

# Timothy Barry

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## EMPLOYMENT

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### University of Pennsylvania

July – December 2023

Postdoctoral researcher, Department of Statistics

Advisor: Eugene Katsevich

### Harvard University

2024 –

Postdoctoral researcher, Department of Biostatistics

Advisor: Xihong Lin

## EDUCATION

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### Carnegie Mellon University (CMU)

2018 – 2023

PhD in Statistics

Advisors: Kathryn Roeder (CMU), Eugene Katsevich (University of Pennsylvania)

Committee: Jing Lei, Jian Ma, F. William Townes

### University of Maryland, College Park

2014 – 2018

BS in Mathematics with high honors

Minor in Computer Science

## AWARDS

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- Howard Hughes Medical Institute Fellowship 2017
- Maryland Summer Scholars Research Grant 2016
- Banneker-Key Scholarship, University of Maryland's most prestigious scholarship 2014

## MENTORING

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

## 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." BioRxiv preprint. [Link](#). (Mihaela Serban Memorial Award, American Statistical Association, Pittsburgh chapter) 2023
- **T Barry**, E Katsevich, K Roeder. "Exponential family measurement error models for single-cell CRISPR screens." Revisions at *Biostatistics*. [Link](#). 2022
- 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](#). (Platform talk, American Society of Human Genetics conference) 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

## SOFTWARE PACKAGES

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- **sceptre**: Robust inference for single-cell CRISPR screens. [Link](#).
- **ondisc (beta)**: Large-scale computing for single-cell data. [Link](#).

## TALKS

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- “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

## PROFESSIONAL SERVICE

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- Reviewer for *Biometrika*, *Nature Biotechnology*

## TEACHING ASSISTANTSHIPS (CMU)

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

## COMPUTING

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- Languages: R, Python, C/C++, Nextflow
- Operating systems: Unix, Linux
- Clusters and clouds: SLURM, Sun Grid Engine, Azure
- Database systems: HDF5
- Version control systems: Git/Github

Updated 2023.