

## Curriculum Vitae

**DYLAN J. TAYLOR**

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## EDUCATION

- 2024      **PhD in Biological Sciences**  
Program in Cellular, Molecular, Developmental Biology, and Biophysics  
Johns Hopkins University, Baltimore, MD  
Advisor: Rajiv McCoy
- 2018      **BS in Biology – Microbiology**  
Minors in Physics and Astronomy  
University of Maryland, College Park, MD

## PROFESSIONAL EXPERIENCE

- 2024 – Present      **Scientist – Human Genetics**  
Arena BioWorks, Cambridge, MA
- 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) 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
- 2024      **Data Science and Machine Learning Intern – StatGen**  
insitro, San Francisco, CA
- 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

## RESEARCH EXPERIENCE

- 2020 – 2024      **PhD Candidate**, Johns Hopkins University, Baltimore, MD  
Advisor: Rajiv McCoy
- Characterized functional genetic variation driving gene expression and splicing differences in diverse human cohorts
  - Benchmarked the advantages of using a complete human reference genome to analyze genetic variation
- 2020      **Graduate Rotation Student**, Johns Hopkins University, Baltimore, MD  
Advisor: William Ludington

- Investigated genetic basis for effective colonization of the *Drosophila melanogaster* gut by *Lactobacillus plantarum*; characterized domain differences in a Mucin-binding gene among *L. plantarum* strains
- 2019 – 2020      **Graduate Rotation Student**, Johns Hopkins University, Baltimore, MD  
 Advisor: Jocelyne DiRuggiero
- Investigated shared sequence-structural motifs in archaeal sRNAs to elucidate potential Argonaute-like binding partner and identify mRNA binding partners
- 2019      **Graduate Rotation Student**, Johns Hopkins University, Baltimore, MD  
 Advisor: James Taylor
- Built a convolutional neural network capable of accurately predicting chromatin compartmentalization from pre-defined epigenetic states across mouse hematopoietic cell types
- 2018-2019      **Research Assistant**, University of Maryland, College Park, MD  
 Advisor: Mihai Pop
- Developed a computational algorithm to generate sets of representative oligomers from metagenomic marker genes to design a high-resolution metagenomic profiling assay
- 2017      **Undergraduate Research Assistant**, University of Florida, Gainesville, FL  
 Advisors: Robert Ferl and Anna-Lisa Paul
- Developed qualitative imaging tools to monitor plant mesophyll health using Normalized Differential Vegetation Index for use in growing crops on the International Space Station.
  - Created predictive MATLAB model of leaf temperature in changing gravity environments to forecast impacts on leaf temperature as spacecraft move into and out of orbit
- 2015      **iGEM Undergraduate Team Member**, University of Maryland, College Park, MD
- As part of the 2015 International Genetically Engineered Machine (iGEM) competition, designed a novel plasmid-maintenance system independent of antibiotic resistance and demonstrated system efficacy in maintaining plasmids
  - Designed and constructed a cheap thermocycler using a hairdryer and soda can that successfully amplified DNA

## PUBLICATIONS

\*      *denotes co-first authors*

### RESEARCH ARTICLES (PEER-REVIEWED)

- 2024      **Taylor, D. J.**, Chhetri, S. B., Tassia, M. G., Biddanda, A., Yan, S. M., Wojcik, G. L., Battle, A., McCoy, R. C. (2024). Sources of gene expression variation in a globally diverse human cohort. *Nature*. DOI: [10.1038/s41586-024-07708-2](https://doi.org/10.1038/s41586-024-07708-2)
- 2024      Xiang, G., He, X., Giardine, B. M., Isaac, K. J., **Taylor, D. J.**, McCoy, R. C., Jansen, C., Keller, C. A., Wixom, A. Q., Cockburn, A., Miller, A., Qi, Q., He, Y., Li, Y., Lichtenberg, J., Heuston, E. F., Anderson, S. M., Luan, J., Vermunt, M. W., ..., Hardison, R. C. (2024). Interspecies regulatory landscapes and elements revealed by novel joint systematic integration of human and mouse blood cell epigenomes. *Genome Research*. DOI: [10.1101/gr.277950.123](https://doi.org/10.1101/gr.277950.123)
- 2023      \*Rhie, A., \*Nurk, S., \*Cechova, M., \*Hoyt, S. J., **\*Taylor, D. J.**, Altemose, N., Hook, P. W., Koren, S., Rautiainen, M., Alexandrov, I. A., Allen, J., Asri, M., Bzikadze, A. v., Chen, N.-C., Chin, C.-S., Diekhans, M., Flicek, P., Formenti, G., Functamman, A., ..., Phillippy, A. M. (2023). The complete sequence of a human Y chromosome. *Nature*. DOI: [10.1038/s41586-023-06457-y](https://doi.org/10.1038/s41586-023-06457-y)

- 2023 Yang, X., Wang, X., Zou, Y., Zhang, S., Xia, M., Vollger, M. R., Chen, N.-C., **Taylor, D. J.**, Harvey, W. T., Logsdon, G. A., Meng, D., Shi, J., McCoy, R. C., Schatz, M. C., Li, W., Eichler, E. E., Lu, Q., & Mao, Y. (2023). Characterization of large-scale genomic differences in the first complete human genome. *Genome Biology*. DOI: [10.1186/s13059-023-02995-w](https://doi.org/10.1186/s13059-023-02995-w)
- 2022 \*Aganezov, S., \*Yan, S. M., \*Soto, D. C., \*Kirsche, M., \*Zarate, S., Avdeyev, P., **Taylor, D. J.**, Shafin, K., Shumate, A., Xiao, C., Wagner, J., McDaniel, J., Olson, N. D., Sauria, M. E. G., Vollger, M. R., Rhie, A., Meredith, M., Martin, S., Lee, J., ... Schatz, M. C. (2022). A complete reference genome improves analysis of human genetic variation. *Science*, 376(6588). DOI: [10.1126/science.abl3533](https://doi.org/10.1126/science.abl3533)
- 2021 Yan, S. M., Sherman, R. M., **Taylor, D. J.**, Nair, D. R., Bortvin, A. N., Schatz, M. C., & McCoy, R. C. (2021). Local adaptation and archaic introgression shape global diversity at human structural variant loci. *ELife*, 10. DOI: [10.7554/eLife.67615](https://doi.org/10.7554/eLife.67615)
- 2019 Sakowski, E., Uritskiy, G., Cooper, R., Gomes, M., McLaren, M. R., Meisel, J. S., Mickol, R. L., Mintz, C. D., Mongodin, E. F., Pop, M., Rahman, M. A., Sanchez, A., Timp, W., Vela, J. D., Wolz, C. M., Zackular, J. P., Chopyk, J., Commichaux, S., Davis, M., ..., **Taylor, D. J.** (28/30), ..., Preheim, S. P. (2019). Current State of and Future Opportunities for Prediction in Microbiome Research: Report from the Mid-Atlantic Microbiome Meet-up in Baltimore on 9 January 2019. *MSystems*, 4(5). DOI: [10.1128/mSystems.00392-19](https://doi.org/10.1128/mSystems.00392-19)
- 2018 Beisel, N. S., Callahan, J. B., Sng, N. J., **Taylor, D. J.**, Paul, A.-L., & Ferl, R. J. (2018). Utilization of single-image normalized difference vegetation index (SI-NDVI) for early plant stress detection. *Applications in Plant Sciences*, 6(10), e01186. DOI: [10.1002/aps3.1186](https://doi.org/10.1002/aps3.1186)

#### REVIEW ARTICLES

- 2023 \***Taylor, D. J.**, \*Eizenga, J. M., \*Li, Q., Das, A., Jenike, K. M., Kenny, E. E., Miga, K. H., Monlong, J., McCoy, R. C., Paten, B., & Schatz, M. C. (2024). Beyond the Human Genome Project: The age of complete human genome sequences and pangenome references. *Annual Reviews*, 25. DOI: [10.1146/annurev-genom-021623-081639](https://doi.org/10.1146/annurev-genom-021623-081639)

#### RESEARCH GRANTS

- 2023-2025 **NIH/NHGRI F31:** Ruth L. Kirschstein Predoctoral Individual National Research Service Award  
PI: Dylan Taylor; Johns Hopkins University  
Title: "Uncovering sources of human gene expression variation in a globally diverse cohort."

#### FELLOWSHIPS, HONORS & AWARDS

- 2024 Stephen & Carolyn Oppenheimer Thesis Award; Johns Hopkins University Department of Biology
- 2023 Ruth L. Kirschstein National Research Service Award (NRSA) Fellowship; NIH/NHGRI
- 2022 Conference Travel Grant; Johns Hopkins University Graduate Representative Organization
- 2021 Fellowship Honorable Mention; NSF Graduate Research Fellowship Program
- 2021 Technology Fellowship Grant; Johns Hopkins University Center for Educational Resources
- 2021 Victor G. Corces Teaching Award; Johns Hopkins University Department of Biology

2018	Student Commencement Speaker; UMD College of Computer, Mathematical, and Natural Sciences
2018	Sigma Alpha Omicron Honors Society for excellence in Microbiology; University of Maryland
2016	Honors College Citation; UMD Integrated Life Sciences Honors College
2015	Gold Medal and Nomination for Best-in-Track; iGEM 2015
2014	Dean's Scholarship; University of Maryland

## PRESENTATIONS

### ORAL PRESENTATIONS

- 2023 **Center for Bioinformatics and Computational Biology Seminar Series**, College Park, MD  
Uncovering sources of human gene expression variation in a globally diverse cohort
- 2022 **T2T-F2F**, Santa Cruz, CA  
A complete reference genome improves analysis of human genetic variation
- 2020 **International Society for Computational Biology: Intelligent Systems for Molecular Biology, Online\***  
Introducing genome assembly to the general public through interactive word games

### POSTER PRESENTATIONS

- 2024 **The Allied Genetics Conference**, Washington, D.C.
- 2023 **American Society of Human Genetics Annual Meeting**, Washington, D.C.
- 2023 **JHU CMDDB Program Retreat**, Hershey, PA
- 2022 **American Society of Human Genetics Annual Meeting**, Los Angeles, CA\*
- 2022 **JHU CMDDB Program Retreat**, Harpers Ferry, VA
- 2022 **Cold Spring Harbor Laboratory: Biology of Genomes**, Cold Spring Harbor, NY
- 2020 **American Society of Human Genetics**, *virtual*
- 2015 **iGEM Giant Jamboree**, Boston, MA

*\* Not presenting author*

## TEACHING EXPERIENCE

- 2024 **Instructor**, Modelling Biological Populations (Undergraduate Level), Johns Hopkins University
- 2021 – Present **Guest Lecturer**, Quantitative Biology Lab (Graduate Level), Johns Hopkins University
- 2021 – Present **Teaching Assistant**, Quantitative Biology Lab (Graduate Level), Johns Hopkins University
- 2020 – Present **Teaching Assistant**, Quantitative Biology Bootcamp (Graduate Level), Johns Hopkins University
- 2022 **Guest Lecturer**, Advanced Sequencing Technologies and Bioinformatics Analysis (Graduate Level and above), Cold Spring Harbor Laboratory
- 2021 – 2022 **Technology Fellow**, Developmental Genetics Lab (Undergraduate Level), Johns Hopkins University
- 2020 – 2021 **Teaching Assistant**, Developmental Genetics Lab (Undergraduate Level), Johns Hopkins University
- 2019 **Instructor**, Trampoline (Undergraduate Level), University of Maryland, College Park

## RESEARCH MENTORSHIP

### GRADUATE

- 2024 Jake Galvin, Rotation Student, Johns Hopkins University

2022 – 2023 Calvin Runnels, Rotation Student, Johns Hopkins University

HIGH SCHOOL

2022 – 2023 Cosima Billotte Bermudez, Ingenuity Project, Baltimore Polytechnic Institute

## ACADEMIC SERVICE & OUTREACH

2019 – Present **BioRep**, CMDB Program, Johns Hopkins University

- Student-elected representative within the CMDB program. Act as a liaison between the graduate student body and the program directors and administration.
- Organize recruitment activities for prospective graduate students, as well as orientation activities for first year students
- Revamped first-year rotation evaluation form to more specifically convey student strengths and weaknesses and facilitate communication between students and their PIs

2021 **Workshop Leader**, Agara Bio, Johns Hopkins University

- Developed a computational biology workshop for Agara Bio, an undergraduate-driven community lab at Johns Hopkins University
- During the two-part workshop, introduced students to Hidden Markov Models (HMMs), helped them develop basic Python programming skills, and had them apply these skills to build their own gene-finding HMM