



Rachel Allison Ungar

Postdoctoral Scholar, Biomedical Ethics

Bio

BIO

Rachel Ungar, PhD, is a Postdoctoral Fellow in the Stanford Training Program in ELSI Research (T32) at the Stanford Center for Biomedical Ethics. Her graduate research was in computational genomics focused on multiomics approaches in Stephen Montgomery's lab. She was an active member of the Undiagnosed Diseases Network, and GREGoR rare disease consortia focused on transcriptomic methods and data standards. She also examined the impact of rare variants and sex on the X-chromosome. During her PhD, she co-created and taught a course expanding ethics education to bioscientists (GENE 220: Genetics, Ethics, and Society) and evaluated its impact. During her postdoc, Rachel aims to use her background to integrate genomics and ethics, beginning with ethical considerations for rare and undiagnosed disorders. Rachel received her PhD in Genetics at Stanford. She earned her Bachelor of Science in Biology at the University of Arkansas with minors in mathematics and computer science.

PROFESSIONAL EDUCATION

- Doctor of Philosophy, Stanford University , GENE-PHD (2024)
- BS, University of Arkansas , Biology (2018)
- PhD, Stanford University , Genetics (2024)

Teaching

COURSES

2022-23

- Introduction to Genetics, Ethics, and Society: GENE 220 (Spr)

Publications

PUBLICATIONS

- **Biallelic Variants in RNU6ATAC Result in a Minor Spliceopathy Characterized by Transcriptome-Wide Minor Intron Retention Events and Short Stature with Variable Multisystem Manifestations.** *HGG advances*
Mendez, R., Arriaga, T. M., Ma, J., Bonner, D. E., Emami, S., Levy, R. J., Alsagheir, A., Alhaddad, B., Bakur, K., Ungar, R. A., Matalon, D. R., Miller, A. M., Nguyen, et al
2026: 100588
- **GREGoR: accelerating genomics for rare diseases.** *Nature*
Dawood, M., Heavner, B., Wheeler, M. M., Ungar, R. A., LoTempio, J., Wiel, L., Berger, S., Bernstein, J. A., Chong, J. X., Délot, E. C., Eichler, E. E., Lupski, J. R., Shojaie, et al
2025; 647 (8089): 331-342
- **Transcriptome-wide outlier approach identifies individuals with minor spliceopathies.** *American journal of human genetics*

Arriaga, T. M., Mendez, R., Ungar, R. A., Bonner, D. E., Matalon, D. R., Lemire, G., Goddard, P. C., Padhi, E. M., Miller, A. M., Nguyen, J. V., Ma, J., Smith, K. S., Scott, et al

2025

- **Transcriptomic signatures of rare variant impacts across sex and the X-chromosome.** *HGG advances*
Ungar, R. A., Li, T., Vetr, N. G., Ersaro, N., Battle, A., Montgomery, S. B.
2025: 100463
- **Integration of transcriptomics and long-read genomics prioritizes structural variants in rare disease.** *Genome research*
Jensen, T. D., Ni, B., Reuter, C. M., Gorzynski, J. E., Fazal, S., Bonner, D., Ungar, R. A., Goddard, P. C., Raja, A., Ashley, E. A., Bernstein, J. A., Zuchner, S., Greicius, et al
2025
- **Transcriptome-wide outlier approach identifies individuals with minor spliceopathies.** *medRxiv : the preprint server for health sciences*
Arriaga, M. T., Mendez, R., Ungar, R. A., Bonner, D. E., Matalon, D. R., Lemire, G., Goddard, P. C., Padhi, E. M., Miller, A. M., Nguyen, J. V., Ma, J., Smith, K. S., Scott, et al
2025
- **GREGoR: Accelerating Genomics for Rare Diseases.** *ArXiv*
Dawood, M., Heavner, B., Wheeler, M. M., Ungar, R. A., LoTempio, J., Wiel, L., Berger, S., Bernstein, J. A., Chong, J. X., Délot, E. C., Eichler, E. E., Gibbs, R. A., Lupski, et al
2024
- **Impact of genome build on RNA-seq interpretation and diagnostics.** *American journal of human genetics*
Ungar, R. A., Goddard, P. C., Jensen, T. D., Degalez, F., Smith, K. S., Jin, C. A., Bonner, D. E., Bernstein, J. A., Wheeler, M. T., Montgomery, S. B.
2024
- **Loss of function of FAM177A1, a Golgi complex localized protein, causes a novel neurodevelopmental disorder.** *Genetics in medicine : official journal of the American College of Medical Genetics*
Kohler, J. N., Legro, N. R., Baldrige, D., Shin, J., Bowman, A., Ugur, B., Jackstadt, M. M., Shriver, L. P., Patti, G. J., Zhang, B., Feng, W., McAdow, A. R., Goddard, et al
2024: 101166
- **Increasing equity in science requires better ethics training: A course by trainees, for trainees.** *Cell genomics*
Patel, R. A., Ungar, R. A., Pyke, A. L., Adimoelja, A., Chakraborty, M., Cotter, D. J., Freund, M., Goddard, P., Gomez-Stafford, J., Greenwald, E., Higgs, E., Hunter, N., MacKenzie, et al
2024: 100554
- **Integration of transcriptomics and long-read genomics prioritizes structural variants in rare disease.** *medRxiv : the preprint server for health sciences*
Jensen, T. D., Ni, B., Reuter, C. M., Gorzynski, J. E., Fazal, S., Bonner, D., Ungar, R. A., Goddard, P. C., Raja, A., Ashley, E. A., Bernstein, J. A., Zuchner, S., Greicius, et al
2024
- **Impact of genome build on RNA-seq interpretation and diagnostics.** *medRxiv : the preprint server for health sciences*
Ungar, R. A., Goddard, P. C., Jensen, T. D., Degalez, F., Smith, K. S., Jin, C. A., Bonner, D. E., Bernstein, J. A., Wheeler, M. T., Montgomery, S. B.
2024
- **Transcriptomics and chromatin accessibility in multiple African population samples.** *bioRxiv : the preprint server for biology*
DeGorter, M. K., Goddard, P. C., Karakoc, E., Kundu, S., Yan, S. M., Nachun, D., Abell, N., Aguirre, M., Carstensen, T., Chen, Z., Durrant, M., Dwaracherla, V. R., Feng, et al
2023