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
2024	**Data Science and Machine Learning Intern – StatGen** insitro, San Francisco, CA

RESEARCH EXPERIENCE

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

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

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

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., Fungtammasan, A., …, Phillippy, A. M. (2023). The complete sequence of a human Y chromosome. *Nature*. DOI: 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

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

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
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
2018	Beisel, N. S., Callaham, 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

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

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

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 CMDB Program Retreat**, Hershey, PA

2022   **American Society of Human Genetics Annual Meeting**, Los Angeles, CA*

2022   **JHU CMDB 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