

## Curriculum Vitae

**DYLAN J. TAYLOR**

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## EDUCATION

- 2019 – Present     **PhD candidate in Biological Sciences**  
Program in Cellular, Molecular, Developmental Biology, and Biophysics  
Johns Hopkins University, Baltimore, MD  
Advisor: Rajiv McCoy
- 2014 – 2018     **BS in Biology – Microbiology**  
Minors in Physics and Astronomy  
University of Maryland, College Park, MD

## RESEARCH EXPERIENCE

- 2020 – Present     **PhD Candidate**, Johns Hopkins University, Baltimore, MD  
Advisor: Rajiv McCoy
- Characterizing functional genetic variation driving gene expression and splicing changes in diverse human cohorts.
  - Extending genetic association studies to diverse human cohorts using the Ancestral Recombination Graph (ARG) to improve mapping quality and cross-population applicability.
- 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

### ARTICLES UNDER REVIEW

- 2023 Xiang, G., He, X., Giardine, B. M., Weaver, 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. (2023). Cross-species regulatory landscapes and elements revealed by novel joint systematic integration of human and mouse blood cell epigenomes. *bioRxiv*, 2023.04.02.535219. DOI: [10.1101/2023.04.02.535219](https://doi.org/10.1101/2023.04.02.535219)
- 2022 \*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. (2022). The complete sequence of a human Y chromosome. *bioRxiv*, 2022.12.01.518724. DOI: [10.1101/2022.12.01.518724](https://doi.org/10.1101/2022.12.01.518724)
- 2022 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. (2022). A refined characterization of large-scale genomic differences in the first complete human genome. *bioRxiv*, 2022.12.17.520860. DOI: [10.1101/2022.12.17.520860](https://doi.org/10.1101/2022.12.17.520860)

### RESEARCH ARTICLES (PEER-REVIEWED)

- 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.abc3533](https://doi.org/10.1126/science.abc3533)
- 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)

## 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

- 2022 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

- 2022 **American Society of Human Genetics**, Los Angeles, CA\*  
Uncovering sources of human gene expression variation in a globally diverse cohort
- 2022 **JHU CMDB Program Retreat**, Harpers Ferry, VA  
Uncovering sources of human gene expression variation in a globally diverse cohort
- 2022 **Cold Spring Harbor Laboratory: Biology of Genomes**, Cold Spring Harbor, NY  
Uncovering sources of human gene expression variation in a globally diverse cohort
- 2020 **American Society of Human Genetics**, *virtual*  
Extending GWAS to diverse cohorts using the ancestral recombination graph
- 2015 **iGEM Giant Jamboree**, Boston, MA  
Hok ‘Em Sok ‘Em Robotics

*\* Not presenting author*

## TEACHING EXPERIENCE

- 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

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

### HIGH SCHOOL

- 2022 – Present 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