Thomas A. Sasani

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Education

8/15-10/19 **Ph.D, Human Genetics**, *University of Utah*, Salt Lake City, UT
advisor: Professor Aaron Quinlan

8/11-6/15 **BA, Biochemistry**, *Lawrence University*, Appleton, WI
advisor: Professor Brian Piasecki
honors: *summa cum laude*

Experience

10/22-pres. **Staff Research Scientist**, *Quinlan Lab*, Univ. of Utah, Dept. of Human Genetics
- Developing new statistical methods to analyze DNA mutation and genome evolution

5/21-10/22. **Senior Data Scientist**, *Recursion Pharmaceuticals*
- Created interactive dashboards to facilitate the interpretation of massive cellular imaging datasets
- Wrote and maintained statistical methods in production-level Python code repositories
- Collaborated with teams of scientists and product managers throughout the company

3/20-5/21 **Postdoctoral Fellow**, *Harris Lab*, Univ. of Washington, Dept. of Genome Sciences
- Applied linear modeling techniques to identify genes that influence mammalian mutation rates
- Created pipelines to process terabytes of whole-genome sequencing data
- Shared research findings in high-profile scientific journals and invited seminars

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

8/12-6/15 **Undergraduate Research Assistant**, *Piasecki Lab*, Lawrence University
- Cloned and visualized the expression of genes involved in sensory cilia structure and function
- Constructed an automated tracking instrument to identify behavioral phenotypes in *C. elegans*

Preprints

2024 Kunisaki J, Goldberg ME, Lulla S, **Sasani TA**, Hiatt L, Nicholas TJ, Liu L, Torres-Arce E, Guo Y, James E, Horns JJ, Ramsay JM, Chen W, Hotaling JM, Aston KI, Quinlan AR. Sperm from infertile, oligozoospermic men have elevated mutation rates. *medRxiv.*

2024 Mokveld T, Dolzhenko E, Dashnow H, Nicholas TJ, **Sasani TA**, van der Sanden B, Jadhav B, Pedersen B, Kronenberg S, Tucci A, Sharp AJ, Quinlan AR, Gilissen C, Hoischen A, Eberle MA. TRGT-denovo: accurate detection of de novo tandem repeat mutations. *bioRxiv.*

2024 Porubsky D, Dashnow H, **Sasani TA**, Logsdon GA, Hallast P, Noyes MD, Kronenberg ZN, Mokveld T, et al. A familial, telomere-to-telomere reference for human *de novo* mutation and recombination from a four-generation pedigree. *bioRxiv.*

2024 Xu K, Zhang Y, Baldwin-Brown J, **Sasani TA**, Phadnis N, Miller MP, Rog O. Decoding chromosome organization using CheC-PLS: chromosome conformation by proximity labeling and long-read sequencing. *bioRxiv.*

2022 Ashbrook DG, **Sasani TA**, Maksimov M, Gunturkun MH, Ma N, Villani F, Ren Y, Rothschild D, Chen H, Lu L, Colonna V, Dumont B, Harris K, Gymrek M, Pritchard JK, Palmer AA, Williams RW. Private and sub-family specific mutations of founder haplotypes in the BXD family reveal phenotypic consequences relevant to health and disease. *bioRxiv.*

Peer-reviewed manuscripts (also see Google Scholar)

2024 **Sasani TA**, Quinlan AR, Harris KE. Epistasis between mutator alleles contributes to germline mutation spectrum variability in laboratory mice. *eLife*. **Code.**

2022 Fixsen SM, Cone KR, Goldstein SA, **Sasani TA**, Quinlan AR, Rothenburg S, Elde NC. Poxviruses capture host genes by LINE-1 retrotransposition. *eLife*.

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.**

2021 Belyeu JR*, **Sasani TA***, Pedersen BS, Quinlan AR. Unfazed: parent-of-origin detection for large and small de novo variants. *Bioinformatics*.

2020 Wallace AD, **Sasani TA**, Swanier J, Gates B, Greenland J, Pedersen BS, Varley KT, Quinlan AR. CaBagE: a Cas9-based Background Elimination strategy for targeted, long-read DNA sequencing. *PLoS One*.

2020 Cawthon RM, Meeks HD*, **Sasani TA***, Smith KR, Kerber RA, O'Brien E, Baird L, Dixon MM, Peiffer AP, Leppert MF, Quinlan AR, Jorde LB. Germline mutation rates in young adults predict longevity and reproductive lifespan. *Scientific Reports*.

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.

2019 Gao Z, Moorjani P, **Sasani TA**, Pedersen BS, Quinlan AR, Jorde LB, Amster G, Przeworski M. Overlooked roles of DNA damage and maternal age in generating human germline mutations. *PNAS*.

2018 **Sasani TA***, Cone KR*, Quinlan AR, Elde NC. Long read sequencing reveals poxvirus evolution through rapid homogenization of gene arrays. *eLife*. **Code.**

2018 Belyeu JR, Nicholas TJ, Pedersen BS, **Sasani TA**, Havrilla JM, Kravitz SN, Conway ME, Lohman BK, Quinlan AR, Layer RM. SV-plaudit: A cloud-based framework for manually curating thousands of structural variants. *GigaScience*.

2018 Jain M*, Koren S*, Miga KM*, Quick J*, Rand AC*, **Sasani TA***, Tyson JR*, Beggs AD, Dilthey AT, Fiddes IT, Malla S, Marriott H, Nieto T, O'Grady J, Olsen HE, Pedersen BS, Rhie A, Richardson H, Quinlan AR, Snutch TP, Tee L, Paten B, Phillippy AM, Simpson JT, Loman NJ, Loose M. Nanopore sequencing and assembly of a human genome with ultra-long reads. *Nature Biotechnology*.

2017 Feusier J, Witherspoon DJ, Watkins WS, Goubert C, **Sasani TA**, Jorde LB. Discovery of rare, diagnostic Alu Yb8/9 elements in diverse human populations. *Mobile DNA*.

2017 Piasecki BP, **Sasani TA**, Lessenger AT, Huth N, Farrell S. MAPK-15 is a ciliary protein required for PKD-2 localization and male mating behavior in *Caenorhabditis elegans*. *Cytoskeleton*.

* indicates equal contribution

Awards and Fellowships

2020-2021 **NIH T32 Postdoctoral Genome Sciences Training Grant**, *University of Washington*

2017-2019 **NIH T32 Predoctoral Genetics Training Grant**, *University of Utah*

2017 & 2018 **Charles J. Epstein Trainee Award for Excellence in Human Genetics**, *Semifinalist, American Society for Human Genetics*

2018 **Lassonde Institute Student Innovator**, *University of Utah*

2015 **Howard and Helen Russell Award for Excellence in Biological Research**, *Lawrence University*

Invited Presentations

2021 *Mapping mutator alleles in mice*. Recent Advances in Biology Lecture Series, Lawrence University. Virtual.

2021 *Mapping mutator alleles in mice*. Pritchard Lab Mini-Conference, Stanford University. Virtual.

2021 *A wild-derived antimutator drives germline mutation spectrum differences in a genetically diverse murine family*. Przeworski Lab Meeting, Columbia University. Virtual.

2019 *A short tale of viral evolution told with long reads*. Society for Molecular Biology and Evolution (Annual Meeting). Manchester, UK.

2017 *Human immune defense mechanisms drive rapid genome evolution in vaccinia virus*. London Calling (Oxford Nanopore Technologies meeting). London, UK.

Contributed Presentations

2023 *Discovering epistasis between germline mutator alleles in mice.* The Biology of Genomes. Cold Spring Harbor, NY, USA.

2018 *Directly measuring the dynamics of the human mutation rate by sequencing large, multi-generational pedigrees*. American Society of Human Genetics, Annual Meeting. San Diego, CA, USA (Plenary Presentation).

2017 *Human immune defense mechanisms drive rapid genome evolution in vaccinia virus.* American Society of Human Genetics Annual Meeting. Orlando, FL, USA (Platform Presentation).

Mentorship

Graduate Students

8/24-10/24 **Taeho K.**, Accuracy of Element AVITI sequencing at homopolymer loci in the human genome, University of Utah

9/20-12/20 **Candice Y.**, Identifying structural variants in a recombinant inbred mouse cross, University of Washington.

10/19-12/19 **Bianca A.**, Patterns of recombination in large Utah pedigrees, University of Utah.

1/20-3/20 **Erica H.**, Regional variation in mutation rates and spectra, University of Utah.

High School Students

7/20-9/20 **Myles F.**, Variation in mutation rates and spectra in a recombinant inbred mouse cross, University of Washington.

Teaching Experience

University of Utah

2024 **Guest Lecturer**, *Applied Computational Genomics*

2019-2020 **Guest Lecturer**, *Salt Lake Learners of Biostatistics*

2017 **Teaching Assistant**, *Applied Computational Genomics*

2016 **Teaching Assistant**, *Programming for Biomedical Science*

2016 **Guest Instructor**, *Summer Data Science Bootcamp*

Cold Spring Harbor Laboratory

2016 & 2017 **Teaching Assistant**, *Advanced Sequencing Technologies and Applications*

Reviewing

ad hoc Genome Biology, Genome Medicine, Molecular Biology and Evolution, Bioinformatics, eLife, Science, Nature Communications, PNAS

Courses and Professional Development

2018 Leena Peltonen School of Human Genomics