

Timothy Barry

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EDUCATION

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| Carnegie Mellon University
PhD in Statistics and Data Science
Advisors: Kathryn Roeder, Eugene Katsevich | <i>2018 – 2023</i> |
| University of Maryland, College Park
BS in Mathematics with high honors
Minor in Computer Science | <i>2014 – 2018</i> |

AWARDS

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

TEACHING ASSISTANTSHIPS

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| • Statistics 36-350: Statistical computing | <i>Fall 2018</i> |
| • Statistics 36-469: Statistical genomics and high-dimensional inference | <i>Spring 2020</i> |

MENTORING

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| • Songcheng Dai (Computational Biology Masters student at CMU). Research topic: algorithmic and statistical tools for large-scale single-cell data. | <i>2021 - 2022</i> |
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PAPERS

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| • T Barry , E Katsevich, K Roeder. "Robust differential expression testing for single-cell CRISPR screens." Preprint. Link . | <i>2022</i> |
| • T Barry , E Katsevich, K Roeder. "Exponential family measurement error models for single-cell CRISPR screens." Revisions at Biostatistics. Link . | |
| • 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) | <i>2021</i> |
| • J Morris, Z Daniloski, J Domingo, T Barry , M Ziosi, D Glinos, S Hao, E Mimitou, P Smibert, K Roeder, E Katsevich, T Lappalainen, N Sanjana. "Discovery of target genes and pathways of blood trait loci using pooled CRISPR screens and single cell RNA sequencing." <i>BioRxiv</i> . Link . | <i>2021</i> |

Undergraduate

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| • 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." <i>Animal Behaviour</i> 166. * <i>Joint first authorship</i> . Link . | <i>2020</i> |
| • T Barry . "Collections in R: Review and Proposal." <i>The R Journal</i> 10.1. Link . | <i>2018</i> |

TALKS

- “Exponential family measurement error models for single-cell CRISPR screens.” *2021*
Joint Statistics meetings. Washington, DC. Contributed.
- “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.” Xin He Lab, University of Chicago. Held virtually. Invited. *2021*

SERVICE AND SCIENCE OUTREACH

- Volunteer math, science, and English tutor to elementary and middle school students through UMD Lakeland STARS program. *2015 – 2018*

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 January 2023.