

# Curriculum Vitae

## Ananth Kalyanaraman

Associate Professor

Boeing Centennial Chair in Computer Science  
School of Electrical Engineering and Computer Science

Washington State University

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## RESEARCH INTERESTS

- Bioinformatics and Computational Biology
- Parallel Algorithms and Applications
- Combinatorial Pattern Matching and String Algorithms

## EDUCATION

**Ph.D.** in Computer Engineering, Summer 2006

Dissertation Title: Large-scale Methods in Computational Genomics  
(Research Excellence Award, Iowa State University)

Adviser: Prof. Srinivas Aluru

**Iowa State University, Ames, IA, USA**

GPA: 3.95/4.0

**M.S.** in Computer Science, Summer 2002

Thesis Title: Parallel Clustering of Expressed Sequence Tags  
(Research Excellence Award, Iowa State University)

Adviser: Prof. Srinivas Aluru

**Iowa State University, Ames, IA, USA**

GPA: 3.92/4.0

**B.E.** in Computer Science and Engineering, May 1998

**Visvesvaraya National Institute of Technology,**

(Formerly, Regional Engineering College, Nagpur)

Nagpur, Maharashtra, India

Grade Percentage: 78%

## EXPERIENCE

Boeing Centennial Chair (2015 - present)	School of Electrical Engineering and Computer Science Washington State University Pullman, WA, USA
Visiting Scholar (sabbatical leave) (Aug 2013 - December 2013)	Department of Computer Science Purdue University West Lafayette, IN, USA
Associate Professor (Aug 2012 - present)	School of Electrical Engineering and Computer Science Paul G. Allen School for Global Animal Health Molecular Plant Sciences Graduate Program Center for Integrated Biotechnology Washington State University Pullman, WA, USA
Affiliate Associate Professor (March 2014 - present)	Paul G. Allen School for Global Animal Health Washington State University Pullman, WA, USA
Assistant Professor (Aug 2006 - Aug 2012)	School of Electrical Engineering and Computer Science Molecular Plant Sciences Graduate Program Center for Integrated Biotechnology Washington State University Pullman, WA, USA
Graduate Assistant (Jan 2001 - Aug 2006)	Department of Electrical and Computer Engineering Iowa State University Ames, IA, USA
Summer Intern (May-Aug 2005)	IBM Research, Yorktown Heights, NY Biomolecular Dynamics and Scalable Modeling
Summer Intern (May-Aug 2004)	IBM, Rochester, MN BlueGene/L Scaling and Performance Team
Summer Intern (Jun-Aug 2003)	Pioneer Hi-Bred International Inc., Johnston, IA Bioinformatics Group
Associate Consultant (Jan-Jul 2000)	Citibank NA, London, UK

Associate Consultant      Citicorp Overseas Software Ltd., Mumbai, India  
(Aug 1998 - Jan 2000)

## HONORS AND AWARDS

1. *2017 DARPA HIVE/IEEE HPEC Graph Challenge Champion*: <http://graphchallenge.mit.edu/champions>, 2017.
2. *Outstanding Teacher Award*. School of EECS, Washington State University, 2017.
3. *Best Student Paper Award*. *Proc. ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM BCB'16)*, 2016.
4. *EECS Early Career Award*, School of EECS, Washington State University, 2013.
5. *ECpE Early Career Impact Award*, Iowa State University, 2012.
6. *U.S. Department of Energy Early Career Research Award*, 2011-2016.
7. *Research Excellence Award*, Iowa State University, Summer 2006.
8. *Best Paper Award*. *Proc. IEEE International Parallel and Distributed Processing Symposium, 2006 (IPDPS'06)*.
9. *Best Paper Award*. *Proc. IEEE Computational Systems Bioinformatics Conference, 2005 (CSB'05)*.
10. *IBM Ph.D. Fellowship*, Fall 2005 - Summer 2006.
11. *IBM Ph.D. Fellowship*, Fall 2004 - Summer 2005.
12. *Pioneer Hi-Bred Graduate Research Fellowship*, January - December 2003.
13. *Best Poster Award for Computing Applications*. *The International Symposium on Modern Computing*, Iowa State University, 2003.
14. *Research Excellence Award*, Iowa State University, Summer 2002.
15. Secured All India Rank 54 (98.03 percentile) in Graduate Aptitude Test in Engineering, 1998.

## PUBLICATIONS

(\* indicates student authors from the lab—i.e., student advisees/co-advisees)

### Book Chapters

- BC1. A. Kalyanaraman. Algorithms for genome assembly. *Encyclopedia of Parallel Computing*, D. Padua (ed.), Springer Science+Business Media LLC, DOI 10.1007/978-0-387-09766-4, 2011.
- BC2. B. Sosinski, V. Shulaev, A. Dhingra, A. Kalyanaraman, R. Bumgarner, D. Rokhsar, I. Verde, R. Velasco, A.G. Abbott. “Rosaceous genome sequencing: Perspectives and progress” in *Genetics and Genomics of Rosaceae*, Vol 6(8):601–615, 2009, DOI: 10.1007/978-0-387-77491-6\_28, Springer New York.
- BC3. A. Kalyanaraman, S. Aluru. “Expressed Sequence Tags: Clustering and applications” in *Handbook of Computational Molecular Biology*, Edited by S. Aluru, Chapman & Hall/CRC Computer and Information Science Series, 2005.

- BC4. S. Emrich, A. Kalyanaraman, S. Aluru. “Algorithms for large-scale clustering and assembly of biological sequence data” in *Handbook of Computational Molecular Biology*, Edited by S. Aluru, Chapman & Hall/CRC Computer and Information Science Series, 2005.
- BC5. R. Raje, A. Kalyanaraman, N. Nayani. “Distributed-object computing tools” in *Tools and Environments for Parallel and Distributed Computing*, Edited by S. Hariri and M. Parashar, Wiley-Interscience, 2004.

## Refereed Journal Publications

- J1. P. Ghosh\*, A. Kalyanaraman. A fast sketch-based assembler for genomes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB)*, In Press. DOI: 10.1109/TCBB.2017.2737999.
- J2. H. Lu\*, M. Halappanavar, D. Chavarria-Miranda, A.H. Gebremedhin, A. Panyala, A. Kalyanaraman. Algorithms for Balanced Graph Colorings with Applications in Parallel Computing. *IEEE Transactions on Parallel and Distributed Systems (TPDS)*, vol. 28, no. 5, pp. 1240-1256, May 1 2017. doi: 10.1109/TPDS.2016.2620142.
- J3. A. Abnoui\*, S.L. Broschat, A. Kalyanaraman. A Fast Alignment-Free Approach for de Novo Detection of Protein Conserved Regions. *PLOS ONE*, 11(8), p.e0161338, 2016. DOI: 10.1371/journal.pone.0161338.
- J4. K. Duraisamy, H. Lu\*, P. Pande, A. Kalyanaraman. High Performance and Energy Efficient Network-on-Chip Architectures for Graph Analytics. *ACM Transactions on Embedded Computing Systems (TECS)*, vol. 15, no. 4, p. 66, 2016. DOI: 10.1145/2961027.
- J5. R. Sharpe, T. Koepke, A. Harper, J. Grimes, M. Galli, M. Satoh-Cruz, A. Kalyanaraman, K. Evans, D. Kramer, A. Dhingra. CisSERS: Customizable *in silico* Sequence Evaluation for Restriction Sites. *PLOS ONE*, 11(4):e0152404, 2016. doi: 10.1371/journal.pone.0152404. eCollection 2016.
- J6. A. Kalyanaraman, M. Halappanavar, D. Chavarria-Miranda, H. Lu\*, K. Duraisamy, P. Pande. Fast uncovering of graph communities on a chip: Toward scalable community detection on multicore and manycore platforms. *Foundations and Trends in Electronic Design Automation (FnTEDA)*, Paperback 118 pages. now Publishers, ISBN-10: 1680831321, ISBN-13: 978-1680831320, 2016.
- J7. T. Wu, S.A.N. Sarmadi, V. Venkatasubramanian, A. Pothan, A. Kalyanaraman. Fast SVD computations for synchrophasor algorithms. *IEEE Transactions on Power Systems*, 31(2):1651-1652, 2016. DOI: 10.1109/TPWRS.2015.2412679
- J8. H. Lu\*, M. Halappanavar, A. Kalyanaraman. Parallel heuristics for scalable community detection. *Parallel Computing*, Vol. 47, pp. 19-37, 2015. DOI: 10.1016/j.parco.2015.03.003 *Journal's top (#1) downloaded paper* from January 2016-Ma 2017.
- J9. J. Daily\*, A. Kalyanaraman, S. Krishnamoorthy, A. Vishnu. A work stealing based approach for enabling scalable optimal sequence homology detection. *Journal of Distributed and Parallel Computing (JPDC)*, Vol. 79-80, pp. 132-142, May 2015. DOI: 10.1016/j.jpdc.2014.08.009
- J10. J. Adam, J. Stephens, S. Chung, M. Brady, R. D. Evans, C. Kruger, B. Lamb, M. Liu, C. Stckle, J. Vaughan, K. Rajagopalan, J. Harrison, C. Tague, A. Kalyanaraman, Y. Chen, A. Guenther, F.-Y. Leung, L. R. Leung, A. Perleberg, J. Yoder, E. Allen, S. Anderson, B. Chandrasekharan, K. Malek, T. Mullis\*, C. Miller, T. Nergui, J. Poinsette, J. Reyes, J. Zhu, J. Choate, X. Jiang, R. Nelson, J.-H. Yoon, G. Yorgey, K. Johnson, K. Chinnayakanahalli,

- A. Hamlet, B. Nijssen, and V. Walden. BioEarth: Envisioning and developing a new regional earth system model to inform natural and agricultural resource management, *Climatic Change*, pp. 1-17, 2014.
- J11. T. Majumder\*, P.P. Pande, A. Kalyanaraman. Hardware Accelerators in Computational Biology: Application, Potential and Challenges. *IEEE Design and Test of Computers: Special Issue on Hardware Acceleration in Computational Biology*, 31(1): 8-18, 2014, DOI: 10.1109/MDAT.2013.2290118
- J12. T. Majumder\*, P.P. Pande, A. Kalyanaraman. Wireless NoC platforms with dynamic task allocation for maximum likelihood phylogeny reconstruction. *IEEE Design and Test of Computers*, 31(3):54-64, 2014, DOI: 10.1109/MDAT.2013.2288778.
- J13. N. Dasgupta, Y. Chen, A. Kalyanaraman, S. Daoud. Comparison of clustering algorithms: An example with proteomic data. *Advances and Applications in Statistics*, 33(1):p63, 2013.
- J14. T. Majumder\*, P.P. Pande, A. Kalyanaraman. High-Throughput, Energy-Efficient Network-on-Chip-Based Hardware Accelerators. *Sustainable Computing: Informatics and Systems (SUSCOM)*, 3(1):36-46, 2013. DOI: 10.1016/j.suscom.2013.01.001.
- J15. I. Rytsareva\*, T. Chapman\*, and A. Kalyanaraman. Parallel algorithms for clustering biological graphs on distributed and shared memory architectures. *International Journal of High Performance Computing and Networking (IJHPCN)*, 7(4):241-257, 2014.
- J16. T. Majumder\*, M. Borgens, P.P. Pande, A. Kalyanaraman. On-Chip Network-Enabled Multi-Core Platforms Targeting Maximum Likelihood Phylogeny Reconstruction. *IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems (TCAD)*, 2012, 31(7):1061-1073.
- J17. C. Wu\*, A. Kalyanaraman, W.R. Cannon. *pGraph*: Efficient parallel construction of large-scale protein sequence homology graphs. *IEEE Transactions on Parallel and Distributed Systems*, 23(10):1923-1933, 2012, DOI <http://doi.ieeecomputersociety.org/10.1109/TPDS.2012.19>.
- J18. T. Majumder\*, S. Sarkar\*, P. Pande, A. Kalyanaraman. NoC-Based Hardware Accelerator for Breakpoint Phylogeny. *IEEE Transactions on Computers*, 2012, 61(6):857-869, doi:10.1109/TC.2011.100.
- J19. A. Kalyanaraman, W.R. Cannon, B. Latt\*, D.J. Baxter. MapReduce implementation of a hybrid spectral library-database search method for large-scale peptide identification. *Bioinformatics*, Advance online access, 2011. doi:10.1093/bioinformatics/btr523.
- J20. A.O.T. Lau, A. Kalyanaraman, I. Echaide, G.H. Palmer, R. Bock, M.J. Pedroni, M. Rameshkumar\*, M.B. Ferreira, T.I. Fletcher, T.F. McElwain. Attenuation of virulence in an Apicomplexan hemoparasite results in reduced genome diversity at the population level. *BMC Genomics*, 12:410, 2011, doi:10.1186/1471-2164-12-410.
- J21. R. Velasco, A. Zharkikh, J. Affourtit, A. Dhingra, A. Cestaro, A. Kalyanaraman, P. Fontana, S.K. Bhatnagar, M. Troggio, D. Pruss, S. Salvi, M. Pindo, P. Baldi, S. Castelletti, M. Cavaiuolo, G. Coppola, F. Costa, V. Cova, A.D. Ri, V. Goremykin, M. Komjanc, S. Longhi, P. Magnago, G. Malacarne, M. Malnoy, D. Micheletti, M. Moretto, M. Perazzolli, A. Si-Ammour, S. Vezzulli, E. Zini, G. Eldredge, L.M. Fitzgerald, N. Gutin, J. Lanchbury, T. Macalma, J.T. Mitchell, J. Reid, B. Wardell, C. Kodira, Z. Chen, B. Desany, F. Niazi, M. Palmer, T. Koepke, D. Jiwan, S. Schaeffer, V. Krishnan\*, C. Wu, V.T. Chu, S.T. King, J. Vick, Q. Tao, A. Mraz, A. Stormo, K. Stormo, R. Bogden, D. Ederle, A. Stella, A. Vecchiatti,

- M.M. Kater, S. Masiero, P. Lasserre, Y. Lespinasse, A.C. Allan, V. Bus, D. Chagna, R.N. Crowhurst, A.P. Gleave, E. Lavezzo, J.A. Fawcett, S. Proost, P. Rouz, L. Sterck, S. Toppo, B. Lazzari, R.P. Hellens, C. Durel, A. Gutin, R.E. Bumgarner, S.E. Gardiner, M. Skolnick, M. Egholm, Y. Peer, F. Salamini, R. Viola. The genome of the domesticated apple (*Malus domestica* Borkh.). *Nature Genetics*, 42: 833-839, 2010, doi:10.1038/ng.654.
- J22. The International Brachypodium Initiative. Genome sequencing and analysis of the model grass *Brachypodium distachyon*. *Nature*, vol. 463, pp. 763-768, 2010. doi:10.1038/nature08747.
- J23. S. Sarkar\*, G. Kulkarni\*, P. Pande, A. Kalyanaraman. Network-on-chip Hardware Accelerators for Biological Sequence Alignment. *IEEE Transactions on Computers*, 59(1):29-41, 2010.
- J24. P.S. Schnable *et al.* The B73 Maize Genome: Complexity, diversity and dynamics. *Science*, 326(5956):1112-1115, 2009.
- J25. F. Wei, J.C. Stein, C. Liang, J. Zhang, R.S. Fulton, R.S. Baucom, E. De Paoli, S. Zhou, L. Yang, Y. Han, S. Pasternak, A. Narechania, L. Zhang, C. Yeh, K. Ying, D.H. Nagel, K. Collura, D. Kudrna, J. Currie, J. Lin, H. Kim, A. Angelova, G. Scara, M. Wissotski, W. Golser, L. Courtney, S. Kruchowski, T.A. Graves, S.M. Rock, S. Adams, L.A. Fulton, C. Fronick, W. Courtney, M. Kramer, L. Spiegel, L. Nascimento, A. Kalyanaraman, C. Chaparro, J. Deragon, P. San Miguel, N. Jiang, S.R. Wessler, P.J. Green, Y. Yu, D.C. Schwartz, B.C. Meyers, J.L. Bennetzen, R.A. Martienssen, W.R. McCombie, S. Aluru, S.W. Clifton, P.S. Schnable, D. Ware, R.K. Wilson and R.A. Wing Detailed analysis of a contiguous 22-Mb region of the maize genome. *PLoS Genetics*, 5(11):e1000728, 2009. doi:10.1371/journal.pgen.1000728.
- J26. A. Kalyanaraman, S.J. Emrich, P.S. Schnable, S. Aluru. Assembling genomes on large-scale parallel computers. *Journal of Parallel and Distributed Computing (JPDC)*, 67(12):1240-1255, 2007.
- J27. A. Kalyanaraman, S. Aluru. Efficient algorithms and software for detection of full-length LTR retrotransposons. *Journal of Bioinformatics and Computational Biology (JBCB)*, 4(2):197-216, 2007.
- J28. M. Mitreva, A.A. Elling, M. Dante, A.P. Kloek, A. Kalyanaraman, S. Aluru, S.W. Clifton, D.M. Bird, T.J. Baum, J.P. McCarter. A survey of SL1-spliced transcripts from the root-lesion nematode *Pratylenchus penetrans*. *Molecular Genetics and Genomics (MGG)*, 272:138-148, 2004.
- J29. A. Kalyanaraman, S. Aluru, V. Brendel, S. Kothari. Space and time efficient parallel algorithms and software for EST clustering. *IEEE Transactions on Parallel and Distributed Systems (TPDS)*, 14(12):1209-1221, 2003.
- J30. A. Kalyanaraman, S. Aluru, S. Kothari, V. Brendel. Efficient clustering of large EST data sets on parallel computers. *Nucleic Acids Research (NAR)*, 31(11):2963-2974, 2003.

## Refereed Conference and Workshop Publications

- C1. A. Panyala, O. Subasi, M. Halappanavar, A. Kalyanaraman, D. Chavarria-Miranda, S. Krishnamoorthy. Approximate computing techniques for iterative graph algorithms. *Proc. IEEE International Conference on High Performance Computing, Data, and Analytics (HiPC'17)*, Accepted, Jaipur, India, December 2017.
- C2. M. Halappanavar, H. Lu\*, A. Kalyanaraman, A. Tumeo. Scalable Static and Dynamic Community Detection Using Grappolo. *Proc. IEEE High Performance Extreme Computing*,

Accepted, Waltham, MA, September 2017.

**2017 DARPA HIVE/IEEE HPEC Graph Challenge Champion:** <http://graphchallenge.mit.edu/champions>.

- C3. K. Duraisamy, H. Lu\*, P. Pande, A. Kalyanaraman. Accelerating Graph Community Detection with Approximate Updates via an Energy-Efficient NoC. *Proc. Design Automation Conference (DAC)*, Accepted, June 18-12, 2017.
- C4. P. Ghosh\*, A. Kalyanaraman. A fast sketch-based assembler for genomes. *Proc. ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB)*, pp. 241-250, 2016. DOI: 10.1145/2975167.2975192. **Best Student Paper Award**.
- C5. P. Pesantez\*, A. Kalyanaraman. Detecting communities in biological bipartite networks. *Proc. ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB)*, pp. 98-107, 2016. DOI: 10.1145/2975167.2975177.
- C6. M. Kamruzzaman\*, A. Kalyanaraman, B. Krishnamoorthy. Characterizing the Role of Environment on Phenotypic Traits using Topological Data Analysis. *Proc. ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB)*, pp. 487-488, 2016. DOI: 10.1145/2975167.2985646.
- C7. J. Daily\*, A. Kalyanaraman, S. Krishnamoorthy, B. Ren. On the Impact of Widening Vector Registers on Sequence Alignment. *Proc. International Conference on Parallel Processing (ICPP)*, pp. 506-515, 2016. DOI: 10.1109/ICPP.2016.65.
- C8. K. Duraisamy, H. Lu\*, P. Pande, A. Kalyanaraman. High Performance and Energy Efficient Wireless NoC-Enabled Multicore Architecture for Graph Analytics. *Proc. International Conference on Compilers, Architectures and Synthesis of Embedded Systems (CASES)*, pp. 147-156, 2015. **Best Paper Finalist**.
- C9. A. Abnoui\*, S. Broschat, A. Kalyanaraman. An alignment-free approach to cluster proteins using frequency of conserved k-mers. *Proc. 6<sup>th</sup> ACM Conference on Bioinformatics, Computational Biology and Health Informatics (ACM-BCB)*, pp. 597-606, 2015. DOI: 10.1145/2808719.2812223
- C10. T. Majumder\*, P. Pande, A. Kalyanaraman. On-Chip Network-Enabled Many-Core Architectures for Computational Biology Applications. *Proc. Design, Automation and Test in Europe (DATE)*, pp. 259-264, 2015.
- C11. H. Lu\*, M. Halappanavar, D. Chavarria, A. Gebremedhin, A. Kalyanaraman. Balanced coloring for parallel computing applications. *Proc. IEEE International Parallel and Distributed Processing Symposium (IPDPS)*, pp. 7-16, 2015. DOI: 10.1109/IPDPS.2015.113
- C12. D. Chavarria, M. Halappanavar, A. Kalyanaraman. Scaling graph community detection on the Tiler Many-core architecture. *Proc. IEEE International Conference on High Performance Computing (HiPC)*, December 17-20, 2014, Goa, India (11 pages).
- C13. H. Lu\*, M. Halappanavar, A. Kalyanaraman, S. Choudhury. Parallel heuristics for scalable community detection. *Proc. International Parallel and Distributed Processing Symposium Workshops (IPDPSW)*, pp. 1374-1385, 2014. DOI: 10.1109/IPDPSW.2014.155
- C14. T. Mullis\*, M. Liu, A. Kalyanaraman, J. Vaughan, C. Tague, J. Adam. Design and implementation of Kepler workflows for BioEarth, pp. 1-10. International Conference on Computational Science (ICCS) *Procedia Computer Science*, vol. 29, pp. 1722-1732, 2014. DOI: 10.1016/j.procs.2014.05.157.

- C15. M.V. Venkatasubramanian, A. Pothan, A. Kalyanaraman, D.J. Sobajic. Computational Challenges in Stability Monitoring of Power Systems using Large Number of PMUs (position paper). *Proc. 2013 National Workshop on Energy Cyber-Physical Systems*, organized by NSF, Arlington, VA, December 16-17, 2013, pp. 1-3.
- C16. D. Deford\*, A. Kalyanaraman. Empirical Analysis of Space-Filling Curves for Scientific Computing Applications. *Proc. International Conference on Parallel Processing (ICPP'13)*, October 1-4, 2013, Lyon, France, pp.170-179. DOI: 10.1109/ICPP.2013.26
- C17. I. Rytsareva\*, A. Kalyanaraman, K. Konwar, S. Hallam. Scalable heuristics for clustering biological graphs. *Proc. IEEE International Conference on Computational Advances in Bio and Medical Sciences (ICCABS'13)*, New Orleans, LA, June 12-14, 2013, pp. 1-6.
- C18. F. Poursabzi\*, A. Kalyanaraman. On clustering heterogeneous networks. *Proc. SIAM Workshop on Network Science (NetSci13)*, Held in conjunction with SIAM Annual Meeting, San Diego, CA, July 7-8, 2013, pp. 1-2.
- C19. T. Majumder\*, P. Pande, A. Kalyanaraman. Network-on-Chip with Long-Range Wireless Links for High-Throughput Scientific Computation. *Proc. 3rd Workshop on Communication Architecture for Scalable Systems (CASS)*, Held in conjunction with IPDPS 2013, pp. 781-790, 2013.
- C20. C. Wu\*, A. Kalyanaraman. GPU-accelerated protein family identification for metagenomics. *Proc. 12<sup>th</sup> IEEE International Workshop on High Performance Computational Biology (HiCOMB)*, Held in conjunction with IPDPS 2013, pp. 559-568, 2013, Invited paper.
- C21. J. Daily\*, S. Krishnamoorthy, A. Kalyanaraman. Towards Scalable Optimal Sequence Homology Detection. *Proc. Workshop on Parallel Algorithms and Software for Analysis of Massive Graphs (ParGraph'12)*, Held in conjunction with HiPC 2012, pp. 1-8, 2012.
- C22. I. Rytsareva\*, Q. Le, E. Conner, A. Kalyanaraman, J. Panchal. c. *Proc. ASME International Design Engineering Technical Conferences & Computers and Information in Engineering Conference (IDETC/CIE)*, pp. 1-10, 2012.
- C23. A. Hugo, D.J. Baxter, W.R. Cannon, A. Kalyanaraman, G. Kulkarni\*, S.J. Callister. Prototyping of microbial communities using high performance optimization of proteome-spectra matches. *Proc. Pacific Symposium on Biocomputing (PSB)*, 2012.
- C24. I. Rytsareva\*, A. Kalyanaraman. An efficient MapReduce algorithm for parallelizing large-scale graph clustering. *Proc. ParGraph - Workshop on Parallel Algorithms and Software for Analysis of Massive Graphs*, Held in conjunction with HiPC'11, Bengaluru, India, 2011.
- C25. T. Chapman\*, A. Kalyanaraman. An OpenMP algorithm and implementation for clustering biological graphs. *Proc. IA<sup>3</sup> - Workshop on Irregular Applications: Architectures & Algorithms*, Held in conjunction with SC|11, pp. 3-10, 2011.
- C26. T. Majumder\*, P. Pande, A. Kalyanaraman. Accelerating Maximum Likelihood based Phylogenetic Kernels using Network-on-Chip. *Proc. International Symposium on Computer Architecture and High Performance Computing (SBAC-PAD)*, pp. 17-24, 2011. <http://doi.ieeecomputersociety.org/10.1109/SBAC-PAD.2011.17>.
- C27. C. Wu\*, A. Kalyanaraman, W. Cannon. A scalable parallel algorithm for large-scale protein sequence homology detection. *Proc. International Conference on Parallel Processing (ICPP)*, San Diego, CA, September 13-16, 2010, pp. 333-342, doi: 10.1109/ICPP.2010.41.
- C28. T. Majumder\*, S. Sarkar\*, P. Pande, A. Kalyanaraman. An optimized NoC Architecture for accelerating TSP kernels in breakpoint median problem. *Proc. IEEE International Con-*



- ference on Application-specific Systems, Architectures and Processors (ASAP), pp. 89-96, 2010.
- C29. S. Sarkar\*, T. Majumder\*, A. Kalyanaraman, P. Pande. Hardware accelerators for biocomputing: A survey. *Proc. IEEE International Symposium on Circuits and Systems (ISCAS)*, pp. 3789-3792, 2010.
- C30. A. Kalyanaraman, D. Baxter, W. Cannon. "Using clouds for data-intensive computing in proteomics", *Proc. Workshop on Using clouds for parallel computations in systems biology*, SC|09, Portland, OR, Nov 16, 2009.
- C31. Md. Muksitul Haque\*, A. Kalyanaraman, A. Dhingra, N. Abu-lail, K. Graybeal. DNAjig: A new approach for building DNA nanostructures. *Proc. IEEE International Conference on Bioinformatics & Biomedicine (BIBM)*, pp. 379-383, Washington D.C., November 1-4, 2009. doi: 10.1109/BIBM.2009.71. (Acceptance rate: 34.7%)
- C32. G. Kulkarni\*, A. Kalyanaraman, W. Cannon, D. Baxter. A scalable parallel approach for peptide identification from large-scale mass spectrometry data. *Proc. International Conference on Parallel Processing Workshops (ICPPW)*, pp. 423-430, Vienna, Austria, Sep. 22-25, 2009, doi: 10.1109/ICPPW.2009.41.
- C33. C. Wu\*, A. Kalyanaraman. An efficient parallel approach for identifying protein families in large-scale metagenomic data sets. *Proc. IEEE/ACM Supercomputing Conference (SC|08)*, Austin, TX, Nov. 15-21, 2008. (Acceptance Rate: 21.2%)
- C34. W. Davis, A. Kalyanaraman, D. Cook. An information theoretic approach for the discovery of irregular and repetitive patterns in genomic data. *Proc. IEEE Computational Intelligence in Bioinformatics and Bioengineering (CIBCB'08)*, pp. 30-37, Sun Valley, Idaho, Sept. 15-17, 2008, doi: 10.1109/CIBCB.2008.4675756.
- C35. S.J. Emrich, A. Kalyanaraman, S. Aluru. Massively parallel clustering of Expressed Sequence Tags, *Proc. ISCA 20th International Conference on Parallel and Distributed Computing Systems (PDCS'07)*, 254-261, 2007.
- C36. A. Kalyanaraman, S. Aluru, P.S. Schnable. Turning repeats to advantage: Scaffolding genomic contigs using LTR retrotransposons. *Proc. Life Sciences Society Computational Systems Bioinformatics Conference (CSB'06)*, 167-178, 2006. (Acceptance Rate: 19.2%)
- C37. A. Kalyanaraman, S.J. Emrich, P.S. Schnable, S. Aluru. Assembling genomes on large-scale parallel computers. *Proc. IEEE International Parallel and Distributed Processing Symposium (IPDPS'06)*, 2006. (Acceptance Rate: 23%) **Best Paper Award.**
- C38. A. Kalyanaraman, S. Aluru. Efficient algorithms and software for detection of full-length LTR retrotransposons. *Proc. IEEE Computational Systems Bioinformatics Conference (CSB'05)*, pp. 56-64, 2005. (Acceptance Rate: 12.2%) **Best Paper Award.**
- C39. P. Ko, M. Narayanan, A. Kalyanaraman, S. Aluru. Space-conserving optimal DNA-protein alignment. *Proc. IEEE Computational Systems Bioinformatics Conference (CSB'04)*, pp. 77-85, 2004. (Acceptance Rate: 31%)
- C40. A. Kalyanaraman, S. Aluru, S. Kothari. Space and time efficient parallel algorithms and software for EST clustering. *Proc. International Conference on Parallel Processing (ICPP'02)*, pp. 331-339, 2002. (Acceptance Rate: 36%)
- C41. A. Kalyanaraman, S. Aluru, S. Kothari. Parallel EST clustering. *Proc. First International Workshop on High Performance Computational Biology (HiCOMB '02)*, held in conjunction with the *IEEE International Parallel and Distributed Processing Symposium*, 2002.

## Extended Abstracts & Technical Reports

- EA1. T. Chapman\*, A. Kalyanaraman. Enabling large-scale metagenomic protein family identification on the NSF TeraGrid. Undergraduate poster in *TeraGrid 2011*, 2011.
- EA2. A. Kalyanaraman, D. Baxter, W.R. Cannon. White Paper on “Using clouds for data-intensive computing in proteomics”, *Proc. Workshop on Using clouds for parallel computations in systems biology*, SC|09, Portland, OR, Nov 16, 2009.
- EA3. C. Wu\*, A. Kalyanaraman, A. Dhingra. Enabling Cost-Effective Sequencing Of Arbitrarily Long Conserved DNA Sequences. *Proc. Plant & Animal Genomes XVI Conference (PAG’08)*, San Diego, January 12-16, 2008.
- EA4. C. Wu\*, A. Kalyanaraman, A. Dhingra. An efficient computational framework for amplifying arbitrarily long conserved DNA sequences. *Proc. LSS Computational Systems Bioinformatics Conference (CSB’07)*, UC San Diego, August 13-17, 2007.
- EA5. W. Davis, A. Kalyanaraman, D. Cook. An information theoretic approach for the discovery of irregular and repetitive patterns in genomic data. *Proc. LSS Computational Systems Bioinformatics Conference (CSB’07)*, UC San Diego, August 13-17, 2007.

## Conference Tutorials and Other Educational Outreach

- Ed1. A. Kalyanaraman. Computational biology education: “Parallel graph algorithms with applications to metagenomics and metaproteomics”. Presented at *SC|11 Education program*, Seattle, WA, November 13, 2011.
- Ed2. A. Kalyanaraman. High school outreach: “Computing & the Art of Problem Solving”. Presented as part of the *Imagine U at WSU* program at the following venues and dates: Sunnyside High School, Sunnyside, WA, November 24, 2008; Wenatchee High School, Wenatchee, WA, March 19, 2009; Bridgeport High School, Bridgeport, WA, March 20, 2009; Lewis & Clark High School, Spokane, WA, November 22, 2010.
- Ed3. A. Kalyanaraman and J. Krause. Computational biology education: “Computational thinking for molecular biology and sequence analysis”. Presented at *SC|09 Education*, Portland, OR, November 14, 2009.
- Ed4. A. Kalyanaraman. Computational biology education: “Transcriptomics: From small-scale to large-scale”. Presented at *SC|09 Education*, Portland, OR, November 14, 2009.
- Ed5. A. Kalyanaraman and J. Krause. Computational biology education: “Molecular Evolution and Phylogeny”. Presented at *SC|09 Education*, Portland, OR, November 15, 2009.
- Ed6. A. Kalyanaraman. “Computational biology for biology educators - Computational thinking & Transcriptomics”, *SC|09 Education Workshop @ UC Merced*, Merced, CA, June 7-13, 2009. Materials available from <http://moodle.sc-education.org>.
- Ed7. A. Kalyanaraman. Computational biology education: “One to many and many to many sequence comparisons: BLAST-ing to metagenomics”. Presented at *SC|08 Education*, Austin, TX, November 17, 2008.
- Ed8. S. Aluru, D.A. Bader, A. Kalyanaraman. Conference tutorial: “High-performance Computing Methods for Computational Genomics”. Presented at the *2007 IEEE International Parallel and Distributed Processing Symposium (IPDPS’07)*, Long Beach, CA, March 26-30, 2007.

Ed9. S. Aluru, D.A. Bader, A. Kalyanaraman. Conference tutorial: “High-performance Computing Methods for Computational Genomics”. Presented at the *2006 IEEE/ACM Supercomputing Conference (SC06)*, Tampa, FL, November 11-17, 2006.

## Software Technologies

- SW1. *PaCE*: Software for parallel clustering of DNA sequences. Copyrighted with Iowa State University.
- SW2. *LTR-par*: Software for parallel identification of full-length LTR retrotransposons in genomes.
- SW3. *pClust*: Parallel software suite for large-scale clustering of metagenomics open reading frames/protein sequences, 2008 (Key citation: Wu *et al.*, SC’08).  
Lead student developer: Changjun Wu  
Open Source Website: <https://code.google.com/archive/p/pclust/>
- SW4. *pGraph*: Parallel software for building large-scale homology graphs for metagenomics open reading frame/protein sequences. (Key citation: Wu *et al.*, TPDS’12).  
Lead student developer: Changjun Wu  
Open Source Website: <https://code.google.com/archive/p/psgraph/>
- SW5. *Grappolo-TK*: Parallel toolkit for Graph Community Detection, and Graph Balanced Coloring. (Key citations: Lu *et al.*, PARCO’15), Lu *et al.*, TPDS’16).  
Lead student developer: Hao Lu  
Open Source Website: <https://github.com/luhowardmark/GrappoloTK>
- SW6. *biLouvain*: A scalable implementation for bipartite graph community detection. (Key citations: Pesantez and Kalyanaraman, ACM-BCB’16).  
Lead student developer: Paola Pesantez  
Open Source Website: <https://github.com/paolapesantez/biLouvain>
- SW7. *FastEtch*: A fast sketch-based assembler for genomes. (Key citations: Ghosh and Kalyanaraman, ACM-BCB’16).  
Lead student developer: Priyanka Ghosh  
Open Source Website: In progress.

## Invited Talks, Panels, and Presentations

1. “On Scaling Graph Algorithms for Parallel Data-Driven Scientific Applications”, Invited talk, Indian Institute of Technology Madras, Chennai, India, December 16, 2016.
2. The “Women in Bioinformatics” panel, *ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB)*, Seattle, WA, October 2-5, 2016.
3. “On Scaling Graph Algorithms for Microbiome Applications,” Special Session talk, Special session on “Molecular Communication and Networking with Applications to Precision Medicine,” Intelligent Systems in Molecular Biology (ISMB), Orlando, FL, July 9-12, 2016.
4. “A parallel graph framework for metagenomics and microbial genomics,” Invited Talk, Workshop on Parallel Software Libraries for Sequence Analysis (pSALSA), Held in conjunction with IPDPS 2016, Chicago, IL, May 22, 2016.
5. “On Scaling Graph Algorithms for the New Age Biological Sciences,” Invited Talk, Workshop on Large Scale Complex Network Analysis (LSCNA 2015), Indian Statistical Institute, Kolkata, December 19-20, 2015.

6. "State of the Art of Large Scale Complex Networks: Problems & Challenges," Panel, Workshop on Large Scale Complex Network Analysis (LSCNA 2015), Indian Statistical Institute, Kolkata, December 19-20, 2015.
7. "Problems, Challenges and Opportunities in Exploring the "Dark Matter" of Life Sciences: The Microbiome," **Keynote address**, IEEE International Workshop on Parallel and Distributed Computing for Large Scale Machine Learning and Big Data Analytics (ParLearning), held in conjunction with IPDPS'15, Hyderabad, India, May 29, 2015.
8. "Emerging Architectural Frameworks for Microbiome Applications," Invited Talk, IEEE International Workshop on High Performance Computational Biology (HiCOMB), held in conjunction with IPDPS'15, Hyderabad, India, May 25, 2015.
9. "Scalable Clustering for Computational Biology: Algorithms and Applications," Department Colloquium, Visvesvaraya National Institute of Technology, Nagpur, India, May 15, 2015.
10. "A Scalable Graph-theoretic Framework for Functional Characterization of Environmental Microbial Communities," Invited Talk, TCS Research, Mumbai, India, May 13, 2015.
11. "DNAjig: A new approach for building DNA nanostructures," Guest lecture in the course *Introduction to bionanotechnology*, The Gene and Linda Voiland School of Chemical Engineering and Bioengineering, Washington State University, Pullman, WA, March 27, 2014.
12. "ECRP: Efficient Graph Kernels for Extreme Scale Analysis of Environmental Community Data," DOE SDMAV PI meeting, Extreme Scale Computing Conference, Walnut Creek, CA, January 13-15, 2015.
13. "On Big Data Analytics for the Next Generation Life Sciences," HiPC14, BOF session on Big Data, Goa, India, December 17-21, 2014.
14. "A Scalable Graph-theoretic Framework for Metagenomics and other Scientific Applications," Colloquium, Department of Computer Science, Boise State University, Boise, ID, December 1, 2014.
15. "Graph algorithms for computational metagenomics," International Workshop on High Performance Computational Biology (HiCOMB'14), Pheonix, AZ, May 19, 2014.
16. "Toward a scalable algorithmic framework for functional characterization of microbial communities," Colloquium, Department of Computer Science, Old Dominion University, Norfolk, VA, April 25, 2014.
17. "Scalable Graph Methods for Functional Characterization of Environmental Microbial Communities," Minisymposium on Graph Analysis for Scientific Discovery, *SIAM Conference on Parallel Processing (SIAM PP'14)*, Portland, OR, February 18-21, 2014.
18. "Scalable Heuristics for Clustering of Large-scale Metagenomics Data," Colloquia presentation at the *San Diego Supercomputing Center*, University of California San Diego, San Diego, CA, July 9, 2013.
19. "Scalable Heuristics for Clustering of Large-scale Metagenomics Data," Colloquia presentation at the *Pacific Northwest National Laboratory*, Richland, WA, April 29, 2013.
20. "DNAjig: A new approach for building DNA nanostructures," Guest lecture in the course *Introduction to bionanotechnology*, The Gene and Linda Voiland School of Chemical Engineering and Bioengineering, Washington State University, Pullman, WA, March 18, 2013.
21. "Theory, Application and Challenges for Graph-theoretic Models in Computational Biology," presented at the Minisymposium on Scalable Graph-theoretic Models for Computational Bi-

- ology, *SIAM Conference on Computational Science and Engineering (CSE'13)*, Boston, MA, February 25-March 1, 2013.
22. “Scalable MapReduce algorithms for proteomics and metaproteomics,” Biopharma Case Study, *Cloud Computing Symposium, Part of Molecular Med TRI-CON 2012*, San Francisco, CA, February 19-20, 2012.
  23. “Parallel Graph-based Techniques for Clustering Large-scale Metagenomics Datasets,” *Dept. Computer Science and Engineering*, Texas A&M University, College Station, TX, October 10, 2011.
  24. “Parallel Algorithms for Graph-theoretic Clustering of Biological Data,” *School of Mechanical and Materials Engineering*, WSU, February 17, 2011.
  25. “Efficient parallel algorithms for data-intensive biocomputing,” *EECS executive board meeting*, Seattle, WA, October 15, 2010.
  26. “Efficient algorithms for large-scale sequence analysis on parallel computers,” *School of Molecular Biosciences seminar*, WSU, August 26, 2010.
  27. Plenary talk, “Data intensive life sciences,” *Data Intensive Research Analytics Center Workshop*, University of Washington, Seattle, WA, January 15, 2010.
  28. Algorithms & Techniques for Parallel Genome Assembly and Sequence Clustering. Department of Biology, University of Utah, Salt Lake City, June 17-18, 2009.
  29. Algorithms & Techniques to Reduce the Computational Burden of Protein Family Detection. J. Craig Venter Institute, Rockville, MD, 2009.
  30. Algorithmic & HPC Issues in Microbial Community Genomics. DOE Exascale Townhall Meeting, Oak Ridge National Laboratory, May 17-18, 2007.
  31. HPC Methods for Large-scale Computational Genomics Applications. Pacific Northwest National Laboratory, March 23, 2007.

## EXTRAMURAL AND INTRAMURAL FUNDING

### Research Grants and Awards

1. **PI**, \$1,249,557, Collaborative Research: ABI Innovation: A Scalable Framework for Visual Exploration and Hypotheses Extraction of Phenomics Data using Topological Analytics, NSF ABI #1661348, 8/1/2017-7/31/2020.  
PI: Ananth Kalyanaraman, Co-PIs: Bala Krishnamoorthy, Zhiwu Zhang @ Washington State University, Bei Wang Phillips @ University of Utah, Patrick Schnable @ Iowa State University.
2. **Co-PI**, \$1,719,179, Model-Driven Surveillance and Intervention Evaluation in Highly Stochastic Healthcare Settings, Center for Disease Control and Prevention (CDC), 8/1/2017-7/31/2020.  
PI: Eric Lofgren, Kalyanaraman, Co-PIs: Margaret Davis, Ananth Kalyanaraman, Sandip Roy @ Washington State University, Deverick Anderson, Rebekah Moehring @ Duke University.
3. **PI** at WSU, \$73,244, Algorithms for Scalable Approximate Graph Clustering on Streaming Data, High Performance Data Analytics (HPDA), Pacific Northwest National Laboratory, 8/16/2016-7/31/2017.

4. **PI**, \$10,000, “Collaborative Research: Student Travel Support: International Workshop on Big Data in Life Sciences, Newport Beach, CA, September 20, 2014”, NSF CCF, 7/1/2014-6/30/2015. PIs: Jaroslaw Zola @ Rutgers, Ananth Kalyanaraman @ WSU.
5. **Co-PI**, \$666,969, ABI Innovation: Next-Gen Clustering: Fast and accurate ways to cluster proteins, NSF ABI #1262664, 8/29/2013-8/28/2018.  
PI: Shira Broschat, Co-PIs: Ananth Kalyanaraman, Doug Call @ Washington State University.
6. **PI**, \$750,000, Early Career Award: Efficient graph kernels for extreme scale analysis of environmental community data, Department of Energy: Early Career Research Program, 8/16/2011 - 8/15/2017.
7. **Co-PI**, \$3,053,000, PMU: Collaborative Research: Type 2: Understanding Biogeochemical Cycling in the Context of Climate Variability Using a Regional Earth System Modeling, USDA, 3/16/2011 - 3/15/2016.  
PI: Jennifer Adam @ Washington State University.
8. **PI**, \$435,000, DC: Small: Efficient algorithms for data-intensive bio-computing, NSF IIS #0916463, 9/1/2009-8/31/2013.  
PI: Ananth Kalyanaraman, Co-PIs: Partha Pande @ Washington State University, William Cannon @ Pacific Northwest National Lab.
9. **PI**, \$16,000, REU supplement: DC: Small: Efficient algorithms for data-intensive bio-computing, NSF IIS #0916463, 5/16/2011-8/31/2012.
10. **Co-PI**, \$224,000, An apple genome sequencing initiative, USDA NRI, 8/16/2008-12/31/2012.  
PI: Amit Dhingra, Co-PIs: Ananth Kalyanaraman @ Washington State University.
11. **PI**, \$14,700, Algorithms & Software for Large-scale Metagenomics, WSU Seed Grant (jointly funded by WSU Office of Research & WSU Foundation), 5/16/2008-8/15/2009.

## Research Infrastructure

1. **PI**, NERSC ERCAP allocation award, “Scalable and accurate construction of large protein sequence homology graphs for environmental community data sets”, 292K CPU hours on Cray XC30 (Edison/Cori), January-December 2017.
2. **PI**, NERSC ERCAP allocation award, “Scalable and accurate construction of large protein sequence homology graphs for environmental community data sets”, 192K CPU hours on Cray XC30 (Edison/Cori), January-December 2016.
3. **PI**, NERSC ERCAP allocation award, “Scalable and accurate construction of large protein sequence homology graphs for environmental community data sets”, 300K CPU hours on Cray XT4 (Hopper), January-December 2015.
4. **PI**, NERSC ERCAP allocation award, “Scalable and accurate construction of large protein sequence homology graphs for environmental community data sets”, 300K CPU hours on Cray XT4 (Hopper), January-December 2014.

5. **PI**, NERSC ERCAP allocation award, “Scalable and accurate construction of large protein sequence homology graphs for environmental community data sets”, 300K CPU hours on Cray XT4 (Hopper), January-December 2013.
6. **PI**, NERSC ERCAP startup allocation, 15K CPU hours, 2012-2013.
7. **PI**, NSF TeraGrid Resource Allocation Program, “Data-intensive Protein Bioinformatics on the TeraGrid”, 30K CPU hours (startup)

## TEACHING ACTIVITIES

### Course Instruction

1. Designed and Taught: “Introduction to Parallel Computing” (Cpt S 411), School of EECS, WSU.  
Has taught every Fall semester since Fall 2014.
2. Designed and Taught: “Fundamental Algorithms in Computational Genomics” (Cpt S 571/471), School of EECS, WSU.  
Has taught every Spring semester since Spring 2007.
3. Designed and Taught: “Automata and Formal Languages” (Cpt S 317), School of EECS, WSU.  
Has taught every Spring semester since Spring 2009.
4. Designed and Taught: “Advanced Data Structures” (Cpt S 223), School of EECS, WSU.  
Fall semesters 2007-2012.
5. Teaching Assistant, Discrete Computational Structures (COM S 330), 3 credit course, Iowa State University, Spring 2001.

### Curriculum Development

1. WSU HPC (Kamiak) training in parallel programming, Summer 2017.
2. (2012) Blue Waters Petascale Undergraduate module: “Suffix trees: How to do Google search in bioinformatics?”, <http://www.shodor.org/petascale/materials/UPModules/suffixTrees/> (peer-reviewed).
3. (2009) Collaborative development of a high school curriculum, “Understanding algorithms for high school bioinformatics”, with Pallavi Ishwad @ Pittsburgh Supercomputing Center and Martha Narro @ University of Arizona, SC|09 Education Workshop @ Merced, CA, June 7-13.
4. (2009) Designed and taught a 1-week workshop, Computational biology for undergraduate biology educators, SC|09 Education Workshop @ UC Merced, Merced, CA, June 7-13.  
Materials available from <http://moodle.sc-education.org>.
5. (2007) Designed and presented a day-long workshop on “High-performance Computing for Bioinformatics”, SC|07 Education program’s UTEP’07: Parallel and Cluster Computing Workshop, University of Texas at El Paso, May 20-26.

## GRADUATE STUDENTS ADVISING

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## Current

1. Neda Zarayeneh, Ph.D. Computer Science, Summer 2017-
2. Marco Minutoli, Ph.D. Computer Science, Fall 2016-
3. Md. Methun Kamruzzaman, Ph.D. Computer Science, Fall 2015-
4. Priyanka Ghosh, Ph.D. Computer Science, Spring 2015-
5. Paola Gabriela Pesantez Cabrera, Ph.D. Computer Science, Fall 2013-
6. Armen Abnoui, Ph.D. (co-advisee; advisor: S. Broschat), Computer Science, Fall 2013-
7. Evan Olds, M.S. Computer Science, Fall 2013-

## Completed

1. Hao Lu, Ph.D. Computer Science, Summer 2012-Spring 2017  
Oak Ridge National Laboratory, TN
2. Jeff Daily, Ph.D. Computer Science, Spring 2012-Spring 2015  
Pacific Northwest National Laboratory, WA
3. Inna Rytsareva, Ph.D. Computer Science, Fall 2010-Summer 2014  
The Weather Channel (formerly @ CDC)
4. Tristan Mullis, M.S. Computer Science, Fall 2012-Spring 2014  
SEL Inc., WA
5. Turbo Majumder (co-advisee), Ph.D. Computer Engineering, Fall 2009-Spring 2013  
Intel, OR
6. Meena Rameshkumar, M.S. Computer Science, Fall 2010-Spring 2012  
Amazon, WA
7. Changjun Wu, Ph.D. Computer Science, Spring 2011  
Palantir, CA
8. Souradip Sarkar (co-advisee), Ph.D. Computer Engineering, Fall 2010  
Bell Labs, Belgium
9. Md. Muksitul Haque, M.S. Computer Science, Fall 2010  
Stryker, FL
10. Gaurav Kulkarni, M.S. Computer Science, Fall 2009  
Microsoft, WA
11. Vandhana Krishnan, M.S. Computer Science, Summer 2009  
Stanford University, CA

## UNDERGRADUATE RESEARCHERS

1. Samuel Schreiber, Lab intern, Summer 2017.
2. Ritche Long, Blue Waters Undergraduate Petascale Research Intern, 2015-2016.
3. Daryl Deford, REU, Summer 2012 (currently a PhD student at Dartmoth)
4. Lyle James Dallas, REU, Summer 2013, Summer 2014



5. Emma Conner, NSF REU site, Summer 2012
6. Joseph Taylor, NSF REU supplement, Summer 2012
7. Timothy Chapman, NSF REU supplement, Summer 2011
8. Michael Borgens, NSF REU supplement, Summer 2011
9. Emma Corner, NSF REU, Summer 2011
10. Hao Lu, Computer Science, Summer 2010-current *Blue Waters Undergraduate Petascale Research Intern*.
11. Benjamin Latt, Computer Science, Fall 2009-Summer 2010

## PROFESSIONAL ACTIVITIES

### Journal Editorial Board and Special Issues

1. Subject Area Editor, *Parallel Computing (PARCO)*, 2017-.
2. Associate Editor, *Journal of Parallel and Distributed Computing (JPDC)*, 2015-.
3. Associate Editor, *IEEE Transactions on Parallel and Distributed Systems (TPDS)*, 2014-.
4. Associate Editor, *Journal of Scientific Programming*, 2014-2016.
5. Journal Special Issue Guest Editor, *IEEE Transactions on Multi-Scale Computing Systems: Special Issue on Advances in Parallel Graph Processing: Algorithms, Architectures, and Application Frameworks*, along with Mahantesh Halappanavar (PNNL), Expected publication date: January 2018.
6. Supplement Editor, *BMC Bioinformatics, BMC Genomics SIs for ICCABS'13*, 2014.
7. Associate Editor, *Frontiers in Systems Microbiology*, 2013-.
8. Journal Special Issue Guest Editor, *IEEE Design & Test: Special Issue on Hardware Acceleration in Computational Biology*, along with Partha Pande, Expected publication date: January/February 2014.

### Conference and Workshop Leadership

1. Algorithms Track Vice-Chair, IEEE International Parallel and Distributed Processing Symposium (IPDPS), Vancouver, BC, Canada, May 2018.
2. Conference Program Co-chair, IEEE International Conference of Contemporary Computing (IC3), Noida, India, August 2017.
3. Applications Track Vice-Chair, "IEEE International Conference on High Performance Computing, Data, and Analytics" (HiPC), Jaipur, India, December 2017.
4. Minisymposium Organizer, "Advances in Dynamic Graphs: Algorithms, Applications and Challenges", SIAM Conference on Computational Science and Engineering (SIAM-CSE'17), Atlanta, GA, February 27-March 3, 2017.

5. Track co-chair for the Big Data in Bioinformatics track, “ACM Conference on Bioinformatics, Computational Biology, and Health Informatics” (ACM-BCB), 2017.
6. Workshop Chair, “ACM Conference on Bioinformatics, Computational Biology, and Health Informatics” (ACM-BCB), 2016.
7. Workshop Program Co-chair, “IEEE International Workshop on High Performance Computational Biology” (HiCOMB’16), 2016.
8. Workshop Co-chair, “IEEE International Workshop on Foundations of Big Data Computing”, in conjunction with HiPC 2015, Bengaluru, India, December 16, 2015.
9. Publicity Chair, “ACM Conference on Bioinformatics, Computational Biology, and Health Informatics” (ACM-BCB), 2015.
10. Workshop Co-chair, “The ACM International Workshop on Big Data in Life Sciences” (BigLS), to be held on September 9, 2015, Atlanta, GA (in conjunction with ACM BCB 2015).
11. Workshop Co-chair, “The ACM International Workshop on Big Data in Life Sciences” (BigLS), September 20, 2014, Newport Beach, CA (in conjunction with ACM BCB 2014).
12. Track chair, Bioinformatics and Computational Biology, ICIT’14.
13. Workshop Co-chair, “The 1<sup>st</sup> International Workshop on Big Data in Life Sciences” (BigLS), held in conjunction with IEEE ICCABS’2013 conference, New Orleans, LA, June 13, 2013.
14. Mini-symposium Organizer, “Scalable Graph-theoretic Models for Computational Biology”, SIAM Conference on Computational Science and Engineering (CSE’13), Boston, MA, February 25-March 1, 2013.
15. Program chair, IEEE International Workshop on High Performance Computational Biology, 2011 (HiCOMB’11).
16. Special session organizer, Session title: “Designing Hardware Accelerators for Biocomputing”, 2010 IEEE International Symposium on Circuits and Systems (ISCAS’10).

### **Conference Program Committee Memberships**

1. SBAC-PAD’17: International Symposium on Computer Architecture and High Performance Computing (SBAC-PAD), Campinas, Brazil, October 2017.
2. KDD bigdas’17: KDD Workshop on Big Data Analytics-as-a-Service: Architecture, Algorithms, and Applications in Health Informatics, Halifax, Canada, August 2017.
3. ParLearning’17 - The 6th International Workshop on Parallel and Distributed Computing for Large Scale Machine Learning and Big Data Analytics, Held in conjunction with IPDPS, 2017, Orlando, FL, USA.
4. International Conference on Parallel Processing (ICPP), 2017.
5. ACM-BCB, ACM Conference on Bioinformatics, Computational Biology and Biomedical Informatics, 2016.

6. International Conference on Computational Science (ICCS), 2016.
7. ACM-BCB, ACM Conference on Bioinformatics, Computational Biology and Biomedical Informatics, 2015.
8. IEEE International Conference on Computational Science and Engineering, 2015, Porto, Portugal.
9. IEEE International Parallel and Distributed Processing Symposium (IPDPS), 2015, Hyderabad, India.
10. ParLearning'15 - The 4th International Workshop on Parallel and Distributed Computing for Large Scale Machine Learning and Big Data Analytics, Held in conjunction with IPDPS, 2015, Hyderabad, India.
11. EduHPC: Workshop on Education for High-Performance Computing, held in conjunction with SC'14, 2014.
12. NSF/TCPP CDER Center Early Adopter Awards for Fall-14, 2014.
13. ACM Compute, Organized by ACM India chapter, October 9-11, 2014.
14. Fourth NSF/TCPP Workshop on Parallel and Distributed Computing Education (EduPar-14), Held in conjunction with IPDPS'14, 2014.
15. ACM International Workshop on Algorithms for Computational Biology, 2014 (ACB-14).
16. IEEE International Workshop on High Performance Computational Biology, 2014 (HiCOMB'14).
17. NSF/TCPP CDER Center Early Adopter Awards for Fall-13, 2013.
18. ACM-BCB'13 - ACM Conference on Bioinformatics, Computational Biology and Biomedical Informatics, 2013.
19. ParGraph'13 - Workshop on Parallel Algorithms and Software for Analysis of Massive Graphs, Held in conjunction with HiPC'13, 2013.
20. 19<sup>th</sup> IEEE International Conference on Parallel and Distributed Systems (ICPADS), 2013.
21. IEEE International Conference on High Performance Computing and Communications (HPCC), 2013.
22. IEEE International Conference on Computational Advances in Bio and Medical Sciences (ICCABS), 2013.
23. IEEE International Symposium on Parallel and Distributed Processing with Applications (ISPA), 2013.
24. International Conference on Parallel Processing (ICPP), 2013.
25. IEEE International Workshop on High Performance Computational Biology, 2013 (HiCOMB'13).
26. Parallel Computational Biology (PBC'13) Workshop, Held in conjunction with PPAM Conference, 2013.

27. The International Conference on High Performance Computing, Networking, Storage and Analysis (aka. Supercomputing 2013 or SC'13).
28. ParGraph'12 - Workshop on Parallel Algorithms and Software for Analysis of Massive Graphs, Held in conjunction with HiPC'12, 2012.
29. 12<sup>th</sup> International Conference on Algorithms and Architectures for Parallel Processing (ICA3PP-12), 2012.
30. 18<sup>th</sup> IEEE International Conference on Parallel and Distributed Systems (ICPADS), 2012.
31. IEEE International Conference on High Performance Computing and Communications (HPCC), 2012.
32. International Conference on Parallel Processing (ICPP), 2012.
33. IEEE International Workshop on High Performance Computational Biology, 2012 (HiCOMB'12).
34. IEEE International Conference on Computational Advances in Bio and Medical Sciences (ICCABS), 2012.
35. Workshop on Emerging Parallel Architectures (held as part of ICCS), 2012.
36. IEEE International Conference on Data Mining (ICDM11), 2011.
37. Workshop on Parallel Programming on Accelerator Clusters (PPAC11), held in conjunction with IEEE Cluster, 2011.
38. IEEE International Conference on High Performance Computing and Communications (HPCC), 2011.
39. HiPC 2011.
40. IEEE International Conference on Computational Advances in Bio and Medical Sciences (ICCABS), 2011.
41. International Conference on Advanced Communications and Computation (INFOCOMP), 2011.
42. Workshop on Using Emerging Parallel Architectures for Computational Science, (held as part of ICCS), 2011.
43. IEEE Cluster Workshop on Parallel Programming and Applications on Accelerator Clusters, 2010.
44. Workshop on Emerging Parallel Architectures (held as part of ICCS), 2010.
45. International Conference on Contemporary Computing, 2009 (IC<sup>3</sup>).
46. Workshop on Using Emerging Parallel Architectures for Computational Science, (held as part of ICCS), 2009.
47. Parallel Bio-Computing Workshop, 2009 (PBC'09).
48. The International Conference on High Performance Computing, Networking, Storage and Analysis (aka. Supercomputing 2008 or SC'08).

49. International Conference on High Performance Computing, 2008 (HiPC-08).
50. ACS/IEEE International Conference on Computer Systems and Applications, 2008 (AICCSA8).
51. IEEE International Workshop on High Performance Computational Biology, 2008 (HiCOMB).
52. International Conference on Parallel Processing, 2007 (ICPP).
53. IEEE International Parallel and Distributed Processing Symposium, 2007 (IPDPS).
54. Parallel Bio-Computing Workshop, 2007 (PBC).

## **Proposal and Paper Reviews**

1. Panelist, NSF, 2017.
2. Panelist, NSF, 2016.
3. Panelist, NIH, 2015
4. Panelist, BIO and MATH directorates, National Science Foundation, 2015.
5. Panelist, US Department of Energy, 2015
6. Panelist, US Department of Energy, 2014 (multiple panels).
7. Panelist, US Department of Energy, 2012.
8. Panelist, CISE directorate, National Science Foundation, 2010.
9. Panelist, BIO directorate, National Science Foundation, 2009.
10. Panelist, CSREES, United States Department of Agriculture, 2009.
11. Panelist, CISE directorate, National Science Foundation, 2008.
12. Other review activities: BMC Bioinformatics, BMC Research Notes, Bioinformatics, IEEE Transactions on Knowledge and Data Engineering, IEEE Transactions on Parallel and Distributed Computing, Journal of Data Mining and Knowledge Discovery, Journal of Parallel and Distributed Computing, Nucleic Acids Research, Parallel Computing, Parallel Processing Letters.

## **Invited Meetings**

1. PNNL Environmental Molecular Science Laboratory (EMSL): Breakthrough Science & Technology Workshop, Richland, WA, 2017.
2. DOE Office of Science Exascale Requirements Reviews, Biological and Environmental Research , Rockville, MD, 2016.
3. DOE Extreme Scale Research Conference, SDMA&V PI meeting, Walnut Creek, CA, January 13-15, 2015.
4. DOE Exascale Research Conference, PI meeting, Washington D.C., October 1-3, 2012.
5. DOE Exascale Research Conference, PI meeting, Portland, OR, April 16-18, 2012.

6. Session organizer, “Data intensive life sciences”, *Data Intensive Research Analytics Center Workshop*, University of Washington, Seattle, WA, January 15, 2010.
7. Microsoft Faculty Summit, Redmond, July 27-29, 2008.
8. DOE Exascale Townhall Meetings at: Oak Ridge National Laboratory (May 17-18, 2007), and Pacific Northwest National Laboratory (July 16-17, 2007).

## Other Academic Service

1. Data Analytics program, Faculty search committee chair, 2017.
2. Review Board, Center for Institutional Research Computing (CIRC), Washington State University, 2017-.
3. Member, Faculty Affairs Committee (Faculty senate sub-committee), Washington State University, 2016-.
4. Chair, Computer Science Curriculum Committee, School of EECS, Washington State University, 2015-.
5. Multiple Faculty Search Committees, School of EECS, Washington State University, 2015-2016.
6. Statistics Faculty search committee, Dept. Mathematics, Washington State University, 2015
7. VCEA cluster search committee, Washington State University, 2015
8. Multiple Faculty Search Committees, School of EECS, Washington State University, 2014-2015.
9. WSU Strategic Plan drafting committee, Washington State University, 2013.
10. Faculty Search Committee, School of EECS, Washington State University, 2013.
11. Senior Diversity Liaison, College of Engineering and Architecture representative, Washington State University, 2012-.
12. Faculty Search Committee, School of EECS, Washington State University, 2012.
13. Reid Miller Teaching Award Committee, School of EECS, Washington State University, 2012.
14. Cpt S Qualifying Exams Committee, School of EECS, Washington State University, 2012-.
15. Cpt S Curriculum Committee, School of EECS, Washington State University, 2011-.
16. Cpt S Faculty Search Committee, School of EECS, Washington State University, 2011-2012.
17. Reid Miller Teaching Award Committee, School of EECS, Washington State University, 2010.
18. Cpt S Faculty Search Committee, School of EECS, Washington State University, 2006-2007.
19. Graduate Advisory Committee, Department of Computer Science, Iowa State University, 2001-2003.
20. Colloquium Committee, Department of Computer Science, Iowa State University, 2001-2003.

## Training and Certification

1. Provost's Leadership Academy, Washington State University, 2012.
2. Preparing Future Faculty (certification), Iowa State University, 2003-2004.
3. Computing Writer's Workshop (training), Department of Computer Science, Iowa State University, 2003.
4. Personal Software Process (certification), Software Engineering Institute, Carnegie Mellon University, 1999.

## Memberships in Professional Societies

1. Association for Computing Machinery (*ACM*) Member, 2002-.
2. International Society for Computational Biology (*ISCB*) Member, 2006-.
3. Institute of Electrical and Electronics Engineers, Inc. (*IEEE*) Member, 2002-.
4. *IEEE* - Computer Society, Inc. (*IEEE-CS*) Member, 2011-.
5. Society for Industrial and Appplied Mathematics (*SIAM*) Member, 2004-.