Kevin Z. Lin

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CV last updated: September 13, 2025

Education

- **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

- **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

- **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

- 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; 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; Statistical Sinica; Statistics and Probability Letters; Statistics in Medicine; Technometrics
- 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)
- Area Chair for the conference Machine Learning in Computational Biology (Autumn 2023, 2024, 2025).

Bibliography

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

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

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

5. Mamde, S., Rose, S. E., Prater, K. E., Cochoit, A., Lin, Y. F., Smith, I., Johnson, C. S., Reid, A. N., Qiu, W., Strohbehn, 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*, pages 2025–03
   DOI: 10.1101/2025.03.16.643481

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)

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)

Funding History

- **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

"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

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

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)

University Service

- Lead coordinator for the Mental Health working group (Winter 2023, Spring 2024)
- 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

Teaching History

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)

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

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 Dr. Wei Sun and Dr. Nancy Zhang (Winter 2022)

Advising and Formal Mentoring

MS and PhD committees in non-chair role

1. Doctoral Committee Member
   (a) Connor Finkbeiner (2023-24), 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), 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. 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. Yifan Lin (2024-25), University of Washington, Department of Biostatistics, Master of Science - Thesis
8. Shirley Mathur (2025), University of Washington, Department of Statistics, PhD

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