagnostic: Visually understanding pairwise variable relationships” January 2018  
*For ASA section: Statistical Computing and Statistical Graphics*
- **PhD TAs of the year** Carnegie Mellon University  
For the Spring 2020 semester (1 of 2 total recipients) May 2020
- **Wikimedia Foundation Research Award of the Year** (Remote)  
For paper “Controlled analyses of social biases in Wikipedia bios” 2023
- **Biometrics Excellent Referee Awards** Atlanta, GA  
For the excellent reviews for the journal Biometrics (1 of 3 total recipients) 2024

## PROFESSIONAL ACTIVITIES

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- Association member for: American Society of Cell Biology (ASCB); American Statistical Association (ASA); American Society of Human Genetics (ASHG); Eastern North American Region (ENAR); International Chinese Statistical Association (ICSA); Institute of Mathematical Statistics (IMS); International Society to Advance Alzheimer's Research and Treatment (ISTAART)
- Peer-Reviewer for: Annals of Applied Statistics; Annals of Statistics; Bayesian Analysis; Biometrics; Biometrika; Cell Genomics; Cell Press Community Review; Electronic Journal of Statistics; Genome Biology; IEEE Transactions of Network Science and Engineering; Information and Inference: A Journal of the IMA; Journal of American Statistical Association; Journal of Machine Learning Research; Journal of Molecular Biology; Journal of the Royal Statistical Society: Series B; Machine Learning in Computational Biology; Nature Communications; Nature Methods; Nature Neuroscience; Nucleic Acids Research; Patterns; PLOS Genetics; Proceedings of the National Academy of Sciences; Statistical Sinica; Statistics and Probability Letters; Statistics in Medicine; Technometrics; Wiley Interdisciplinary Reviews: Computational Statistics
- Grant Reviewer for:
  - National Science Foundation (Methodology, Measurement, and Statistics): 2024
- Reviewer for Student Paper Award for the American Statistical Association's Section on Statistics in Genomics and Genetics (December in 2023, 2024, 2025)
- Area Chair for the conference Machine Learning in Computational Biology (Autumn 2023, 2024, 2025).
- Poster judge for International Society for Stem Cell Research's AI and Digital Biology Symposium (Autumn 2025).

## BIBLIOGRAPHY

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**Bold** denotes PI and his mentored students. Items are ordered in chronological order.

### Refereed research articles

1. Vanderbei, R., **Lin, K. Z.**, Liu, H., and Wang, L. (2016). Revisiting compressed sensing: Exploiting the efficiency of simplex and sparsification methods. *Mathematical Programming Computation*, 8(3):253–269  
[DOI: 10.1007/s12532-016-0105-y](https://doi.org/10.1007/s12532-016-0105-y)
2. **Lin, K. Z.**, Sharpnack, J., Rinaldo, A., and Tibshirani, R. J. (2017). A sharp error analysis for the fused lasso, with application to approximate changepoint screening. In *Advances in Neural Information Processing Systems*, pages 6884–6893  
[DOI: 10.5555/3295222.3295432](https://doi.org/10.5555/3295222.3295432)
3. An, J.-Y., **Lin, K. Z.**, Zhu, L., Werling, D. M., Dong, S., Brand, H., Wang, H. Z., Zhao, X., Schwartz, G. B., Collins, R. L., Currall, B. B., Dastmalchi, C., Dea, J., Duhn, C., Gilson, M. C., Klei, L., Liang, L., Markenscoff-Papadimitriou, E., Pochareddy, S., Ahituv, N., Buxbaum, J. D., Coon, H., Daly, M. J., Shin Kim, Y., Marth, G. T., Neale, B. M., Quinlan, A. R., Rubenstein, J. L., Sestan, N., State, M. W., Willsey, A. J., Talkowski, M. E., Devlin, B.,

- Roeder, K., and Sanders, S. J. (2018). Genome-wide de novo risk score implicates promoter variation in autism spectrum disorder. *Science*, 362(6420)  
DOI: 10.1126/science.aat6576
4. Lei, J. and **Lin, K. Z.** (2020). Discussion of ‘Network cross-validation by edge sampling’. *Biometrika*, 107(2):285–287  
DOI: 10.1093/biomet/asaa009
5. Wang, D., Zhao, Z., **Lin, K. Z.**, and Willett, R. (2021). Statistically and computationally efficient changepoint localization in regression settings. *Journal of Machine Learning Research*, 22:248–1  
DOI: 10.5555/3546258.3546506
6. Hyun, S., **Lin, K. Z.**, G’Sell, M., and Tibshirani, R. J. (2021). Post-selection inference for changepoint detection algorithms with application to copy number variation data. *Biometrics*, 77(3):1037–1049  
DOI: 10.1111/biom.13422
7. **Lin, K. Z.**, Liu, H., and Roeder, K. (2021b). Covariance-based sample selection for heterogeneous data: Applications to gene expression and autism risk gene detection. *Journal of the American Statistical Association*, 116(533):54–67  
DOI: 10.1080/01621459.2020.1738234
8. **Lin, K. Z.**, Lei, J., and Roeder, K. (2021a). Exponential-family embedding with application to cell developmental trajectories for single-cell RNA-seq data. *Journal of the American Statistical Association*, 116(534):457–470  
DOI: 10.1080/01621459.2021.1886106
9. Field, A., Park, C. Y., **Lin, K. Z.**, and Tsvetkov, Y. (2022). Controlled analyses of social biases in Wikipedia bios. In *Proceedings of the ACM Web Conference 2022*, pages 2624–2635  
DOI: 10.1145/3485447.3512134
10. Lei, J. and **Lin, K. Z.** (2023). Bias-adjusted spectral clustering in multi-layer stochastic block models. *Journal of the American Statistical Association*, 118(544):2433–2445  
DOI: 10.1080/01621459.2022.2054817
11. Guan, P. Y., Lee, J. S., Wang, L., **Lin, K. Z.**, Mei, W., Chen, L., and Jiang, Y. (2023). Destin2: Integrative and cross-modality analysis of single-cell chromatin accessibility data. *Frontiers in Genetics*, 14  
DOI: 10.3389/fgene.2023.1089936
12. **Lin, K. Z.** and Zhang, N. R. (2023). Quantifying common and distinct information in single-cell multimodal data with Tilted Canonical Correlation Analysis. *Proceedings of the National Academy of Sciences*, 120(32)  
DOI: 10.1073/pnas.2303647120
13. Chen, S., Zhu, B., Huang, S., Hickey, J. W., **Lin, K. Z.**, Snyder, M., Greenleaf, W. J., Nolan, G. P., Zhang, N. R., and Ma, Z. (2024). Integration of spatial and single-cell data across modalities with weakly linked features. *Nature Biotechnology*, 42(7):1096–1106  
DOI: 10.1038/s41587-023-01935-0
14. **Lin, K. Z.**, Qiu, Y., and Roeder, K. (2024). eSVD-DE: Cohort-wide differential expression in single-cell RNA-seq data using exponential-family embeddings. *BMC Bioinformatics*, 25(1):113  
DOI: 10.1186/s12859-024-05724-7

15. Prater, K. E. and **Lin, K. Z.** (2025). All the single cells: Single-cell transcriptomics/epigenomics experimental design and analysis considerations for glial biologists. *Glia*, 73(3):451–473  
DOI: 10.1002/glia.24633

#### Other refereed scholarly publications

1. **Lin, K. Z.** (2017). We, the millennials: The statistical significance of political significance. *Significance*, 14(5):28–33  
DOI: 10.1111/j.1740-9713.2017.01073.x

#### Other non-refereed scholarly publications

1. **Lin, K. Z.** and Lei, J. (2024). Dynamic clustering for heterophilic stochastic block models with time-varying node memberships. *arXiv preprint arXiv:2403.05654*  
Arxiv: 2403.05654 (*In revision*)
2. **Yang, S. J.**, Wang, Y., and **Lin, K. Z.** (2024). LCL: Contrastive learning for lineage barcoded scRNA-seq data. *bioRxiv*  
DOI: 10.1101/2024.10.28.620670
3. **Wu, W.**, Kennedy, T., Arguello-Miranda, O., and **Lin, K. Z.** (2024). Measuring regulatory network inheritance in dividing yeast cells using ordinary differential equations. *bioRxiv*  
DOI: 10.1101/2024.11.23.624995
4. **Li, Y.**, Wei, Z. J., Chen, Y.-C., and **Lin, K. Z.** (2024). Assessing RNA velocity stability across synthetic replicates using count splitting. *bioRxiv*  
DOI: 10.1101/2024.11.23.625009 (*In revision*)
5. Mamde, S., Rose, S. E., Prater, K. E., Cochoit, A., Lin, Y. F., Smith, I., Johnson, C. S., Reid, A. N., Qiu, W., Strohhahn, S., Keene, C. D., Rolf, B. A., **Lin, K. Z.**, Lee, S. I., Garden, G. A., Blue, E. E., Young, J. E., and Jayadev, S. (2025). Genetic risk in endolysosomal network genes correlates with endolysosomal dysfunction across neural cell types in Alzheimer’s disease. *bioRxiv*  
DOI: 10.1101/2025.03.16.643481
6. Fu, Y., Mathew, D., Wang, M., Chen, X. E., **Lin, K. Z.**, Schaff, D., Shaffer, S. M., Pardoll, D. M., Jackson, C., and Zhang, N. R. (2025). Deciphering cell fate and clonal dynamics via integrative single-cell lineage modeling. *bioRxiv*  
DOI: 10.1101/2025.09.01.673503
7. **Du, J. T.** and **Lin, K. Z.** (2025). Integrating morphology and gene expression of neural cells in unpaired single-cell data using GeoAdvAE. *bioRxiv*  
DOI: 10.1101/2025.11.19.689368

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#### PATENTS AND OTHER INTELLECTUAL PROPERTY

Below are publicly available software made by me and my lab.

1. **covarianceSelection**: R package for selecting datasets with similar high-dimensional covariance matrices. (<https://github.com/linnykos/covarianceSelection>)
2. **selectiveModel**: R package for selective inference via binary segmentation for changepoint detection. (<https://github.com/linnykos/selectiveModel>, developed jointly with Sangwon Hyun)

3. **eSVD**: R package for performing dimension reduction for matrices with respect to an exponential-family distribution. (<https://github.com/linnykos/esvd>)
4. **networkSoSD**: R package for performing spectral clustering to estimate node communities based on a collection of networks. (<https://github.com/linnykos/networkSoSD>)
5. **tiltedCCA**: R package for estimating the shared and distinct geometry in paired multimodal data. (<https://github.com/linnykos/tiltedCCA>)
6. **eSVD2**: R package that extends the functionality of the previous eSVD package, and also implements specialized functions to perform subject-level differential expression for single-cell data. (<https://github.com/linnykos/eSVD2>)
7. **Lineage-aware\_CL**: Python package to isolate the lineage-specific gene expression signatures from lineage-tracing scRNA-seq data ([https://github.com/SZ-yang/Lineage-aware\\_CL](https://github.com/SZ-yang/Lineage-aware_CL))
8. **ODEinherit**: R package to quantify the amount of inheritance of protein regulatory networks during cell division from live imaging microscopy data (<https://github.com/WenbinWu2001/ODEinherit>)
9. **veloUncertainty**: Python package to perform inference on RNA velocity methods based on count-splitting scRNA-seq data (<https://github.com/linnykos/veloUncertainty>)
10. **GeoAdvAE**: Python package to diagonally integrate cells' morphology with cell's single-cell RNA-seq transcriptome (<https://github.com/turbodu222/GeoAdvAE>)

## FUNDING HISTORY

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- **Royalty Research Fund** 03/16/2025 - 03/15/2026  
 University of Washington PI: Lin  
 Title: Quantifying population-wide genomic markers of Alzheimer's resiliency from cohort-wide single-cell RNA-sequencing data  
 Role: PI, Amount: \$40,000

## CONFERENCES AND SYMPOSIUMS

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"id." denotes identical title as the item above. Items are grouped by talks, and then ordered by chronological order.

### Invited departmental seminars

1. **University of California, Los Angeles: Department of Statistics** (12/2021).  
 Exponential-family embedding with application to cell developmental trajectories for single-cell data
2. **University of California, Irvine: Department of Statistics** (12/2022). Tilted-CCA:  
 Quantifying common and distinct information in multiomic single-cell data
3. **University of Washington: Department of Biostatistics** (01/2023). id.
4. **University of Chicago: Department of Statistics** (01/2023). id.
5. **University of California, Riverside: Department of Statistics** (01/2023). id.
6. **University of Waterloo: Department of Statistics** (01/2023). id.

7. **Pennsylvania State University: Department of Statistics** (01/2023). id.
8. **University of North Carolina: Department of Biostatistics** (01/2023). id.
9. **University of Michigan: Department of Statistics** (01/2023). id.
10. **University of Michigan: Department of Biostatistics** (02/2023). id.
11. **University of Illinois, Urbana-Champaign: Department of Statistics** (02/2023). id.
12. **Emory University: Department of Biostatistics** (02/2023). id.
13. **McGill University: Department of Epidemiology, Biostatistics, and Occupational Health** (09/2023). id.
14. **University of California, Santa Cruz: Department of Statistics** (10/2023). id.
15. **University of Washington: Department of Statistics** (05/2024). id.
16. **Michigan State University: Department of Statistics** (02/2024). Single-cell paired RNA & ATAC: Surveying broad multi-modal coordination in development and cancer resistance
17. **University of Pennsylvania: Biostatistics Division of Department of Biostatistics, Epidemiology, and Informatics** (03/2024). id.
18. **Duke University: Computational Biology and Bioinformatics** (04/2024). id.
19. **Brown University: Center for Computational Molecular Biology** (12/2024). eSVD-DE: Cohort-level differential expression in single-cell data via matrix factorization
20. **University of Wisconsin - Madison: Department of Statistics** (11/2025). Unexplored corners of multi-modal integration in cell biology

#### Conference/Seminar presentations

Note: (\*) denotes invited talks.

1. Modeling and Optimization: Theory and Applications (08/2014, Bethlehem, PA). Optimization for compressed sensing: New insights and alternatives
2. American Society of Human Genetics (10/2015, Baltimore, MD). Gaussian graphical model integrating microarray and sequencing data for autism risk gene detection
3. Joint Statistical Meeting (08/2016, Chicago, IL). id.
4. Conference on Neural Information Processing Systems (12/2017, Long Beach, CA). A sharp error analysis for the fused lasso, with application to approximate changepoint screening
5. Joint Statistical Meeting (08/2017, Baltimore, MD). Hypothesis testing for simultaneous variable clustering and correlation network estimation
6. Joint Statistical Meeting (08/2018, Vancouver, Canada). Dependency diagnostic: Visually understanding pairwise variable relationships
7. Joint Statistical Meeting (08/2019, Denver, CO). Exponential-family embedding with application to cell developmental trajectories for single-cell data

8. **Joint Statistical Meeting\*** (08/2020, Remote). id.
9. American Society of Human Genetics (10/2020, Remote). id.
10. Joint Statistical Meeting (08/2020, Remote). Time-varying stochastic block models via kernel smoothing, with application to RNA-seq data
11. **StatScale Seminar\*** (07/2021, Remote). id.
12. Symposium on Data Science and Statistics (06/2022, Pittsburgh, PA). Spectral clustering for multi-layer stochastic block models: Analysis of dynamic heterophilic networks
13. **International Chinese Statistical Association Applied Statistical Symposium\*** (06/2023, Ann Arbor, MI). id.
14. **International Conference on Econometrics and Statistics \*** (08/2025, Tokyo, Japan). id.
15. Joint Statistical Meetings (08/2022, Washington DC). Tilted-CCA: Quantifying common and distinct information in multiomic single-cell data
16. Institute of Mathematical Statistics New Researchers Conference 2023 (08/2023, Toronto, Canada). id.
17. **Scripps Research: Computational Biology and Bioinformatics Seminar\*** (08/2023, Remote). id.
18. Cell Symposia: The conceptual power of single-cell biology (08/2023, San Diego, CA). id.
19. American Society of Human Genetics (11/2023, Washington DC). id.
20. Keystone Symposia: Regulatory RNA - Emerging Mechanisms (12/2023, Banff, Canada). id.
21. **Joint Statistical Meeting\*** (08/2024, Portland, OR). id.
22. International Indian Statistical Association (06/2025, Lincoln, NE). id.
23. Joint Statistical Meeting (08/2023, Toronto, Canada). eSVD: Cohort-level differential expression in single-cell data via matrix factorization
24. **UW Genome Science: Combi Seminar\*** (01/2024, Seattle, WA). Single-cell paired RNA & ATAC: Surveying broad multi-modal coordination in development and cancer resistance
25. **Fred Hutch Cancer Center: Biostatistics Seminar Series\*** (01/2024, Seattle, WA). id.
26. **International Chinese Statistical Association Applied Statistical Symposium\*** (06/2024, Nashville, TN). eSVD-DE: Cohort-level differential expression in single-cell data via matrix factorization
27. American Society of Cell Biology (12/2024, San Diego, CA). Measuring inheritance of regulatory networks in dividing yeast cells using statistical ODE networks
28. **Eastern North American Region\*** (03/2025, New Orleans, LA). Dissecting cellular stress response through lineage barcoded multiome experiments
29. **UW Genome Science: Combi Seminar\*** (02/2025, Seattle, WA). LCL: Contrastive Learning for Lineage Barcoded scRNA-seq Data

30. **Statgen: Conference on Statistics in Genomics and Genetics\*** (05/2025, Minnesota, MN). id.
31. **International Chinese Statistical Association Applied Statistical Symposium\*** (06/2025, Storrs, CT). id.
32. Gordon Research Conference: Alzheimer's Disease (06/2025, Venutra, CA). Cohort-level differential distributional analysis for studying microglia in Alzheimer's disease via single-cell RNA-sequencing
33. American Society of Human Genetics (10/2025, Boston, MA). Integration of microglial morphology-gene expression via microscopy and snRNA-seq data to understand trajectory in Alzheimer's disease

#### **Organized conference sessions**

1. Statgen: Conference on Statistics in Genomics and Genetics (05/2024, Pittsburgh, PA). Session title: New mathematical paradigms behind single-cell biology
2. Joint Statistical Meeting (08/2024, Portland, OR). Session title: Single-cell Biology: New frontiers to understand gene expression through other omics
3. Eastern North American Region (03/2025, New Orleans, LA). Session title: New frontiers of single-cell biology, fueled by advancements in technology
4. Statgen: Conference on Statistics in Genomics and Genetics (05/2025, Minnesota, MN). Session title: Single-cell biology: New statistical frontiers across different omics

#### **Webinars**

1. Institute of Mathematical Statistics – New Researchers Group: Navigating the academic job market (11/2024)

#### **Session moderator at conference**

1. American Society of Human Genetics (10/2025, Boston, MA). Session Title: All That and a Bag of Variants: Functional Genomics of Brain Disorders  
Session moderator with Hongyu Zhao

#### **UNIVERSITY SERVICE**

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- Lead coordinator for the Mental Health working group (Winter 2023 - Spring 2025)
- UW Department of Biostatistics: Teaching track assistant professor search; Member (2023)
- UW School of Public Health: Mock Interview; Interviewer (Winter 2023)
- UW School of Public Health: Resume Clinic; Reviewer (2023: Autumn, 2024: Spring, Autumn)
- UW Department of Biostatistics: Seminar Committee; Member (2024 - Present), Chair (2025 - Present)
- UW Alzheimer's Disease Research Center (ADRC) Workshop; Co-lead with Katherine E. Prater (Summer 2025).  
Title: Hands-on single-nucleus RNA-seq analysis workshop for AD researchers

- Fred Hutchinson Cancer Center, Biostatistics Division: Assistant/associate/full professor professor search; Member (2025)
- Coordinator for UW Biostatistics Book Club on Caretaking in Alzheimer's disease (Fall 2025)  
Discussed: "Travelers to Unimaginable Lands: Stories of Dementia, the Caregiver, and the Human Brain" by Dasha Kiper

## TEACHING HISTORY

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### At Princeton University

1. Course designer for ORF 350: Analysis of Big Data (Spring 2012, Spring 2013, Spring 2014)

### At Carnegie Melon University

1. Teaching assistant for 46-921 & 46-923: Financial Data Analysis I and II (Spring 2014)
2. Teaching assistant for 36-217: Probability Theory and Random Processes (Spring 2015)
3. Teaching assistant for 36-350: Statistical Computing (Fall 2015, Fall 2016, Fall 2017)
4. Guest lecturer for 36-750: Statistical Computing (Fall 2016, Fall 2017, Fall 2018, Fall 2019, Fall 2020)
5. Assistant instructor for 36-350: Statistical Computing (Spring 2018)
6. Instructor for 36-350: Statistical Computing (Summer 2018)
7. Data science initiative project fellow for 36-490: Undergraduate Research (Spring 2019)
8. Co-instructor for 36-469: Statistical Genomics and High-Dimensional Inference (Spring 2020).  
With Kathryn Roeder

### At University of Washington

1. Instructor for BIOST 582: Student Seminar (Autumn 2023)
2. Instructor for BIOST 561: Computational Skills for Biostatistics (Spring 2024, Spring 2025)
3. Instructor for BIOST 545: Biostatistical Methods for Big Omics Data (Winter 2025)  
Course website: <https://linnykos.github.io/scOmicNotes/>.

### Independent study supervision

1. Yuhong Li (2023-25), University of Washington, Department of Biostatistics, Master of Science - Thesis
2. Zhaoheng Li (2023-25), University of Washington, Department of Biostatistics, PhD candidate
3. Yimin Zhao (2023-25), University of Washington, Department of Biostatistics, PhD candidate
4. Wenjing (Tati) Zhang (2023-25), University of Washington, Department of Biostatistics, Master of Science - Thesis
5. Amy Watt (2024-25), University of Washington, Department of Biostatistics, PhD candidate

6. Yifan Lin (2024-25), University of Washington, Department of Biostatistics, Master of Science - Thesis
7. Shirley Mathur (2025), University of Washington, Department of Statistics, PhD candidate
8. Michael Yung (2025), University of Washington, Department of Biostatistics, PhD candidate

## **Teaching and other professional development**

Short courses and tutorials taught at conferences:

1. ENAR 2024 (03/2024, Baltimore, MA) Teaching RNA-velocity for single-cell trajectory analysis and discussing its future research directions (Tutorial)
2. JSM 2025 (08/2025, Nashville, TN). From Faculty Hiring to Collaborative Success: Building a Thriving Academic Career (Roundtable) Co-lead with: Ahmad Talafha

Other professional development:

- Certified by CMU's Eberly Center's Future Faculty Program, which included two observed lectures in two different semesters (Fall 2019 to Summer 2020)
- Certified with Gatekeeper certificate by the QPR's (Question, Persuade, Refer) suicide prevention program (February 2020)
- Certified by Mental Health First Aid USA (Fall 2020)
- Teaching assistant for the Section on Statistical Genomics and Genetics (SSGG)'s online short course (Title: An Introduction to Deep Learning in Omics). Taught by Wei Sun and Nancy Zhang (Winter 2022)

## **ADVISING AND FORMAL MENTORING**

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### **MS and PhD committees in non-chair role**

1. Doctoral Committee Member
  - (a) Connor Finkbeiner (2023-25), University of Washington, Department of Genome Sciences, PhD candidate. (Chair: Manu Setty, at Fred Hutchinson Cancer Center)
2. Graduate School Representative
  - (a) Clifford Rostomily (2024-25), University of Washington, Department of Genome Sciences, PhD candidate. (Chair: Cole Trapnell)
  - (b) Rachel Ng (2025), University of Washington, Department of Bioengineering, PhD candidate. (Chair: Jim Heath, at Institute for Systems Biology)
  - (c) Wenyu Zeng (2025), University of Washington, Department of Biomedical and Health Informatics, PhD candidate. (Chair: Jim Phuong)
3. Qualifying Exam Member
  - (a) Anna Spiro (2023), University of Washington, Department of Computer Science, PhD candidate. (Chair: Sara Mostafavi)

### **Other mentoring**

Project Supervision (outside of independent study supervision)

1. Zeyu (Jerry) Wei (2023), University of Washington, Department of Statistics, PhD (on project jointly with Yen-Chi Chen)
2. Wenbin Wu (2023-25), University of Washington, Department of Statistics, Master of Science - Advanced Methods and Data Analysis
3. Haoye Yang (2023), University of Washington, Department of Statistics, Master of Science - Advanced Methods and Data Analysis
4. Shizhao (Joshua) Yang (2023-25), University of Washington, Department of Biostatistics, Master of Science - Capstone
5. Jinqiu (Turbo) Du (2024-25), University of Washington, Department of Biostatistics, Master of Science - Capstone
6. Jingyi Guan (2024-25), University of Washington, Department of Biostatistics, PhD candidate
7. Rita Li (2025), University of Washington, Department of Biostatistics, Master of Science - Capstone

### **Department-assigned Academic Advisor**

1. Alejandro Hernandez (2023-24), University of Washington, Department of Biostatistics, Master of Science - Capstone
2. Yutong Jin (2023-24), University of Washington, Department of Biostatistics, Master of Science - Capstone
3. Mohamad D. Bairakdar (2024-25), University of Washington, Department of Biostatistics, PhD candidate
4. Bojun Chen (2025), University of Washington, Department of Biostatistics, PhD candidate