

# Timothy Barry

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## EDUCATION

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| <b>Carnegie Mellon University</b><br>PhD in Statistics and Data Science<br>Advisors: Kathryn Roeder, Eugene Katsevich | <i>2018 – 2023</i> |
| <b>University of Maryland, College Park</b><br>BS in Mathematics with high honors<br>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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| • <b>T Barry</b> , K Roeder, E Katsevich. "Robust differential expression testing for single-cell CRISPR screens." Preprint. <a href="#">Link</a> .  | <i>2023</i> |
| • <b>T Barry</b> , E Katsevich, K Roeder. "Exponential family measurement error models for single-cell CRISPR screens." Revisions at Biostatistics. <a href="#">Link</a> .   | <i>2022</i> |
| • <b>T Barry</b> , X Wang, J Morris, K Roeder, E Katsevich. "SCEPTRE improves calibration and sensitivity in single-cell CRISPR screen analysis." Genome Biology. <a href="#">Link</a> . ( <a href="#">Reviewers' choice, American Society of Human Genetics conference, 2021</a> )                            | <i>2021</i> |
| • J Morris, Z Daniloski, J Domingo, <b>T Barry</b> , 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." BioRxiv. <a href="#">Link</a> . | <i>2021</i> |

### Undergraduate

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| • <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> . | <i>2020</i> |
| • <b>T Barry</b> . "Collections in R: Review and Proposal." <i>The R Journal</i> 10.1. <a href="#">Link</a> .  | <i>2018</i> |

## SOFTWARES

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- **sceptre**: Robust inference for single-cell CRISPR screens. [Link](#).
- **ondisc**: Large-scale computing for single-cell data. (This software currently is in beta version and undergoing testing by several research groups.)

## TALKS

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- “Exponential family measurement error models for single-cell CRISPR screens.” 2022  
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

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

## 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 January 2023.