Daniel J. Geiszler

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SKILLS

Data Science

Machine learning, Probability and statistics, Scientific computing, Algorithm development

Bioinformatics

Computational proteomics, Post-translational modifications, Transcriptomics, Multi-omics integration, Mass spectrometry

Biology

Oncology, Immunology, Virology, Cell biology

Software development

Python, Java, R, C++, Bash, Pipeline development, Git/GitHub, Continuous integration (CI/CD), Linux, High-performance computing

EDUCATION

Ph.D., Bioinformatics   Aug 2022
    University of Michigan, Ann Arbor

B.S., Biotechnology; B.S., Chemistry; Minor, Mathematics   May 2017
    California State University San Marcos

EXPERIENCE

Koç Üniversitesi – Dr. Nurhan Özlü   2022 – Present
Postdoctoral Fellow – Proteome Informatics   **Istanbul, Turkey**

- Utilized machine learning and Bayesian statistics to develop noise-robust method for post-translational modification localization that achieves near-theoretically optimal performance
- Led bioinformatics efforts to identify 13 universal biomarkers of cytokinesis in a multi-cell line, multi-cell phase experiment with factorial design and identified ontology-enriched patterns across cell cycle phases
- Collaborated in cross-functional teams with biologists, leading bioinformatics efforts in 4 projects to create tailored workflows for complex proteomics projects spanning biomarker discovery, protein-protein interactions, and phosphoproteomics

University of Michigan Department of Pathology – Dr. Alexey Nesvizhskii   Jan 2018 – Aug 2022
Graduate Researcher – Proteome Informatics   **Ann Arbor, MI, USA**

- Published and maintained software packages for proteomics analysis with more than 75,000 downloads that are widely used in production environments in both academia and industry
- Developed automated methods to mine for post-translational modification signature identification in mass spectra that increase identified peptides by up to 100% in some cases
- Spearheaded collaborations for inter-university, cross-functional projects in engineering chemoproteomics probe fragmentation patterns resulting in 2 publications
- Provided end-user support for FragPipe, promptly troubleshooting hundreds of IT and configuration issues
- Integrated 110 cancer patient transcriptomic and proteomic samples with multi-omics approaches to identify neo-antigens as part of the Clinical Proteomics Tumor Analysis Consortium

GRANTS

European Molecular Biology Organization Postdoctoral Fellowship   Sep 2023 – Present
    €115,200 (ALTF 109-2023)

HONORS AND AWARDS

Rackham Graduate Travel Award	2021
Proteomics Data Mining Challenge 2020 winning team	2020
IREU Summer Scholarship Recipient	2017
Magna Cum Laude – CSUSM	2017
Outstanding Chemistry Graduate	2017
HyperCube Scholar in Computational Chemistry	2016
Outstanding Senior at CSUSM	2016

INVITED TALKS

A new statistical model for open search localization   Oct 2024
TuPA International Proteomics Congress // 6th National Proteomics Congress

Illuminate Your Open Search: Comprehensive PTM Identification   Oct 2022
TuPA International Proteomics Congress // 4th National Proteomics Congress

SCIENTIFIC SOFTWARE CONTRIBUTIONS

PTM-Shepherd (https://ptmshepherd.nesvilab.org/)
        A tool for mass-tolerant search annotation
        Roles: creator, technical support, software maintenance

FragPipe (https://fragpipe.nesvilab.org/)
        A pipeline for analyzing mass-spectrometry proteomics data with 75,000 downloads
        Roles: contributor, technical support, software maintenance

EzRAG (https://github.com/danielgeiszler/EzRAG/)
        A lightweight program for testing retrieval-augmented generation
        Roles: creator

FragRAG (private)
        A retrieval augmented generation-powered chatbot for FragPipe questions
        Roles: creator

PUBLICATIONS

Detecting diagnostic features in MS/MS spectra of post-translationally modified peptides
Geiszler, D. J., Polasky, D. A., Yu, F., Nesvizhskii, A. I. Nature Communications (2023).

Solid-phase compatible silane-based cleavable linker enables custom isobaric quantitative chemoproteomics
Burton, N. R, Polasky, D. P., Shikwanna, F., Ofori, S., Yan, T., **Geiszler, D. J.**, da Veiga Leprevost, F.,
Nesvizhskii, A. I., Backus, K. M. Journal of the American Chemical Society (2023).

MSFragger Labile Mode: A Flexible Method to Improve PTM Search in Proteomics
Polasky, D. A., **Geiszler, D. J**., Yu, F., Teo, G. C., Nesvizhskii, A. I. (2023). Molecular & Cellular Proteomics,
22(5), 100538.

Multiattribute Glycan Identification and FDR Control for Glycoproteomics
Polasky, D. A., **Geiszler, D. J**., Yu, F., Nesvizhskii, A. I. (2022). Molecular & Cellular Proteomics, 21(3), 100205.

Enhancing Cysteine Chemoproteomic Coverage Through Systematic Assessment of Click Chemistry Product Fragmentation
Yang, T., Palmer, A. B., **Geiszler, D. J**., Polasky, D. A., Boatner, L. M., Burton, N. R., Armenta, E., Nesvizhskii, A. I., Backus, K. M. (2022). Analytical Chemistry, 94(9), 3800-3810.

PTM-Shepherd: analysis and summarization of post-translational and chemical modifications from open search results
Geiszler, D. J., Kong, A. T., Avtonomov, D. M., Yu, F., da Veiga Leprevost, F., & Nesvizhskii, A. I. (2021). Molecular & Cellular Proteomics, 20, 100018.

Identification of modified peptides using localization-aware open search
Yu, F., Teo, G. C., Kong, A. T., Haynes, S. E., Avtonomov, D. M., **Geiszler, D. J.**, & Nesvizhskii, A. I. (2020). Nature Communications, 11(1), 1-9.

Integrated proteogenomic characterization of clear cell renal cell carcinoma
Clark, D. J., [39 authors], **Geiszler, D.**, [39 authors]. (2019). Cell, 179(4), 964-983.

UNDER REVIEW

Proximity labeling and SILAC based proteomic approach identifies proteins at the interface of homotypic and heterotypic cancer cell interactions
Saner, N., Uzun, C., Akarlar, B., Ozkan, S. N., Ozturk, E., **Geiszler**, **D. J.**, Ozlu, N. (Under review). Molecular & Cellular Proteomics.

IN PREPARATION

A new statistical model for open search localization
Geiszler, D. J., Ozlu, N. (in preparation).

A multi-cell line phosphoproteomic atlas of cell cycle regulation
Ceyhan, C. S.,* **Geiszler, D. J.**,* Dittmann, A., Grossman, J., Ozlu, N. (in preparation).
*These authors contributed equally

Investigating the regulatory roles of protein palmitoylation during cell division
Ozkan, N. E., Yapici, G. N., **Geiszler, D. J.**, Ozlu, N. (in preparation).

PRESENTATIONS AND OTHER WORK

A new statistical model for open search localization
Daniel J. Geiszler, Nurhan Ozlu [Poster]. American Society for Mass Spectrometry (2024).

The Urinary Post-Translational Modification Landscape and Applications in Clear Cell Renal Cell Carcinoma Biomarker Discovery
Daniel J. Geiszler, Nazli Ozkan, Gamze Yapici, Meral Kiremit, Nurhan Ozlu [Poster]. American Society for Mass Spectrometry (2023).

Computational Methods for Characterizing Post-translational and Chemical Modifications Found in Open Searches
Daniel J. Geiszler. [Dissertation]. University of Michigan (2022).

Automated modification-specific spectral feature detection
Daniel J. Geiszler, Daniel A Polasky, Fengchao Yu, Alexey I. Nesvizhskii. [Poster]. American Society for Mass Spectrometry (2021).

Multi-Level Post-Translational Modification Classification with PTM-Shepherd
Daniel J. Geiszler, Andy T. Kong, Dmitry M. Avtonomov, Felipe da Veiga Leprevost, Hui-Yin Chang, Fengchao Yu, Alexey I. Nesvizhskii. [Poster]. American Society for Mass Spectrometry (2020).

Exploring the Open Proteome: Proteomics Open Search Analysis with PTM-Shepherd
Daniel J Geiszler, Andy T Kong, Dmitry M Avtonomov, Felipe V Leprevost, Guo Ci Teo, Hui-Yin Chang, Alexey I Nesvizhskii. [Poster]. American Society for Mass Spectrometry (2019).

SCIENTIFIC BLOG POSTS

Daniel Geiszler. (2025) *Retrieval Augmented Generation with DeepSeek*
https://danny.bio/posts/20250125-retrieval-augmented-generation/RagSystem.html

Daniel Geiszler. (2024) *How to Make a Rolling Blog Post with Continuous Integration*
https://danny.bio/posts/20241221-rolling-blog-posts/

Daniel Geiszler. (2024) *Machine Learning Basics*
https://danny.bio/posts/20241219-machine-learning-basics/

Daniel Geiszler. (2024) *Learning Pyro for Better Content Sorting*
https://danny.bio/posts/20241215-testing-pyro/testing_pyro.html

LANGUAGES

English (native)

Turkish (limited working proficiency)

Spanish (recoverable)