Jason A Wulff, Ph.D.
Principal Scientist
Bioinformatics and Molecular Biology
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Education

- Ph.D., Entomology, University of Kentucky, Lexington, Kentucky
- BA, English, University of Minnesota, Minneapolis, Minnesota

Clearance

- Cleared for Top Secret information and granted access to Sensitive Compartmented Information based on a Single Scope Background Investigation completed on July 28, 2020

Specialties

- Ph.D. scientist with over 10 years of experience in bioinformatics, microbiology, and molecular biology, leading projects in various domains such as infectious disease/biothreat/select agents diagnostics, plant, insect, bacterial, viral, and fungal systems
- Principal Scientist for laboratory techniques: Illumina, PACBIO, and ONT MinION NGS library prep and sequencing of DNA and RNA, CRISPR gene editing, RT-PCR, immunoassay based toxin detection all within an ISO 9001 and ISO 17025 certified laboratory focused on biothreat agent detection
- Principal Scientist for bioinformatics (assembly, mapping, annotation, gene ontology, visualization, supervised/unsupervised machine learning, RNA-Seq, microbiome/metagenomic programs, snakemake workflows, database development, synthetic biology detection), Python, and R pipeline scripting with implementation on low resource hardware and high performance clusters
- Extensive experience distilling complex ideas to diverse audiences through academic teaching, bioinformatics trainings, collaborations, mentoring, national and international meeting presentations, and Peace Corps/Nepal service; expertise evidenced by presentations at >20 national and international venues and peer-reviewed publications

Experience

Lead Engineer, July 2023 – Present
Booz Allen Hamilton, Charlottesville, Virginia

- Manage a team of data scientists, overseeing the ingestion of diverse data types and ensuring quality and completeness for complex datasets
- Lead the development and training of machine learning tools to uncover patterns within large-scale data and enhancing data interpretation

- Advise on user interface (UI) enhancements, tailoring solutions to meet specific client requests and improving interactions with a big data infrastructure

Microbiologist V, October 2022 – June 2023
Amentum, Ruckersville, Virginia

- Managed teams of staff scientists in biological threat detection and biodefense mission areas, with a focus on high-throughput genomics, microbial diagnostics in high complexity backgrounds, molecular biology, and bioinformatics research
- Developed and implemented strategic planning initiatives for the laboratory, including workforce training and identification of new methods for trace detection of biothreat agents
- Managed a new laboratory setup and protocol development for a genomics and proteomics core capability
- Provided technical expertise and serve as subject matter expert for wet lab and bioinformatics activities including Illumina, PACBIO, and ONT MinION sequencing, qPCR, Maldi-TOF, LCMS, and Immunoassays, as well as, the data analysis capabilities including developing open-source software snakemake pipelines for sequencing data analysis

Principal Scientist / Capability Manager II, October 2020 – October 2022
MRIGlobal, Charlottesville, Virginia

- Principal Scientist and Team Lead for microbial forensics molecular and bioinformatics group; led efforts on machine learning model development, bioinformatics pipeline development, and database development efforts for deep sample characterization
- Led and trained staff on Illumina, PACBIO, and ONT MinION NGS library prep/sequencing of DNA and RNA and on diagnostic assays using CRISPR, RT-PCR, immunoassay based, LCMS and MALDI-TOF all within an ISO 9001 and ISO 17025 certified laboratory focused on viral, bacterial, and fungal select agent detection and characterization
- Coordinated bioinformatics development with molecular biology R&D across teams of molecular biologist and bioinformaticians
- Responsible for all deliverables, including reports and scripts
- Maintained core bioinformatics and laboratory team through interviewing, hiring, and managing staff
- Advanced capabilities by exploring and developing diverse cutting-edge supervised/unsupervised machine learning approaches using TensorFlow and Scikit-learn
- Distilled method development and validation efforts into Standard Operating Procedures (SOPs)
- Implemented a laboratory information management system (LIMS) by developing workflows and training staff on its usage within a ISO17025 certified laboratory
- Experience with and knowledge of the Federal Select Agent Program from managing BSL 2 and BSL 3 laboratory tasks involving pathogens and toxins.

Senior Scientist / Capability Manager I, May 2018 – September 2020
MRIGlobal, Charlottesville, Virginia

- Senior Scientist and Team Lead for 26 scientists in a client driven laboratory that focuses on the detection and characterization of nucleic acids and protein targets for the purposes of biodefense
- Managed and implemented continuous improvements and validation of bioinformatics tools to cover expanded requirements, including contextual signatures for synthetic biology and bio-processing
- Established custom databases for biological threat agents, genetic near-neighbors, simulants, environmental backgrounds, 16s, mitochondrial, and chloroplasts, and synthetic biology components
- Provided subject matter expertise in molecular biology, NGS, genomics, bioinformatics, select agents, biosafety, and synthetic biology for a DoD client
- Identified requirements, quotes, purchased, and set up high-side computational hardware and software at the behest of the government

Postdoctoral Scholar, April 2016 – 2018
Sword Lab, Texas A&M University, College Station, Texas

- Innovated a high-throughput sequencing DNA barcoding bulk detection assay to identify exotic species, *Helicoverpa armigera,* and discriminate hybrids from closely related, and morphologically similar, species within the United States
- Adapted the portable high-throughput sequencing technology, Oxford Nanopore MinION, to a rapid and field ready, exotic pest DNA bulk detection assay
- Developed and maintain the computational resources for collaborators, including RADSeq and metagenomic software pipelines and databases
- Quantified changes in plant defense gene induction using RT-qPCR

Postdoctoral Scholar, April 2014 – 2016
Eubanks Lab, Texas A&M University, College Station, Texas

- Implemented both reference-based and *de novo* RNA-Seq using the Linux shell environment, High Performance Computing, cloud computing, python scripts, and R based bioinformatics tools to identify differentially expressed plant defense genes in spider mite and pesticide treated maize (*Zea mays*) and soybean (*Glycines max*)
- Developed a high-throughput (Illumina and Oxford nanopore MinION) DNA metabarcoding and molecular taxonomy technique to resolve prey DNA within the gut of fire ant (*Solenopsis invicta*)

Graduate Research Assistant 2008 -2014
White Lab, University of Kentucky, Dept. of Entomology, Lexington, Kentucky
Dissertation: The Role of the Bacterial Endosymbiont, *Arsenophonus*, in the Soybean Aphid, Aphis glycines

- Manipulated bacterial infection in five soybean aphid genotypes using antibiotic microinjection and microsatellite genotyping to determine the impact of an aphid bacterial endosymbiont on aphid susceptibility to biological control, resistant soybean cultivars, and plant hormonal defense

- Surveyed bacterial endosymbiont infection frequency, strain diversity and titer in native and introduced soybean aphid populations using sequencing, qPCR and PCR

Select Publications

1. Wulff J., M. K. Kjeldgaard, M. D. Eubanks, G. A. Sword (2021). From the bellies of babes: a larval-based approach to ant molecular gut content analysis. Insectes Sociaux, 2-3: 245-253.
2. Holt J., A. Styer, J. White, J. Armstrong, S. Nibouche, L. Costet, A. Malacrinò, J. Antwi, J. Wulff, G. Peterson, N. Mclaren, R. Medina (2020). Differences in Microbiota Between Two Multilocus Lineages of the Sugarcane Aphid (Melanaphis sacchari) in the Continental United States. Annals of the Entomological Society of America. 113. 1-9.
3. Wulff J., M. Kiani, K. Regan, M. Eubanks, A. Szczepaniec, (2019). Neonicotinoid Insecticides Alter the Transcriptome of Soybean and Decrease Plant Resistance. International Journal of Molecular Sciences. 20. 783.
4. Wulff J. A., J. A.White (2015). The endosymbiont *Arsenophonus* provides a general benefit to its host soybean aphid (Hemiptera:Aphididae) regardless of host plant resistance (Rag). Environmental Entomology. 44(3): 574-581.
5. Hoot S. B., K. M.Wefferling, J. A.Wulff (2015). Phylogeny and Character Evolution of Papaveraceae s.l. (Ranunculales). Systematic Botany 40(2): 474-488.
6. Brady C. M., M. K. Asplen, N. Desneux, G. E. Heimpel, K. R. Hopper, C. R. Linnen, K. M. Oliver, J. A. Wulff, J. A.White (2014). Worldwide populations of the aphid, *Aphis craccivora*, are infected with diverse facultative bacterial symbionts. Microbial Ecology. 67(1): 195-204
7. Wulff J. A., K. Buckman, K. Wu, G.E.Heimpel, J. A. White (2013). The endosymbiont *Arsenophonus* is widespread in soybean aphid, *Aphis glycines,* but doesn't provide protection from parasitoids or a fungal pathogen. PLoS ONE 8:e62145.