

SUMMARY.....

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 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.

SKILLS.....

Science	Computing	Chemistry	Bio/Chem-informatics
<ul style="list-style-type: none"> • Experimental design • Manuscript & grant preparation • Experienced educator & communicator 	<ul style="list-style-type: none"> • Python, R, Bash, Groovy, L^AT_EX • Machine Learning, Probabilistic Programming • Git, continuous integration • Workflows, HPC, AWS, Slurm • Nextflow, Docker, Singularity 	<ul style="list-style-type: none"> • Organic Synthesis • Purification & characterization • Chromatography • Mass spectrometry • Nuclear Magnetic Resonance 	<ul style="list-style-type: none"> • <i>in-silico</i> compound generation • Feature selection. • Generalized Linear Models • Bayesian statistics • Advanced visualizations

SELECTED PROJECTS & KEY CONTRIBUTIONS.....

<i>Metabolomics of wine and wildfire</i>	<ul style="list-style-type: none"> • Utilized and expanded upon an untargeted metabolomics approach to evaluate critical molecules associated with smoke taint in wine. • Developed an in-silico library of potential smoke-associated compounds created by permuting known enzyme transformations upon suspected smoke contaminants.
<i>Terabyte scale workflow development</i>	<ul style="list-style-type: none"> • Assisted in the design and development of this nextflow workflow script. • Wrote and containerized, with Docker and Singularity, scripts for use within the workflow. This involved programming in bash, Groovy, Python, and R.
<i>Profiling complex phenotypes in apples</i>	<ul style="list-style-type: none"> • Analyzed apple transcriptomics and scald data and identified gene expression patterns associated with increased scald risk. • Provided writings, figures, and analyses for grant applications.
<i>Synthetic Organic Chemistry</i>	<ul style="list-style-type: none"> • In my dissertation I investigated novel synthetic methods using S-Nitrosothiols. • Planned and ran synthetic organic chemistry reactions. • Purified and characterized products using LCMS, NMR, and mass-spectroscopy. • Ordered chemical reagents and lab supplies.
<i>Statistics Consulting</i>	<ul style="list-style-type: none"> • Consulted on data analysis for consumer trials. • Wrote generalized linear models in R. • Wrote Bayesian model using PyMC.

REFERENCES.....

Available upon request.

PROFESSIONAL EXPERIENCE & EDUCATION

2018 - 2024	Postdoctoral Researcher to Dr. Stephen Ficklin. Department of Horticulture, Washington State University, Pullman WA, 99163
2017 - 2018	Postdoctoral Researcher joint appointment with Dr. Aurora Clark & Dr. Stephen Ficklin. Washington State University, Pullman WA, 99163
2012 - 2017	Ph.D. Synthetic Organic Chemistry. Dissertation on the <i>Synthetic Applications of S-Nitrosothiols</i>
2009 - 2012	Research Assistant to Ming Xian. Washington State University, Pullman WA, 99163
2012 - 2017	Ph.D. in <i>Organic Chemistry</i> , Dissertation: Synthetic uses of S-Nitrosothiols in Organic Chemistry Washington State University, Pullman WA, 99163
2006 - 2012	Bachelors of Science in <i>Chemistry</i> Washington State University, Pullman WA, 99163

TEACHING EXPERIENCE AT W.S.U.

2022	Instructor AFS 505 Topics in Computational and Analytical Methods for Scientists. Introduction to data science using Python. Created course content and gave lectures.
2018	Co-Instructor HORT 503 Advanced Topics: Data Analytics for Scientists. Introduction to data science using Python. Assisted in course creation and gave lectures.
2013 - 2016	Teaching Assistant of first and second semester organic chemistry.
2013	Teaching Assistant of second semester organic chemistry.
2010	Tutor of general & organic chemistry
2009, 2016	Teaching Assistant of Organic Qualitative Analysis Laboratory

SELECTED 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

OPEN SOURCE SOFTWARE

- GEMmaker: a Nextflow workflow for large-scale gene expression sample processing, expression-level quantification and Gene Expression Matrix (GEM) construction. Results from GEMmaker are useful for differential gene expression (DGE) and gene co-expression network (GCN) analyses. The GEMmaker workflow currently supports Illumina RNA-seq datasets.
Contribution: Assisted in development and testing.
- Pynome: a product of the NSF-funded SciDAS project; It is used to automate retrieval and preparation of whole genome sequences for a variety of Eukaryotic species. Pynome integrates with iRODs to prepare large-scale genomic analytics workflows.
Contribution: Assisted in design, and primary contributor to version 1.0.