PATRICK J. LAWRENCE

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EDUCATION

THE Ohio State University, Columbus, OH 2020-present
Biomedical Sciences Graduate Program | Computational Biology and Bioinformatics

Washington and Lee University, Lexington, VA 2015-2019
Bachelor of Arts, Chemistry | Minor in Philosophy | GPA: 3.647

- *Honors and Awards*: Dean's List, Honor Roll, Scholar-Athlete
- *Honors Societies*: Beta Beta Beta, Phi Sigma Tau, Alpha Epsilon Delta
- *Relevant Coursework*: Applied Bayesian Regression, Data Science, Statistics, Endocrinology, Genetics, Immunology, Biochemistry, Inorganic/Bioinorganic Chemistry, Physical Chemistry: Quantum and Computational Chemistry

RESEARCH AND WORK EXPERIENCE

Bioinformatics Analyst 2019-present
Nationwide Children's Hospital, Institute for Genomic Medicine Columbus, OH

- Analyzed and interpreted whole genome and whole exome sequence data for a study of over 1000 patients with congenital heart defects
- Discovered a novel pathogenic variant in GATA6 responsible for tricuspid atresia using genetic variant analysis techniques and a knowledge of bioinorganic chemistry
- Developed high-throughput image analysis software to assist with the functional analysis of candidate variants using wound-healing assays
- Utilized my analysis software to determine that, *in vitro*, a NRP2 variant significantly reduces cellular migration, an effect which may partially explain the molecular etiology of an instance of familial bicuspid aortic valve.
- Expanded tertiary analysis annotations through the addition of heart enhancer region scores to identify candidate variants for functional analysis in whole genome sequence data from subjects for which the genetic etiology of their heart defect(s) has not been explained by protein coding variation
- Modeled protein folding to assess the impact variants may have on conformation, stability, and disease etiology
- Evaluated the electrostatic surface potential and pH of a protein's microenvironment to elucidate the mechanism by which a variant in CASZ1 reduced its relative expression
- Executed scripts in Bash and Python to perform numerous bioinformatics tasks, including efficient processing of data in AWS S3 buckets and parsing of data from in-house pipelines
- Assisted in the preparation of both grant applications and manuscripts for publication

Research Aide 2017-2019
Nationwide Children's Hospital, Institute for Genomic Medicine Columbus, OH

- Utilized an in-house sequence analysis pipeline (Churchill) to analyze whole exome sequence data and locate genetic variants responsible for the etiology of observed phenotypes
- Automated the processing of FASTQ files from an on-going, multi-site, genetic study on familial congenital heart defects containing over 1000 subjects using Bash and Python
- Scripted programs to automate the generation of quality control metrics for collected and processed genetic data to identify sample swaps, non-paternity issues, and unknown consanguinities

Research Aide 2016-2017
Nationwide Children's Hospital, Autism Treatment Network Columbus, OH

- Entered quantitative data gathered from several multi-site, national studies involving the care, treatment, and diagnosis of children with autism spectrum disorder
- Referenced diagnostic tools to evaluate inclusion or exclusion criteria
- Employed mass marketing and community outreach techniques to increase participation in clinical studies
- Acquired familiarity with Institutional Review Board (IRB) protocols involving bias and subject risk

PUBLICATIONS

Lawrence P, Gordon D, White P, McBride K. "WHAAP: A Comprehensive Wound Healing Automated Analysis Pipeline to Reduce the Burden of Genetic Variant Functional Analysis." *In Preparation.*

Gordon D, Cunningham D, Zender G, Neinast R, **Lawrence P**, Corsmeier D, Garg V, White P, McBride K. "Exome Sequencing in Multiplex Families with Left Sided Cardiac Defects has High Yield for Disease Gene Discovery." *In Preparation.*

POSTER PRESENTATIONS

Lawrence P, Zender G, White P, McBride K. Reducing the Burden of Genetic Functional Analysis: The Use of Image Recognition in Automating the Analysis of Wound Healing Assays. Poster session presented at: The Ohio State University's Center for Clinical and Translational Science's 9th Annual Meeting; 2019 Dec 3; Columbus, OH.

Bennett J, Gordon D, **Lawrence P**, McBride K, White P, Garg V. Use of Machine Learning to Identify High Risk Variants of Uncertain Significance in Lamin A/C Cardiomyopathy. Poster session presented at: The Ohio State University's Center for Clinical and Translational Science's 9th Annual Meeting; 2019 Dec 3; Columbus, OH.

Lawrence P, Gordon D, Kelly B, White P. Implementing Quality Control Metrics in Congenital Heart Defect Variant Analysis with Big Data. Poster session presented at: Nationwide Children's Hospital Summer Student Poster Competition; 2018 Aug 3; Columbus, OH.

INTELLECTUAL PROPERTY DISCLOSURES

Lawrence P, Gordon D, White P, McBride K. WHAAP: A Comprehensive Wound Healing Automated Analysis Pipeline to Reduce the Burden of Genetic Variant Functional Analysis. March 2020. Office of Technology Commercialization, The Research Institute at Nationwide Children's Hospital.

SKILLS AND CERTIFICATIONS

Bioinformatics Tools: Experience using Blast, Chimera, Churchill, Ensembl, I-Tasser, PDB, PRIMUS, PyMOL, PyRosetta, String-DB, UCSU Genome Browser, U-Net, Varhouse

Programming Languages: Experience using Bash, Linux, Python, R

Phlebotomy Technician: Certification Obtained from Ohio School of Phlebotomy (2017)