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 NIH T32 grant that funded my research was terminated.)

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

- Uplifting Athletes rare disease foundation Young Investigator Award *2025*
- National Science Foundation STATGEN Travel Award (declined) *2025*
- 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

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.

GRANT ACTIVITY

Awarded

Name	Organization	Mechanism	Role	Funds	Dates
"Statistical methods to evaluate the precision of therapeutic gene editing for rare diseases"	Uplifting Athletes rare disease foundation	Young investigator award	PI	$20,000	02/01/2026 - 01/31/2027

Submitted

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

PROFESSIONAL SERVICE

- *Reviewer*, Annals of Applied Statistics, Biometrika, Nature Biotechnology, Nature Methods
- *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

- "Measuring off-target effects in CRISPR based gene editing" Shwachman-Diamond Syndrome Global Patient Advocacy and Partnering Summit. Virtual. Invited. *2025*
- "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*