

# Timothy Barry

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## INTERESTS

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Statistics, genomics, and computer science

## EDUCATION

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**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

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

## TEACHING ASSISTANTSHIPS

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

## 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. 2021 - 2022

## PAPERS

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- **T Barry**, K Roeder, E Katsevich. "Robust differential expression testing for single-cell CRISPR screens." Pre-submission. [Link](#). 2023
- **T Barry**, E Katsevich, K Roeder. "Exponential family measurement error models for single-cell CRISPR screens." Revisions at *Biostatistics*. [Link](#). 2022
- **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) 2021
- 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." Revision and resubmission requested at *Science*. [Link](#). 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

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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, undergoing preliminary use and testing by several research groups. A stable release will be available in 2023.) [Link](#).

## 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.” *2021*  
RECOMB-Seq. Held virtually. Contributed.
- “Conditional resampling improves calibration and sensitivity in single-cell CRISPR screen analysis.” *2021*  
Xin He Lab, University of Chicago. Held virtually. Invited.

## SERVICE AND SCIENCE OUTREACH

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

## 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.