

Timothy (Tim) Barry

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EMPLOYMENT

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|---|----------------------|
| Harvard University
Postdoctoral researcher, Department of Biostatistics
Advisor: Xihong Lin | 2024 – |
| University of Pennsylvania
Postdoctoral researcher, Department of Statistics
Advisor: Eugene Katsevich | July – December 2023 |

EDUCATION

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

AWARDS

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| • 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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| • T Barry , K Mason, E Katsevich, K Roeder. "Robust differential expression testing for single-cell CRISPR screens at low multiplicity of infection." <i>Genome Biology</i> . 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." <i>Biostatistics</i> . 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." <i>Science</i> . Link . | 2023 |
| • T Barry , X Wang, J Morris, K Roeder, E Katsevich. "SCEPTRE improves calibration and sensitivity in single-cell CRISPR screen analysis." <i>Genome Biology</i> . 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." <i>Animal Behaviour</i> 166. *Joint first authorship. Link . | 2020 |
| • T Barry . "Collections in R: Review and Proposal." <i>The R Journal</i> 10.1. Link . | 2018 |

BOOK

- **T Barry**, J Deutsch, E Katsevich. "Hands-on single-cell CRISPR screen analysis." e-book preprint. [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 CRISPR screen kits.
- **ondisc**: out-of-core and cluster-scale computing on single-cell data. [Link](#).

PROFESSIONAL SERVICE

- *Reviewer*, Annals of Applied Statistics, Biometrika, Nature Biotechnology
- *Judge*, New England Statistical Society (NESS) student paper competition

MENTORING

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

TALKS

- * "Robust negative binomial regression by adaptively permuting score test statistics." 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

TEACHING ASSISTANTSHIPS (CMU)

- Statistics 36-350: Statistical computing *Fall 2018*
- Statistics 36-469: Statistical genomics and high-dimensional inference *Spring 2020*

COMPUTING

- Languages: R, Python, C/C++, Nextflow
- Clusters and clouds: SLURM, Sun Grid Engine, Azure
- Database systems: HDF5

Updated October 2024.