

Sage M. Wright

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Education

- 2021 **M.Sc. Bioinformatics and Genomics**, *Penn State University*, Hershey, PA.
Thesis Title: The Effect of CK2 Inhibition on Heterochromatin in AML
Advisor - Dr. Sinisa Dovat
- 2017 **B.S. Bioinformatics**, *Brigham Young University*, Provo, UT.
Minors: Computer Science, English, Music

Experience

Work

- 2022–now **Bioinformatics Scientist**, *Theiagen Genomics*, Highlands Ranch, CO.
- Maintained bioinformatic pipelines for the analysis of viral, bacterial, and fungal pathogens (see the Theiagen Genomics GitHub repositories).
 - Developed the Mercury_Prep_N_Batch workflow that helps prepare SARS-CoV-2 and mpox genomic data for submission to national and international repositories.
 - Developed the Terra_2_NCBI workflow that prepares *and* submits genomic data for submission to NCBI's BioSample and SRA data repositories.
 - Maintained and responded to user feature-requests and bug-reports promptly.
 - Trained public health scientists around the world on how to perform bioinformatic analyses on their locally-collected pathogen data. Virtual trainings were performed in many countries, including: the United States, Oman, Mozambique, Ukraine, Georgia, etc.
- 2021–2022 **Bioinformatician**, *Pennsylvania Department of Health Bureau of Laboratories*, Exton, PA.
- Set up a cloud-based bioinformatic infrastructure for data analysis.
 - Analyze SARS-CoV-2 genomes to ensure proper quality, identify their lineages, and create phylogenetic trees.
 - Contribute SARS-CoV-2 genomes and associated metadata to national and international databases, such as NCBI and GISAID.
 - Analyze PulseNet pathogens; PulseNet WGS Analysis Certified.
 - Prepare for genomic epidemiology on outbreaks of state-wide communicable diseases.

Research

- 2020–2021 **Graduate Student Researcher**, *Dr. Sinisa Dovat Lab*, Hershey, PA.
- Analyze occupancy patterns of heterochromatin histone modifications after inhibition of the protein CK2 using RNA-Seq and ChIP-Seq.
- 2019–2020 **Graduate Student Researcher**, *Dr. James Broach Lab*, Hershey, PA.
- Identify variants associated with disease phenotype in newborn infant from the whole-genome sequencing data of a family.
 - Analyze data produced from optical mapping technology.
 - Identify genomic variants in HPV-integrated cancer samples.

- 2017–2019 **Graduate Student Researcher**, *Dr. Feng Yue Lab*, Hershey, PA.
- Identify structural variants in alternative sequencing technologies, such as Hi-C, Bionano optical mapping, and long-read sequencing.
 - Develop a machine learning algorithm to identify TAD regions in 3D genomics data.
- 2015–2017 **Bioinformatics Research Assistant**, *Dr. John Kauwe Lab*, Provo, UT.
- Prepare a pipeline to automate the process of running Natural Selection analyses from aligned genome sequence files.
 - Calculate correlation between IL6R and CRP cerebral spinal fluid levels in Alzheimer's Disease patients.
 - Determine relationship between rare variants and Alzheimer's Disease status and progression.
 - Conduct GWAS analyses for Alzheimer's Disease
- 2016 **Summer Undergraduate Research Intern**, *Dr. Feng Yue Lab*, Hershey, PA.
- Examine the effect of structural and copy number variations in both Osteosarcoma and Parkinson's Disease.
 - Propose a plan for further investigation in certain loci for validation of duplicated genes identified.
 - Prepare and present a poster in addition to several oral presentations to explain results of the analyses.

Teaching

- 2017 **Teaching Assistant**, *CS 312 - BYU Computer Science Department*, Provo, UT.
"Algorithm Analysis and Design"
- Teach students about different programming concepts and algorithms, including linear and dynamic programming, and various NP-complete and NP-hard computational problems.
 - Aid students on programming projects implementing algorithms under both complexity and time constraints. Grade homework assignments and coding project reports.
- 2015 **Teaching Assistant**, *BIO 165 - BYU Biology Department*, Provo, UT.
"Introduction to Bioinformatics"
- Coach students learning Python and understanding programming concepts, such as conditionals, logic, and loops, with regard to bioinformatic algorithms, including finding the reverse complement of a sequence, translation, etc.

Volunteering

- 2022–now **Violinist**, *Narragansett Bay Symphony Community Orchestra*, East Providence, RI.
- Attend weekly rehearsals in the first violin section.
 - Perform concerts with orchestra.
- 2020–2021 **Student Organizer**, *B2D2K NIH Training Grant*, Penn State University, PA.
- Organize monthly meetings and events for trainees.
 - Coordinate with faculty.
- 2019–2021 **Treasurer**, *Science Policy Society*, Penn State Hershey – Hershey, PA.
- Plan and organize monthly public outreach programs ("Science on Tap") that focus on the latest ideas in science and policy.

2017–2021 **Violinist**, *West Shore Symphony Orchestra*, Mechanicsburg, PA.

- Attend weekly rehearsals in the first violin section.
- Perform concerts with orchestra.

2019 **Retreat Organizer**, *Bioinformatics and Genomics Retreat*, State College, PA.

- Plan and organize the 2019 Annual Bioinformatics and Genomics Retreat held at Penn State University with three other students.
- Contact and arrange speakers, develop the conference schedule, organize and run a two-hour workshop for retreat attendees.
- Coordinate individuals with logistical matters.
- Prevent a sorority from disrupting and entering the conference hall during a talk.
- Retreat workshop topic: "Science Communication: How to Explain Your Job"

Publications

Smith EA, Libuit KG, Kapsak CJ, Scribner MR, **Wright SM**, Bell J, Morales C, Crumpler M, Messenger S, Hacker JK, Ledin K, Glaser C, Jacobson K, Sevin-sky JR, Wadford DA. 2023. Pathogen genomics in public health laboratories: successes, challenges, and lessons learned from California's SARS-CoV-2 Whole-Genome Sequencing Initiative, California COVIDNet. *Microb Genom* 9:001027. <https://doi.org/10.1099/mgen0.001027>

LaBarge B, Hennessey M, Zhang L, Goldrich D, Chartrand S, Purnell C, **Wright SM**, Goldenberg D, Broach JR. 2022. Human Papillomavirus Integration Strictly Correlates with Global Genome Instability in Head and Neck Cancer. *Mol Cancer Res* 20(9):1420-1428. <https://doi.org/10.1158/1541-7786.MCR-21-0831>

Salameh T, Wang X, Song F, Zhang B, **Wright SM**, Khunsriraksakul C, Yue F. 2020. A supervised learning framework for chromatin loop detection in genome-wide contact maps. *Nat Comm* 11:3428. <https://doi.org/10.1101/739698>

Wright SM, Jensen SL, Cockriel KL, Davis B, Tschanz JT, Munger RG, Corcoran CD, Kauwe JSK. 2019. Association study of rs3846662 with Alzheimer's disease in a population-based cohort: the Cache County Study. *Neurobiol Aging* 84:242e1-242e6. <https://doi.org/10.1016/j.neurobiolaging.2019.03.004>

Miller JB, Hippen AA, **Wright SM**, Morris C, Ridge PG. 2017. Human viruses have codon usage biases that match highly expressed proteins in the tissues they infect. *Biomed Genet Genomics* 2(2):1-5. <https://doi.org/10.15761/BGG.1000134>.

Wright SM, Carroll C, Walters A, Newell PD, Chaston JM. 2017. Genome sequence of *Leuconostoc citreum* DmW_111, isolated from wild *Drosophila*. *Genome Announc* 5:e00507-17. <https://doi.org/10.1128/genomeA.00507-17>.

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