

Eugene Katsevich

Assistant Professor of Statistics

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Employment

University of Pennsylvania, Department of Statistics, Assistant Professor, 2020-present.

Carnegie Mellon University, Department of Statistics and Data Science, Postdoctoral Researcher, 2019-2020.

Advisors: Kathryn Roeder and Aaditya Ramdas.

Education

Stanford University, Ph.D. in Statistics, 2019.

Thesis Advisor: Chiara Sabatti.

Princeton University, A.B. in Mathematics (with Highest Honors), 2014.

Thesis Advisor: Amit Singer.

Industry Experience

- *Research intern*, 23andMe computational biology team (Summer 2018).
- *Research intern*, Toshiba Medical Research Institute USA, (Summer 2013).
- *Research intern*, Virginia Tech Biomedical Imaging Division, (Summer 2011).

Funding

- Wharton Analytics Fund, awarded for "Statistical Software for Single Cell CRISPR Screens." \$75,000 (2021-2023).

Awards

- Jerome H. Friedman Applied Statistics Dissertation Award (2019).
- Statistics Department Teaching Assistant Award (2016).
- Hertz Fellowship (2014-2019).
- National Defense Science and Engineering Fellowship (2014-2017).
- George B. Covington Thesis Prize in Mathematics (2014).
- Early election to Phi Beta Kappa (2013).
- Barry Goldwater Scholarship (2012).

- Shapiro Prize for Academic Excellence (2011, 2012).
- Freshman First Honor Prize (2011).

Teaching and Training

Courses Taught at University of Pennsylvania

- STAT 471: Modern Data Mining, Spring '21 – Undergraduate Level.

Courses Taught at Stanford

- STATS 302: Qualifying Exams Workshop, Summer '17 – Graduate Level.

Doctoral Student Supervision

- Timothy Barry; jointly with Kathryn Roeder (Spring 2020 – present)

Professional Service Activities

- *Reviewer*, Annals of Statistics, Journal of the Royal Statistical Society (Series B), Journal of the American Statistical Association, Annals of Applied Statistics, Statistical Science, Proceedings of the National Academy of Sciences, Statistics and Probability Letters, Journal of Computational and Graphical Statistics, Electronic Journal of Statistics, Genetics.
- *Organizer*, Stanford statistics department orientation program for PhD students (2018).
- *Organizer*, Hertz West Coast Retreat (2017).
- *Academic chair*, Princeton Math Club (2012).
- *Head problem writer*, Princeton University Math Competition (2011).

Presentations

Invited talks

- *Statistical Analysis of Single Cell CRISPR Screens*.
Biostatistics seminar at Yale University,
February 2, 2021, held virtually.
- *Statistical Analysis of Single Cell CRISPR Screens*.
Open Insights in Biomedical Data Science Seminar at the University of Pennsylvania,
November 13, 2020, held virtually.
- *Finite-sample optimality and large-sample power analysis of the conditional randomization test*.
Young Data Science Researcher Seminar at ETH Zurich, November 6, 2020, held virtually.
- *Statistical analysis of single cell CRISPR screens*.
Stanford Biostatistics Workshop, October 8, 2020, held virtually.

- *The conditional randomization test in theory and in practice.*
International Seminar on Selective Inference, Aug. 20, 2020, held virtually.
- *A theoretical treatment of conditional independence testing under Model-X.*
Joint Statistical Meetings, Aug. 2–6, 2020, held virtually.
- *Multiple testing for modern data: structure, curation, and replicability.*
U.C. San Diego Halicioglu Data Science Institute Special Seminar, Feb. 12, 2019.
- *Multiple testing for modern data: structure, curation, and replicability.*
Rutgers University Statistics Seminar, Feb. 5, 2019.
- *Multiple testing for modern data: structure, curation, and replicability.*
Wharton Statistics Seminar, University of Pennsylvania, Jan. 30, 2019.
- *Multiple testing for modern data: structure, curation, and replicability.*
University of Chicago Statistics Colloquium, Jan. 24, 2019.
- *Controlling FDR while highlighting distinct discoveries, with applications to GO enrichment analysis.*
Stanford University Biostatistics Workshop, Oct. 11, 2018.
- *Controlling FDR while highlighting distinct discoveries, with applications to GO enrichment analysis.*
U.C. Berkeley Statistics and Genomics Seminar, Sep. 27, 2018.

Contributed talks

- *A theoretical treatment of conditional independence testing under Model-X.*
Bernoulli-IMS One World Symposium, Aug. 24–28, 2020, held virtually.
- *Simultaneous High-Probability Bounds on the False Discovery Proportion for Nested Sequences of Rejection Sets.*
International Conference on Multiple Comparison Procedures, Dec. 13–15, 2019, in Taipei, Taiwan.
- *Gene Ontology enrichment testing: Reconciling FDR control with filtering.*
Joint Statistical Meetings, Jul. 28–Aug. 2, 2018, in Vancouver, Canada.
- *The multilayer knockoff filter: Controlled multi-resolution variable selection.*
International Conference on Multiple Comparison Procedures, Jun. 20–23, 2017, in Riverside, California.

Poster Presentations

- *Conditional resampling improves sensitivity and specificity of genome-wide CRISPR regulatory screens.*
American Society for Human Genetics, Oct. 27–30, 2020, held virtually.
- *Controlling FDR While Highlighting Selected Discoveries.*
International Conference on Multiple Comparison Procedures, Dec. 13–15, 2019, in Taipei, Taiwan.
- *Multi-resolution association analysis for exome-wide sequencing.*
American Society for Human Genetics, Oct. 16–20, 2018, in San Diego, California.
- *Controlling FDR while highlighting distinct discoveries.*
Workshop on Higher-Order Asymptotics and Post-Selection Inference, Sep. 8–10 2018, in St. Louis, Missouri.
- *Multilayer FDR control for genetic association studies.*
Graybill Conference on Statistical Genomics and Genetics, Jun. 5–7 2017, in Fort Collins, Colorado.
Best student poster award.
- *The multilayer knockoff filter: Multilayer FDR control for association studies.*
Probabilistic Modeling in Genomics, Sep. 12–14, 2016, in Oxford, United Kingdom.

Workshop Participation

- *Participant*, Simons Institute Workshop on Robust and High-Dimensional Statistics (October 2018).
- *Participant*, Joint UCLA and Stanford Statistical Genetics Programming Workshop (Summer 2016).
- *Participant*, UCLA Computational Genomics Summer Institute short course (Summer 2016).

Preprints

- [1] E. Katsevich and A. Ramdas. A theoretical treatment of conditional independence testing under Model-X. Available on [arXiv](#).
- [2] M. Liu, E. Katsevich, L. Janson, and A. Ramdas. Fast and powerful conditional randomization testing via distillation. Available on [arXiv](#).
- [3] T. Barry, X. Wang, J. A. Morris, K. Roeder, and E. Katsevich. Conditional resampling improves calibration and sensitivity in single-cell CRISPR screen analysis. Available on [bioRxiv](#).
- [4] J. Tian, X. Chen, E. Katsevich, J. Goeman, and A. Ramdas. Large-scale simultaneous inference under dependence. Available on [arXiv](#).
- [5] J. A. Morris, Z. Daniloski, J. Domingo, T. Barry, M. Ziosi, D. A. Glinos, S. Hao, E. Mimitou, P. Smibert, K. Roeder, E. Katsevich, T. Lappalainen, and N. E. Sanjana. Discovery of target genes and pathways of blood trait loci using pooled CRISPR screens and single cell RNA sequencing. Available on [bioRxiv](#).

Publications

- [1] E. Katsevich, A. Katsevich, and G. Wang. Stability of the interior problem for polynomial region of interest. *Inverse Problems*, 28(6), 2012. Available on [PubMed](#).
- [2] B. Shi, E. Katsevich, B. Chiang, A. Katsevich, and A. Zamyatin. Image registration for motion estimation in cardiac CT. In *SPIE Medical Imaging*, San Diego, California, February 2014. Available on [SPIE digital library](#).
- [3] E. Katsevich, A. Katsevich, A. Singer. Covariance matrix estimation for the cryo-EM heterogeneity problem. *SIAM Journal on Imaging Sciences*, 8(1):126–185, 2015. Available on [PubMed](#).
- [4] J. Anden, E. Katsevich, and A. Singer. Covariance estimation using conjugate gradient for 3D classification in cryo-EM. In *IEEE Int Symp Biomed Imaging*, New York, New York, April 2015. Available on [PubMed](#).
- [5] E. Katsevich and C. Sabatti. Multilayer Knockoff Filter: Controlled variable selection at multiple resolutions. *Annals of Applied Statistics*, 13(1):1–33, 2019. Available on [Project Euclid](#).
- [6] J. Zhu, Q. Zhao, E. Katsevich, C. Sabatti. Exploratory Gene Ontology Analysis with Interactive Visualization. *Nature Scientific Reports*, 9:7793, 2019. Available at [nature.com](#).
- [7] M. Sesia, E. Katsevich, S. Bates, E. Candès, C. Sabatti. Multi-resolution localization of causal variants across the genome. *Nature Communications*, 11:1093, 2020. Available at [nature.com](#).
- [8] E. Katsevich and A. Ramdas. Simultaneous high-probability bounds on the false discovery proportion in structured, regression, and online settings. *Annals of Statistics*, 48(6):3465–3487, 2020. Available on [Project Euclid](#).

- [9] **E. Katsevich**, C. Sabatti, and M. Bogomolov. Filtering the rejection set while preserving false discovery rate control. *Journal of the American Statistical Association*, to appear, 2021. Available on [arXiv](#).

Last updated: April 28, 2021