Timothy Barry

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EMPLOYMENT

University of Pennsylvania *July – December 2023*
Postdoctoral researcher, Department of Statistics
Advisor: Eugene Katsevich

Harvard University *2024 –*
Postdoctoral researcher, Department of Biostatistics
Advisor: Xihong Lin

EDUCATION

Carnegie Mellon University (CMU) *2018 – 2023*
PhD in Statistics
Advisors: Kathryn Roeder (CMU), Eugene Katsevich (University of Pennsylvania)
Committee: Jing Lei, Jian Ma, F. William Townes

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*

PAPERS

- **T Barry**, K Mason, E Katsevich, K Roeder. "Robust differential expression testing for single-cell CRISPR screens at low multiplicity of infection." BioRxiv preprint. Link. (Mihaela Serban Memorial Award, American Statistical Association, Pittsburgh chapter) *2023*
- **T Barry**, K Roeder, E Katsevich. "Exponential family measurement error models for single-cell CRISPR screens." Major revision submitted at *Biostatistics*. Link. *2022*
- J Morris, C Caragine, Z Daniloski, J Domingo, **T Barry**, 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." **Science**. Link. *2023*
- **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*
- **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*

SOFTWARE PACKAGES

- `sceptre`: Robust inference for single-cell CRISPR screens. Link.
- `ondisc` (beta): Large-scale computing for single-cell data. Link.

PROFESSIONAL SERVICE

- Reviewer for Biometrika, Nature Biotechnology

MENTORING

• Songcheng Dai (Computational Biology Masters student at CMU). Topic: algorithms, data structures, and software for large-scale single-cell data.	*2021 - 2022*

TALKS

• "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)

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

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 2023.