

# Andrew E. Bruno

Center for Computational Research  
SUNY at Buffalo  
New York State Center of Excellence  
in Bioinformatics & Life Sciences  
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## Current Position

Senior Programmer Analyst, Center for Computational Research, State University of New York at Buffalo

## Education

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

## Professional Experience

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

- Software Engineer (50%) - Support research groups from a wide variety of disciplines utilizing CCR's high-performance computing infrastructure. Design and implement scientific software applications for processing and analyzing Bioinformatics datasets.
- System Administrator (50%) - Administer high performance Linux based compute clusters. Perform automated software installations across thousands of nodes, maintain user account management systems (Kerberos/LDAP), develop system monitoring tools for tracking resource utilization and energy consumption. Administer private cloud infrastructure running Eucalyptus.
- Provide computational and system administration support for SUNY Buffalo's Next-Generation Sequencing and Expression Analysis Core running Illumina GAIIX for high throughput sequencing.

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

- Designed and implemented web based data visualization, graphing 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. 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
2. **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
3. 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/rna.055160.115
4. 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
5. **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
6. Sreevidya 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
7. **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
8. 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
9. **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
10. 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
11. 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

### Current

- **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

### Completed

- **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

## Teaching

- BCH519 – Introduction to Bioinformatics and Computational Biology

## Software

- mokey – FreeIPA self-service account management portal
- Harrier – Screen to beam image targeting
- TREAT – Trypanosome RNA Editing Alignment Tool
- xtuition – An expert crystallization knowledge system
- iquota – Linux CLI tools for Isilon OneFS SmartQuota reporting
- Cockatoo – A similarity metric for macromolecular crystallization conditions
- FUSIM – Software tool for simulating fusion transcripts
- miRdSNP – A database of disease-associated SNPs and microRNA target sites on 3'UTRs of human genes
- UBMoD – 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.

## Conference and Seminar Presentations

- *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

- 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.