Andrew E. Bruno

Software Engineer

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About me ——————

I'm a software engineer at the University at Buffalo Center for Computational Research, where I work with computers that are occasionally called *super*. I help organizations solve complex, computationally intensive problems and administer infrastructure both physical and in the clouds. I live perilously in the trenches between full stack web developer and DevOps engineer. I enjoy building applications from inception through deployment and running them on GNU/Linux systems with various forms of duct tape. I'm interested in privacy and owning my data, writing free software, gadgets that monitor my vital signs, and trying to be a good dad.

Skills ——————

Go, Python, Linux

Java, PHP, Perl, QML, C, C++

DevOps, Puppet, Foreman

MySQL, Redis, Elasticsearch

AWS, OpenStack administration

Full stack web development

HTML, CSS, JavaScript

Education

| 2013 | M.Sc. Bioinformatics and Biostatistics *Fusion transcript simulation and application in testing fusion discovery methods* | University at Buffalo |
| 2003 | B.Sc. Computer Science magna cum laude | University at Buffalo |

Recent Publications

| 2018 | Bruno et al. Classification of crystallization outcomes using deep convolutional neural networks | PLoS ONE |
| 2016 | Simpson et al. High-throughput sequencing of partially edited trypanosome mRNAs reveals barriers to editing progression and evidence for alternative editing | RNA |

Experience

2007-	Center for Computational Research High performance computing System administrator and Software engineer specializing in distributed systems , bioinformatics, and web development	University at Buffalo
2005-	Consulting Consultant providing custom web development and Amazon Web Services administration	Buffalo, NY
2003-2007	O'Reilly Media Software engineer developing web applications, SafariU print-on-demand publishing platform, and business intelligence software	Sebastopol, CA

Selected Projects

Xtuition

🌐 http://xtuition.org/

Developed an expert crystallization knowledge system and web-based user interface to optimize conditions and factors that drive the crystallization of macromolecular samples. Database contains more than 16 million experimental outcomes. Tech stack: Go, MariaDB, Python, Nginx, D3.js

Mokey

⭘ https://github.com/ubccr/mokey

Designed and built a self-service identity management portal for FreeIPA. Tech stack: Go, MariaDB, Redis, OAuth 2.0/OpenID Connect

Coldfront

⭘ https://github.com/ubccr/coldfront

Lead developer of an open source resource allocation system designed to provide a central portal for administration, reporting, and measuring scientific impact of HPC resources. Tech stack: Python, Django, MariaDB/PostgreSQL, Nginx, Bootstrap

Teaching/Presentations

- Course Instructor for BCH 519 Bioinformatics and Computational Biology
- Speaker at OpenStack Summit, Vancouver, BC 2018. [video]