

Timothy Barry

tbarry2@andrew.cmu.edu • <https://timothy-barry.github.io>

INTERESTS

Statistics, genomics, computer science

EDUCATION

Carnegie Mellon University (CMU) 2018 – 2023

PhD in Statistics and Data Science

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

• Howard Hughes Medical Institute Fellowship 2017

• Maryland Summer Scholars Research Grant 2016

• Banneker-Key Scholarship, University of Maryland's most prestigious scholarship 2014

MENTORING

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

PAPERS

• **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

Undergraduate

• **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

SOFTWARES

- `sceptre`: Robust inference for single-cell CRISPR screens. [Link](#).
 - Example studies that use this method: [Science 2023](#), [Genome Biology 2023](#)
- `ondisc` (beta): Large-scale computing for single-cell data. [Link](#).

TALKS

- “Robust inference by resampling score statistics, with application to single-cell CRISPR screens.” ASA Pittsburgh chapter spring banquet. Pittsburgh, PA. Contributed. 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

- 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
- Operating systems: Unix, Linux
- Clusters and clouds: SLURM, Sun Grid Engine, Azure
- Database systems: HDF5
- Version control systems: Git/Github

Updated 2023.