

# Timothy (Tim) Barry

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## EMPLOYMENT

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| <b>Harvard University</b><br>Postdoctoral researcher, Department of Biostatistics<br>Advisor: Xihong Lin            | 2024 –               |
| <b>University of Pennsylvania</b><br>Postdoctoral researcher, Department of Statistics<br>Advisor: Eugene Katsevich | July – December 2023 |

## EDUCATION

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| <b>Carnegie Mellon University (CMU)</b><br>PhD in Statistics<br>Advisors: Kathryn Roeder (CMU), Eugene Katsevich (University of Pennsylvania) | 2018 – 2023 |
| <b>University of Maryland, College Park</b><br>BS in Mathematics with high honors<br>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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| • <b>T Barry</b> , K Mason, E Katsevich, K Roeder. "Robust differential expression testing for single-cell CRISPR screens at low multiplicity of infection." <i>Genome Biology</i> , to appear. <a href="#">Link</a> . (Mihaela Serban Memorial Award, American Statistical Association, Pittsburgh chapter)         | 2024+ |
| • <b>T Barry</b> , K Roeder, E Katsevich. "Exponential family measurement error models for single-cell CRISPR screens." <i>Biostatistics</i> . <a href="#">Link</a> .  | 2024  |
| • J Morris, C Caragine, Z Daniloski, J Domingo, <b>T Barry</b> , 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> . <a href="#">Link</a> . | 2023  |
| • <b>T Barry</b> , X Wang, J Morris, K Roeder, E Katsevich. "SCEPTRE improves calibration and sensitivity in single-cell CRISPR screen analysis." <i>Genome Biology</i> . <a href="#">Link</a> . (Reviewers' choice, American Society of Human Genetics conference)  | 2021  |
| • <b>T Barry</b> *, 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. <a href="#">Link</a> .   | 2020  |
| • <b>T Barry</b> . "Collections in R: Review and Proposal." <i>The R Journal</i> 10.1. <a href="#">Link</a> .  | 2018  |

## BOOK

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- **T Barry**, J Deutsch, E Katsevich. "Hands-on single-cell CRISPR screen analysis." e-book preprint. [Link](#) 2024

## SOFTWARE PACKAGES

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- **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

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

## 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

## TALKS

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- "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)

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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 April 2024.