

TYLER BIGGS, PH.D

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RESEARCH SCIENTIST: BIOINFORMATICS, CHEMINFORMATICS, METABOLOMICS

With a Ph.D. in synthetic organic chemistry and over five years of experience conducting Bioinformatics research, I bring a unique perspective to Bioinformatics research. I excel in end-to-end analysis of large datasets from diverse sources, including transcriptomics, metabolomics, cheminformatics, and metabolomic assays. I am an expert in Python and workflow development and experienced in containerization (Docker), Git, and continuous integration practices. I have deployed machine learning, generalized linear models, and custom hierarchical Bayesian models (via PyMC) for hypothesis generation in statistical and exploratory analysis. Most importantly, I can communicate complex results to various audiences, including commodity stakeholders, private industry, and scientific collaborators.

- **Expert in:** Python, R, Bash, Groovy (Java), Machine Learning, Probabilistic Programming (PyMC), Git, Workflow development and containerization, Nextflow, Docker, and Singularity.
- **Finely honed written & verbal communication**, analytical, experimental design, project management, and research skills.
- **Proven ability to communicate and collaborate effectively** with internal & external stakeholders at all levels.
- **Adept at prioritizing, multi-tasking, and pivoting** to adapt to ever-changing work environments.
- **Equal ability to perform autonomously**, as a team leader, and as a supportive team player.

CORE COMPETENCIES

Experimental Design | Generalized Linear Models | Bayesian Statistics | Research | Grant Writing | Metabolomics | Bioinformatics
Cheminformatics | Transcriptomics | Organic Synthesis | Chromatography | Mass Spectrometry | Nuclear Magnetic Resonance
Programming | Next-Generation Sequencing | RNA-seq data | Feature Selection | Dimensional Reduction

PROFESSIONAL EXPERIENCE

WASHINGTON STATE UNIVERSITY

2017-Present

Postdoctoral Researcher to Dr. Stephen Ficklin, Department of Horticulture

Conduct Bioinformatics research focused on agricultural applications. Use NGS/RNAseq data to inform experimental design, execution, and analysis. Collaborate with stakeholders in commodities, USDA, and private industry. Conduct statistical analysis and interpret results for Scientists. Drive pipeline development, write papers and grants, and create custom scientific software.

- Assisted in developing and testing GEMmaker: Nextflow workflow for large-scale gene expression sample processing, expression-level quantification, and Gene Expression Matrix (GEM) construction.
- Instrumental in the design and served as the primary contributor to NSF-funded SciDAS project, Pynome version 1.0, which is used to automate retrieval and preparation of whole genome sequences for Eukaryotic species and integrates with iRODs to prepare large-scale genomic analytics workflows.
- Utilized an untargeted metabolomics approach to evaluate critical molecules associated with smoke taint in wine and developed an in-silico library of potential smoke-associated compounds created by permuting known enzyme transformations upon suspected smoke contaminants.
- Applied machine learning and generalized linear models for prediction and feature selection to biological data (such as RNA-seq and untargeted LCMS assays) with multifaceted experimental designs and time series.

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ACADEMIC BACKGROUND

Doctor of Philosophy in Organic Chemistry | Washington State University, Pullman, WA

Dissertation: Synthetic uses of S-Nitrosothiols in Organic Chemistry

Bachelor of Science in Chemistry | Washington State University, Pullman, WA

SELECTED PUBLICATIONS

Peer-Reviewed Publications

1. John Hadish, Tyler Biggs, Ben Shealy, M. Reed Bender, Coleman B. McKnight, Connor Wytko; Melissa C. Smith; F. Alex Feltus; Loren Honaas, Stephen Ficklin. GEMmaker: process massive RNA-seq datasets on heterogeneous computational infrastructure (2022), *BMC Bioinformatics*
2. Cameron Ogle, David Reddick, Coleman McKnight, Tyler Biggs, Rini Pauly, Stephen P. Ficklin, F. Alex Feltus, and Susmit Shannigrahi. Named Data Networking for Genomics Data Management and Integrated Workflows. *Front. Big Data*. (2021) doi:10.3389/fdata.2021.582468
3. Craig McConnel, Sierra Crisp, Tyler Biggs, Lindsay Parrish, William Sischo, Amber Adams-Progar, Stephen Ficklin. Transcriptomic analysis of peripheral leukocytes in dairy cows with and without evidence of early postpartum disease. *Frontiers in Veterinary Science* (2020) doi:10.15232/aas.2020-02092
4. Craig McConnel, Sierra Crisp, Tyler Biggs, Stephen Ficklin, Lindsay M. Parrish, Sophie Trombetta, William M. Sischo, Amber Adams-Progar. A fixed cohort field study of gene expression in circulating leukocytes from dairy cows with and without mastitis. *Journal of Dairy Science* (2020) doi:10.3389/fvets.2020.559279
5. Caihong Zhang, Tyler Biggs, Nelmi Devarie-Baez, Shaomin Shuang, Chuan Dong, Ming Xian. S-Nitrosothiols: Chemistry and Reactions. *Chem. Commun.* (2017) doi:10.1039/C7CC06574D
6. Tyler Biggs, Laksiri Weerasinghe, Chung-Min Park, Ming Xian. Phosphine mediated conjugation of S- nitrosothiols and aldehydes. *Tetrahedron Letters* (2015) doi:10.1016/j.tetlet.2015.04.017
7. Yu Zhao, Tyler Biggs, Ming Xian. Hydrogen sulfide (H₂S) releasing agents: chemistry and biological applications. *Chemical Communications*. (2014) doi:10.1039/C4CC00968A
8. Chung-Min Park, Wei Niu, Chunrong Liu, Tyler Biggs, Jiantao Guo, Ming Xian. A Proline-Based Phosphine Template for Staudinger Ligation. *Organic Letters* (2012) doi:10.1021/ol3022484

REFERENCES AVAILABLE ON REQUEST