

William Maxwell Alexander, MS

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PROFESSIONAL EXPERIENCE

Independent – Alexander Bioinformatics

2023-2024

Independent bioinformatics consulting venture. Additional public-facing scientific projects developed in this period include:

- ProteoFlow – Proprietary end-to-end cloud-based analysis workflow for LC-MS proteomics
- BioReport – Web service using LLM-based analysis of scientific papers to summarize knowledge of genes and proteins
- Accessive – Python library and web service for translating between 12+ bioinformatic accession formats for genes, transcripts, and proteoforms

Computational Biologist – Kernal Biologics

2021-2023

- Designed and implemented a cloud-based, high-throughput LC-MS proteomics analysis pipeline optimized for detecting products of non-standard protein translation events
- Analyzed Ribo-seq, SHAPE-seq, and other specialized transcriptomic data aimed at characterizing mRNA in-vivo structure and functional properties
- Performed combined analyses of multi-omic, multi-tissue and single-cell datasets to discover cell-specific translation dynamics
- Collaborated with wet lab scientists to iteratively design and evaluate mRNA sequence elements applicable to novel therapeutics

Software Engineer – Radix Labs

2020-2021

- 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

Bioinformatics Engineer – Dana-Farber Cancer Institute

2014-2020

- 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-labeled 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.

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

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.
- Zhu H, Ficarro SB, **Alexander WM**, Fleming LE, Adelmant G, Zhang T, Willetts M, Decker J, Brehmer S, Krause M, East MP. PRM-LIVE with trapped ion mobility spectrometry and its application in selectivity profiling of kinase inhibitors. *Analytical chemistry*. 2021 Oct 4;93(41):13791-9.
- Ficarro SB, **Alexander WM**, Tavares I, Marto JA. Open source fraction collector/MALDI spotter for proteomics. *HardwareX*. 2022 Apr 1;11:e00305.