Curriculum Vitae: Tamer Kahveci

Associate Professor

Department of Computer and Information Science and Engineering University of Florida, Gainesville, FL 32611-6120, USA

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URL: http://www.cise.ufl.edu/~tamer/Lab-URL: http://bioinformatics.cise.ufl.edu

Phone: 1-352-505 1554 **Fax:** 1-352-392 1220

Research Interests: Bioinformatics. Computational Biology. Indexing, querying, and mining bioinformatics data. Comparison and analysis of genomic, metabolomic, proteomic data and biological networks.

Education

1999 - 2004 Doctor of Philosophy in Computer Science

University of California, Santa Barbara

Dissertation: Indexing and querying of sequence databases.

1993 - 1997 B.S. in Computer Engineering and Information Science

University of Bilkent, Ankara, Turkey

Teaching Experience

2010-now	Associate Professor, CISE, University of Florida
2004-2010	Assistant Professor, CISE, University of Florida
1999-2000	Teaching Assistant, University of California, Santa Barbara
1997-1999	Teaching Assistant, University of Bilkent, Ankara, Turkey

Positions

2010-now	Associate Professor, CISE, University of Florida
2004-2010	Assistant Professor, CISE, University of Florida

Graduate Advisor

Ambuj Singh, Computer Science Department, University of California, Santa Barbara

Honors

2011	Honorary best paper award at the ACM International Conference on Bioinformatics and Computational Biology
2010	Best student paper award at the ACM International Conference on Bioinformatics and
	Computational Biology
2009	NSF Career Award
2008	University of Florida, Research Initiative Award.
2008	Best paper award at the International Conference on Computational Systems Biology.
2006	ORAU Powe Junior Faculty Enhancement Award
1993	Silver medal at International Mathematics Olympiads

Professional Organizations

Member of ACM, IEEE, ICSB, SIG-BIO

Journal publications

- 1. Ahmet Ay, Dihong Gong, <u>Tamer Kahveci</u>. *Network-based Prediction of Cancer under Genetic Storm*. Cancer Informatics. 2014 (42 pages) (accepted)
- Andrei Todor, Haitham Gabr, Alin Dobra, <u>Tamer Kahveci</u>. Large scale analysis of signal reachability. Bioinformatics. In press. (International Conference on Intelligent Systems for Molecular Biology (ISMB)) 2014.
- Andrei Todor, Alin Dobra, <u>Tamer Kahveci</u>. Characterizing topology of probabilistic biological networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics Journal (IEEE/ACM TCBB). 10:4, 2013.
- 4. Mahmudul Hasan, Yusuf Kavurucu and <u>Tamer Kahveci</u>. *A scalable method for discovering significant subnetworks*. BMC Systems Biology. 7:4, 2013.
- 5. Saad Sheikh, <u>Tamer Kahveci</u>, Sanjay Ranka, Gordon Burleigh. *Stability Analysis of Phylogenetic Trees*, Bioinformatics, 29:2, 2013.
- 6. Jesse F. Gregory III*, Youngja Park, Yvonne Lamers, Nirmalya Bandyopadhyay, Yueh-Yun Chi, Kichen Lee, Steven Kim, Vanessa da Silva, Nicholas Hove, Sanjay Ranka, <u>Tamer Kahveci</u>, Keith E. Muller, Robert D. Stevens, Christopher B. Newgard, Peter W. Stacpoole, and Dean P. Jones. *Metabolomic Analysis Reveals Extended Metabolic Consequences of Marginal Vitamin B-6 Deficiency in Healthy Human Subjects*. PloS ONE, 8:6, 2013.
- 7. Andrei Todor, Alin Dobra, <u>Tamer Kahveci</u>. *Probabilistic Biological Network Alignment*, IEEE/ACM Transactions on Computational Biology and Bioinformatics Journal (IEEE/ACM TCBB). 10:1, 2013.
- Seyedsasan Hashemikhabir, Eyup Serdar Ayaz, Yusuf Kavurucu, Tolga Can, <u>Tamer Kahveci</u>. Large scale signaling network reconstruction. IEEE/ACM Transactions on Computational Biology and Bioinformatics Journal. 9:6, 2012.
- 9. Gunhan Gulsoy, Nirmalya Bandhyopadhyay, <u>Tamer Kahveci</u>. *HIDEN: Hierarchical decomposition of regulatory networks*. BMC Bioinformatics, 13:250, 2012.
- 10. Avinash Ramu, Gordon Burleigh, <u>Tamer Kahveci</u>. A scalable method for identifying frequent subtrees in sets of large phylogenetic trees, BMC Bioinformatics, 13:250, 2012.
- 11.Gunhan Gulsoy, Bhavik Gandhi, <u>Tamer Kahveci</u>. *TOPAC: Alignment of gene regulatory networks using topology aware coloring*, Journal of Bioinformatics and Computational Biology (JBCB), 10:1, 2012.
- 12. Daniel Marbach, Sushmita Roy, Ferhat Ay, Patrick E. Meyer, Rogerio Candeias, <u>Tamer Kahveci</u>, Christopher A. Bristow, and Manolis Kellis. *Predictive regulatory models in Drosophila melanogaster by integrative inference of transcriptional networks*, Genome Research, 22 (7): 1334-49, 2012.
- 13. Nirmalya Bandyopadhyay, Manas Somaiya, Sanjay Ranka, <u>Tamer Kahveci</u>. *CMRF: Analyzing Differential Gene Regulation in Two Group Perturbation Experiments*, BMC Genomics, 13:2, 2012.
- 14. Michael Dang, Ferhat Ay, <u>Tamer Kahveci</u>. *Metabolic network alignment in large scale by network compression*, BMC Bioinformatics vol 13, 2012.
- Gunhan Gulsoy, <u>Tamer Kahveci</u>. RINQ: Reference-based Indexing for Network Queries, Bioinformatics, 27 (13): i149-i158. (International Conference on Intelligent Systems for Molecular Biology (ISMB), 2011)
- 16.Basma El Yacoubi, Isabelle Hatin, Christopher Deutsch, <u>Tamer Kahveci</u>, Jean-Pierre Rousset, Dirk Iwata-Reuyl, Alexey G Murzin and Valerie de Crecy-Lagard. *A role for the universal Kae1/Qri7/YgjD (COG0533) family in tRNA modification*, The EMBO Journal advance online

- publication 1 February 2011; doi:10.1038/emboj.2010.363.
- 17. Ferhat Ay, Manolis Kellis, <u>Tamer Kahveci</u>. SubMAP: Aligning metabolic pathways with subnetwork mappings, Journal of Computational Biology, 18(3):1-17, 2011.
- 18.Bin Song, I. Esra Buyuktahtakin, Sanjay Ranka, <u>Tamer Kahveci</u>. *Manipulating the steady state of metabolic pathways*, IEEE/ACM Transactions on Computational Biology and Bioinformatics (IEEE TCBB), 8(3), pages 732-747, 2011.
- 19. Jayendra Venkateswaran, Bin Song, <u>Tamer Kahveci</u>, Christopher Jermaine. *TRIAL: A Tool for Finding Distant Structural Similaritie*, IEEE/ACM Transactions on Computational Biology and Bioinformatics (IEEE TCBB), 8(3), pages 819-831, 2011.
- 20. Nirmalya Bandyopadhyay, Sanjay Ranka, Y. Sun, Steve Goodison, <u>Tamer Kahveci</u>. *Pathway based Feature Selection for Cancer Microarray Data*, Journal of Advances in Bioinformatics, accepted for publication.
- 21. Nirmalya Bandyopadhyay, <u>Tamer Kahveci</u>. *GBA Manager*: An online tool for querying low complexity regions in proteins, Journal of Computational Biology, 17(1):73-7, 2010.
- 22. Ferhat Ay, Fei Xu, <u>Tamer Kahveci</u>. Scalable Steady State Analysis of Boolean Biological Regulatory Networks, PLoS ONE 4(12), pages e7992, 2009.
- 23. Jun Liu, Nirmalya Bandyopadhyay, Sanjay Ranka, Michael Baudis, <u>Tamer Kahveci.</u> Inferring Progression Models for CGH data, Bioinformatics, 25:15, pages 2208-2215, 2009.
- 24. Ferhat Ay, <u>Tamer Kahveci</u>, Valerie de Crecy-Lagard. *A Fast And Accurate Algorithm For Comparative Analysis Of Metabolic Pathways*, Journal of Bioinformatics and Computational Biology (JBCB), 7:3, pages 389-428, 2009.
- 25.Bin Song, Padmavati Sridhar, <u>Tamer Kahveci</u> and Sanjay Ranka. *Double Iterative Optimization for Metabolic Network-Based Drug Target Identification*, International Journal of Data Mining and Bioinformatics, 3:2, pages 145-159, 2009.
- 26.Jun Liu, Sanjay Ranka, <u>Tamer Kahveci</u>. Classification and Feature Selection Algorithms for Multi-class CGH data, Bioinformatics, 24 (13): i86-i95. (International Conference on Intelligent Systems for Molecular Biology (ISMB), 86-95, 2008)
- 27. Xuehui Li, <u>Tamer Kahveci</u>, and A. Mark Settles. *A Novel Genome-Scale Repeat Finder Geared towards Transposons*, Bioinformatics, 24(4): 468-476, 2008.
- 28. Jayendra Venkateswaran, Deepak Lachwani, <u>Tamer Kahveci</u>, Christopher Jermaine. *Reference-Based Indexing for Metric Spaces with Costly Distance Measures*, the VLDB Journal, 17:5, pages 1231 - 1251, 2008.
- 29. Xu Zhang, <u>Tamer Kahveci.</u> *QOMA: Quasi-Optimal Multiple Alignment of Protein Sequences*, Bioinformatics, 23:2, pages 162-168, 2007.
- 30. Jun Liu, Sanjay Ranka, <u>Tamer Kahveci.</u> *Markers improve clustering of CGH data*, Bioinformatics, 23:4, pages 450-457, 2007.
- 31. Xuehui Li, <u>Tamer Kahveci</u>. A novel algorithm for identifying low-complexity regions in a protein sequence, Bioinformatics, 22:24, pages 2980-2987, 2006.
- 32. Jun Liu, Jaaved Mohammed, James Carter, Sanjay Ranka, <u>Tamer Kahveci</u>, Michael Baudis. *Distance-based Clustering of CGH Data*, Bioinformatics, 22:16, pages 1971-1978, 2006.
- 33. <u>Tamer Kahveci</u> and Ambuj K. Singh. *Optimizing Similarity Search for Arbitrary Length Time Series Queries*, IEEE Transactions on Knowledge and Data Engineering (TKDE), 16:4, pages 418-433, 2004.
- 34. Orhan Camoglu, <u>Tamer Kahveci</u> and Ambuj K. Singh. *Towards Index-based Similarity Search for Protein Structure Databases*, Journal of Bioinformatics and Computational Biology (JBCB),

- 2:1, pages 99-126, 2004.
- 35. <u>Tamer Kahveci</u>, Vebjorn Ljosa and Ambuj K. Singh. *Speeding up Whole Genome Alignment by Indexing Frequency Vectors*, Bioinformatics, 20:13, pages 2122-2134, 2004.
- 36. <u>Tamer Kahveci</u> and Ambuj K. Singh. *Progressive Searching of Biological Sequences*, IEEE Database Engineering Bulletin, 2004.
- 37.Orhan Camoglu, <u>Tamer Kahveci</u>, Ambuj K. Singh. *PSI: Indexing Protein Structures for Fast Similarity Search*, Bioinformatics (2003) 19: i81-i83. (International Conference on Intelligent Systems for Molecular Biology (ISMB), 2003)

Peer reviewed conference publications

- 38. Haitham Gabr, <u>Tamer Kahveci</u>. Characterization of probabilistic signaling networks through signal propagation. IEEE International Conference on Computational Advances in Bio and medical Sciences (ICCABS), 2014.
- 39. Mahmudul Hasan, <u>Tamer Kahveci</u>. Color distribution can accelerate network alignment. International Conference on Bioinformatics and Computational Biology (ACM-BCB), 2013.
- 40. Haitham Gabr, Andrei Todor, Helia Zandi, Alin Dobra, <u>Tamer Kahveci</u>. *PReach: Reachability in Probabilistic Signaling Networks*. International Conference on Bioinformatics and Computational Biology (ACM-BCB), 2013.
- 41. Haitham Gabr, Alin Dobra, <u>Tamer Kahveci</u>, *From uncertain protein interaction networks to signaling pathways through intensive color coding*, Pacific Symposium on Biocomputing (PSB), 2013.
- 42. Gunhan Gulsoy, <u>Tamer Kahveci</u>. *Inferring gene functions from metabolic reactions*. IEEE International Workshop on Genomic Signal Processing and Statistics (GENSIPS), 2012.
- 43. Andrei Todor, Alin Dobra, <u>Tamer Kahveci</u>, <u>Uncertain interactions affect degree distribution of biological networks</u>, International Conference On Bioinformatics and Computational Biology (IEEE-BIBM), 2012.
- 44. Mahmudul Hasan, Yusuf Kavurucu, <u>Tamer Kahveci</u>, *SiS: Significant Subnetworks in Massive Number of Network Topologies, International Conference*, On Bioinformatics and Computational Biology (IEEE-BIBM), 2012.
- 45. Nirmalya Bandyopadhyay, Manas Somiya, Sanjay Ranka, <u>Tamer Kahveci</u>. *SSLPred : Predicting Synthetic Sickness Lethality*, Pacific Symposium on Biocomputing (PSB), 2012.
- 46.Gunhan Gulsoy, Bhavik Gandhi, <u>Tamer Kahveci</u>, *Topology aware coloring of gene regulatory networks*, International Conference On Bioinformatics and Computational Biology (ACM-BCB), 2011.
- 47. Michael Dang, Ferhat Ay, <u>Tamer Kahveci</u>, *A Novel Framework for Large Scale Metabolic Network Alignments by Compression*, International Conference On Bioinformatics and Computational Biology (ACM-BCB), 2011. **(Honorary best paper)**
- 48. Nirmalya Bandyopadhyay, Manas Somiya, Sanjay Ranka, <u>Tamer Kahveci</u>, *Identifying Differentially Regulated Genes*, IEEE International Conference on Computational Advances in Bio and medical Sciences (ICCABS), 2011.
- Ferhat Ay, Gunhan Gulsoy, <u>Tamer Kahveci</u>, *Finding Steady States of Large Scale Regulatory Networks through Partitioning*, IEEE International Workshop on Genomic Signal Processing and Statistics (GENSIPS), 2010.
- 50.Nirmalya Bandyopadhyay, Manas Somiya, Sanjay Ranka, <u>Tamer Kahveci</u>, <u>Modeling</u> Perturbations using Gene Networks, International Conference on Computational Systems

- Biology (CSB), 2010.
- 51. Ferhat Ay, <u>Tamer Kahveci</u>, *SubMAP: Aligning metabolic pathways with subnetwork mappings*, International Conference on Research in Computational Biology (RECOMB), 2010.
- 52.Bin Song, Sanjay Ranka, <u>Tamer Kahveci</u>, *Enzymatic target identification with dynamic states*, International Conference On Bioinformatics and Computational Biology (ACM-BCB), 2010. (Best student paper award)
- 53. Ferhat Ay, <u>Tamer Kahveci</u>, *Functional Similarities of Reaction Sets in Metabolic Pathways*, International Conference On Bioinformatics and Computational Biology (ACM-BCB), 2010.
- 54.Nirmalya Bandyopadhyay, Mark Settles, <u>Tamer Kahveci</u>, RepFrag: A Graph based Method for Finding Repeats and Transposons from Fragmented Genomes, International Conference On Bioinformatics and Computational Biology (ACM-BCB), 2010.
- 55. Ferhat Ay, Thang N. Dinh, My T. Thai, <u>Tamer Kahveci</u>, *Finding Dynamic Modules of Biological Regulatory Networks*, IEEE International Conference on Bioinformatics and Bioengineering (BIBE), 2010.
- 56. Fei Xu, Ravi Jampani, Mingxi Wu, Chris Jermaine, <u>Tamer Kahveci</u>, Surrogate Ranking for Very Expensive Similarity Queries, International Conference on Data Engineering (ICDE), 848-859, 2010.
- 57. Ferhat Ay, Fei Xu, <u>Tamer Kahveci</u>, *Scalable Steady State Analysis of Boolean Biological Regulatory Networks*, RECOMB RG/SB/DREAM, 2009.
- 58. Ferhat Ay, <u>Tamer Kahveci</u>, Valerie de Crecy-Lagard, *Consistent alignment of metabolic pathways without any abstraction in modeling*, International Conference on Computational Systems Biology (CSB), 2008. **(Best paper award)**
- 59. Padmavati Sridhar, Bin Song, <u>Tamer Kahveci</u> and Sanjay Ranka, *Mining metabolic networks for optimal drug targets*, Pacific Symposium on Biocomputing (PSB), 13: 291-302, 2008.
- 60.Xu Zhang, <u>Tamer Kahveci</u>, *QOMA2: Optimizing the alignment of many sequences*, IEEE International Conference on Bioinformatics and Bioengineering (BIBE), 780-787, 2007.
- 61. Padmavati Sridhar, <u>Tamer Kahveci</u>, Sanjay Ranka, *An iterative algorithm for metabolic network-based drug target identification*, Pacific Symposium on Biocomputing (PSB), 88-99, 2007.
- 62. Xuehui Li, <u>Tamer Kahveci</u>, *Quality-based similarity search for biological sequence databases*, BIOCOMP, 567-573, 2007.
- 63. Jun Liu, Sanjay Ranka, and <u>Tamer Kahveci</u>, *A web server for mining Comparative Genomic Hybridization (CGH) data*, Data mining, systems analysis and optimization in biomedicine, pages 144-131, 2007.
- 64. Jayendra Venkateswaran, Deepak Lachwani, <u>Tamer Kahveci</u>, Christopher Jermaine, *Reference-based Indexing of Sequence Databases*, International Conference on Very Large Databases (VLDB), 906-917, 2006.
- 65. Jayendra Venkateswaran, <u>Tamer Kahveci</u>, Orhan Camoglu, *Finding Data Broadness via Generalized Nearest Neighbors*, International Conference on Extending Database Technologies (EDBT), 645-663, 2006.
- 66.Xu Zhang, <u>Tamer Kahveci</u>. A New Approach for Alignment of Multiple Proteins, Pacific Symposium on Biocomputing (PSB), 339-350, 2006.
- 67. Yue Li, Lan Luo, Tao Li and <u>Tamer Kahveci</u>, *Microarchitecture Characteristics and Implications of Alignment of Multiple Bioinformatics Sequences*, Workshop on Unique Chips and Systems (Held in conjunction with IEEE International Symposium on Performance Analysis of Systems and Software), 2006.

- 68. <u>Tamer Kahveci</u>, Venkatakrishnan Ramaswamy, Han Tao, Tao Li, *Approximate Global Alignment of Sequences*, IEEE International Conference on Bioinformatics and Bioengineering (BIBE), 81-88, 2005.
- 69. Abhijit Pol, <u>Tamer Kahveci</u>, *Highly Scalable and Accurate Seeds for Subsequence Alignment*, IEEE International Conference on Bioinformatics and Bioengineering (BIBE), 27-31, 2005.
- 70. Yue Li, Tao Li, <u>Tamer Kahveci</u>, Jose Fortes, *Workload Characterization of Bioinformatics Applications on Pentium 4 Architecture*, MASCOTS, 15-22, 2005.
- 71.Arnab Bhattacharya, Tolga Can, <u>Tamer Kahveci</u>, Ambuj K. Singh, Yuan-Fang Wang, *ProGreSS: Simultaneous Searching of Protein Databases by Sequence and Structure*, Pacific Symposium on Biocomputing (PSB), 264-275, 2004.
- 72. Orhan Camoglu, <u>Tamer Kahveci</u>, Ambuj K. Singh, *Towards Index-based Similarity Search for Protein Structure Databases*, International Conference on Computational Systems Biology (CSB), 148-158, 2003.
- 73. <u>Tamer Kahveci</u>, Christian Lang, Ambuj K. Singh, *Joining Massive High-Dimensional Databases*, International Conference on Data Engineering (ICDE), 264-276, 2003.
- 74. <u>Tamer Kahveci</u>, Ambuj K. Singh, *MAP: Searching Large Genome Databases*, Pacific Symposium on Biocomputing (PSB), 303-314, 2003.
- 75. <u>Tamer Kahveci</u>, Ambuj K. Singh, and Aliekber Gurel, *Similarity Searching for Multi-Attribute Sequences*, Statistical and Scientific Database Management (SSDBM), 2002.
- 76. <u>Tamer Kahveci</u> and Ambuj K. Singh. *An Efficient Index Structure for String Databases*, International Conference on Very Large Databases (VLDB), 2001.
- 77. <u>Tamer Kahveci</u> and Ambuj K. Singh, *Variable Length Queries for Time Series Data*, International Conference on Data Engineering (ICDE), 2001, pages 273-282.
- 78. Tuba Yavuz-Kahveci, <u>Tamer Kahveci</u> and Ambuj K. Singh, *Buffering of Index Structures*, SPIE, 2000.

Book chapters

- Bin Song, I. Esra Büyüktahtakin, Nirmalya Bandyopadhyay, Sanjay Ranka and Tamer Kahveci, Identifying Enzyme Knockout Strategies on Multiple Enzyme Associations, Bioinformatics - Trends and Methodologies, Mahmood A. Mahdavi (Ed.), ISBN: 978-953-307-282-1, InTech 2011.
- Ferhat Ay, Gunhan Gulsoy, Tamer Kahveci, Mining biological networks for similar patterns, in "DATA MINING: Foundations and Intelligent Paradigms-- Volume 3", editor Dawn E. Holmes and Lakhmi Jain, Springer, 2011.
- Tamer Kahveci, Ambuj K. Singh, Index Structures for Approximate Matching in Sequence Databases, in "Handbook on Computational Biology", editor Srinivas Aluru, CRC Press

Other Publications

- Andrei Todor, Haitham Gabr, Alin Dobra, <u>Tamer Kahveci</u>. Reachability Analysis in Large Probabilistic Biological Networks. International Conference on Bioinformatics and Computational Biology (ACM-BCB), 2013 (poster paper).
- Xu Zhang, Tamer Kahveci, A New Approach for Multiple Sequence Alignment, RECOMB, 2005 (poster paper).
- Arnab Bhattacharya, Tamer Kahveci, Ambuj K. Singh, Motif Finding and Multiple Alignment through Vector-Space Embeddings of Protein Sequences, RECOMB, 2004 (poster paper).

- Tamer Kahveci, Ambuj K. Singh, Fast Alignment of Large Genome Databases, International Conference on Data Engineering (ICDE), pages 768-770, 2003 (demo paper).
- Tamer Kahveci, Ambuj K. Singh, and Aliekber Gurel, An Efficient Index Structure for Shift and Scale Invariant Search of Multi-Attribute Time Sequences, International Conference on Data Engineering (ICDE), 2002 (poster paper)

Professional Activities

Editorial activities

- Associate Editor, EURASIP Journal on Bioinformatics and Systems Biology.
- Editorial review board, International Journal of Knowledge Discovery in Bioinformatics.
- Editorial Board, ISRN Bioinformatics.
- Editorial Board, Frontiers in Cancer Genetics.
- Editorial Board, Frontiers in Genomic Assay Technology
- Editorial Board, Network Modeling and Analysis in Health

Informatics and Bioinformatics

- Guest editor, Journal of Advances in Bioinformatics.
- Guest editor, IEEE/ACM Transactions on Computational Biology and Bioinformatics.

Program Committee Chair

- Workshop on Epigenomics and Cell Function (ECF) 2013
- International Conference On Bioinformatics and Computational Biology (ACM-BCB), 2012
- Bio-KDD, 2012

• Program Committee Member

• 2013

- IEEE International Conference on Bioinformatics and Biomedicine (BIBM)
- International Conference on Intelligent Systems on Molecular Biology (ISMB),
- International Conference on Research in Computational Molecular Biology (RECOMB)
- International Conference on Bioinformatics and Computational Biology (BICoB)
- ASE/IEEE International Conference on BioMedical Computing (BioMedCom)
- Asia Pacific Bioinformatics Conference (APBC)
- IEEE International Workshop on Genomic Signal Processing and Statistics (GENSIPS)
- Biotechnology and Bioinformatics Symposium (BIOT)

• 2012

- IEEE International Conference on Bioinformatics and Biomedicine (BIBM)
- International Conference on Bioinformatics and Computational Biology (BICoB)
- International Conference on Intelligent Systems on Molecular Biology (ISMB)
- International Symposium on Health Informatics and Bioinformatics (HIBIT)
- IEEE International Conference on Data Mining (ICDM)
- The International Conference on Very Large Data Bases (VLDB).
- IEEE International Workshop on Genomic Signal Processing and Statistics (GENSIPS)

• 2011

- IEEE International Conference on Bioinformatics and Biomedicine (BIBM)
- International Conference On Bioinformatics and Computational Biology (ACM-BCB)
- International Conference on Intelligent Systems on Molecular Biology (ISMB)
- International Symposium on Health Informatics and Bioinformatics (HIBIT)
- IEEE International Conference on Data Engineering (ICDE)
- IEEE International Conference on Data Mining (ICDM)

International Conference on Computational Systems Biology (CSB)

• 2010

- International Conference on Intelligent Systems on Molecular Biology (ISMB)
- International Conference on Computational Systems Biology (CSB)
- IEEE International Conference on Data Engineering (ICDE)
- International Symposium on Computer and Information Sciences (ISCIS),
- International Conference On Bioinformatics and Computational Biology (ACM-BCB)
- International Symposium on Health Informatics and Bioinformatics (HIBIT)
- Pacific-Asia Conference on Knowledge Discovery and Data Mining (PAKDD)
- The International Conference on Very Large Data Bases (VLDB).

• 2009

- International Workshop on Biological Data Management (BIDM)
- International Conference on Computational Systems Biology (CSB)
- IEEE International Conference on Data Mining (ICDM)
- International Symposium on Computer and Information Sciences (ISCIS)
- International Symposium on Health Informatics and Bioinformatics (HIBIT)
- Pacific-Asia Conference on Knowledge Discovery and Data Mining (PAKDD)
- The International Journal on Very Large Data Bases (VLDB)

2008

- Biotechnology and Bioinformatics Symposium (BIOT),
- International Conference on Intelligent Systems for Molecular Biology (ISMB)
- International Conference on Data Warehousing and Knowledge Discovery (DAWAK),
- IEEE International Conference on Data Mining (ICDM),
- ACM SIGKDD International Conference on Knowledge Discovery and Data Mining (KDD)
- International Symposium on Health Informatics and Bioinformatics (HIBIT)
- Machine Learning in Biomedicine and Bioinformatics (MLBB)
- IEEE International Conference on Data Mining (ICDM)

• 2007

- IEEE International Conference on Data Engineering (ICDE)
- International Conference on Data Warehousing and Knowledge Discovery (DAWAK)
- Pacific-Asia Conference on Knowledge Discovery and Data Mining (PAKDD)
- Database Systems for Advanced Applications (DASFAA)
- International Symposium on Health Informatics and Bioinformatics (HIBIT)
- The International Journal on Very Large Data Bases (VLDB)

• 2006

- IEEE International Conference on Data Mining (ICDM)
- IEEE Workshop on High Performance Computing in Medicine and Biology (HiPCoMB)
- International Conference on Data Warehousing and Knowledge Discovery (DAWAK)
- ACM SIGKDD International Conference on Knowledge Discovery and Data Mining (KDD)

• 2005

- IEEE International Conference on Data Mining (ICDM)
- International Workshop on Biological Data Management (BIDM)

Reviewer in scholarly journals

- IEEE Transactions on Parallel and Distributed Systems (TPDS)
- Very Large Data Base Journal (VLDBJ)
- IEEE Transactions on Knowledge and Data Engineering (TKDE)
- ACM/IEEE Transactions on Computational Biology and Bioinformatics (TCBB)
- Transactions on Database Systems (TODS)

- Data & Knowledge Engineering (DKE)
- International Journal of Knowledge Discovery in Bioinformatics (IJKDB)
- Journal of Bioinformatics and Computational Biology (JBCB)
- Journal of Computational Biology (JCB)
- PLoS Computational Biology
- Bioinformatics Journal
- BMC Bioinformatics
- Journal of Advances in Bioinformatics.

Reviewer of research proposals

- ABI panel, National Science Foundation
- IIS panel, National Science Foundation
- National Institute of Health

Professional Committees

- ISCB Publications Committee Member.
- ACM SIG-Bio Awards Committee Member.

Outreach and Community Services

 Founder and vice chair of the Sweetwater Branch Academy Elementary and Middle School.

Ph.D. students

(Chronological order of graduation date)

- Jayendra Venkateswaran, "Indexing techniques for metric databases with costly searches", 2007.
- Xu Zhang, "Multiple sequence alignment solutions and applications", 2007.
- Xuehui Li, "Identification and application of repetitive biological sequences", 2007.
- Jun Liu, "Mining comparative genomic hybridization data", 2007 (co-chair).
- Bin Song, "New in silico approaches for metabolic engineering", 2010.
- Ferhat Ay, "A comparative study on biological networks: alignment and structural properties", 2011.
- Nirmalya Bandyopadhyay, "Modeling perturbations in gene regulatory and signaling networks", 2011 (co-chair).
- Gunhan Gulsoy, Querying of large biological network databases, 2013.
- Andrei Todor, Querying probabilistic networks, 2014 (expected).
- Md. Mahmudul Hasan, Network motif identification, 2015 (expected)
- Haitham Gabr, Pathway identification in uncertain networks, 2015 (expected)

M.S. students

• Padmavati Sridhar, Mining metabolic networks, 2006.

Research support

- UF Informatics Institute Seed Fund, "Integrating Omics Data with Domain Specific Knowledge for Predicting Cellular Sensitivity to Chemotherapy And Radiotherapy", 08/01/2014 – 07/31/2015, \$49,000 (Co-PI).
- UF Informatics Institute Seed Fund, "Identification of phylogenetic and functional networks of prokaryotes that control methane production in peatlands", 08/01/2014 – 07/31/2015, \$39,000 (Co-PI).
- 3. AFE, "Gene mining in impatiens for resistance to infection by the downy", 07/01/2014 06/30/2015, \$29,033 (Co-PI).
- 4. NSF (CCF-1251599), "CIF: EAGER: Modeling and Querying of Probabilistic Biological Networks", 08/01/13 07/31/15, \$174,925 (PI).

- 5. NSF (DBI-1262451), "ABI Innovation: Querying Massive Dynamic Biological Network Databases", 07/01/13 06/30/16, \$492,584 (PI).
- 6. NSF (CCF-1048217), "CiC: EAGER: Inferring Pattern and Processes of Genome Evolution Through Cloud Computing Beyond", 01/01/11 12/31/13, \$300,000 (Co-PI).
- 7. NSF (IIS-1244794), "Student Travel Sponsorship for Third ACM BCB Conference, 2012", 09/01/12 08/31/13, \$24,000 (Co-PI).
- 8. NSF (IIS-0845439), "CAREER: New technologies for querying pathway databases", 06/01/09 05/31/14, \$400,000 (PI)
- 9. NSF (CCF-0829867), "EMT/BSSE: Biological networks as a communication model for entities with complex interactions", 09/01/08 08/31/11, \$300,000 (PI).
- 10. NSF (DUE-0920151), "Sequencing Gators: Building a Genome Science Curriculum at the University of Florida and Beyond", 01/01/10 12/31/13, \$499,888 (Co-PI)
- 11. NSF (IOS-0606607), "Dosage dependent genes affecting seed composition and weight", 09/2006-08/2010, \$1,227,302, (major collaborator).
- 12. UF Research Initiative Grant, "Constructing Stable Phylogenetic Trees", 05/2010-04/2012, \$100,000, (co-PI)
- 13. UF Research Initiative Grant, "Identification of repeats in genomes in the presence of transposons", 05/2008-04/2010, \$80,000, (PI)
- 14. UFGI Seed Grant, "Sequence Indexed Maize Transposon Insertion Sites for Cereal Functional Genomics", 06/2006 05/2008, \$100,000 (co-PI).
- 15. Oak Ridge Associated Universities (OARU) Ralph E. Powe Junior Faculty Enhancement Award, 06/2006 01/2007, \$10,000, (PI).