David C. Gemperline

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HIGHLIGHTS

Software development in C#, Perl, and Java

Extensive experience in proteomic sample preparation and development of quantitative proteomic analysis software for high resolution mass spectrometry

Experience with independent biological research designs (included next generation sequencing, genomic, proteomic, and phenotypic data analysis) and broad knowledge of computational data anlysis techniques

Knowledge of Solid software design principles and algorithmic complexity

EDUCATION

Doctor of Philosphy in Genetics, 2016
University of Wisconsin-Madison, Madison, WI

Bachelor of Arts in Chemistry and Biology, 2009
Carthage College, Kenosha, WI
GPA: 3.92/4.00, *Summa Cum Laude*

TECHNICAL SKILLS

Project lead developing a novel label-free quantitative proteomics pipeline: I developed an open-source C# command line application with a WinForms front-end to extend user friendliness.

Language experience in R, C#, Perl, Java   GitHub http://dcgemperline.github.io

Software Development Tools: Visual Studio 2017, Resharper, Git, SVN, EMACS
Knowledge: Object-Oriented and functional programming design, Test-Driven Development (TDD), OS Experience with Windows and Linux
Continued Profesional Development: Coursera - Algorithms Part I and Machine Learning by Andrew Ng

RELEVANT SKILLS

Leadership and mentoring experience
Experience working on interdisciplinary research teams
Excellent oral and written communication skills: **Invited speaker at an international Gordon Research Conference on Post-Translational Modifications**

EXPERIENCE

Postdoc Immunology - Bioinformatics Eli Lilly and Company   Oct 2016 - Present
Indianapolis, IN
Analyzed and integrated multi-omic clinical data for patient stratification using blah

Research Assistant   University of Wisconsin-Madison   Aug 2009 - Oct 2016
Madison, WI

- Performed data analysis and custom software development for biological data analysis pipelines with a focus on mass spectrometry-based label-free quantitative proteomics
- Laboratory expert on using and configuring next generation sequencing (NGS) data analysis software from Linux Command line
- Generation of transgenic plants expressing tagged epitope variants