JAROSLAW **ZOLA**

University at Buffalo, SUNY
Department of Computer Science and Engineering
Department of Biomedical Informatics
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Research Interests

Addressing challenging problems, and accelerating scientific discovery through:

- Development of scalable algorithms and software for big data in life sciences
- Novel bioinformatics methods in the context of next-gen sequencing technologies
- High performance, parallel and distributed computing on emerging architectures
- Data driven large-scale scientific computing

Education

2002 - 2005: Ph.D. in Computer Science (these en cotutelle)
Grenoble Institute of Technology, Grenoble, France

2001 - 2005: Ph.D. in Computer Science
Czestochowa University of Technology, Czestochowa, Poland

2000: Study abroad (Computer Science, Erasmus Program)
Grenoble Institute of Technology, Grenoble, France

1996 - 2001: M.Sc. in Computer Science
Czestochowa University of Technology, Czestochowa, Poland
Specialization: Software Engineering and Information Systems

Professional Experience

Aug 2014 - present: Assistant Professor
Department of Computer Science and Engineering
Department of Biomedical Informatics
University at Buffalo, Buffalo, NY

Oct 2012 – Aug 2014:	Associate Research Professor Department of Electrical and Computer Engineering Rutgers Discovery Informatics Institute Rutgers University, Piscataway, NJ
Aug 2010 – Oct 2012:	Research Assistant Professor Department of Electrical and Computer Engineering Iowa State University, Ames, IA
Jun 2006 – Aug 2010:	Postdoctoral Research Associate Department of Electrical and Computer Engineering Iowa State University, Ames, IA
Nov 2001 – Jun 2006:	Research Assistant Institute of Computer and Information Sciences Czestochowa University of Technology, Czestochowa, Poland

Honors and Awards

2018:	Early Career Faculty Teaching Award, Department of Computer Science and Engineering, University at Buffalo
2012:	IEEE Senior Member
2007:	Best paper award nomination, ACM/IEEE Supercomputing Conference
2002:	Ph.D. scholarship award of the French government

Research Grants

Current

1. Co-PI, NSF, "OAC Core: Small: Scalable Non-linear Dimensionality Reduction Methods to Accelerate Scientific Discovery." Duration 36mos. Starting date: 05/01/2019. Amount: $499,814.
2. PI, NSF, "CAREER: Scalable Software and Algorithmic Infrastructure for Probabilistic Graphical Modeling." Duration 60 mos. Starting date: 02/15/2019. Amount: $487,569.
3. PI, XSEDE, "Scalable Algorithms for Bayesian Graphical Modeling." Duration 12 mos. Starting date: 06/01/2018. Resource Allocation: 1,600 node-hours.
4. PI, NSF, "Collaborative Research: Mentoring the Next Generation of Parallel Processing Researchers at IPDPS and other IEEE-CSTCPP Sponsored Conferences." Duration 12 mos. Starting date 05/01/2018. Amount $25,000.
5. Co-I, NIH, "Buffalo Clinical and Translational Research Center." Duration 43 mos. Starting date: 08/12/2015. Amount: $13,151,902.

Completed

6. Co-PI, VA, "Precision Oncology Tumor Board." Duration 13 mos. Starting date: 09/01/2017. Amount: $985,630.
7. PI, UB IMPACT, "OneBioStore: Distributed Smart Storage and Scalable Algorithms for Collaborative Biomedical Discovery." Duration: 12 mos. Starting date: 09/01/2016. Amount: $18,560.
8. PI, NSF/CCF, "Student Travel Support: ACM International Workshop on Big Data in Life Sciences, Seattle, WA, October 2, 2016." Duration: 12 mos. Starting date: 07/01/2016. Amount: $10,000.
9. PI, NSF/CBET, "Collaborative Research: CDS&E: Sculpting Fluid Flow Using a Programmed Sequence of Micro-pillars." Duration: 36 mos. Starting date: 09/01/2013. Amount: $59,842 plus $8,000 REU Supplement.
10. PI, AWS Cloud Credits for Research, "Long DNA reads analysis in Amazon cloud." Amazon Cloud Resource Allocation, Duration: 12 mos. Starting date: 04/01/2016. Amount: $10,000.
11. Co-PI, NSF/IIS, "BIGDATA: Mid-Scale: DA: Collaborative Research: Genomes galore – Core Techniques, Libraries, and Domain Specific Languages for High-throughput DNA Sequencing." Duration: 36 mos. Starting date: 01/01/2013. Amount: $1,300,000.
12. PI, Argonne Leadership Computing Facility, "ELaSTIC – Similarity Graphs from Large-scale Biological Sequence Collections." Mira Supercomputer Resource Allocation, Duration: 12 mos. Starting date: 01/01/2015. Amount: 2M core-hours.
13. PI, NSF/CCF, "Collaborative Research: Student travel support: International Workshop on Big Data in Life Sciences, Newport Beach, CA, September 20, 2014." Duration: 12 mos. Starting date: 09/01/2014. Amount: $10,000.
14. PI, NSF/IIP (sub-award from Optimal Solutions, Inc.), "STTR Phase I: Using Big Data to Support Supply Chain Analytics and Optimization." Duration: 12 mos. Starting date: 01/01/2014. Amount: $112,500.

Publications and Talks

† – joint first authors.

Journal Publications

1. P. Du, A. Zebrowski, **J. Zola**, B. Ganapathysubramanian, O. Wodo, "Microstructure Design Using Graphs", Nature Computational Materials, 4(50), 2018. DOI: s41524-018-0108-5
2. O. Wodo, **J. Zola**, B.S.S. Pokuri, P. Du, B. Ganapathysubramanian, "Automated, High Throughput Exploration of Process-structure-property Relationships Using the MapReduce Paradigm," Materials Discovery, 1, pp. 21-28, 2015. DOI: 10.1016/j.md.2015.12.001

3. N. Clauvelin, P. Lo, O. I. Kulaeva, E.V. Nizovtseva, J. Diaz-Montes, **J. Zola**, M. Parashar, V.M. Studitsky, W.K. Olson, "Nucleosome Positioning and Composition Modulate In Silico Chromatin Flexibility," Journal of Physics: Condensed Matter, 27(6):064112, 2015. DOI: 10.1088/0953-8984/27/6/064112 PMID: 25564155

4. S.K. Samudrala, **J. Zola**, S. Aluru, B. Ganapathysubramanian, "Parallel Framework for Dimensionality Reduction of Large-Scale Datasets," Scientific Programming, 2015. DOI: 10.1155/2015/180214

5. J. Diaz-Montes, B. Ganapathysubramanian, M. Parashar, I. Rodero, Y. Xie, **J. Zola**: "Federated Computing for the Masses – Aggregating Resources to Tackle Large-scale Engineering Problems," IEEE Computing in Science & Engineering, 16(4), pp. 62–72, 2014. DOI: 10.1109/MCSE.2013.134

6. O. Nikolova, **J. Zola**, S. Aluru: "Parallel Globally Optimal Structure Learning of Bayesian Networks," Journal of Parallel and Distributed Computing, 73(8), pp. 1039–1048, 2013. DOI: 10.1016/j.jpdc.2013.04.001

7. X. Yang†, **J. Zola†**, S. Aluru: "Large-Scale Metagenomic Clustering on Map-Reduce Clusters," Journal of Bioinformatics and Computational Biology, 11(1):1340001, 2013. DOI: 10.1142/S0219720013400015 PMID: 23427983

8. M. Aluru†, **J. Zola†**, D. Nettleton, S. Aluru: "Reverse Engineering and Analysis of Large Genome-Scale Gene Networks," Nucleic Acids Research, 41(1):e24, 2013. DOI: 10.1093/nar/gks904 PMID: 23042249

9. A. Sarje†, **J. Zola†**, S. Aluru: "Accelerating Pairwise Computations on Cell Processors," IEEE Transactions on Parallel and Distributed Systems, 22(1), pp. 69–77, 2011. DOI: 10.1109/TPDS.2010.65

10. X. Yu, L. Li, **J. Zola**, M. Aluru, H. Ye, A. Foudree, H. Guo, S. Anderson, S. Aluru, P. Liu, S. Rodermel, Y. Yin: "A Brassinosteroid Transcriptional Network Revealed by Genome-Wide Identification of BESI Target Genes in Arabidopsis thaliana," Plant Journal, 65(4), pp. 634–646, 2011. DOI: 10.1111/j.1365-313X.2010.04449.x PMID: 21214652

11. **J. Zola**, M. Aluru, A. Sarje, S. Aluru: "Parallel Information-Theory-Based Construction of Genome-Wide Gene Regulatory Networks," IEEE Transactions on Parallel and Distributed Systems, 21(12), pp. 1721–1733, 2010. DOI: 10.1109/TPDS.2010.59

12. M. Aluru, **J. Zola**, A. Foudree, S.R. Rodermel: "Chloroplast Photooxidation Induced Transcriptome Reprogramming in Arabidopsis immutans White Leaf Sectors," Plant Physiology, 150(2), pp. 904–923, 2009. DOI: 10.1104/pp.109.135780 PMID: 19386811

13. M. Ott, **J. Zola**, S. Aluru, A.D. Johnson, D. Janies, A. Stamatakis: "Large Scale Phylogenetic Analysis on Current HPC Architectures," Scientific Programming, 16(2-3), pp. 255–270, 2008. DOI: http://dx.doi.org/10.3233/SPR-2008-0247

14. D. Trystram, G. Parmentier, **J. Zola**: "Large Scale Multiple Sequence Alignment with Simultaneous Phylogeny Inference," Journal of Parallel and Distributed Computing, 66(12), pp. 1534–1545, 2006. DOI: 10.1016/j.jpdc.2006.03.003

Peer-reviewed Conference Publications

15. S. Karan, M. Eichhorn, B. Hurlburt, G. Iraci, **J. Zola**, "Fast Counting in Machine Learning Applications," In Proc. of Conference on Uncertainty in Artificial Intelligence (UAI 2018), 2018. arXiv: 1804.04640

16. S. Karan, **J. Zola**: "Scalable Exact Parent Sets Identification in Bayesian Networks Learning with Apache Spark," In Proc. of IEEE Int. Conference on High Performance Computing, Data, and Analytics (HiPC 2017), pp. 33–41, 2017. DOI: 10.1109/HiPC.2017.00014

17. F. Schoeneman, S. Mahapatra, V. Chandola, N. Napp, **J. Zola**, "Error Metrics for Learning Reliable Manifolds from Streaming Data," In Proc. of SIAM International Conference on Data Mining (SDM 2017), pp. 750–758, 2017. DOI: 10.1137/1.9781611974973.84

18. S. Karan, **J. Zola**: "Exact Structure Learning of Bayesian Networks by Optimal Path Extension," In Proc. of IEEE Int. Conference on Big Data (BigData), pp. 48–55, 2016. DOI: 10.1109/BigData.2016.7840588

19. R. Nihalani, **J. Zola**, S. Aluru: "Resolving Read Assignment Ambiguities in Metagenomic Clustering," In Proc. of ISCA Int. Conference on Bioinformatics and Computational Biology (BICoB 2013), 2013.

20. X. Yang, **J. Zola**, S. Aluru: "Parallel Metagenomic Sequence Clustering via Sketching and Maximal Quasi-Clique Enumeration on Map-Reduce Clouds," In IEEE Proc. of Int. Parallel and Distributed Processing Symposium (IPDPS 2011), pp. 1210–1220, 2011. DOI: 10.1109/IPDPS.2011.116

21. **J. Zola**†, A. Sarje†, S. Aluru: "Constructing Gene Regulatory Networks on Clusters of Cell Processors," In IEEE Proc. of Int. Conference on Parallel Processing (ICPP 2009), pp. 108–115, 2009. DOI: 10.1109/ICPP.2009.35

22. O. Nikolova, **J. Zola**, S. Aluru: "Parallel Algorithm for Exact Bayesian Network Inference," In IEEE Proc. of Int. Conference on High Performance Computing (HiPC 2009), pp. 342–349, 2009. DOI: 10.1109/HIPC.2009.5433194

23. **J. Zola**, M. Aluru, S. Aluru: "Parallel Information-Theory-Based Construction of Gene Regulatory Networks," In Proc. of Int. Conference on High Performance Computing (HiPC 2008), LNCS vol. 5374, pp. 336–349, 2008. DOI: 10.1007/978-3-540-89894-8_31

24. M. Ott, **J. Zola**, S. Aluru, A. Stamatakis: "Large Scale Maximum Likelihood-Based Phylogenetic Analysis on the IBM BlueGene/L," In Proc. of ACM/IEEE Supercomputing Conference (SC 2007), 2007 **(best paper finalist)**. DOI: 10.1145/1362622.1362628

25. **J. Zola**, X. Yang, S. Rospondek, S. Aluru: "Parallel T-Coffee: A Parallel Multiple Sequence Aligner," In Proc. of ISCA Int. Conference on Parallel and Distributed Computing and Systems (PDCS 2007), pp. 248–253, 2007.

26. D. Trystram, **J. Zola**: "Parallel Multiple Sequence Alignment with Decentralized Cache Support," In Proc. of Int. European Conference on Parallel and Distributed Computing (Euro-Par 2005), LNCS vol. 3648, pp. 1217–1226, 2005. DOI: 10.1007/11549468_133

27. G. Parmentier, D. Trystram, **J. Zola**: "Cache-Based Parallelization of Multiple Sequence Alignment Problem," In Proc. of Int. European Conference on Parallel and Distributed Computing (Euro-Par 2004), LNCS vol. 3149, pp. 1005–1012, 2004. DOI: 10.1007/978-3-540-27866-5_135

28. **J. Zola**, L. Lacinski, R. Wyrzykowski: "An Object-Oriented Library for Evolution Programs with Applications for Partitioning of Finite Element Meshes," IUTAM Symp. on Evolutionary Methods in Mechanics, Solid Mechanics and its Applications, vol. 117, pp. 351–360, 2004.

29. R. Wyrzykowski, A. Tomas, K. Karczewski, **J. Zola**, T. Kuczynski: "Development, Administration and Use of Eltoro Cluster," In Proc. of Pionier 2002, pp. 273–280, 2002 (in Polish).

30. **J. Zola**, R. Wyrzykowski: "EPL-Julia, the High Performance Library for Evolutionary Computations," In Proc. of Int. Conference on Parallel Processing and Applied Mathematics (PPAM 2001), LNCS vol. 2328, pp. 633–639, 2002. DOI: 10.1007/3-540-48086-2_72

Peer-reviewed Workshop Publications

31. S. Ko, L. Sassoubre, **J. Zola**: "Applications and Challenges of Real-time Mobile DNA Analysis," In Proc. of ACM Int Workshop on Mobile Computing Systems and Applications (HotMobile 2018), pp. 1-6, 2018. DOI: 10.1145/3177102.3177114

32. **J. Zola**: "Constructing Similarity Graphs from Large-scale Biological Sequence Collections," In Proc. of IEEE Int. Workshop on High Performance Computational Biology (HiCOMB 2014), pp. 500–507, 2014. DOI: 10.1109/IPDPSW.2014.63

33. J. Diaz-Montes, Y. Xie, I. Rodero, **J. Zola**, B. Ganapathysubramanian, M. Parashar: "Exploring the Use of Elastic Resource Federations for Enabling Large-Scale Scientific Workflows," In Proc. of Workshop on Many-Task Computing on Clouds, Grids, and Supercomputers (MTAGS 2013), 2013 **(best paper finalist)**.

34. **J. Zola**, D. Trystram, A. Tchernykh, C. Brizuela: "Parallel Multiple Sequence Alignment with Local Phylogeny Search by Simulated Annealing," In Proc. of IEEE Int. Workshop on High Performance Computational Biology (HiCOMB 2006), 2006. DOI: 10.1109/IPDPS.2006.1639536

Book Chapters

35. **J. Zola**: "Parallel Computing for Gene Networks Reverse Engineering," Chapter in "Approaches in Integrative Bioinformatics – Towards Virtual Cell," M. Chen, R. Hofestaedt (eds.), Springer, 2014. DOI: 10.1007/978-3-642-41281-3_12

36. **J. Zola**, S. Aluru: "Network Inference in Systems Biology," Chapter in "Encyclopedia of Parallel Computing," D. Padua (ed.), Springer, 2011. DOI: 10.1007/978-0-387-09766-4_466

37. A. Sarje, **J. Zola**, S. Aluru: "Pairwise Computations on the Cell Processor with Applications in Computational Biology," Chapter in "Scientific Computing with Multicores and Accelerators," J. Kurzak, D.A. Bader, J. Dongarra (eds.), Chapman & Hall/CRC, 2010.

38. D. Trystram, **J. Zola**: "Multiple Sequence Alignment and Phylogenetic Inference," Chapter in "Grids for Bioinformatics and Computational Biology," A. Zomaya, E. Talbi (eds.), John Wiley & Sons, 2007. DOI: 10.1002/9780470191637.ch6

Edited Proceedings

39. A. Kalyanaraman, **J. Zola**, D.A. Bader, S. Aluru (eds.): "Proceedings of the Fifteenth IEEE International Workshop on High Performance Computational Biology (HiCOMB 2016)," IEEE Computer Society, 2016.

40. **J. Zola**, D.A. Bader, S. Aluru (eds.): "Proceedings of the Twelfth IEEE International Workshop on High Performance Computational Biology (HiCOMB 2013)," IEEE Computer Society, 2013.

41. D.A. Bader, D. Trystram, **J. Zola** (eds.): "Proceedings of the Parallel Bio-Computing Workshop (PBC 2005)," Springer Verlag, 2005.

Technical Reports

42. J. Diaz-Montes, B. Ganapathysubramanian, M. Parashar, I. Rodero, Y. Xie, **J. Zola**: "Federated Computing for the Masses – Aggregating Resources to Tackle Large-scale Engineering Problems," Tech. Report, Rutgers Discovery Informatics Institute, TR-RDI2-20130515-0, 2013.

Invited Talks and Lectures

1. Invited talk: "Big Data Analytics." Presented at UB CTSI Biomedical Informatics Workshop Series, October 2017.
2. Invited talk: "Sketching Biological Sequences for Storage and Computation." Presented at Workshop on Parallel Software Libraries for Sequence Analysis (pSALSA) in Seattle, October 2016.
3. Invited talk: "Parallel Computing for Large-scale Computational Biology." Presented at Pharmacology and Toxicology Seminar Series at University at Buffalo, October 2015.
4. Invited talk: "Similarity Detection in Large Sequence Collections." Presented at Workshop on Parallel Software Libraries for Sequence Analysis (pSALSA) in Atlanta, September 2015.
5. Three-hours tutorial: "How to Find Who Lives in Your Belly Button: Not Too Short Introduction to Metagenomics." Presented at DIMACS Center for Discrete Mathematics and Theoretical Computer Science, June 2014.
6. Invited talk: "Constructing Similarity Graphs from Large-scale Biological Sequence Collections." Presented at Drexel University, March 2013.
7. Panelist: "Big Data Standards and the Potential Long Term Benefits for Research and Clinical Development." Webinar organized by NGSLeaders, December 2012.
8. Invited talk: "Large Scale Metagenomic Clustering." Presented at International Conference on the Bioinformatics of Genome Regulation and Structure/Systems Biology in Novosibirsk, Russia, June 2012.
9. Three-hours tutorial: "Not Too Short Introduction to Metagenomics." Presented at Czestochowa University of Technology, Poland, December 2011.

10. Invited talk: “Computational Biology: Can We Do Without Parallel Computing?” Presented at Corporacion Universitaria para el Desarrollo de Internet meeting in Puebla, Mexico, April 2009.
11. Invited lectures: “Introduction to Bioinformatics.” and “High Performance Computational Biology.” Presented at Pannon University, Hungary, May 2006.
12. Two-hours talk with Denis Trystram: “Bio-Computing Today: What to Expect from Parallel and Distributed Systems?” Presented at 4th Franco-Mexican School on Distributed Systems in Grenoble, France, July 2005.
13. Seminar: “Parallel Server for Large Scale Multiple Sequence Alignment.” Presented at Poznan University of Technology, Institute of Computing Science, Poland, May 2005.
14. Invited talk with Roman Wyrzykowski and Tomasz Olas: “Parallel FEM Computations on PC-Based Cluster Using Myrinet.” Presented at Myrinet User’s Group Conference in Vienna, Austria, May 2002.

Teaching

Curriculum Development

1. CSE/BMI 577 “Processing of Strings and Sequences,” University at Buffalo.
2. CSE 470/570 “Introduction to Parallel and Distributed Processing,” University at Buffalo.
3. BMI 503 “Biomedical Informatics Systems, Databases and Software Methods,” University at Buffalo.

Courses Taught

1. CSE/BMI 577 “Processing of Strings and Sequences,” University at Buffalo, Spring 2019.
2. CSE 470/570 “Introduction to Parallel and Distributed Processing,” University at Buffalo, Fall 2017, Fall 2018.
3. BMI 503 “Biomedical Informatics Systems, Databases and Software Methods,” University at Buffalo, Fall 2015, Fall 2016, Fall 2017, Fall 2018.
4. CSE 250 “Data Structures in C++,” University at Buffalo, Spring 2015, Fall 2016, Spring 2018.
5. CSE 603 “Parallel and Distributed Processing,” University at Buffalo, Fall 2015.
6. CprE 426/526 “Introduction to Parallel Algorithms and Programming” (co-instructor), Iowa State University, Spring 2011 and 2012.
7. CS Graduate Level “Introduction to High Performance Computing,” Czestochowa University of Technology, Spring 2006.
8. CS Undergraduate Level “Computer Languages and Programming Methods,” Czestochowa University of Technology, Spring 2001-2005.

9. CS Undergraduate Level "Selected Topics in Combinatorial Optimization," Czestochowa University of Technology, Fall 2001.

Mentoring

Postdoctoral Supervisor

1. Vamsi Krishna Potluru (co-supervised with Manish Parashar), Rutgers University, 2014.

Ph.D. Advisor

2. Subhadeep Karan, University at Buffalo, 2015-present.
3. Frank Schoeneman, University at Buffalo, 2015-present.
4. Vicky Zheng, University at Buffalo, 2016-present.

M.Sc. Advisor

5. Marc Greenbaum, Thesis: "GPGPU–Based Fast Counting in Machine Learning Applications," University at Buffalo, 2018-2019.
6. Vinay Ashokkumar, Independent study, University at Buffalo, 2016.
7. Kushal Bhandari, Independent study, University at Buffalo, 2016.
8. Jeban Ephrim Gnanaraj Kanagarajan, Independent study, University at Buffalo, 2016.
9. Ajay Sudhakar Deshpande, Independent study, University at Buffalo, 2015-2016.
10. Dhanasekar Karuppasamy, Independent study, University at Buffalo, 2015-2016.
11. Piotr Dziubecki, Thesis: "A User-Oriented Grid Portal For Large Scale Multiple Sequence Alignment," Czestochowa University of Technology, 2005-2006.
12. Adrian Rospondek, Thesis: "Parallel-*-Coffee: Parallel Implementation of 3D/T-Coffee Method," Czestochowa University of Technology, 2005-2006.
13. Malgorzata Sikorska, Thesis: "A Practical Comparison of 2PC and 3PC Mechanisms for Distributed Databases," Czestochowa University of Technology, 2005-2006.
14. Monika Zagala, Thesis: "Rational Arithmetic of High Precision for C++," Czestochowa University of Technology, 2005-2006.

Thesis Committee

1. Pavan Kumar Behara, University at Buffalo.
2. Wei Zheng, University at Buffalo, 2019.

3. Suchismit Mahapatra, University at Buffalo, 2018.
4. Sai Kiranmayee Samudrala, Iowa State University, 2012.

Outreach Activities

Undergraduate Mentoring

1. Timothy Chase, Research Internship, University at Buffalo, 2019.
2. Patrick Iwaszko, Research Internship, University at Buffalo, 2019.
3. Michael Klein, Research Internship, University at Buffalo, 2019.
4. Manmeet Singh, Research Internship, University at Buffalo, 2019.
5. Feng-Mao Tsai, Research Internship, University at Buffalo, 2018.
6. Daniel Bosah, Research Internship, University at Buffalo, 2018.
7. Jon Goodrum, Research Internship, University at Buffalo, 2017.
8. Matthew Eichhorn, Research Internship, University at Buffalo, 2016-2017.
9. Blake Hurlburt, Research Internship, University at Buffalo, 2016-2017.
10. Grant Iraci, Research Internship, University at Buffalo, 2016-2017.
11. Jacob Ekstrum, Research Internship, University at Buffalo, 2016-2017.
12. Adithya Narayanan, Research Internship, University at Buffalo, 2016.
13. Ashish Tyagi, Research Internship, University at Buffalo, 2015-2016.
14. Paul Kowalski, NSF REU, University at Buffalo, 2015-2016.
    (CSE Undergraduate Research Award, 2016)
15. Vicky Zheng, Research Internship, University at Buffalo, 2015-2016.
    (CSE Undergraduate Research Award, 2016)
16. William Spoth, Research Internship, University at Buffalo, 2015.
17. David Bryant, Research Internship, University at Buffalo, 2015.
18. Hannah Graesser, Summer Research Internship, Canisius College, 2015.
19. Manikandan Sundararajan, Research Internship, University at Buffalo, 2015.
20. Vidita Gawade, Aresty Summer Research Program, Rutgers University, 2014.
21. Kush Oza, NSF REU, Rutgers University, 2014.
22. Dylan Quinta, NSF REU, Carnegie Mellon University, 2014.
23. Mariam Tsilosani, NSF REU, Rutgers University, 2014.
24. Walter Hummel, Aresty Research Assistant Program, Rutgers University, 2013-2014.
25. Alexio Mota, Aresty Research Assistant Program, Rutgers University, 2013-2014.

Early Education and K12 Outreach

1. Presenter, The Eric Pitman Annual Summer Workshop in Computational Science, Center for Computational Research, 2015-2018.
2. Instructor, Liberty Partnerships Program, University at Buffalo, 2015-2018.
3. Group Leader, "Science is Elementary" Outreach Program Westminster Community Charter School, Buffalo, 2014-2015.
4. Advisor, Chaitanya Aluru, "Research Internship in Bioinformatics and Computational Biology," Ames High School, IA (Extended Learning Program), 2011-2012.

Professional Service and Activities

Advisory Functions

1. Panelist, Gryphon Scientific/AAAS/FBI Roundtable on Enhancing the Research and Educational Environment at U.S. Universities, 2015.
2. Member, AAAS/FBI Working Group on Big Data in Life Sciences and National Security, 2014.

Organizing Committees

1. Founding co-chair, ACM International Workshop on Big Data in Life Sciences (BigLS).
2. Founding co-chair, Parallel Bio-Computing Workshop (PBC).
3. Workshops vice-chair, IEEE International Parallel and Distributed Processing Symposium (IPDPS), 2018 and 2019.
4. Advancing Algorithms and Methods track co-chair, ACM Conference on Bioinformatics, Computational Biology and Biomedical Informatics (ACM BCB), 2017.
5. Student travel award co-chair, ACM Conference on Bioinformatics, Computational Biology and Biomedical Informatics (ACM BCB), 2016.
6. Program chair, IEEE International Workshop on High Performance Computational Biology (HiCOMB), 2013 and 2016.
7. Co-organizer, ACM/IEEE Supercomputing workshop: Computational and Data Challenges in Genomic Sequencing, 2015.
8. Publicity chair, IEEE International Conference on Computational Advances in Bio and Medical Sciences (ICCABS), 2013.
9. Publicity co-chair, ISCA International Conference on Bioinformatics and Computational Biology (BICoB), 2013.
10. Co-organizer, IEEE Cluster Workshop: Parallel Programming and Applications on Accelerator Clusters (PPAAC), 2010.

Program Committees

1. International Conference on Parallel Processing and Applied Mathematics (PPAM), 2013, 2015, 2017 and 2019.
2. IEEE International Parallel and Distributed Processing Symposium (IPDPS), 2015, 2016 and 2018.
3. IEEE International Conference on High Performance Computing (HiPC), 2015, 2017 and 2018.
4. International Symposium on Computer Architecture and High Performance Computing (SBAC-PAD), 2013, 2016, 2017 and 2018.
5. ISCA International Conference on Bioinformatics and Computational Biology (BICoB), 2012 and 2018.
6. ACM Conference on Bioinformatics, Computational Biology and Biomedical Informatics (ACM BCB), 2013, 2015 and 2016.
7. Workshop on Accelerator-Enabled Algorithms and Applications in Bioinformatics (WACEBI), 2016.
8. International Workshop on Data Intensive Distributed Computing (DIDC), 2016.
9. ACM/IEEE Supercomputing, Posters Committee, 2015.
10. IEEE Cluster 2015.
11. IEEE International Workshop on Foundations of Big Data Computing, 2015.
12. International Conference on Parallel Processing (ICPP), 2012 and 2014.
13. ASE/IEEE International Conference on Big Data, 2013 and 2014.
14. International Conference on Contemporary Computing (IC3), 2011 and 2014.
15. IEEE International Conference on Parallel and Distributed Systems (ICPADS), 2012 and 2013.
16. Workshop on Using Emerging Parallel Architectures (WEPA) 2009, 2010 and 2012.
17. ACM/IEEE Supercomputing, 2008.

Referee

Proposals

1. National Science Foundation, 2016, 2017, 2018.
2. Great Lakes Consortium for Petascale Computation, 2015-2018.
3. Israeli Ministry of Science, 2018.
4. AAAS Peer Review Committee for KACST, 2014.
5. Austrian Science Fund, 2013.
6. Polish National Science Centre, 2013.

Journals

1. IEEE Transactions on Parallel and Distributed Systems
2. Journal of Parallel and Distributed Computing
3. ACM Transactions on Parallel Computing
4. Parallel Computing
5. Future Generation Computer Systems
6. International Journal of Parallel Programming
7. Concurrency and Computation: Practice and Experience
8. International Journal of High Performance Computing
9. IEEE/ACM Transactions on Computational Biology and Bioinformatics
10. Bioinformatics
11. PLOS ONE
12. IET Systems Biology
13. International Journal of Data Mining and Bioinformatics
14. BMC Bioinformatics
15. BMC Research Notes
16. Software: Practice and Experience

Professional Societies Membership

1. Institute of Electrical and Electronics Engineers (IEEE), 2006-present (senior member since 2012).
2. IEEE Computer Society, 2006-present.
3. Association for Computing Machinery (ACM), 2007-present.
4. ACM Special Interest Group on High Performance Computing (SIGHPC), 2014-present.
5. ACM Special Interest Group on Bioinformatics, Computational Biology, and Biomedical Informatics (SIGBio), 2014-present.
6. American Association for the Advancement of Science (AAAS), 2013-2018.

Professional Societies Service

1. ACM Special Interest Group on Bioinformatics, Computational Biology, and Biomedical Informatics, Director of Web Communications, 2017-present.
2. IEEE Computer Society Technical Committee on Parallel Processing, Student Travel Awards Chair, 2016-present.

University Service – University at Buffalo

University Level

1. Faculty Advisory Committee, Center for Computational Research, 2014-present.

Department of Computer Science and Engineering

1. Member, Student Outcomes Assesment Committee, 2018-present.
2. Member, Undergraduate Affairs Committee
   (chair of Data-Driven Decisions sub-committee), 2015-present.
3. Member, Teaching Effectiveness and TA Training Committee, 2016.
4. Member, Student Awards Committee, 2015-2016.
5. Member, Colloquium Committee, 2014-2016.
6. Member, Graduate Admission Committee, 2014.

Media Coverage

1. "Middle schoolers say I Can! to college" – "UB SEAS News," A story summarizing "I Can!" program run by the UB's Liberty Partnership Program in which I participate as an instructor.
2. "Kudos: Zola member of 'big data' working group" – "UB Reporter," A short story highlighting my participation in the AAAS/FBI Working Group on Big Data in Life Sciences and National Security.
3. "Big Biological Impacts From Big Data" – "Science Magazine," A story about how big data impacts life sciences, featuring my comments on the subject.
4. "Our Bodies, Our Data" – "Quanta Magazine" and "Wired.com," A story about the current status of big data in life sciences, featuring my comments on the topic.
5. "Sculpting Flow" – "NSF News From the Field" and "Science 2.0," A brief report on the computational aspects of sculpting fluid flows in microfluidic channels. The report covers the HPC experiment I led at Rutgers. It has been featured on the main NSF News web page.
6. "Understanding Fluid Flow in Microchannels" – "Digital Manufacturing Report" and "HPC in the Cloud," Article about using a cloud-like federation of HPC resources to solve pressing engineering problems. The story is based on the experiment I led at Rutgers to analyze a parameter space in microfluidic flow.

Software Development

All projects are open source.

1. **SABNA**: High performance, exact structure learning of Bayesian networks under different scoring criteria. The framework implements several novel algorithms and data structures to enable BN learning on large data. Developed together with Subhadeep Karan (Ph.D. student) – https://gitlab.com/SCoRe-Group/SABNA-Release.
2. **SABNAtk**: Efficient library for fast counting in Machine Learning applications. Developed together with Subhadeep Karan (Ph.D. student) and Matthew Eichhorn, Blake Hurlburt and Grant Iraci (undergraduate students) – https://gitlab.com/SCoRe-Group/SABNAtk.
3. **ELaSTIC**: Similarity graphs construction from massive biological sequence collections. The method is design to detect pairwise similarities in data sets with millions of DNA/RNA or protein sequences without aligning all sequences against each other – http://www.jzola.org/elastic.
4. **CLOSET**: Cloud-enabled framework based on map-reduce for large scale metagenomic data clustering. The software handles data sets consisting of millions of reads and can be used to classify data at different taxonomic levels – http://www.jzola.org/closet.
5. **TINGe**: Systems biology parallel framework for gene networks inference. The software can handle whole genome microarray expression data, and it has been successfully used to reconstruct the largest to date gene network of *Arabidopsis thaliana* – http://www.jzola.org/tinge.
6. **GeNA**: Cytoscape plugin and standalone application for analysis of gene regulatory networks using approach akin to the PageRank algorithm – http://www.jzola.org/tinge.
7. **Parallel T-Coffee**: Parallel multiple sequence aligner able to align thousands of sequences using the T-Coffee scoring method (more than 400 downloads, web portal built by researchers from Spain and England) – http://www.jzola.org/ptc.
8. **Libpnorm**: A C/C++ high performance library for scheduling pairwise computations on Cell processors taking into account local memory limitations – http://www.jzola.org/libpnorm.