**Summary:**

Master of Science with computational and experimental experience. Currently a Ph.D. candidate in microbiology. Proven skills with organization, Python programming, R programming, teamwork, figure generation, writing, and undergraduate mentorship.

**Education**

* Bachelor’s of Science: Northern Arizona University Biomedical Science May 2014
* Bachelor’s of Science: Northern Arizona University Chemistry Health Professional May 2014
* Master’s of Science: Boise State University Computational Biochemistry Aug 2016
* Doctor of Philosophy: Northern Arizona University Biology Expected May 2023

**Recently Performed and Upcoming Experimentation**

* Conducting machine learning experiments to better understand genetic causes of antibiotic resistance in *Burkholderia pseudomallei.*
* Conducting resampling experimentation on RNAseq differential expression data.
* Meta-analysis/review of current state of the art GWAS programs for bacteria.

**Relevant Expertise**

* **M.S. degree in computational biochemistry**
* **Python:** Five years’ experience using python for machine learning on top of two years’ experience with general python programming (7 total years).
* **R**: Three years' experience with statistical analysis including tuning machine learning models.
* **Containers**: Have used many programs with Docker and singularity containers. Have experience writing snakemake bioinformatic pipelines.
* **High-Performance Computing (HPC):** Over 3 years of experience with HPC. Most currently used in predicting genotype-phenotype relationships using machine learning algorithms with next-generation sequence data.
* **Machine Learning:** Sufficiently trained in the most current standard practices as well as troubleshooting real-world research problems in both R and python (Currently learning Julia).
* **Large Data**: My current research utilizes whole genome sequences (WGS) from bacteria, meaning hundreds of thousands to millions of predictors.
* **Github**:https://github.com/PaulDanPhillips
* **Analysis of next-generation sequencing data:** Have used known pipelines (UGAP, NASP, LS-BSR) to analyze raw sequence read files.
* **Coordinating multiple projects simultaneously:** Have experience coordinating multiple separate projects simultaneously, including delegating tasks to other researchers.
* **Bioinformatic and Phylogenetic analysis skills:** Have built and analyzed phylogenetic trees.
* **Self-starter:** Have always been self-motivated, especially on scientific topics of interest to me.
* **Multi-tasking:** Have experience working on multiple research projects simultaneously, which requires efficient multi-tasking
* **Efficiently Learn:** Through graduate studies have learned how to digest large amounts of relevant peer-reviewed scientific literature.
* **Independent Experimental Hypothesis:** I have devised and tested my own scientific hypothesis through my Master’s and Ph.D.
* **Training Researchers:** Have trained both graduate and undergraduate students to perform high- and low-level experimentation.
* **Collaboration:** I am always willing to collaborate to increase the knowledge gained on any project.
* **Writing and Communication:** I have good writing experience with several publications. I am also practiced at presenting to scientific conferences. I am always excited to improve through more practice via grant reports, publications, and presentations

**Software Knowledge**

* **Machine Learning:** Sufficiently trained in the most current standard practices as well as troubleshooting real-world research problems.
* **Linux:** Proficient in the use of terminal, VI text editor, and installation of programs.
* **Python:** Five years’ experience using python for machine learning on top of two years’ experience with general python programming.
* **GROMACS:** Experienced running short and long Molecular Dynamic simulations.
* **Pymol:** Extensive experience generating high-resolution images of peptide structures.
* **Mathmatica:** Solved complex quantum chemical problems

**Publications**

Roe, C., Williamson, C., Vazquez, A., Kyger, K., Valentine, M., Bowers, J., **Phillips, P. D.**, et al. (2020). Bacterial Genome wide association studies (bGWAS) and transcriptomics identifies cryptic antimicrobial resistance mechanisms in Acinetobacter baumannii. 8, 1–19. doi:10.1101/864462. [frontiersin.org](https://www.frontiersin.org/articles/10.3389/fpubh.2020.00451/full)

Greene, J. R., Merrett, K. L., Heyert, A. J., Simmons, L. F., Migliori, C. M., Vogt, K. C., Castro, R. S., **Phillips, P. D.**, et al. (2019). Scope and efficacy of the broad-spectrum topical antiseptic choline geranate. 1–22. [PLOS](https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0222211)

Bartee, D., Sanders, S., **Phillips, P. D.**, Harrison, M. J., Koppisch, A. T., and Meyers, C. L. F. (2019). Enamide Prodrugs of Acetyl Phosphonate Deoxy- D -xylulose-5- phosphate Synthase Inhibitors as Potent Antibacterial Agents. doi:10.1021/acsinfecdis.8b00307. [pubs.acs.org](https://pubs.acs.org/doi/10.1021/acsinfecdis.8b00307)

Turner, M. W., Marquart, L. A., **Phillips, P. D.**, and Mcdougal, O. M. (2019). Mutagenesis of α-Conotoxins for Enhancing Activity and Selectivity for Nicotinic Acetylcholine Receptors. doi:10.3390/toxins11020113. [mdpi](https://www.mdpi.com/2072-6651/11/2/113" \t "_blank)

Sanders, S., Bartee, D., Harrison, M. J., **Phillips, P. D.**, Koppisch, A. T., and Freel Meyers, C. L. (2018). Growth medium-dependent antimicrobial activity of early stage MEP pathway inhibitors. PLoS One 13, 1–20. doi:10.1371/journal.pone.0197638. [journals.plos.org](https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0197638)

**Daniel Phillips**, P., Andersen, T., and M. McDougal, O. (2016). Assessing the utility and limitations of high throughput virtual screening. AIMS Mol. Sci. 3, 238–245. doi:10.3934/molsci.2016.2.238. [AIMS Press](https://www.aimspress.com/article/10.3934/molsci.2016.2.238)

King, M. D., **Phillips, P.**strong>, Turner, M. W., Katz, M., Lew, S., Bradburn, S., et al. (2015). Computational Exploration of a Protein Receptor Binding Space with Student Proposed Peptide Ligands w. 63–67. doi:10.1002/bmb.20925. [iubmb](https://iubmb.onlinelibrary.wiley.com/doi/full/10.1002/bmb.20925" \t "_blank)

Fox, D. T., Schmidt, E. N., Tian, H., Dhungana, S., Valentine, M. C., Warrington, N. V, **Phillips, P. D.**, et al. (2014). Sub-Inhibitory Fosmidomycin Exposures Elicits Oxidative Stress in Salmonella enterica Serovar typhimurium LT2. 9. doi:10.1371/journal.pone.0095271. [PLOS](https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0095271)

**Presentations**

Honorable mention at American Association for the Advancement of Science Pacific Division 97th annual meeting.

The Joint Science and Technology Office of the Chemical and Biological Defense Program (JSTO-CBD) two-day virtual workshop:  Artificial Intelligence Medical Discovery (AIMED)

ASM AZ/S. NV Branch & AZ Wellbeing Commons meeting, April 16th, 2022

**References:** Upon Request