

MICHAEL G. TASSIA, PH.D.

bioinformatics | data science | statistical genetics

 [Github](#)  [LinkedIn](#)  [Google Scholar](#)  michaeltassia@gmail.com

SUMMARY

- Computational biologist with 10+ years of experience in human genetics, statistical learning, & data science.
- Deep subject matter expertise in somatic mosaicism across human tissues with aging and disease, with specialization in hematology and cancer.
- Proficiency in rapid development of innovative techniques to analyze large and complex genetic data sets, both as a leader and collaborative team-member.
- Productive scientific career underscored by 16 publications, 6 awarded grants, & 18 talks at academic conferences.

EDUCATION & TRAINING

Johns Hopkins University

Postdoctoral Fellow with joint appointments in Biology and Hematology

2022 – Present

Baltimore, MD

Auburn University

Ph.D. in Biological Sciences

2015 – 2021

Auburn, AL

University of Washington

B.S. in Biology (General)

2011 – 2014

Seattle, WA

TECHNICAL SKILLS/EXPERIENCE

Genetics: WGS/WES/RNA-seq data analysis (study design, pre-processing, QC), somatic/germline variant calling (SNVs, SVs, CNVs), phylogenetics, population genetics, QTL mapping/GWAS, differential gene expression

Data science: Regression, inference & prediction, regularization, model validation, unsupervised learning

Public datasets: 1000 Genomes, All of Us, ClinVar, COSMIC, GENCODE, gnomAD, GTEx, TOPMed, UK Biobank

Programming: R, Bash, Python, Snakemake, Git, high-performance computing and resource scheduling (e.g., slurm)

Bioinformatics software: GATK, bcftools, bedtools, IGV, SLiM, plink, DESeq2, phytools, iqtree

SELECTED AWARDS & HONORS

- [2025] *ASH Abstract Achievement Award*; American Society of Hematology
- [2024-2026] *NIH T32 in Hematology*; Johns Hopkins Division of Hematology & NIH NHLBI
- [2024-2026] *ASH Scholar Award*; American Society of Hematology

HIGHLIGHTED RESEARCH EXPERIENCE

Modeling evolutionary complexity across hematopoietic progenitors | Johns Hopkins University 2022 – pres.

- Leading an international, multi-institution collaboration to develop and apply novel algorithms to detect and quantify complex evolutionary histories (e.g., recurrent mutations) among somatic lineages with aging and disease.
- Head developer of Bayesian algorithms tailored to technological advances in single-cell DNA sequencing data.
- Research funded through fellowships from the American Society of Hematology and NIH (T32).

Characterizing the role of telomeres in the evolution of clonal hematopoiesis | Johns Hopkins University 2022 – pres.

- Leveraged expertise in genomics, phylogenetics, and population genetics to reconstruct the evolutionary history of hematopoietic lineages and inform the genetic context of cancer risk.
- Demonstrated that inherited defects in telomere genes affects the evolutionary landscape of hematopoietic stem cells, modulating somatic mutation burden and lifetime risk of cancer.
- Co-first author publication in *NEJM*, establishing a collaboration between labs of co-mentors in the Department of Biology and Department of Oncology at Johns Hopkins School of Medicine.

Studying genetic variation at multiple scales of evolution | Auburn University & Johns Hopkins University 2015 – 2025

- Led and contributed to research studying evolution across diverse timescales, from somatic evolution within human individuals to species divergence across >500 million years.
- *Selected studies include:* Quantification of gene expression variation across human populations; detection of positive selection in complete primate genomes; characterization of innate immunity pathways across the animal tree of life.