Andrew E. Bruno

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Current Position

Assistant Director, Software Engineering, Center for Computational Research, University at Buffalo

Education

M.Sc. Bioinformatics and Biostatistics, University at Buffalo 02/2013

- Thesis: *Fusion transcript simulation and application in testing fusion discovery methods*

B.Sc. Computer Science, University at Buffalo 06/2003

- Honors: *magna cum laude*

Teaching Experience

BCH519 Bioinformatics and Computational Biology, University at Buffalo Spring 2013 - 2021

- Co-taught introductory computational biology course in a large class lab format to graduate students majoring in biochemistry, genomics, and bioinformatics. Prepared and delivered lectures, designed accompanying coding exercises and lab homework

Professional Experience

Assistant Director, Software Engineering, Center for Computational Research, University at Buffalo – Buffalo, NY 04/2025 – present

- Development, implementation, and management of HPC infrastructure, including hardware, software, and networking
- Design and deployment of high performance layer 3 data center networks using BGP, EVPN, VXLAN
- Lead software engineering and project management of high-impact research projects that require HPC resources
- Collaborate with researchers across disciplines to facilitate faculty-led research

Senior Systems Administrator, Center for Computational Research, University at Buffalo – Buffalo, NY 03/2007 – 04/2025

- Design, architect, and administer the infrastructure that runs large high performance Linux based compute clusters. Administer Slurm workload manager.
- 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 using Prometheus and Grafana
- Provide computational and system administration support for UB Genomics and Bioinformatics Core running Illumina high throughput sequencing platforms
- Administer private cloud infrastructure running OpenStack

Software Engineer, O'Reilly Media – Sebastopol, CA 07/2003 – 03/2007

- 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.
- 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

1. **Andrew E. Bruno**, Dori Sajdak. ColdFront: Resource Allocation Management System. *In Practice and Experience in Advanced Research Computing (PEARC '21)*. Association for Computing Machinery, New York, NY, USA, 1-5, 2021. doi:10.1145/3437359.3465585
2. **Andrew E. Bruno**, Salvatore J. Guercio, Doris Sajdak, Tony Kew, and Matthew D. Jones. Grendel: Bare Metal Provisioning System for High Performance Computing. *In Practice and Experience in Advanced Research Computing (PEARC '20)*. Association for Computing Machinery, New York, NY, USA, 13-18, 2020. doi:10.1145/3311790.3396637
3. **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
4. 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
5. **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
6. 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
7. 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
8. **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 Hierarchal Visualization Applied to Macromolecular Crystallography. *PLoS ONE*, 9(6): e100782, 2014. doi:10.1371/journal.pone.0100782
9. 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.
10. 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
11. **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
12. 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
13. **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
14. 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
15. 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

16. 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)

Conference and Seminar Presentations

Expanding Research Computing to Multiple Data Centers October 16, 2025
Campus Research Computing Consortium (CaRCC), Systems-Facing Track 📹

XDMoD, ColdFront, OnDemand HPC Toolset Overview September 15, 2022
Campus Research Computing Consortium (CaRCC), Systems-Facing Track 📹

ColdFront: Resource Allocation Management System July 20, 2021
Practice & Experience in Advanced Research Computing (PEARC) ’21, Boston, MA 📹

HPCSYSPROS SC20 Workshop Panel: Cluster Management November 13, 2020
SIGHPC Systems Professionals Workshop, Super Computing ’20, Atlanta, GA

Grendel: Bare Metal Provisioning System for High Performance Computing July 29, 2020
Practice & Experience in Advanced Research Computing (PEARC) ’20, Portland, OR 📹

Federated Keystone Single Sign-On with FreeIPA and OpenID Connect May 21, 2018
OpenStack Summit, Vancouver, BC 📹

Research Experience

POSE: Phase I: ColdFront: HPC Community Allocation & Resource Ecosystem (HPC CARE) 07/2025 - 06/2026

The University at Buffalo Center for Computational Research has developed an open source software tool for managing the access and allocations for cyberinfrastructure resources. This proposal aims to scope out the next steps required to transition this software project into an open source ecosystem

- Role: Co-PI
- National Science Foundation
- Award #: 2517857 PI: Sajdak, Doris

Advanced CI Coordination Ecosystem: Monitoring and Measurement Services 05/2022 - 04/2027

This project builds upon and expands XDMoD, the cyberinfrastructure measurement and optimization tools which serve as the foundation for measuring and monitoring services for the large NSF investment in the Advanced Cyberinfrastructure Coordination Ecosystem: Services & Support program

- Role: Key Personnel/Systems Administrator
- National Science Foundation
- Award #: 2137603 PI: Furlani, Thomas

High-Resolution Molecular Recognition of Ligands using Solution X-Ray Scattering 08/2019 - 07/2023

Develop a collection of new algorithms combining solution scattering with structural information obtained by methods such as crystallography for the determination of high-resolution structure and dynamics of protein-ligand complexes in solution

- Role: Key Personnel/Software Engineer
- National Institutes of Health / NIGMS
- Award #: R01GM133998 PI: Grant, T.D.

Frameworks: Software - Open OnDemand 2.0: Advancing Accessibility and Scalability for Computational Science through Leveraged Software Cyberinfrastructure 11/2018 - 10/2023

The project develops Open OnDemand 2.0, an open-source software that enables access to high-performance computing, cloud, and remote computing resources via the web, and lower the barriers to access HPC systems

- Role: Key Personnel/Systems Administrator
- National Science Foundation
- Award #: 1835725 PI: Hudak, David

Regulation of RNA Editing in Trypanosoma Brucei 08/2012 - 07/2016

Understand the molecular mechanisms of RNA editing in kinetoplastid parasites, which cause African sleeping sickness, Chagas' disease, and leishmaniasis.

- Role: Key Personnel/Software Engineer
- National Institute of Allergy & Infectious Disease
- Award #: 2R01AI061580-06A1 PI: Read, Laurie

Western New York Stem Cell Culture and Analysis Center 11/2011 - 10/2015

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.

- Role: Key Personnel/Data Manager
- New York State Department of Health
- Award #: C026714 PI: Gronostajski, Richard

Technology Audit and Insertion Service for TeraGrid 07/2010 - 06/2015

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.

- Role: Key Personnel/System Administrator
- National Science Foundation
- Award #: 1025159 PI: Furlani, Thomas

Development of An Expert Crystallization Knowledge System 01/2010 - 12/2014

Development of an expert crystallization knowledge system and web-based user interface to optimize conditions and factors that drive the crystallization of macromolecular samples.

- Role: Key Personnel/Software Engineer
- National Institutes of Health (subcontract from Hauptman Woodward Institute)
- Award #: 1R01GM088396 PI: Snell, Edward H

NYSERDA Data Center and Server Efficiency Proposal - Category A: Demonstration Projects 09/2008 - 12/2010

Demonstration of substantial energy conservation through installation of energy efficient compute servers

- Role: Key Personnel/Programmer
- New York State Energy Research and Development Authority (NYSERDA)
- PI: T. Furlani

Software

ColdFront - HPC Resource Allocation System coldfront.dev

- 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

Grendel - Bare Metal Provisioning system github.com/ubccr/grendel

- Lead developer of an open source bare metal provisioning system for high performance computing
- Tech Stack: Go, sqlite

MARCO - MAchine Recognition of Crystallization Outcomes marco.ccr.buffalo.edu

- Founding member of MARCO. 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

Mokey - Self-service Identity Management Portal github.com/ubccr/mokey

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

DENSSWeb - DENsity from Solution Scattering (DENSS) web front-end denss.ccr.buffalo.edu

- Designed and built a web based front end for DENSS, an algorithm used for calculating ab initio electron density maps directly from solution scattering data allowing users to run complex DENSS pipelines and view results interactively via a browser.
- Tech Stack: Go, Python, LiteMol

TREAT - Trypanosome RNA Editing Alignment Tool 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

Xtuition - Expert Crystallization Knowledge System 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

Professional Affiliations

Research Computing Facilitator, Campus Champions 2020 - present

Last updated: October 22, 2025