Timothy Barry

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INTERESTS

Statistics, genomics, and computer science

EDUCATION

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

- 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

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

MENTORING

- Songcheng Dai (Computational Biology Masters student at CMU). Research topic: algorithmic and statistical tools for large-scale single-cell data. *2021 - 2022*

PAPERS

- **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

- `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

- "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*

SERVICE AND SCIENCE OUTREACH

- Tutored math, science, and English 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.