Tyler Biggs, Ph.D.

Pullman Washington
https://biggstd.github.io/

Summary

With a Ph.D. in synthetic organic chemistry and over seven years of experience conducting bioinformatics research, I bring a unique perspective to applied data science. 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
- Experimental design
- Manuscript & grant preparation
- Experienced educator & communicator

Computing
- Python, R, Bash, Groovy, LaTeX
- Machine Learning, Probabilistic Programming
- Git, continuous integration
- Workflows, HPC, AWS, Slurm
- Nextflow, Docker, Singularity

Chemistry
- Organic Synthesis
- Purification & characterization
- Chromatography
- Mass spectrometry
- Nuclear Magnetic Resonance

Bio/Chem-informatics
- *in-silico* compound generation
- Feature selection.
- Generalized Linear Models
- Bayesian statistics
- Advanced visualizations

Selected Projects & Key Contributions

Metabolomics of wine and wildfire
- 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.

Terabyte scale workflow development
- 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.

Profiling complex phenotypes in apples
- Analyzed time-series apple transcriptomics and scald data and identified gene expression patterns associated with increased scald risk.
- Provided writings, figures, and analyses for grant applications.

Synthetic Organic Chemistry
- 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.

Statistics Consulting
- 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 *Synthetic Applications of S-Nitrosothiols*
2009 - 2012	**Research Assistant** to Ming Xian. Washington State University, Pullman WA, 99163
2012 - 2017	**Ph.D.** in *Organic Chemistry*, Dissertation: Synthetic uses of S-Nitrosothiols in Organic Chemistry Washington State University, Pullman WA, 99163
2006 - 2012	**Bachelors of Science** in *Chemistry* 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 Diary 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 (H_2S) 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.