UMA ARORA

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CORE COMPETENCIES

- **Omics and Data Analysis**: RNA-seq (bulk and single-cell), WGS (Illumina, PacBio), methylation, ChIP-seq, ATAC-seq, 3D genomics, Multi-omics data integration
- **Tools & Resources**: UK Biobank, All of Us, ClinVar, gnomAD, GEO, UCSC
- **Population and Statistical Genetics**: GWAS (common and rare), ExWAS, Statistical and functional fine mapping, Heritability, Polygenic risk scores, Multi-ancestry population analysis
- **Data & Programming**: Python (pandas, NumPy, scikit-learn), R (Seurat, DESeq2), bash, Git, Nextflow, SQL basics
- **Cloud & Computing**: HPC environments, Docker, AWS, GCP

WORK EXPERIENCE

FOUNDATION MEDICINE, Boston, MA 05/2024 – 05/2025

Computational Biologist 1 Research & Development, Computational Discovery

Drove feature discovery and innovation towards the development of a new product as part of a highly interdisciplinary team.

- Led biomarker discovery efforts as part of a cross-functional R&D team; collaborated closely with clinical annotation, assay development, and data engineering groups.
- Improved and implemented reproducible pipelines for biomarker discovery using whole-genome methylation sequencing for early cancer detection and tissue-of-origin prediction.
- Contributed to translational product development through analysis of large-scale genomic and clinical datasets.

BOSTON CHILDREN'S HOSPITAL and THE BROAD INSTITUTE, Boston, MA 02/2023 – 05/2024

Postdoctoral Research Fellow

Led independent projects and collaborated with experimental scientists to uncover the mechanistic role of genetic variation on hematopoietic stem cell function. Applied population genomics approaches to quantify the germline factors underlying risk for blood disorders.

- Designed and executed GWAS and fine mapping in large biobank cohorts (UK Biobank and All of Us) to identify novel genetic risk loci for myeloid malignancies.
- Collaborated with experimental biologists to validate computationally generated hypotheses in hematopoietic stem cells.
- Co-led multi-omics integration analyses (RNA-seq, ChIP-seq, 3D genomics, ATAC-seq) to link genetic variation and 3D genome changes contributing to fetal hemoglobin regulation during erythropoiesis.
- Harnessed scRNA-seq datasets to uncover changes in transposable element expression in hematopoietic stem and progenitor cells.
- Performed statistical modeling to identify rare ClinVar variants associated with myeloproliferative neoplasms.

TUFTS UNIVERSITY and THE JACKSON LABORATORY, Bar Harbor, ME 06/2017 – 01/2023

Graduate Research Fellow

Designed, executed, and analyzed experiments to uncover the evolutionary patterns of centromere DNA, a repetitive and rapidly evolving region of the genome that is challenging to investigate with existing tools. Combined computational and experimental methods to uncover the scope of diversity at mouse centromeres and the impact of centromere genetic variation on function.

- Developed customized k-mer based pipelines to quantify genetic and epigenetic sequence variation at diverse mouse centromeres.

- Bridged computational insights and functional validation with the following molecular biology techniques: fluorescence in-situ hybridization, fluorescence microscopy, ChIP-seq, CUT&Tag, quantitative-PCR, cell culture, bacterial transfection, western blotting.
- Discovered the centromere repeat sequence for the species Mus Pahari and collaborated with an external lab to quantitatively characterize the scope of genetic variation.
- Collaborated with external labs and mentored junior researchers; awarded NIH F31 fellowship and multiple scientific honors.

EDUCATION

Doctor of Philosophy (PhD), Genetics, TUFTS UNIVERSITY AND THE JACKSON LABORATORY, Bar Harbor, ME

Bachelor of Science (BS), Psychobiology and Marine Biology, UNIVERSITY OF CALIFORNIA, Los Angeles, CA

PUBLICATIONS

Michael Poeschla, **Uma P. Arora** et. al. "Polygenic modifiers impact penetrance and expressivity in telomere biology disorders" *The Journal of Clinical Investigation*, June 2025.

Jorge Diego Martin-Rufino*, Alexis Caulier*, …, **Uma P. Arora** et. al. "Transcription factor networks disproportionately enrich for heritability of blood cell phenotypes" *Science*, April 2025.

Jiawei Zhao*, Liam D. Cato*, **Uma P. Arora** et. al. "Inherited blood cancer predisposition through altered transcriptional elongation" *Cell*, February 2024.

Craig W. Gambogi*, Nootan Pandey*, Jennine M. Dawicki-McKenna*, **Uma P. Arora** et. al. "Centromere innovations within a mouse species" *Science Advances*, November 2023.

Uma P. Arora, Beth Sullivan, Beth L. Dumont. "Variation in the CENP-A sequence association landscape across diverse inbred strains" *Cell Reports*, October 2023.

Uma P. Arora & Beth L. Dumont. "Meiotic drive in house mice: Mechanisms, Consequences, and Insight for Human Biology" *Chromosome Research*, July 2022.

Raman Akinyanju Lawal, **Uma P. Arora**, Beth L. Dumont. "Selection shapes the landscape of functional variation in wild house mice" *BMC Biology*, November 2021.

Uma P. Arora, Caleigh Charlebois, Raman Akinyanju Lawal, Beth L. Dumont. "Population and subspecies diversity at mouse centromere satellites" *BMC Genomics*, April 2021.

PROFESSIONAL DEVELOPMENT

Conservation Education Volunteer, NEW ENGLAND AQUARIUM — 2025 - CURRENT

Carpentries Instructor, THE CARPENTRIES — 2020 - CURRENT

Postbaccalaureate Student Mentor, THE JACKSON LABORATORY — 2021-2022

Ruth L. Kirschstein National Research Service Award F31, NATIONAL CANCER INSTITUTE — 2022

DeLill Nasser Award for Professional Development in Genetics, GENETICS SOCIETY OF AMERICA — 2021

Lorraine Flaherty Award for Outstanding Oral Presentation, IMGS — 2020