

# Curriculum Vitae

## Ananth Kalyanaraman

Assistant Professor

School of Electrical Engineering and Computer Science

Washington State University

P.O Box 642752 Pullman, WA 99164

Office: EME 237

Phone: (509) 335-6760

Fax: (509) 335-3818 (departmental)

Email: [ananth@eecs.wsu.edu](mailto:ananth@eecs.wsu.edu)

Web: <http://www.eecs.wsu.edu/~ananth>

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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

Assistant Professor (Aug 2006 - present)	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 (Aug 1998 - Jan 2000)	Citicorp Overseas Software Ltd., Mumbai, India

## HONORS AND AWARDS

1. *Department of Energy Early Career Research Award*, 2011-2016.
2. *Research Excellence Award*, Iowa State University, Summer 2006.
3. *Best Paper Award. Proc. IEEE International Parallel and Distributed Processing Symposium, 2006 (IPDPS'06)*.
4. *Best Paper Award. Proc. IEEE Computational Systems Bioinformatics Conference, 2005 (CSB'05)*.
5. *IBM Ph.D. Fellowship*, Fall 2005 - Summer 2006.
6. *IBM Ph.D. Fellowship*, Fall 2004 - Summer 2005.
7. *Pioneer Hi-Bred Graduate Research Fellowship*, January - December 2003.
8. *Best Poster Award for Computing Applications. The International Symposium on Modern Computing*, Iowa State University, 2003.
9. *Research Excellence Award*, Iowa State University, Summer 2002.
10. Secured All India Rank 54 (98.03 percentile) in Graduate Aptitude Test in Engineering, 1998.

## PUBLICATIONS

### 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. 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)*, Accepted, 2012.
- J2. 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*, Preprint, 2012, DOI <http://doi.ieeecomputersociety.org/10.1109/TPDS.2012.19>.
- J3. **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.
- J4. 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.
- J5. T. Majumder, S. Sarkar, P. Pande, **A. Kalyanaraman**. NoC-Based Hardware Accelerator for Breakpoint Phylogeny. *IEEE Transactions on Computers*, 2011, In Press, doi:10.1109/TC.2011.100.
- J6. R. Velasco, A. Zharkikh, J. Affourtit, A. Dhingra, A. Cestaro, **A. Kalyanaraman**, P. Fontana, S.K. Bhatnagar, M. Troggo, 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. Chagn, 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.
- J7. 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.
- J8. 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.
- J9. P.S. Schnable *et al.* The B73 Maize Genome: Complexity, diversity and dynamics. *Science*, 326(5956):1112-1115, 2009.
- J10. 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. Col-lura, 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 Miguel1, 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.
- J11. **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.
- J12. **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.
- J13. 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.
- J14. **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.
- J15. **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. I. Rytsareva, Q. Le, E. Conner, **A. Kalyanaraman**, J. Panchal. Evaluating socio-technical coordination in open-source communities: A cluster-based approach. *Proc. ASME Interna-*

*tional Design Engineering Technical Conferences & Computers and Information in Engineering Conference (IDETC/CIE)*, Accepted, 2012.

- C2. 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.
- C3. 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.
- C4. T. Chapman, **A. Kalyanaraman**. An OpenMP algorithm and implementation for clustering biological graphs. *Proc. IA<sup>3</sup> - Workshop on Irregular Applications: Architectures & Algorithms*, To be held in conjunction with SC|11, pp. 3-10, 2011.
- C5. Turbo Majumder, Partha Pande, **Ananth 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>.
- C6. 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.
- C7. 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.
- C8. 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.
- C9. **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.
- C10. 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%)
- C11. 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.
- C12. 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%)
- C13. 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.

- C14. 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.
- C15. **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%)
- C16. **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.
- C17. **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.
- C18. 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%)
- C19. **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%)
- C20. **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**. 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.

- Ed2. **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.
- Ed3. **A. Kalyanaraman**. Computational biology education: “Transcriptomics: From small-scale to large-scale”. Presented at *SC|09 Education*, Portland, OR, November 14, 2009.
- Ed4. **A. Kalyanaraman** and J. Krause. Computational biology education: “Molecular Evolution and Phylogeny”. Presented at *SC|09 Education*, Portland, OR, November 15, 2009.
- Ed5. **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>.
- Ed6. **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.
- Ed7. 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.
- Ed8. 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.
- SW2. *LTR-par*: Software for parallel identification of full-length LTR retrotransposons in genomes.

## Invited Talks and Presentations

1. “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.
2. “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.
3. “Parallel Algorithms for Graph-theoretic Clustering of Biological Data”, *School of Mechanical and Materials Engineering*, WSU, February 17, 2011.
4. “Efficient parallel algorithms for data-intensive biocomputing”, *EECS executive board meeting*, Seattle, WA, October 15, 2010.

5. “Efficient algorithms for large-scale sequence analysis on parallel computers”, *School of Molecular Biosciences seminar*, WSU, August 26, 2010.
6. Plenary talk, “Data intensive life sciences”, *Data Intensive Research Analytics Center Workshop*, University of Washington, Seattle, WA, January 15, 2010.
7. Algorithms & Techniques for Parallel Genome Assembly and Sequence Clustering. Department of Biology, University of Utah, Salt Lake City, June 17-18, 2009.
8. Algorithms & Techniques to Reduce the Computational Burden of Protein Family Detection. J. Craig Venter Institute, Rockville, MD, 2009.
9. Algorithmic & HPC Issues in Microbial Community Genomics. DOE Exascale Townhall Meeting, Oak Ridge National Laboratory, May 17-18, 2007.
10. 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**, \$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 - 8/15/2016.
2. **PI**, \$16,000, REU supplement: DC: Small: Efficient algorithms for data-intensive bio-computing, NSF IIS #0916463, 5/16/2011-8/31/2012.
3. **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.
4. **PI**, \$435,000, DC: Small: Efficient algorithms for data-intensive bio-computing, NSF IIS #0916463, 9/1/2009-8/31/2012.
5. **Co-PI**, \$224,000, An apple genome sequencing initiative, USDA NRI, 8/16/2008-8/15/2010.
6. **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**, NSF TeraGrid Resource Allocation Program, “Data-intensive Protein Bioinformatics on the TeraGrid”, 30K CPU hours (startup)

## TEACHING ACTIVITIES

### Course Instruction

1. Designed and Taught: “Automata and Formal Languages” (Cpt S 317), School of EECS, WSU.

Spring 2009, Spring 2010, Spring 2011.

2. Designed and Taught: “Advanced Data Structures” (Cpt S 223), School of EECS, WSU. Fall 2007, Fall 2008, Fall 2009, Fall 2010.
3. Designed and Taught: “Fundamental Algorithms in Computational Genomics” (Cpt S 571/471), School of EECS, WSU. Spring 2007, Spring 2008, Spring 2009, Spring 2010, Spring 2011.
4. Teaching Assistant, Discrete Computational Structures (COM S 330), 3 credit course, Iowa State University, Spring 2001.

## Curriculum Development

1. (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.
2. (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>.
3. (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. Jeff Daily, Ph.D. Computer Science, Spring 2012-
2. Inna Rytsareva, Ph.D. Computer Science, Fall 2010-
3. Turbo Majumder (co-advisee), Ph.D. Computer Engineering, Fall 2009-
4. Hao Lu, M.S. Computer Science, Spring 2012-
5. George Gruber, M.S. Computer Science, Spring 2012-

### Completed

1. Meena Rameshkumar, M.S. Computer Science, Fall 2010-Spring 2012  
To join VMWare, Inc.
2. Changjun Wu, Ph.D. Computer Science, Spring 2011  
Currently a researcher at Xerox Research, Webster, NY
3. Souradip Sarkar (co-advisee), Ph.D. Computer Engineering, Fall 2010  
Currently a researcher at ExaScience Lab, Intel Labs, Leuven, Belgium
4. Md. Muksitul Haque, M.S. Computer Science, Fall 2010  
Currently a PhD student at WSU

5. Gaurav Kulkarni, M.S. Computer Science, Fall 2009  
Currently a software developer SEL Inc. (First job after graduation: Pacific Northwest National Laboratory)
6. Vandhana Krishnan, M.S. Computer Science, Summer 2009  
Currently a PhD student at University of Idaho

## **UNDERGRADUATE RESEARCHERS**

1. Timothy Chapman, NSF REU supplement, Summer 2011
2. Michael Borgens, NSF REU supplement, Summer 2011
3. Emma Corner, NSF REU, Summer 2011
4. Hao Lu, Computer Science, Summer 2010-current  
*Blue Waters Undergraduate Petascale Research Intern.*
5. Benjamin Latt, Computer Science, Fall 2009-Summer 2010

## **PROFESSIONAL ACTIVITIES**

### **Conference and Workshop Leadership**

1. Program chair, IEEE International Workshop on High Performance Computational Biology, 2011 (HiCOMB'11).
2. 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. ParGraph - Workshop on Parallel Algorithms and Software for Analysis of Massive Graphs, Held in conjunction with HiPC'12, 2012.
2. 12<sup>th</sup> International Conference on Algorithms and Architectures for Parallel Processing (ICA3PP-12), 2012.
3. 18<sup>th</sup> IEEE International Conference on Parallel and Distributed Systems (ICPADS), 2012.
4. IEEE International Conference on High Performance Computing and Communications (HPCC), 2012.
5. International Conference on Parallel Processing (ICPP), 2012.
6. IEEE International Conference on Computational Advances in Bio and Medical Sciences (ICCABS), 2012.
7. Workshop on Emerging Parallel Architectures (held as part of ICCS), 2012.
8. IEEE International Conference on Data Mining (ICDM11), 2011.
9. Workshop on Parallel Programming on Accelerator Clusters (PPAC11), held in conjunction with IEEE Cluster, 2011.

10. IEEE International Conference on High Performance Computing and Communications (HPCC), 2011.
11. HiPC 2011.
12. IEEE International Conference on Computational Advances in Bio and Medical Sciences (ICCABS), 2011.
13. International Conference on Advanced Communications and Computation (INFOCOMP), 2011.
14. Workshop on Using Emerging Parallel Architectures for Computational Science, (held as part of ICCS), 2011.
15. IEEE Cluster Workshop on Parallel Programming and Applications on Accelerator Clusters, 2010.
16. Workshop on Emerging Parallel Architectures (held as part of ICCS), 2010.
17. International Conference on Contemporary Computing, 2009 (IC<sup>3</sup>).
18. Workshop on Using Emerging Parallel Architectures for Computational Science, (held as part of ICCS), 2009.
19. Parallel Bio-Computing Workshop, 2009 (PBC'09).
20. Supercomputing 2008 (SC|08).
21. International Conference on High Performance Computing, 2008 (HiPC-08).
22. ACS/IEEE International Conference on Computer Systems and Applications, 2008 (AICCSA8).
23. IEEE International Workshop on High Performance Computational Biology, 2008 (HiCOMB).
24. International Conference on Parallel Processing, 2007 (ICPP).
25. IEEE International Parallel and Distributed Processing Symposium, 2007 (IPDPS).
26. Parallel Bio-Computing Workshop, 2007 (PBC).

## **Proposal and Paper Reviews**

1. Panelist, CISE directorate, National Science Foundation, 2010.
2. Panelist, BIO directorate, National Science Foundation, 2009.
3. Panelist, CSREES, United States Department of Agriculture, 2009.
4. Panelist, CISE directorate, National Science Foundation, 2008.
5. 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. DOE Exascale Research Conference, PI meeting, Portland, OR, April 16-18, 2012.
2. Session organizer, “Data intensive life sciences”, *Data Intensive Research Analytics Center Workshop*, University of Washington, Seattle, WA, January 15, 2010.
3. Microsoft Faculty Summit, Redmond, July 27-29, 2008.
4. 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. Reid Miller Teaching Award Committee, School of EECS, Washington State University, 2012.
2. Cpt S Qualifying Exams Committee, School of EECS, Washington State University, 2012-.
3. Cpt S Curriculum Committee, School of EECS, Washington State University, 2011-.
4. Cpt S Faculty Search Committee, School of EECS, Washington State University, 2011-2012.
5. Reid Miller Teaching Award Committee, School of EECS, Washington State University, 2010.
6. Cpt S Faculty Search Committee, School of EECS, Washington State University, 2006-2007.
7. Graduate Advisory Committee, Department of Computer Science, Iowa State University, 2001-2003.
8. Colloquium Committee, Department of Computer Science, Iowa State University, 2001-2003.

## Training and Certification

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

## Memberships in Professional Societies

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