

Thomas A. Sasani

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GitHub: [@tomsasani](#)

Education

- 2019 **Ph.D, Human Genetics**, *University of Utah*, Salt Lake City, UT
2015 **B.A, Biochemistry**, *Lawrence University*, Appleton, WI, *summa cum laude*

Experience

- 10/22-pres. **Staff Research Scientist**, *Quinlan Lab*, Univ. of Utah, Dept. of Human Genetics
○ Developing new methods to analyze germline mutation and genome evolution
- 5/21-10/22 **Senior Data Scientist**, *Recursion Pharmaceuticals*
○ Developed new computational methods to analyze data from massive cellular imaging experiments
- 3/20-5/21 **Postdoctoral Fellow**, *Harris Lab*, Univ. of Washington, Dept. of Genome Sciences
○ Discovered alleles that influence the germline mutation rate using whole-genome sequencing data
○ Analyzed single-cell sequencing data to characterize the mutational landscape of spermatogenesis
- 4/16-3/20 **Graduate Research Assistant**, *Quinlan Lab*, Univ. of Utah, Dept. of Human Genetics
○ Analyzed whole-genome sequencing data from large multi-generational families to identify post-zygotic mosaicism and variability in human germline mutation rates
○ Used the Oxford Nanopore Technologies platform to sequence DNA virus genomes under strong selective pressure during experimental evolution

Skills

- Programming **Python (proficient), R (familiar), SQL (familiar)**
Computing **Unix, git, Sun Grid Engine, Amazon EC2**
Data analysis **numpy, scipy, sklearn, pandas, jupyter, unit testing frameworks (pytest)**
Visualization **matplotlib, ggplot2, plotly + Dash**

Selected Academic Publications (full list at [Google Scholar](#))

- 2023 **Sasani TA**, Quinlan AR, Harris KE. Epistasis between mutator alleles contributes to germline mutation rate variability in laboratory mice. *bioRxiv*. [Code](#).
- 2022 **Sasani TA**, Ashbrook DG, Beichman AC, Lu L, Palmer AA, Williams RW, Pritchard JK, Harris K. A natural mutator allele shapes mutation spectrum variation in mice. *Nature*. [Code](#).
- 2019 **Sasani TA**, Pedersen BS, Gao Z, Baird L, Przeworski M, Quinlan AR, Jorde LB. Large, three-generation human families reveal post-zygotic mosaicism and variability in germline mutation accumulation. *eLife*. [Code](#). [Interview on the Naked Scientists podcast](#).

Funding and Awards

- 2020 - 2021 **NIH T32 Postdoctoral Genome Sciences Training Grant**
2017 - 2019 **NIH T32 Predoctoral Genetics Training Grant**
2017 **Lassonde Student Innovator**, *University of Utah*