Timothy (Tim) Barry

tbarry@hsph.harvard.edu • https://timothy-barry.github.io

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

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**, K Roeder, E Katsevich. "Exponential family measurement error models for single-cell CRISPR screens." Major revision submitted 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. *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." eBook draft. Link. *2023*

SOFTWARE PACKAGES

- `sceptre`: single-cell CRISPR screen data analysis. [Link](#).

AWARDS

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

PROFESSIONAL SERVICE

- Reviewing for Nature Biotechnology, Biometrika, Annals of Applied Statistics

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 differential expression analysis for single-cell CRISPR screens". Impact of Genomic Variation on Function (IGVF) Consortium second annual 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

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

COMPUTING

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