Jason M. Gilmore PhD

Department of Genome Sciences, University of Washington, Seattle, WA 98105

(603) 306 6313, jmg44@u.washington.edu

**EDUCATION**

**PhD, Genetics**, May 2014

Geisel School of Medicine at Dartmouth College

Research Advisor: Dr. Scott A. Gerber

Thesis Title: Analytical and computational approaches for quantitative phosphoproteomics

BA, Computational Biology, May 2007

University of Pennsylvania

**RESEARCH EXPERIENCE**

**Senior Fellow,** University of Washington, Seattle, WA 2016-present

Molecular phenotyping of Alzheimer’s disease in post-mortem-biospecimen samples via data independent acquisition

Advisor: Dr. Michael MacCoss

* DIA-MS analysis of soluble and insoluble factions from human brain tissue samples
* Statistical analysis to determine protein expression by region in healthy controls and Alzheimer’s disease patients

Greenland meltwater proteomics

Advisor: Dr. Brook Nunn

* Developed and optimized bacterial extraction from glacial water samples containing fine glacial flour
* DIA-MS analysis of bacterial proteins to probe metabolic pathways related to glacial weathering
* DNA extraction on glacial bacteria samples for metagenome creation

**Senior Fellow,** University of Washington, Seattle, WA 2014-2016

Washington Research Foundation Innovation Fellows Program

High-throughput validation of designed proteins via Mass Spectrometry
Advisors: Dr. David Baker and Dr. Michael MacCoss

* Designed a set of small disulfide-stabilized *de novo* mini-proteins using Rosetta design software
* Expressed, purified and validated designed proteins using an *E.coli* system
* Multi-stage mass spectrometry to evaluate disulfide connections in small proteins
* DIA mass spectrometry on pools of designed proteins for rapid screening

**Graduate Researcher**, Dartmouth College, Hanover, NH, 2008-2014

Analysis of protein phosphorylation

Advisor: Dr. Scott A. Gerber

* Developed and assessed novel protein digestion methodologies for increasing access to phosphorylation sites in proteins
* Designed and implemented a computational tool for the interpolation of peptide quantification results in cases with missing standard data
* Quantitative analysis of the effects of posttranslational modification on peptide shotgun sequencing

**Intern**, Pacific Northwest National Laboratory, Richland, WA, 2006-2008

Protein-Protein interaction network analysis

Advisor: Don Daly

* Implementation of a Bayesian estimator of protein interaction posterior probabilities
* Preparation of end-user documentation for this software tool and for displaying the output with existing freely available network visualization tools

**Undergraduate Researcher**, Pacific Northwest National Laboratory, Richland, WA, 2006-2008

Quality control assessment of high throughput proteomics pipeline

Advisor: Dr. Joshua Adkins

* Established a linear mixed effects model to gauge overall process integrity using protein standards run over several months
* Produced a programming script to monitor certain process characteristics which inform need for recalibration
* Advised on establishment of new practices to document anomalous processing events

**RESEARCH INTERESTS**

Application of computational methods to expand analysis of complex biological datasets

Technique development for proteomics with mass spectrometry

**SKILLS AND TECHNIQUES**

Cell culture including heavy isotope amino acid incorporation

Animal tissue/organ processing

Protein design and modeling with Rosetta

Protein expression and purification in an *E.coli* system

LC-MS/MS sample preparation and analyses

DDA, DIA, and targeted mass spectrometry method design and implementation

Bioinformatic and statistical analyses on large biological datasets

Programming experience with Java, SQL, R, Python, and C++

**TEACHING & TUTORING EXPERIENCE**

**Teaching Assistant**, Dartmouth College

Gene Expression and Inheritance, Summer 2009

* Provided lab instruction of sophomore level biology students.

**PROFESSIONAL ASSOCIATIONS**

American Society for Mass Spectrometry

Human Proteome Organization

**PEER-REVIEWED PUBLICATIONS**

Bhardwaj G, Mulligan VK, Bahl CD, **Gilmore JM**, Harvey PJ, Cheneval O, Buchko GW, Pulavarti SVSRK, Kaas Q, Eletsky A, Huang P, Johnsen WA, Greisen PJ, Rocklin GJ, Song Y, Linsky TW, Watkins A, Rettie SA, Xu X, Carter LP, Bonneau R, Olson JM, Coutsias E, Correnti CE, Szyperski T, Craik DJ & Baker D. Accurate *de novo* design of hyperstable constrained peptides. Nature. 2016; 538, 329-335

Boyken SE, Chen Z, Groves B, Langan RA, Oberdorfer G, Ford A, **Gilmore JM**, Xu C, DiMaio F, Pereira JH, Sankaran B, Seelig G, Zwart PH, Baker D. De novo design of protein homo-oligomers with modular hydrogen-bond network-mediated specificity. Science. 2016 May 6;352(6286):680-7

**Gilmore JM**, Milloy JA, Gerber SA. SILAC surrogates: rescue of quantitative information for orphan analytes in spike-in SILAC experiments. Anal Chem. 2013;85(22):10812-9.

**Gilmore JM**, Kettenbach AN, Gerber SA. Increasing phosphoproteomic coverage through sequential digestion by complementary proteases. Anal Bioanal Chem. 2012;402(2):711-20.

**Gilmore JM**, Greene CS, Andrews PC, Kiralis J and Moore JH. An analysis of new expert knowledge scaling methods for biologically inspired computing. Advances in Artificial Life. Darwin Meets von Neumann. Springer Berlin Heidelberg, 2011. 286-293.

Greene CS, **Gilmore JM**, Kiralis J, Andrews PC, and Moore JH. Optimal use of expert knowledge in ant colony optimization for the analysis of epistasis in human disease. In Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics. Springer Berlin Heidelberg, 2009. 92-103

**Gilmore JM**, Auberry DL, Sharp JL, White AM, Anderson KK, Daly DS. A Bayesian estimator of protein-protein association probabilities. Bioinformatics. 2008;24(13):1554-5.

**REVIEW ARTICLES**

Taylor RC, Singhal M, Daly DS, **Gilmore J**, Cannon WR, Domico K, White AM, Auberry DL, Auberry KJ, Hooker BS, Hurst G, McDermott JE, McDonald WH, Pelletier DA, Schmoyer D, Wiley HS. An analysis pipeline for the inference of protein-protein interaction networks. Int J Data Min Bioinform. 2009;3(4):409-30.

**CONFERENCE PRESENTATIONS**

**Gilmore JM,** Merrihew G, Egertson J, Bollinger J, Grewall A, Montine K, Montine T, MacCoss MJ (2017) Molecular phenotyping of Alzheimer’s disease in post-mortem-biospecimen samples via data independent acquisition

Oral presentation delivered at the American Society for Mass Spectrometry meeting, Indianapolis, IN, June, 2017

**Gilmore JM**, Fallas J, Ueda G, Baker D, and MacCoss MJ (2016). Data Independent Acquisition for the rapid screening of *de novo* protein designs

Oral presentation delivered at the Cascadia Proteomics Symposium, Seattle, WA, July, 2016

**Gilmore JM**, Fallas J, Ueda G, Baker D, and MacCoss MJ (2016). Data Independent Acquisition for the rapid screening of *de novo* protein designs

Oral presentation delivered at the American Society for Mass Spectrometry meeting, San Antonio, TX, June, 2016

**Gilmore JM** and Gerber SA (2012). Surrogate analysis of orphan analytes in Super-SILAC experiments for quantitative proteomics of tumors and tissues

Poster presentation delivered at the 11th Human Proteome Organization World Congress, Boston, MA, September, 2012.

**Gilmore JM**, Kettenbach AN and Gerber SA (2011) Increasing phosphoproteomic coverage through sequential digestion by complementary proteases

Poster presentation delivered at the American Society for Mass Spectrometry meeting, Denver, CO, July, 2011.

**Gilmore JM**, Greene CS, Andrews PC, Kiralis J and Moore JH (2009) An Analysis of New Expert Knowledge Scaling Methods for Biologically Inspired Computing

Oral presentation delivered at the 10th European Conference on Artificial Life meeting, Budapest, Hungary, September, 2009.