

Ananth Kalyanaraman: Curriculum Vitae

(Revised July, 2017)

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

PUBLICATIONS¹

Publication Summary:

Peer-reviewed Publication Record

	Published or accepted		
	Total	Since joining WSU (2006)	Since tenure (2012)
Book chapters/encyclopedia articles	5	2	0
Journal articles	29	26	16
Conference/Workshop proceedings	39	34	21

Citation Report (as of June 2017)²

Citation Indices	All (or life-time)	Since 2012
Citations	5,232	4,185
h-index	17	14
i10-index	22	21

List of Publications:

- Downloadable PDFs for all peer-reviewed publications are available or can be accessed at: <http://eecs.wsu.edu/~ananth/publications.htm>
- * indicates student authors from the lab—i.e., authored/co-authored by student advisees/co-advisees.

Manuscripts Under Review or Revision

- R1. A. Panyala, O. Subasi, M. Halappanavar, A. Kalyanaraman and S. Krishnamoorthy. Approximation Techniques for Iterative Graph Algorithms. *2017 IEEE International Conference on High Performance Computing, Data, and Analytics (HiPC)*, Under review.
- R2. M. Kamruzzaman*, A. Kalyanaraman, B. Krishnamoorthy, P. S. Schnable. Toward A Scalable Exploratory Framework for Complex High-Dimensional Phenomics Data. *Bioinformatics*, Under Review.
bioRxiv Preprint: <http://www.biorxiv.org/content/early/2017/07/05/159954>.
- R3. P. Ghosh*, A. Kalyanaraman. A fast sketch-based assembler for genomes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB)*, Under revision.
- R4. P. Pesantez*, A. Kalyanaraman. Detecting communities in biological bipartite networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB)*, Under review.
bioRxiv Preprint: <http://www.biorxiv.org/content/early/2017/02/02/105197>.

¹Please see the section on “Supporting Information” at the end of this CV for more details about journal impact factors, conference rankings, and additional notes on my contributions.

²All data as reported by Google Scholar; Name variations under which I have published: “Ananth Kalyanaraman”, “Anantharaman Kalyanaraman”, “A. Kalyanaraman”

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. 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.
- J2. A. Abnousi*, 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.
- J3. 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.
- J4. 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.
- J5. 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.
- J6. 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
- J7. 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–May 2017.

- J8. 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
- J9. 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.
- J10. 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
- J11. 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.
- J12. 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.
- J13. 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.
- J14. 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.
- J15. 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.
- J16. 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>.
- J17. 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.
- J18. 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.
- J19. 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.

- J20. 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. Vecchietti, 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.
- J21. 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.
- J22. 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.
- J23. P.S. Schnable *et al.* The B73 Maize Genome: Complexity, diversity and dynamics. *Science*, 326(5956):1112-1115, 2009.
- J24. 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. Scarra, 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. Aluru¹, 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.
- J25. 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.
- J26. 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.
- J27. 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.
- J28. 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.
- J29. 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. 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)*, p.89, 2017.
- C2. 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**.
- C3. 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.
- C4. 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.
- C5. 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.
- C6. 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**.
- C7. A. Abnoui*, S. Broschat, A. Kalyanaraman. An alignment-free approach to cluster proteins using frequency of conserved k-mers. *Proc. 6th ACM Conference on Bioinformatics, Computational Biology and Health Informatics (ACM-BCB)*, pp. 597-606, 2015. DOI: 10.1145/2808719.2812223
- C8. 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.
- C9. 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
- C10. 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).
- C11. 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
- C12. 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.
- C13. M.V. Venkatasubramanian, A. Pothan, A. Kalyanaraman, D.J. Sobajic. Computational Challenges in Stability Monitoring of Power Systems using Large Number of PMUs (position pa-

- per). *Proc. 2013 National Workshop on Energy Cyber-Physical Systems*, organized by NSF, Arlington, VA, December 16-17, 2013, pp. 1-3.
- C14. 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
- C15. 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.
- C16. 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.
- C17. 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.
- C18. C. Wu*, A. Kalyanaraman. GPU-accelerated protein family identification for metagenomics. *Proc. 12th IEEE International Workshop on High Performance Computational Biology (HiCOMB)*, Held in conjunction with IPDPS 2013, pp. 559-568, 2013, Invited paper.
- C19. 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.
- C20. 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.
- C21. 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.
- C22. 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.
- C23. T. Chapman*, A. Kalyanaraman. An OpenMP algorithm and implementation for clustering biological graphs. *Proc. IA³ - Workshop on Irregular Applications: Architectures & Algorithms*, Held in conjunction with SC'11, pp. 3-10, 2011.
- C24. 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>.
- C25. 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.
- C26. T. Majumder*, S. Sarkar*, P. Pande, A. Kalyanaraman. An optimized NoC Architecture for accelerating TSP kernels in breakpoint median problem. *Proc. IEEE International Conference on Application-specific Systems, Architectures and Processors (ASAP)*, pp. 89-96, 2010.

- C27. S. Sarkar*, T. Majumder*, A. Kalyanaraman, P. Pande. Hardware accelerators for bio-computing: A survey. *Proc. IEEE International Symposium on Circuits and Systems (ISCAS)*, pp. 3789-3792, 2010.
- C28. 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.
- C29. 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.
- C30. 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.
- C31. 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.
- C32. 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.
- C33. 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.
- C34. 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.
- C35. 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. **Best Paper Award.**
- C36. 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. **Best Paper Award.**
- C37. 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.
- C38. 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.
- C39. 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 (SC’06)*, Tampa, FL, November 11-17, 2006.

Software Technologies

- SW1. *PaCE*: Software for parallel clustering of DNA sequences. Copyrighted with Iowa State University. Software has been publicly available since 2006, by contacting ananth@eecs.wsu.edu. Key Citation(s): Kalyanaraman *et al.*, NAR 2003, Kalyanaraman *et al.* TPDS 2003.
- SW2. *LTR-par*: Software for parallel identification of full-length LTR retrotransposons in genomes. Software has been publicly available since 2006, by contacting ananth@eecs.wsu.edu. It has also been available publicly in the open source domain at the DAWGPAWS tool distribution site: <http://dawgpaws.sourceforge.net/man.html>. Key Citation(s): Kalyanaraman *et al.*, JBCB 2007.
- 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.
- SW8. *Hyppo-X*: A Scalable Exploratory Framework for Complex High-Dimensional Data. (Key citations: Kamruzzaman, Kalyanaraman, Krishnamoorthy, ACM-BCB’16).
Lead student developer: Md. Methun Kamruzzaman
Open Source Website: <https://xperthut.github.io/HYPP0-X/>

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), Phoenix, 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 Biology, *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

Funding Activity

Over the course of the past 11 years, I have secured funding, either in the capacity of the lead Principal Investigator (PI) or a Co-Principal Investigator (Co-PI), from a number of funding venues. Below is a summary (in dollars) for those proposals which have been successfully awarded or approved.

PS: The numbers cited below represent the grand totals from those awards. The individual project amounts and my role in those projects are elaborated below the table.

	As the Lead PI	As a Co-PI	Total
Extramural	\$2,533,801	\$6,574,799	\$9,108,600
Intramural	\$14,700	\$5,000,000	\$5,014,700

Extramural Research Grants and Awards

- Co-PI**, \$1,719,179 (WSU part \$1,284,077), “Model-Driven Surveillance and Intervention Evaluation in Highly Stochastic Healthcare Settings”
Funding agency: Center for Disease Control and Prevention (CDC)
Funding program: Creation of a Healthcare-Associated Infectious Disease Modeling Network to Improve Prevention Research and Healthcare Delivery
Status: Recommended for funding (Expected start date: 8/1/2017, Expected end date: 7/31/2020).
PI: Eric Lofgren (Paul G. Allen School for Global Animal Health, WSU)
Co-PIs: Deverick Anderson (Duke University), Margaret Davis (Paul G. Allen School for Global Animal Health, WSU), Rebekah Moehring (Duke University), Ananth Kalyanaraman (School of EECS, WSU), Sandip Roy (School of EECS, WSU).
Project Role: The goal of this interdisciplinary project is to to construct a flexible, high-fidelity model of Healthcare-Associated Infectious (HAI) disease transmission. My role in the project is to develop the computational genomics and high performance computing capabilities that are needed to analyze the large swaths of genomic and clinical data to be generated by the Duke hospital facilities in this project.
- PI**, \$1,249,557 (WSU part \$761,428), “Collaborative Research: ABI Innovation: A Scalable Framework for Visual Exploration and Hypotheses Extraction of Phenomics Data using Topological Analytics”
Funding agency: National Science Foundation (NSF)
Funding program: Advances in Biological Informatics (ABI)
Dates: 8/1/2017-7/31/2020
Co-PIs: Bala Krishnamoorthy (Dept. Mathematics, WSU), Bei Wang Phillips (Scientific Computing and Imaging Institute, University of Utah), Patrick Schnable (Dept. Agronomy, Iowa State University), Zhiwu Zhang (Dept. Crop Soil Sciences, WSU)
Senior Personnel: Lawrence Holder (School of EECS, WSU).
Project Role: The goal of this interdisciplinary project is to develop novel visual analytics capabilities and hypothesis extraction methods for analyzing complex, high-dimensional phenomics data sets. I am the lead PI for this project.

3. **Co-PI**, \$911,651, “Development of an online course suite in tools for analysis of sensor-based behavioral health data (AHA!)”
Funding Agency: National Institutes of Health (NIH)
Funding Program: BD2K R25 program
Dates: 5/15/2017-4/30/2020
PI: Diane Cook (School of EECS, WSU)
Co-PIs: Roschelle Fritz (College of Nursing, WSU), Ananth Kalyanaraman (School of EECS, WSU), Maureen Schmitter-Edgecombe (Dept. Psychology, WSU) Gina Sprint (School of EECS, WSU), Douglas Weeks (St. Luke’s Rehabilitation Institute).
Project Role: This project aims to develop new online course and training materials for analyzing sensor-based health behavioral data. My role in the project is to lead the development of training materials pertaining to high performance computing and big data analytics of health behavioral data.
4. **PI**, \$73,244, “Algorithms for Scalable Approximate Graph Clustering on Streaming Data”
Funding Agency: Department of Defense (DOD): Pacific Northwest National Laboratory (PNNL) subcontract
Funding Program: High Performance Data Analytics (HPDA)
Dates: 8/16/2016-7/31/2017
PI: Mahantesh Halappanavar (PNNL)
Co-PIs: Ananth Kalyanaraman (WSU), Sriram Krishnamoorthy (PNNL), Arun Sathanur (PNNL).
Project Role: This is a collaborative project funded through the DOD HPDA program. My role in the project is to lead the algorithm development effort pertaining to dynamic graph clustering and in exploring approximation techniques into those methods.
5. **PI**, \$10,000, “Collaborative Research: Student Travel Support: International Workshop on Big Data in Life Sciences, Newport Beach, CA, September 20, 2014”
Funding Agency: National Science Foundation (NSF)
Funding Program: Computing and Communication Foundations (CCF)—Algorithmic Foundations (AF)
Dates: 7/1/2014-6/30/2015
Co-PI: Jaroslaw Zola (Dept. Computer Science and Engg., University of Buffalo).
Project Role: This is a student travel grant from NSF for attending the ACM-BCB BigLS workshop and the main conference. Both Jaroslaw Zola and I are co-organizers of the workshop.
6. **Co-PI**, \$666,969, ‘ ‘ABI Innovation: Next-Gen Clustering: Fast and accurate ways to cluster proteins”
Funding Agency: National Science Foundation (NSF)
Funding Program: Advances in Biological Informatics (ABI)
Dates: 8/29/2013-8/28/2018 (includes two years extension period)
PI: Shira Broschat (School of EECS, WSU)
Co-PIs: Doug Call (Paul G. Allen School for Global Animal Health, WSU), Ananth Kalyanaraman (School of EECS, WSU)
Project Role: This project aims to develop and implement scalable protein sequence clustering tools and port them to cloud computing platforms. My role in this project is to lead the algorithm development and high performance computing components of the project.

7. **PI**, \$750,000, “Early Career Award: Efficient graph kernels for extreme scale analysis of environmental community data”
Funding agency: Department of Energy (DOE)
Funding program: Early Career Research Program (DOE CAREER/ECRP), Advanced Scientific Computing Research (ASCR)
Dates: 8/16/2011 - 8/15/2018 (includes two years extension period)
Project Role: The goal of this career project is to develop parallel algorithms and software for extreme scale graph analytics, with applications to the analysis of large-scale environmental microbial community data (aka. metagenomics data), and other domains where similar graph applications arise.
8. **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”
Funding Agency: United States Department of Agriculture (USDA)
Funding Program: Earth Systems Modeling (EaSM)
Dates: 3/16/2011 - 3/15/2016
PI: Jennifer Adam (Dept. Civil & Environmental Engg., WSU)
Co-PIs: Michael Brady (School of Economic Sciences, WSU), Serena Chung (Dept. Civil & Environmental Engg., WSU), Raymond Evans (School of Biological Sciences, WSU), John Harrison (School of the Environment, WSU), Ananth Kalyanaraman (School of EECS, WSU), Chad Kruger (CSANR), Brian Lamb (Dept. Civil & Environmental Engg., WSU), Fok-Yan Leung (Dept. Civil & Environmental Engg., WSU), Andrew Perleberg (Forestry, WSU), Claudio Stockle (Biological Systems Engg., WSU), Joseph Vaughan (Dept. Civil & Environmental Engg., WSU), Jonathan Yoder (Dept. Biological Sciences, WSU).
Project Role: The goal of this project was this to develop a comprehensive set of earth system models for understanding biogeochemical cycling in the context of climate variability. My role as a Co-PI in this large project was to lead to the development and implementation of the cyberinfrastructure components of the project.
9. **PI**, \$451,000, “DC: Small: Efficient algorithms for data-intensive bio-computing”
Funding Agency: National Science Foundation (NSF)
Funding Program: IIS
Dates: 9/1/2009-8/31/2013
Co-PIs: Partha Pande (School of EECS, WSU), William Cannon (Computational Biology, PNNL).
Project Role: The goal of this project was to develop parallel graph and sequence algorithms, software, and high performance manycore architectures for several data-intensive computational biology applications. The project included a \$16,000 REU supplement. I was the lead PI of the project.
10. **Co-PI**, \$224,000, “An apple genome sequencing initiative”
Funding Agency: United States Department of Agriculture (USDA)
Funding Program: National Research Initiative (NRI)
Dates: 8/16/2008-12/31/2012
PI: Amit Dhingra (Dept. Horticulture, WSU)
Co-PI: Ananth Kalyanaraman (School of EECS, WSU)
Project Role: The goal of the project was to sequence the apple genome. My role was to lead all the computational components of the project including genome assembly, genome annotation, and comparative genomics.

Intramural Research Grants and Awards

1. **Co-PI**, \$5,000,000, “Community Health Analytics Initiative (CHAI)”
Funding Agency: Washington State University (WSU)
Funding Program: WSU Grand Challenges Initiative
Dates: 7/1/2016-6/30/2021
PI: Behrooz Shirazi (School of EECS, WSU)
Co-PIs: Shira Broschat (School of EECS, WSU), Douglas Call (Paul G. Allen School for Global Animal Health, WSU), Nairanjana Dasgupta (Dept. Mathematics, WSU), Glen Duncan (Elson S. Floyd College of Medicine, WSU), Ananth Kalyanaraman (School of EECS, WSU), Eric Lofgren (Paul G. Allen School for Global Animal Health, WSU), Guy Palmer (Paul G. Allen School for Global Animal Health, WSU), John Roll (Elson S. Floyd College of Medicine, WSU).
Project Role: This is one of the few grand challenge initiatives that were funded by the WSU Office of Research, as a long-term strategic investment to initiate and grow the area of community-based health analytics at WSU, in partnership with the Paul G. Allen School for Global Animal Health and the newly formed medical school (Elson S. Floyd College of Medicine). Most of the funds will be used to cluster hire faculty and other research staff members, along with grooming a new interdisciplinary cohort of PhD students. I am a Co-PI and a core faculty in this initiative.
2. **PI**, \$14,700, “Algorithms and Software for Large-scale Metagenomics”
Funding Agency: Washington State University (WSU)
Funding Program: WSU Seed Grant Program (jointly funded by WSU Office of Research and WSU Foundation)
Dates: 5/16/2008-8/15/2009
Project Role: The goal of this seed grant project is to develop preliminary methods for modeling and analyzing metagenomics data.

Pending Proposals

1. **Co-PI**, “CATALYST: Center for Architectures and Algorithms for Living Computing Systems”
Funding Agency: Defense Advanced Research Projects Agency (DARPA)
Funding Program: SRC JUMP
2. **PI**, “BIGDATA: F: Design Space Exploration for Scalable, Precise, and Cost-effective Combinatorial Big Data Applications”
Funding Agency: National Science Foundation (NSF)
Funding Program: BIGDATA
3. **Co-PI**, “Collaborative Research: Expeditions in Computational Science Behind Global Epidemic Phenomena: Models, Algorithms and Systems”
Funding Agency: National Science Foundation (NSF)
Funding Program: Expeditions in Computing
4. **Co-PI**, “Identifying Predictors of Antimicrobial Exposure for Application in the Standardized Antimicrobial Administration Ratio Risk Adjustment Strategy”
Funding Agency: Center for Disease Control and Prevention (CDC)

5. **Co-PI**, “NRT: Interdisciplinary Graduate Training in Community Health Data Analytics”
Funding Agency: National Science Foundation (NSF)
Funding Program: NSF Research Traineeship (NRT)
6. **Co-PI**, “MRI: Acquisition of a GPU and Coprocessor Expansion for Multidisciplinary Scientific Computing”
Funding Agency: National Science Foundation (NSF)
Funding Program: Major Research Instrumentation (MRI)

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. *CPTS 411: Introduction to Parallel Computing*³, School of EECS, WSU.
Semesters taught: Fa'14, Fa'15, Fa'16, Fa'17.
This is a senior elective for undergraduate students. It is one of the electives for students in the Data Science, Systems & Networking, and Artificial Intelligence tracks. I introduced this course to the curriculum.
Course website: <http://www.eecs.wsu.edu/~ananth/CptS411>.
2. *CPTS 471/571: Computational Genomics*⁴, School of EECS, WSU.
Semesters taught: Sp'07, Sp'08, Sp'09, Sp'10, Sp'11, Sp'13, Sp'14, Sp'15, Sp'16, Sp'17.
This is a course with conjoint listing for graduate students and undergraduates. It is one of the electives for students in the Data Science and General tracks. I introduced this course to the curriculum.
Course website: <http://www.eecs.wsu.edu/~ananth/CptS571>.
3. CPTS 317: Automata and Formal Languages, School of EECS, WSU.
Semesters taught: Sp'09, Sp'10, Sp'11, Sp'12, Sp'13, Sp'14, Sp'15, Sp'17.
This is a core undergraduate course. I developed this course from scratch when I taught it first time and have been refining it since.
Course website: <http://www.eecs.wsu.edu/~ananth/CptS317>.
4. CPTS 223: Advanced Data Structures, School of EECS, WSU.
Semesters taught: Fa'07, Fa'08, Fa'09, Fa'10, Fa'11, Fa'12.
This is a core undergraduate course. I co-developed this course with Prof. Larry Holder.
Course website: <http://www.eecs.wsu.edu/~ananth/CptS223>.
5. Graduate Teaching Assistant, Discrete Computational Structures (COM S 330), 3 credit course, Iowa State University, Spring 2001.

Curriculum Development

1. (2017) 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.

³Course listed as CPTS 483 until Fa'16.

⁴Course listed as CPTS 580 until Sp'11.

GRADUATE STUDENTS ADVISING

	Current	Completed
PhD thesis advisees/co-advisees	6	6
MS thesis advisees/co-advisees	0	5
Undergraduate researchers	2	10

Current Thesis Advisees

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 Ghosh⁵, 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: Shira Broschat), Computer Science, Fall 2013-

Completed Thesis Advisees

1. Hao Lu⁶, 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, Richland, WA
3. Inna Rytsareva, Ph.D. Computer Science, Fall 2010-Summer 2014
The Weather Channel (formerly at CDC), Atlanta, GA
4. Tristan Mullis, M.S. Computer Science, Fall 2012-Spring 2014
SEL Inc., Pullman, WA
5. Turbo Majumder (co-advisee; advisor: Partha Pande), Ph.D. Computer Engineering, Fall 2009-Spring 2013
Intel, Portland, OR (formerly, faculty at Indian Institute of Technology-Delhi (IIT), India)
6. Meena Rameshkumar, M.S. Computer Science, Fall 2010-Spring 2012
Amazon, Seattle, WA (formerly at VMWare, Inc.)
7. Changjun Wu, Ph.D. Computer Science, Spring 2011
Palantir, San Francisco, CA (formerly at Xerox Research)
8. Souradip Sarkar (co-advisee; advisor: Partha Pande), Ph.D. Computer Engineering, Fall 2010
Bell Labs, Belgium
9. Md. Muksitul Haque, M.S. Computer Science, Fall 2010
Stryker, Fort Lauderdale, FL
10. Gaurav Kulkarni, M.S. Computer Science, Fall 2009
Microsoft, Seattle, WA
11. Vandhana Krishnan, M.S. Computer Science, Summer 2009
Stanford University, Palo Alto, CA

⁵Priyanka Ghosh is a recipient of the WSU-PNNL Distinguished Graduate Research Fellowship effective Fall 2017.

⁶Hao Lu received the EECS Outstanding RA award in computer science for his dissertation research in Spring 2017.

UNDERGRADUATE RESEARCHERS

1. Samuel Schreiber, Lab intern, Summer 2017.
2. Matthew Green, Lab intern, Summer 2017.
3. Ritche Long, Blue Waters Undergraduate Petascale Research Intern, 2015-2016.
4. Daryl Deford, REU, Summer 2012 (currently a PhD student at Dartmoth)
5. Lyle James Dallas, REU, Summer 2013, Summer 2014
6. Emma Conner, NSF REU site, Summer 2012
7. Joseph Taylor, NSF REU supplement, Summer 2012
8. Timothy Chapman, NSF REU supplement, Summer 2011
9. Michael Borgens, NSF REU supplement, Summer 2011
10. Emma Corner, NSF REU, Summer 2011
11. Hao Lu, Computer Science, Summer 2010-current *Blue Waters Undergraduate Petascale Research Intern*.
12. Benjamin Latt, Computer Science, Fall 2009-Summer 2010

PROFESSIONAL ACTIVITIES

Journal Editorial Board and Special Issues

1. Associate Editor, *Journal of Parallel and Distributed Computing (JPDC)*, 2015-.
2. Associate Editor, *IEEE Transactions on Parallel and Distributed Systems (TPDS)*, 2014-.
3. Associate Editor, *Journal of Scientific Programming*, 2014-2016.
4. 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.
5. Supplement Editor, *BMC Bioinformatics, BMC Genomics SIs for ICCABS'13*, 2014.
6. Associate Editor, *Frontiers in Systems Microbiology*, 2013-.
7. 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, 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 1st 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, 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. 19th 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. 12th International Conference on Algorithms and Architectures for Parallel Processing (ICA3PP-12), 2012.
30. 18th 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 (IC³).
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).

University 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*), 2006-.
3. Institute of Electrical and Electronics Engineers, Inc. (*IEEE*) Member, 2002-.
4. Society for Industrial and Appplied Mathematics (*SIAM*) Member, 2004-.