Timothy (Tim) Barry

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EMPLOYMENT

Boston Children's Hospital and Massachusetts General Hospital *2025 –*
Postdoctoral researcher
Advisors: Daniel Bauer, Luca Pinello, Danilo Pellin

Harvard University, Department of Biostatistics *2024 – 2025*
Postdoctoral researcher
Advisor: Xihong Lin
(The Trump administration illegally terminated the grant that funded my research.)

University of Pennsylvania, Department of Statistics *2023*
Postdoctoral researcher
Advisor: Eugene Katsevich

EDUCATION

Carnegie Mellon University *2018 – 2023*
PhD in Statistics
Advisors: Kathryn Roeder, Eugene Katsevich (University of Pennsylvania)

University of Maryland, College Park *2014 – 2018*
BS in Mathematics with high honors
Minor in Computer Science

AWARDS

- Harvard Chan Postdoctoral Association Travel Award *2025*
- Howard Hughes Medical Institute Fellowship *2017*
- Maryland Summer Scholars Research Grant *2016*
- Banneker-Key Scholarship, University of Maryland's highest academic scholarship *2014*

PAPERS

- **T Barry**, Z Niu, E Katsevich, X Lin. "The permuted score test for robust differential expression analysis." Preprint. Link. *2025*
- L Fischer, **T Barry**, A Ramdas. "Multiple testing with anytime-valid Monte-Carlo p-values." Preprint. Link. *2024*
- **T Barry**, K Mason, E Katsevich, K Roeder. "Robust differential expression testing for single-cell CRISPR screens at low multiplicity of infection." *Genome Biology*. Link. (Mihaela Serban Memorial Award, American Statistical Association, Pittsburgh chapter) *2024*
- **T Barry**, K Roeder, E Katsevich. "Exponential family measurement error models for single-cell CRISPR screens." *Biostatistics*. Link. *2024*

- J Morris, C Caragine, Z Daniloski, J Domingo, **T Barry**, L Lu, K Davis, M Ziosi, D Glinos, S Hao, E Mimitou, P Smibert, K Roeder, E Katsevich, T Lappalainen, N Sanjana. "Discovery of target genes and pathways at GWAS loci by pooled single-cell CRISPR screens." *Science*. Link. *2023*
- **T Barry**, X Wang, J Morris, K Roeder, E Katsevich. "SCEPTRE improves calibration and sensitivity in single-cell CRISPR screen analysis." *Genome Biology*. Link. (Reviewers' choice, American Society of Human Genetics conference) *2021*
- **T Barry***, E Gurarie*, F Cheraghi, I Kajola, W Fagan. "Does dispersal make the heart grow bolder? Avoidance of anthropogenic habitat elements across wolf life history." *Animal Behaviour* 166. **Joint first authorship*. Link. *2020*
- **T Barry**. "Collections in R: Review and Proposal." *The R Journal 10.1*. Link. *2018*

BOOK

T Barry, J Deutsch, E Katsevich. "Hands-on single-cell CRISPR screen analysis." e-book. Link *2024*

GRANT ACTIVITY

Submitted

Name	Agency	Mechanism	Role	Requested funds	Dates
"Statistical advances in CRISPR profiling and screening"	NIH	K99/R00	PI	$1,015,000	4/01/2026 - 3/30/2031

(Due to the Trump Administration's embargo on new grants to Harvard, I will resubmit this grant from Boston Children's Hospital in the October 2025 cycle.)

SOFTWARE PACKAGES

- `sceptre`: statistically rigorous and massively scalable single-cell CRISPR screen analysis. Link.

  (`sceptre` is the first package for single-cell CRISPR screen analysis endorsed by 10x Genomics, the main commercial supplier of single-cell experimental kits.)

- `ondisc`: out-of-core and cluster-scale computing on single-cell data. Link.

PROFESSIONAL SERVICE

- *Reviewer*, Annals of Applied Statistics, Biometrika, Frontiers in Genetics, Nature Biotechnology
- *Judge*, NESS student paper competition (2024), ENAR student poster competition (2025)

MENTORING

- Songcheng Dai (Computational Biology Masters student at CMU). Topic: algorithms, data structures, and software for large-scale single-cell data. *2021 - 2022*

TALKS

- "The permuted score test for robust differential expression analysis." ASA Conference on Statistics in Genomics and Genetics. Minneapolis, MN. Contributed. *2025*
- "The permuted score test for robust differential expression analysis." International Biometric Society ENAR meeting. New Orleans, LA. Invited. *2025*

• "Massive-scale perturb-seq analysis." IGVF conference. Seattle, WA. Contributed poster. *2024*

• "Massive-scale perturb-seq analysis." Joint Statistics Meetings. Portland, OR. Contributed. *2024*

• "Massive-scale perturb-seq analysis." Monash University Genomics & Bioinformatics Platform seminar series. Held virtually. Invited. *2024*

• "Robust inference by resampling score statistics, with application to single-cell CRISPR screens." NESS conference. Storrs, CT. Invited. *2024*

• "Let it SNO: massive-scale perturb-seq analysis using `sceptre`, `Nextflow`, and `ondisc` (SNO)." IGVF CAMP working group. Held virtually. Invited. *2024*

• "Let it SNO: massive-scale perturb-seq analysis using `sceptre`, `Nextflow`, and `ondisc` (SNO)." RECOMB-seq conference. Boston, MA. Contributed poster. *2024*

• "Robust inference by resampling score statistics, with application to single-cell CRISPR screens." IGVF conference. St Louis, MO. Contributed poster. *2023*

• "Robust inference by resampling score statistics, with application to single-cell CRISPR screens." Bioconductor Conference. Boston, MA. Contributed poster. *2023*

• "Robust inference by resampling score statistics, with application to single-cell CRISPR screens." ASA Pittsburgh chapter spring banquet. Pittsburgh, PA. Contributed poster. *2023*

• "Robust differential expression analysis for single-cell CRISPR screens." Hicks and Hansen Labs, Department of Biostatistics, Johns Hopkins University. Baltimore, MD. Invited. *2023*

• "Exponential family measurement error models for single-cell CRISPR screens." Joint Statistics Meetings. Washington, DC. Contributed. *2022*

• "Conditional resampling improves calibration and sensitivity in single-cell CRISPR screen analysis." RECOMB-Seq. Held virtually. Contributed. *2021*

• "Conditional resampling improves calibration and sensitivity in single-cell CRISPR screen analysis." He Lab, Department of Human Genetics, University of Chicago. Held virtually. Invited. *2021*

Updated July 2025.