

# Timothy (Tim) Barry

timothy.barry@childrens.harvard.edu • <https://timothy-barry.github.io>

## EMPLOYMENT

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| <b>Boston Children's Hospital and Massachusetts General Hospital</b><br>Postdoctoral researcher<br>Advisors: Daniel Bauer, Luca Pinello, Danilo Pellin   | 2025 –      |
| <b>Harvard University, Department of Biostatistics</b><br>Postdoctoral researcher<br>Advisor: Xihong Lin<br>(The Trump administration illegally terminated the grant that funded my research.) | 2024 – 2025 |
| <b>University of Pennsylvania, Department of Statistics</b><br>Postdoctoral researcher<br>Advisor: Eugene Katsevich  | 2023        |

## EDUCATION

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|---|-------------|
| <b>Carnegie Mellon University</b><br>PhD in Statistics<br>Advisors: Kathryn Roeder, Eugene Katsevich (University of Pennsylvania) | 2018 – 2023 |
| <b>University of Maryland, College Park</b><br>BS in Mathematics with high honors<br>Minor in Computer Science                    | 2014 – 2018 |

## AWARDS

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| • 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

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