Dylan Taylor

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Summary

- Computational biologist and statistical geneticist with 6+ years of experience analyzing and integrating large-scale multi-omics datasets to power biological insight and guide data-driven discovery
- Proven track record of building robust, reproducible analysis pipelines from the ground up, including platforms for target nomination and credentialing to support drug discovery efforts
- Deep expertise in statistical modeling and integrative data analysis of complex biological systems, including GWAS and post-GWAS methods
- Collaborative scientist and clear communicator, effective at bridging computational and experimental disciplines in multi-institutional research environments

Education

Johns Hopkins University **2019 – 2024**
Ph.D. in Biological Sciences *Baltimore, MD*

University of Maryland, College Park **2014 – 2018**
B.S. in Biology *College Park, MD*

Technical Skills

Programming & Scripting	Python, R, bash; experience with Java
Cloud Computing & Workflow Dev	AWS, Terra/AnVIL, Nextflow, WDL, SLURM
Statistical Genetics	GWAS, QTL mapping, fine-mapping, colocalization, LDSC, linear modeling
Bioinformatics Software	Plink, bcftools/samtools, Hail, GATK, VEP, bedtools, IGV
RNA-seq & Transcriptomics	FastQC, Salmon, DESeq2, Leafcutter, PEER, CellRanger, Scanpy
Databases & Resources	1000 Genomes, UK Biobank, GTEx, GWAS Catalog, Open Targets, ENCODE; querying with SQL/GraphQL

Selected Honors & Awards

Stephen and Carolyn Oppenheimer Thesis Award | *Johns Hopkins University* **2024**
- Awarded to two Ph.D. graduates each year for promise in research and teaching in Biological Sciences

Ruth L. Kirschstein National Research Service Award (F31) | *NIH NHGRI* - $90,000 **2023**
- Awarded to two Ph.D. graduates each year for promise in research and teaching in Biological Sciences

Graduate Research Fellowship Honorable Mention — Genomics | *NSF* **2021**
- Honorable mention for the NSF GRFP – a prestigious federally-funded graduate fellowship

Institutional Enhancement Grant | *JHU Center for Teaching Excellence & Innovation* - $4,000 **2021**
- Developed programming curriculum for undergraduate biology students to build computational research skills

Student Commencement Speaker | *UMD College of Computer, Mathematical & Natural Sciences* **2018**

Professional Experience

Scientist – Human Genetics | *Arena BioWorks* **2024 – present**
- Lead the development and deployment of a scalable Nextflow-based platform for human genetics–driven target discovery
- Integrate GWAS and post-GWAS analyses (fine-mapping, colocalization) into the pipeline to prioritize targets and provide mechanistic insight
- Build comprehensive genetic evidence packages for putative targets, integrating GWAS, rare variant studies, and pheWAS to inform target prioritization and safety assessment
- Collaborate cross-functionally with functional genomics and cell models teams to translate genetic insights into actionable therapeutic hypotheses

Data Science and Machine Learning Intern | *insitro* **2024**

- Processed raw single cell RNA sequencing dataset to identify distinct cell states in a disease-relevant model
- Applied this processed scRNA-seq data to discover and quantify shared and state-specific expression-associated genetic variation, with a focus on disease relevance

Academic Research Experience

Discovery of regulatory genetic variation in diverse cohorts **2024**

- Led the generation of an open-access RNA-seq dataset from 731 individuals across 26 globally diverse populations, addressing Eurocentric bias in human genetics research
- Mapped >15,000 expression QTLs (eQTLs) and >16,000 splicing QTLs (sQTLs) by integrating RNA-seq with whole-genome sequencing data
- Discovered >1,300 eQTLs and >1,600 sQTLs specific to underrepresented populations, some co-localizing with complex trait GWAS loci
- Demonstrated consistency of QTL effects across populations, enabling predictive applications such as TWAS for target prioritization

Trait-relevance of hematopoietic cis-regulatory machinery **2024**

- Assessed trait relevance of hematopoietic cis-regulatory element (cCRE) annotations generated by collaborators
- Applied linkage disequilibrium score regression (LDSC) to quantify the relevance (measured as enrichment in heritability) of these cCREs to 587 complex traits from the UK Biobank, including 56 blood-related traits
- Determined that cCREs were highly specific to blood traits, with significant enrichment in 52/56 blood traits, establishing a trait-relevant regulatory annotation.

Variant-calling pipeline development with a telomere-to-telomere (T2T) reference genome **2022–2023**

- Developed a scalable alignment and variant calling pipeline on the cloud-based AnVIL/Terra platform, and applied this pipeline to call variants in 3,202 individuals on the first complete T2T human reference genome
- Generated a high-confidence "accessibility" mask, defining regions suitable for short-read variant calling; T2T reference adds >19 million bases of accessible sequence relative to the previous assembly
- Benchmarked read alignment and variant-calling on the Y chromosome assembly, demonstrating significant improvement in both metrics in complex genomic regions
- Lifted databases of genetic variation (including >700 million clinically relevant variants) to T2T reference, enabling analysis of this variation with the new assembly.
- Characterized biological relevance of newly added sequence in T2T by exploring LD with known trait-associated variation; identified 113 GWAS hits in tight LD with novel sequence, suggesting potential causal loci.

Selected Publications

Taylor DJ, Chhetri SB, Tassia MG, Biddanda A, Yan SM, *et al.* (2024). Sources of gene expression variation in a globally diverse human cohort. *Nature.* DOI: 10.1038/s41586-024-07708-2

Taylor DJ*, Eizenga JM*, Li Q*, Das A, Jenike KM, *et al.* (2024). Beyond the Human Genome Project: The age of complete human genome sequences and pangenome references. *Annu Rev Genomics Hum Genet.* DOI: 10.1146/annurev-genom-021623-081639

Xiang GH, He X, Giardine BM, Isaac KJ, **Taylor DJ** (5/34), *et al.* (2024) Interspecies regulatory landscapes and elements revealed by novel joint systematic integration of human and mouse blood cell epigenomes. *Genome Res.* DOI: 10.1146/annurev-genom-021623-081639

Rhie A*, Nurk S*, Cechova M*, Hoyt SJ*, **Taylor DJ***, *et al.* (2023) The complete sequence of a human Y chromosome. *Nature.* DOI: 10.1038/s41586-023-06457-y

Aganezov S*, Yan SM*, Soto DC*, Kirsche M*, Zarate S*, Avdeyev P, **Taylor DJ** (7/33), *et al.* (2022). A complete reference genome improves analysis of human genetic variation. *Science.* DOI: 10.1126/science.abl3533.

* *denotes co-first authors*