

# Andrew E. Bruno

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## Current Position

Senior Programmer Analyst, Center for Computational Research, University at Buffalo

## Education

- M.Sc. Bioinformatics and Biostatistics, University at Buffalo, February 2013.  
Thesis: *Fusion transcript simulation and application in testing fusion discovery methods*
- B.Sc. Computer Science, University at Buffalo, June 2003.  
Honors: *magna cum laude*

## Professional Experience

*3/2007 - , Sr. Programmer Analyst, Center for Computational Research, University at Buffalo*

- Software Engineer - Provide custom software development support for faculty-led research across a wide variety of disciplines utilizing CCR's high-performance computing infrastructure. Design and implement scientific software applications for processing and analyzing Bioinformatics datasets. Provide computational and system administration support for UB Genomics and Bioinformatics Core running Illumina high throughput sequencing platforms.
- System Administrator - Design, architect, and administer the infrastructure that runs high performance Linux based compute clusters. Develop core configuration management using Puppet and automated software installations using Foreman. Maintain single sign-on and identity management systems using FreeIPA and OAuth2/OpenID connect. Develop system monitoring tools for tracking resource utilization and energy consumption. Administer private cloud infrastructure running OpenStack.

*7/2003 - 3/2007, Software Engineer, O'Reilly Media, Inc., Sebastopol, CA*

- Designed and implemented web based business intelligence and reporting tools which analyzed point of sale data for the technical book market. The applications provided O'Reilly's editorial team with vital information for deciding which books to publish in a given area of the market and helped to identify new upcoming trends in technology.
- Designed and implemented a data visualization application using Treemaps which displayed the category hierarchy and sales data for thousands of books across the technical book market in a single interface. The Treemap application was presented at several public events including the O'Reilly Open Source Convention.
- SafariU - Designed and built a print-on-demand publishing platform which enabled college professors to assemble custom text books using O'Reilly's book chapters and article content.
- Designed and implemented an internal web application which managed the workflow of all O'Reilly books from inception to editorial all the way through manufacturing, design, and marketing. The application was used by almost every department internal to O'Reilly and became an integral part of the production process.

## Publications

### Peer-reviewed

1. **Andrew E. Bruno**, Patrick Charbonneau, Janet Newman, Edward H. Snell, David R. So, Vincent Vanhoucke, Christopher J. Watkins, Shawn Williams, Julie Wilson. Classification of crystallization outcomes using deep convolutional neural networks. *PLoS ONE*, 2018. doi:10.1371/journal.pone.0198883
2. Rachel M. Simpson, **Andrew E. Bruno**, Runpu Chen, Kaylen Lott, Brianna L. Tylec, Jonathan E. Bard, Yijun Sun, Michael J. Buck, Laurie K. Read. Trypanosome RNA Editing Mediator Complex proteins have distinct functions in gRNA utilization. *Nucleic Acids Research*, 2017. doi:10.1093/nar/gkx458
3. **Andrew E. Bruno**, Alexei S. Soares, Robin L. Owen and Edward H. Snell. The use of haptic interfaces and web services in crystallography: an application for a 'screen to beam' interface. *Journal of Applied Crystallography*, 2016. doi:10.1107/S160057671601431X
4. Rachel M. Simpson, **Andrew E. Bruno**, Jonathan E. Bard, Michael J. Buck and Laurie K. Read. High-throughput sequencing of partially edited trypanosome mRNAs reveals barriers to editing progression and evidence for alternative editing. *RNA*, 2016. doi:10.1261/ma.055160.115
5. Diana Fusco, Timothy J. Barnum, **Andrew E. Bruno**, Joseph R. Luft, Edward H. Snell, Sayan Mukherjee, Patrick Charbonneau. Statistical Analysis of Crystallization Database Links Protein Physico-Chemical Features with Crystallization Mechanisms. *PLoS ONE*, 9(7): e101123, 2014. doi:10.1371/journal.pone.0101123
6. **Andrew E. Bruno**, Amanda M. Ruby, Joseph R. Luft, Thomas D. Grant, Jayaraman Seetharaman, Gaetano T. Montelione, John F. Hunt, Edward H. Snell. Comparing Chemistry to Outcome: The Development of a Chemical Distance Metric, Coupled with Clustering and Hierarchical Visualization Applied to Macromolecular Crystallography. *PLoS ONE*, 9(6): e100782, 2014. doi:10.1371/journal.pone.0100782
7. Sreevidya Sadananda Sadasiva Rao, Lori A. Shepherd, **Andrew E. Bruno**, Song Liu and Jeffrey C. Miecznikowski. Comparing imputation procedures for Affymetrix gene expression datasets using MAQC datasets. *Advances in Bioinformatics*, vol. 2013, Article ID 790567, 2013. doi:10.1155/2013/790567
8. **Andrew E. Bruno**, Jeffrey C. Miecznikowski, Maochun Qin, Jianmin Wang and Song Liu. FUSIM: a software tool for simulating fusion transcripts. *BMC Bioinformatics*, 14:13, 2013. doi:10.1186/1471-2105-14-13
9. Thomas R. Furlani, Matthew D. Jones, Steven M. Gallo, **Andrew E. Bruno**, Charng-Da Lu, Amin Ghadersohi, Ryan J. Gentner, Abani Patra, Robert L. DeLeon, Gregor von Laszewski, Lizhe Wang and Ann Zimmerman. Performance metrics and auditing framework using application kernels for high-performance computer systems. *Concurrency and Computation: Practice and Experience*, 2012. doi:10.1002/cpe.2871
10. **Andrew E. Bruno**, Li Li, James L. Kalabus, Yuzhuo Pan, Aiming Yu, Zihua Hu. miRdSNP: a database linking human disease-associated SNPs to microRNA target sites. *BMC Genomics*, 13(1):44, 2012. doi:10.1186/1471-2164-13-44
11. Zihua Hu and **Andrew E. Bruno**. The Influence of 3'UTRs on MicroRNA Function Inferred from Human SNP Data. *Comparative and Functional Genomics*, 2011:910769, 2011. doi:10.1155/2011/910769
12. Daniel P. Gaile, Lori A. Shepherd, **Andrew E. Bruno**, Song Liu, Carl D. Morrison, Lara E. Sucheston, Jeffrey C. Miecznikowski. iGenomicViewer: R package for visualisation of high dimension genomic data. *International Journal of Bioinformatics Research and Applications*, 6:584-593, 2010. doi:10.1504/IJBRA.2010.038739

### Conference Papers

1. J.U. Patel, S. J. Guercio, **A. E. Bruno**, M. D. Jones, and T. R. Furlani. Implementing Green Technologies and Practices in a High Performance Computing Center. *International Green Computing Conference*, June 2013, Arlington, VA USA.
2. J. A. Delmerico, N. A. Byrnes, **A.E. Bruno**, M. D. Jones, S. M. Gallo, and V. Chaudhary. Comparing the performance of clusters, Hadoop, and Active Disks on microarray correlation computations. In *Proc. International High Performance Computing (HiPC) Conference*, pages 378-387, 2009. doi:10.1109/HIPC.2009.5433190 (Acceptance rate: 18.8%, 49/261)

## Research Support

### Completed

- **Regulation of RNA Editing in Trypanosoma Brucei**  
*Understand the molecular mechanisms of RNA editing in kinetoplastid parasites, which cause African sleeping sickness, Chagas' disease, and leishmaniasis*  
 2R01AI061580-06A1      PI: Read, Laurie  
 National Institute of Allergy & Infectious Disease  
 08/2012 - 07/2016  
 Role: Data Analyst/Programmer
- **Western New York Stem Cell Culture and Analysis Center**  
*Provide facilities that will make it faster and more efficient for researchers currently using stem cells to generate, culture, analyze and test these cells both in vitro and in therapeutic non human models.*  
 C026714      PI: Gronostajski, Richard  
 New York State Department of Health  
 11/2011 - 10/2015  
 Role: Data Manager
- **Technology Audit and Insertion Service for TeraGrid**  
*Development of an active set of tools and services to monitor the advanced TG:XD cyberinfrastructure and insure its ability to meet the research needs of the end user as well as an advanced web-based interface to present role-specific views of audit results.*  
 OCI1025159      PI: Furlani, Thomas  
 National Science Foundation  
 07/2010 - 06/2015  
 Role: System Administrator
- **Development of An Expert Crystallization Knowledge System**  
*Development of an expert crystallization knowledge system and web-based user interface to optimize conditions and factors that drive the crystallization of macromolecular samples.*  
 1R01GM088396      PI: Snell, Edward H  
 National Institutes of Health (subcontract from Hauptman Woodward Institute)  
 01/2010 - 12/2014  
 Role: Software Engineer
- **Regulation of RNA Editing in Trypanosoma Brucei**  
*Determine the scope and mechanism of RBP16 RNA editing regulation.*  
 1R01AI061580      PI: Read, Laurie  
 National Institute of Allergy & Infectious Disease  
 02/2011 - 11/2011  
 Role: Data Analyst/Programmer
- **ARRA: NYSERDA/University at Buffalo Energy Efficiency Project: Energy Efficient Compute Servers for a High Performance Computing Environment**  
*Implementing Green IT in an HPC environment through the utilization of highly efficient compute servers.*  
 New York State Energy Research and Development Authority (NYSERDA)  
 12/2009 - 12/2010      PI: T. Furlani  
 Role: Sr. Personnel/Programmer
- **NYSERDA Data Center and Server Efficiency Proposal - Category A: Demonstration Projects**  
*Demonstration of substantial energy conservation through installation of energy efficient compute servers*  
 New York State Energy Research and Development Authority (NYSERDA)  
 09/2008 - 01/2010      PI: T. Furlani  
 Role: Sr. Personnel/Programmer

## Software

### *Coldfront*

🌐 <http://coldfront.io>

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, MySQL/PostgreSQL, Nginx, Bootstrap

### *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 from the Hauptman-Woodward Medical Research Institute (HWI) High-Throughput Crystallization Screening Center. Tech stack: Go, MySQL, Python, Nginx, D3.js

### *Mokey*

🌐 <https://github.com/ubccr/mokey>

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

### *MARCO*

🌐 <https://marco.ccr.buffalo.edu>

Founding member of MARCO (MACHINE Recognition of Crystallization Outcomes). This effort aims to collect a large collection of representative images of protein crystallization cocktails along with their metadata, and to share them with image analysis experts beyond the crystallography community. Tech stack: Go, Python, TensorFlow

### *TREAT*

🌐 <https://github.com/ubccr/treat>

Lead developer of TREAT, a multiple sequence alignment and visualization tool specifically designed to analyze variation in sequences caused by Uridine insertion/deletion RNA editing. This phenomenon occurs in trypanosomes, a group of unicellular parasitic flagellate protozoa such the subspecies of *Trypanosoma brucei* which are the causative agents of Human African Trypanosomiasis (HAT or African Sleeping Sickness). Tech stack: Go, BoltDB

### *Harrier*

🌐 <http://harrier.ccr.buffalo.edu>

Designed and built Harrier for "Screen to beam image targeting" in collaboration with Hauptman-Woodward Medical Research Institute. Harrier is a web application optimized for touch screen devices that provides a haptic interface to the visualization, classification, and notation of experimental crystallization data. Harrier links the analysis of crystallization outcomes to the subsequent diffraction analysis eliminating an initial optimization step and enabling crystallization screening plates to be analyzed in the beam efficiently. Tech stack: Python, Flask, Sqlite, MySQL

### *iquota*

🌐 <https://github.com/ubccr/iquota>

Created a set of Linux CLI tools for Isilon OneFS SmartQuota reporting. Tech stack: Go

### Cockatoo

🔗 <https://github.com/ubccr/cockatoo>

Lead developer for Cockatoo, a similarity metric for macromolecular crystallization conditions. Tech stack: Python

### FUSIM

🔗 <https://github.com/aebruno/fusim>

Developed a software tool for simulating fusion transcripts. The simulation of events known to create fusion genes and their resulting chimeric proteins is supported, including inter-chromosome translocation, trans-splicing, complex chromosomal rearrangements, and transcriptional read through events. Tech stack: Java

### miRdSNP

🔗 <http://mirdsnp.ccr.buffalo.edu>

Developed a database of disease-associated SNPs and microRNA target sites on 3'UTRs of human genes. Tech stack: PHP, MongoDB

### UBMoD

🔗 <http://ubmod.sf.net>

An open source data warehouse and web portal for mining statistical data from resource managers (TORQUE, SLURM, SGE) in high-performance computing environments. Predecessor of XDMoD. Tech stack: Java, Spring

## Teaching

- Course instructor for [BCH519 Introduction to Bioinformatics and Computational Biology](#)

## Conference and Seminar Presentations

- *Federated Keystone Single Sign-On with FreeIPA and OpenID Connect* [[video](#)]  
OpenStack Summit, Vancouver, BC, May 21, 2018.
- *SafariU custom publishing platform*  
Mark Logic User Conference, Burlingame, CA, May 24, 2006.
- *Content Analysis and Visualization using O'Reilly Books and Articles*  
Mark Logic User Conference, Burlingame, CA, June 8, 2005.

## Conferences and Workshops Attended

- OpenStack Summit Vancouver, BC, May 21–24, 2018.
- ACM International Conference on Bioinformatics and Computational Biology, Niagara Falls, New York, August 2–4, 2010.
- International Conference for High Performance Computing, Networking, Storage, and Analysis (SC07) Reno-Sparks Convention Center, November 10–16, 2007.
- O'Reilly Open Source Convention (OSCON) Portland, OR, July 24–28, 2006.
- Mark Logic User Conference, Burlingame, CA, May 23–25, 2006.
- O'Reilly Open Source Convention (OSCON) Portland, OR, August 1–5, 2005.

- Mark Logic User Conference, Burlingame, CA, June 7–9, 2005.
- MySQL Conference and Expo, Santa Clara, CA, April 18–21, 2005.
- O'Reilly Emerging Technology Conference, San Diego, CA, March 14–17, 2005.
- O'Reilly Open Source Convention (OSCON) Portland, OR, July 26–30, 2004.

Last updated: December 10, 2018