Thomas A. Sasani

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Experienced computational biologist interested in using programming and statistics to extract meaningful insights from large datasets. Passionate about sharing results in accessible and engaging ways.

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

5/21-pres. **Senior Data Scientist**, *Recursion Pharmaceuticals*.
- Developing new computational methods to analyze data from massive cellular imaging experiments
- Collaborating with product managers and scientists to disseminate results to wide audiences
- Leading regular sprint planning sessions and delegating project goals to teams of ICs

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
- Developed reproducible workflows for processing large DNA sequencing datasets

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)

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*.