

William Maxwell Alexander, MS

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EDUCATION

Master of Science in Computer Science

Tufts University

2011-2013

Concentration in Artificial Intelligence

Master's Thesis: Multi-Step Hindsight Optimization Planning for Real-Time Performance in Partially-Observable Worlds

Bachelor of Arts in Liberal Arts

Bennington College

2007-2010

Concentration in Computer Science and Biology

Senior Project: Spike-Timing-Dependent Neural Network Model for Adaptive Control

PROFESSIONAL EXPERIENCE

Software Engineer

2020

Radix Labs

- Software development on multiple components of the Radix Labs platform for coordinated biological laboratory automation
- Designed and maintained multi-platform build, deployment, and update systems
- Designed interfaces between the automation platform and external utilities and resources, e.g. Opentrons robots and Slack messaging

Bioinformatics Engineer

2013-2020

Blais Proteomics Center, Dana-Farber Cancer Institute

- Published the open-source *multiplierz 2.0* toolset for proteomic mass spectrometry data analysis.
- Developed and maintained the Proteomics Center's automated bioinformatics pipeline.
- Designed custom analysis algorithms for label-free and isotopically-labelled proteomic quantitation.
- Designed MS/MS data pre-processing algorithms to leverage novel HCD chemical fragmentation processes, as part of efforts to develop analytical techniques for the identification of proteins bound by covalent probes.
- Developed novel mass spectrometry acquisition routines for real-time detection of peptides modified by covalent probes
- Contributed to writing and data analysis/presentation for multiple publications and grant proposals.

SKILLS AND TECHNOLOGIES

■ LANGUAGES and KEY LIBRARIES

- **Python**

- ★ **Scientific Computation** - Pandas, NumPy, SciPy, Statsmodels
- ★ **Data Visualization** - Matplotlib, Seaborn
- ★ **Data Pipelines** - Luigi
- ★ **Machine Learning** - Scikit-learn, Tensorflow, Keras

- **Scala**

- ★ **Functional Programming** - Cats, Matryoshka
- ★ **Actor-Model Concurrency** - Akka

- **C/C++/C#**

- **Haskell**

- **R**

■ TOOLS

- **IDEs and Notebooks** - Pycharm, IntelliJ, Wing, Jupyter
- **DevOps** - Docker, Hashicorp Nomad/Consul/Terraform
- **Version Control** - Git, Mercurial, Gitlab, Github
- **Build Systems** - Bazel, Make

SELECTED PUBLICATIONS

- **Alexander WM**, Ficarro SB, Adelmant G, Marto JA. Multiplierz 2.0: A Python-based ecosystem for shared access and analysis of native mass spectrometry data. *Proteomics* 2017;17:1700091.
- Kang UB, **Alexander WM**, Marto JA. Interrogating the hidden phosphoproteome. *Proteomics* 2017;17:1600437.
- Ficarro SB, **Alexander WM**, Marto JA. mzStudio: A dynamic digital canvas for user-driven interrogation of mass spectrometry data. *Proteomes* 2017;5:pii: 20.
- Chu N, Salguero, AL, Liu, AZ, Chen Z, Dempsey DR, Ficarro SB, **Alexander WM**, Marto JA, Li Y, L. Amzel M, Gabelli SB, Cole PA. Akt Kinase Activation Mechanisms Revealed Using Protein Semisynthesis. *Cell* 2018; 174(4):897-907.
- Browne, CM, Jiang B, Ficarro SB, Doctor ZM, Johnson JL, Card JD, Sivakumaren CS, **Alexander WM**, Yaron TM, Murphy CJ, Kwiatkowski NP, Zhang T, Cantley LC, Gray NS, Marto JA. A Chemoproteomic Strategy for Direct and Proteome-wide Covalent Inhibitor Target-site Identification. *J. Am. Chem. Soc* 2019; 141(1):191-203