

Timothy (Tim) Barry

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EMPLOYMENT

Harvard University

2024 –

Postdoctoral researcher, Department of Biostatistics

Advisor: Xihong Lin

University of Pennsylvania

July – December 2023

Postdoctoral researcher, Department of Statistics

Advisor: Eugene Katsevich

EDUCATION

Carnegie Mellon University (CMU)

2018 – 2023

PhD in Statistics

Advisors: Kathryn Roeder (CMU), 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 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

- * “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

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 January 2025.