

Curriculum Vitae for Mehmet Koyutürk

- CONTACT INFORMATION** T. & D. Schroeder Assistant Professor of Computer Science and Engineering
Case Western Reserve University
(1) Department of Electrical Engineering & Computer Science
(2) Center for Proteomics & Bioinformatics
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- RESEARCH INTERESTS**
- Bioinformatics / Computational Biology
 - Parallel & Distributed Systems
 - Scientific Computing, Data Mining
- EDUCATION**
- Purdue University**, West Lafayette, IN, USA
- Ph.D., Computer Science, December 2006
Dissertation: Comparative analysis of biological networks
Advisory Committee: Ananth Grama (co-chair), Wojciech Szpankowski (co-chair), Shankar Subramaniam, Alberto Apostolico, Daisuke Kihara, Robert D. Skeel
- Bilkent University**, Ankara, Turkey
- M.S., Computer Engineering, September 2000
Thesis: Hypergraph-based declustering for multi-disk databases
Advisor: Cevdet Aykanat
- B.S., Electrical & Electronics Engineering, May 1998
Senior Project: Detection of mass lesions on mammograms using multi-resolution snake algorithm
Advisor: Enis Çetin
- POSITIONS HELD**
1. Center for Proteomics & Bioinformatics, School of Medicine
Case Western Reserve University, Cleveland, OH, USA
Assistant Professor (Secondary Appointment)
January 2009 - present
 2. Department of Electrical Engineering & Computer Science
Case Western Reserve University, Cleveland, OH, USA
T. & D. Schroeder Assistant Professor of Computer Science & Engineering
November 2007 - present
 3. Department of Electrical Engineering & Computer Science
Case Western Reserve University, Cleveland, OH, USA
Assistant Professor
August 2007 - October 2007
 4. Department of Computer Science, Purdue University, West Lafayette, IN, USA
Post-Doctoral Research Associate
September 2006 - July 2007

Peer-reviewed Articles in Scientific Journals

1. R. K. Nibbe, M. Koyutürk, and M. R. Chance, “An integrative -omics approach to identify functional subnetworks in human colorectal cancer”, *PLoS Computational Biology*, in press.
2. M. Koyutürk, “Algorithmic and analytical methods in network biology”, *Wiley Interdisciplinary Reviews: Systems Biology and Medicine*, in press.
3. G. Yavaş, M. Koyutürk, M. Özsoyoğlu, M. Gould, and T. LaFramboise, “An optimization framework for unsupervised identification of rare copy number variation from SNP array data”, *Genome Biology*, in press.
4. S. Erten, X. Li, G. Bebek, J. Li, and M. Koyutürk, “Phylogenetic analysis of modularity in protein interaction networks”, *BMC Bioinformatics*, 10:333, 2009.
5. B. Cărbunar, M. K. Ramanathan, M. Koyutürk, S. Jagannathan, and A. Grama, “Efficient tag detection in RFID systems”, *Journal of Parallel and Distributed Computing*, 69(2):180–196, 2009.
6. R. A. Ferreira, M. Koyutürk, S. Jagannathan, and A. Grama, “Semantic indexing in structured peer-to-peer networks”, *Journal of Parallel and Distributed Computing*, 68(1):64–77, 2008.
7. M. Koyutürk, A. Grama, and W. Szpankowski, “Assessing significance of connectivity and conservation in protein interaction networks”, *Journal of Computational Biology*, 14(6), 747–764, 2007.
8. M. Koyutürk, Y. Kim, S. Subramaniam, W. Szpankowski, and A. Grama, “Detecting conserved interaction patterns in biological networks”, *Journal of Computational Biology*, 13(7), 1299–1322, 2006.
9. M. Koyutürk, Y. Kim, U. Topkara, S. Subramaniam, W. Szpankowski, and A. Grama, “Pairwise alignment of protein interaction networks”, *Journal of Computational Biology*, 13(2), 182–189, 2006.
10. M. Koyutürk, A. Grama, and N. Ramakrishnan, “Non-orthogonal decomposition of binary matrices for bounded-error data compression and analysis”, *ACM Transactions on Mathematical Software*, 32(1), 33–69, 2006.
11. Y. Kim, M. Koyutürk, U. Topkara, A. Grama, and S. Subramaniam, “Inferring functional information from domain co-evolution”, *Bioinformatics*, 22(1), 40–49, 2006.
12. J. Chi, M. Koyutürk, and A. Grama, “CONQUEST: A coarse-grained parallel algorithm for constructing summaries of distributed binary datasets”, *Algorithmica*, 45(3), 377–401, 2006.
13. M. Koyutürk, A. Grama and N. Ramakrishnan, “Compression, clustering and pattern discovery in very high dimensional discrete-attribute datasets”, *IEEE Transactions on Knowledge and Data Engineering*, 17(4), 447–461, 2005.
14. M. Koyutürk and C. Aykanat, “Iterative-improvement-based declustering heuristics for multi-disk databases”, *Information Systems*, 30(1), 47–70, 2005.
15. M. N. Gürçan, M. Koyutürk, H. S. Yıldız, R. Ç. Atalay and A. E. Çetin, “Identification of relative protein bands in Polyacrylamide Gel Electrophoresis (PAGE) images using multiresolution snake algorithm”, *Biotechniques*, 26, 1162–1169, 1999.

16. M. Manguoğlu, M. Koyutürk, A. Grama, and A. H. Sameh, “Weighted matrix reordering and banded preconditioners for non-symmetric linear system solvers,” *SIAM Journal on Scientific Computing*, **under review**.

Peer-reviewed Conference Articles in Journal Special Issues

17. J. Pandey, M. Koyutürk, and A. Grama, “Functional characterization and topological modularity in molecular interaction networks”, *BMC Bioinformatics Special Issue on 8th Asia-Pacific Bioinformatics Conf. (APBC’10)*, in press.
18. J. Pandey, M. Koyutürk, S. Subramaniam, and A. Grama, “Functional coherence in domain interaction networks”, *Bioinformatics Special Issue on 7th European Conf. on Computational Biology (ECCB’08)*, 24(16):i28-i34, 2008.
19. J. Pandey, M. Koyutürk, Y. Kim, W. Szpankowski, S. Subramaniam, and A. Grama, “Functional annotation of regulatory pathways”, *Bioinformatics Special Issue on 15th Int’l Conf. on Intelligent Systems for Molecular Biology & 6th European Conf. on Computational Biology (ISMB/ECCB’07)*, 23(13), i377-i386, 2007.
20. M. Koyutürk, A. Grama, and W. Szpankowski, “An efficient algorithm for detecting frequent subgraphs in biological networks”, *Bioinformatics Special Issue on 12th Intern’l Conf. on Intelligent Systems for Molecular Biology & 3rd European Conf. on Computational Biology (ISMB/ECCB’04)*, 20, i200-i207, 2004.

Peer-reviewed Articles in Conference Proceedings

21. S. A. Chowdhury and M. Koyutürk, “Identification of coordinately dysregulated subnetworks in complex phenotypes”, *Pacific Symposium on Biocomputing (PSB’10)*, in press.
22. G. Yavaş, M. Koyutürk, M. Özsoyoğlu, M. Gould, and T. LaFramboise, “ÇOKGEN: A software for the identification of rare copy number variation from SNP microarrays”, *Pacific Symposium on Biocomputing (PSB’10)*, in press.
23. X. Li, S. Erten, G. Bebek, M. Koyutürk and J. Li, “Comparative analysis of modularity in biological systems”, *Fourth Ohio Collaborative Conf. in Bioinformatics (OCCBIO’09)*, 104–109, 2009.
24. M. K. Ramanathan, M. Koyutürk, A. Grama, and S. Jagannathan, “PHALANX: A graph theoretic framework for test case prioritization”, *23rd Annual ACM Symposium on Applied Computing (SAC’08)*, 667–673, 2008.
25. J. Pandey, M. Koyutürk, W. Szpankowski, and A. Grama, “Annotating pathways in interaction networks”, *Pacific Symposium on Biocomputing (PSB’08)*, 13:153-165, 2008.
26. J. Pandey, M. Koyutürk, W. Szpankowski, and A. Grama, “A statistical model for functional characterization of regulatory pathways, *Workshop on Data Mining for Biomedical Informatics, 7th SIAM Int’l Conf. Data Mining (SDM’07)*, 2007.
27. M. Koyutürk, A. Grama, and W. Szpankowski, “Assessing significance of connectivity and conservation in protein interaction networks”, In *10th Intl. Conf. Research in Computational Molecular Biology (RECOMB’06)*, LNBI 3909, 45-59, 2006.
28. M. Koyutürk, A. Grama, and W. Szpankowski, “Pairwise local alignment of protein interaction networks guided by models of evolution”, In *9th Intl. Conf. Research in Computational Molecular Biology (RECOMB’05)*, LNCS 3500, 48-65, 2005.

29. B. Cărbunar, M. K. Ramanathan, M. Koyutürk, C. Hoffmann, and A. Grama, “Redundant reader elimination in RFID systems”, *2nd Annual IEEE Communications Society Conf. Sensor and Ad Hoc Communications and Networks (SECON’05)*, 2005.
30. J. Chi, M. Koyutürk and A. Grama, “CONQUEST: A distributed tool for constructing summaries of high-dimensional discrete-attributed datasets”, *Proc. 4th SIAM Intl. Conf. Data Mining (SIAM DM’04)*, 154-165, 2004.
31. M. Koyutürk and A. Grama, “PROXIMUS: A framework for analyzing very high dimensional discrete-attributed datasets”, *Proc. 9th ACM SIGKDD Intl. Conf. Knowledge Discovery and Data Mining (KDD’03)*, 147-156, 2003.
32. M. Koyutürk, A. Grama and N. Ramakrishnan, “Algebraic techniques for analysis of large discrete-valued datasets”, *Proc. 6th European Conf. Principles of Data Mining and Knowledge Discovery (PKDD’02)*, 311-324, 2002.
33. M. N. Gürcan, M. Koyutürk, H. S. Yıldız, R. Ç. Atalay and A. E. Çetin, “Identification of relative protein bands in Polyacrylamide Gel Electrophoresis (PAGE) using multiresolution snake algorithm”, *Proc. IEEE-SP Intl. Symp. Time-Frequency/Time-Scale Analysis (TFTS’98)*, 277-280, 1998.
34. S. A. Chowdhury, R. K. Nibbe, M. R. Chance, and M. Koyutürk, “Subnetwork state functions define coordinately dysregulated subnetworks in cancer”, *14th Int’l Conf. Research in Computational Molecular Biology (RECOMB’10)*, **under review**.
35. S. Erten and M. Koyutürk, “Role of centrality in network-based prioritization of disease genes”, *8th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics (EVOBIO’10)*, **under review**.

Books

1. M. Koyutürk, S. Subramaniam, and A. Grama (Eds.), *Functional Coherence of Biological Networks*, Springer, in preparation.

Invited Book Chapters

1. B. Cărbunar, M. K. Ramanathan, M. Koyutürk, S. Jagannathan, and A. Grama, “Optimal tag coverage and tag report elimination”, *RFID Systems, Research Trends and Challenges*, John Wiley & Sons, in press.
2. S. Erten and M. Koyutürk, “Identification of modules in protein interaction networks”, In L. S. Heath and N. Ramakrishnan (Eds.), *Problem Solving Handbook in Computational Biology and Bioinformatics*, Springer, in press.

Invited Talks

1. Functional characterization of molecular interaction networks. *Department of Computer Science, Texas Tech University, Lubbock, TX, October 21, 2008.*
2. Functional coherence in molecular interaction networks. *Department of Computer Science, Kent State University, Kent, OH, October 1, 2008.*
3. Functional characterization of molecular interaction networks. *Workshop on Modeling, Analysis, and Integration of Biological Networks, Bertinoro International Center for Informatics, Bertinoro, Italy, September 17, 2008 (Organized by R. Pinter, Technion & S. Batzoglou, Stanford).*

4. Phylogenetic analysis of molecular interaction networks. *Minisymposium on Algorithms for Systems Biology, SIAM Conference on Discrete Mathematics*, Burlington, VT, June 16, 2008 (Organized by C. Şahinalp, Simon Frasier).
5. Discovering commonalities in interaction networks: from alignment to canonical modules. *Workshop on Mathematics for Biological Networks, Institut Henri Poincaré*, Paris, France, December 17, 2007 (Organized by Université d'Evry) .
6. Discovering commonalities in interaction networks: from alignment to canonical modules. *Case Center for Proteomics and Bioinformatics*, Cleveland, OH, December 6, 2007.
7. Algorithmic and analytical methods for functional characterization of molecular interaction networks. *Invited Session on Biological Networks, 39th Symposium on the Interface: Computing Science & Statistics, Systems Biology*, Philadelphia, PA, May 25, 2007 (Organized by N. Przulj, UC-Irvine).

Other Posters & Presentations in Scientific Conferences

1. R. Ewing, Y. Skomorovska-Prokvolit, K. Tamai, S. Saha, J. Song, A. Galante, T. Roman, M. Koyutürk, and J. Wang, “Adventures in the interactome: discovery of novel regulators of the Wnt signaling pathway”, *EMBO Workshop on Wnt Signaling in Development & Disease*, Arolla, Switzerland, 2009.
2. A. Galante, T. Roman, S. Saha, M. Koyutürk, and R. Ewing, “*In silico* modeling of Wnt signaling network”, *Int'l Conf. on Mathematical Biology*, Vancouver, BC, Canada, 2009. **(Won one of the 3 honorable mentions among 120 posters in the conference)**
3. S. Erten, M. Koyutürk, R. Nibbe, and M. Chance, “Characterizing crosstalk in protein interaction networks”, *7th Int'l Conf. on Pathways, Networks, and Systems Medicine*, Corfu, Greece, 2009.
4. R. K. Nibbe, M. Koyutürk, and M. R. Chance, “Network algorithms for the identification of multiple markers in human colorectal cancer”, *5th Annual US Human Proteome Organization Conf.*, San Diego, CA, 2009.
5. M. Manguoğlu, M. Koyutürk, A. Grama, and A. H. Sameh, “Weighted matrix reordering and parallel banded preconditioners for nonsymmetric linear systems”, *SIAM Conf. on Parallel Processing for Scientific Computing*, Toulouse, France, 2008.
6. M. Koyutürk, W. Szpankowski, and A. Grama, “Biclustering gene-feature matrices for statistically significant dense patterns”, *IEEE Computational Systems Bioinformatics Conf. (CSB'04)*, 480-484, Palo Alto, CA, 2004.
7. M. Koyutürk, A. Grama, and W. Szpankowski, “Algorithms for bounded-error correlation of high dimensional data in microarray experiments”, *IEEE Computational Systems Bioinformatics Conf. (CSB'03)*, 575-580, Palo Alto, CA, 2003.

FUNDING

1. M. Koyutürk (PI) and T. LaFramboise (Co-PI), “III: Small: Computational Infrastructure for the Identification of Copy Number Variations from SNP Microarrays”, National Science Foundation, IIS-0916102, \$497,603.00, 09/01/2009 – 08/31/2012.
2. M. Chance (PI), M. Koyutürk (Co-PI), R. Ewing (Co-PI), and G. Bebek (Co-I), “Supplement to Clinical and Translational Science Collaborative: Systems Medicine Data Analysis”, National Institutes of Health, UL1-RR024989 Supplement, \$1,200,000.00, 10/01/2009–09/30/2011.

3. M. Koyutürk (PI), “Learning Bioinformatics Together: Active Learning Strategies to Face the Challenges of Interdisciplinary Education”, CWRU Center for Innovation in Teaching & Education (UCITE), Glennan Fellowship Program, \$6,500.00, 08/01/2009 – 07/31/2010.

SYNERGISTIC
ACTIVITIES

Grant Review

1. Panel Member, NSF CDI Program, 2009.
2. Grant Reviewer, Israel Science Foundation, 2009.
3. Panel Member, NSF CISE IIS Program, 2008.

Program Committees

1. 8th European Conf. on Evolutionary Computation, Machine Learning, and Data Mining in Bioinformatics (EVOBIO), 2010.
2. 14th Pacific-Asia Conference on Knowledge Discovery and Data Mining (PAKDD), 2010.
3. 7th European Conf. on Evolutionary Computation, Machine Learning, and Data Mining in Bioinformatics (EVOBIO), 2009.
4. 13th Pacific-Asia Conference on Knowledge Discovery and Data Mining (PAKDD), 2009.
5. 4th IAPR Int’l Conf. on Pattern Recognition in Bioinformatics (PRIB), 2009.
6. SIAM Int’l Conf. on Data Mining (SIAMDM), 2008.
7. 8th International Workshop on Data Mining in Bioinformatics (BIOKDD), 2008.
8. 6th European Conf. on Evolutionary Computation, Machine Learning, and Data Mining in Bioinformatics (EVOBIO), 2008.
9. 1st Workshop on Data Mining in Functional Genomics (DMFG), 2008.
10. The 6th ACS/IEEE Int’l Conf. on Computer Systems and Applications (Algorithms & Bioinformatics Track), 2008.

Review for Scientific Journals

1. IEEE Transactions on Computational Biology & Bioinformatics, 2008 (2), 2009 (3).
2. PLoS Computational Biology, 2009 (3).
3. Physical Review Letters, 2009.
4. BMC Bioinformatics, 2007, 2008 (4), 2009 (3).
5. Parallel Computing 2005, 2007, 2008 (2), 2009 (2).
6. The Computer Journal, 2009.
7. Bioinformatics, 2005, 2006, 2007, 2008.
8. Statistical Analysis & Data Mining, 2008.
9. Journal of Biomedical Informatics, 2008.
10. Data and Knowledge Engineering, 2008 (2).
11. Biotechnology Progress, 2008.
12. Genome Biology, 2006, 2007.
13. BMC Systems Biology, 2007 (2).

14. International Journal of Bioinformatics Research & Applications, 2007.
15. IEEE Transactions on Knowledge and Data Engineering, 2005.
16. Theoretical Computer Science, 2005.
17. Information Sciences, 2005.
18. Information Processing Letters, 2004.

Review for Scientific Conferences

1. Bioinformatics: PSB (2009), CSB (2008), HiCOMB (2007), RECOMB (2005, 2007).
2. Data Mining: KDD(2007), SIAM DM (2005, 2007), ICDM (2002, 2003, 2004).
3. Algorithms: SODA (2009)
4. Parallel & Distributed Computing: IPDPS (2006), PPOPP (2006), ICPP (2004, 2005).
5. Scientific/High Performance Computing: SC(2008), ICS (2005), HiPC (2004, 2005).
6. Other: CEC (2004).

Other Synergistic Activities

1. Publicity chair, 4th Ohio Collaborative Conference on Bioinformatics (OCCBIO'09), Cleveland, OH, June 15-17, 2009.
2. Session chair, "Graphs/Networks", SIAM Int'l Conference on Data Mining, Atlanta, GA, April 24-26, 2008.

EDUCATIONAL ACTIVITIES

Graduate Students

1. Sinan Erten, Ph.D. Student, 2007-present.
2. Gökhan Yavaş, Ph.D. Student, 2008-present (with M. Özsoyoğlu and T. LaFramboise).
3. Salim A. Chowdhury, Ph.D. Student, 2009-present.

Undergraduate Research Students

1. Matthew M. Ruffalo (Computer Engineering)
2. Theodore Roman (Computer Science/Mathematics, with R. Ewing)
3. Alex Galante (Biology, with R. Ewing)

Teaching

1. EECS 458: Introduction to Bioinformatics, CWRU, Fall 2009.
2. EECS 359: Bioinformatics in Practice, CWRU, Spring 2009 (Introduced with J. Li).
3. EECS 600: Systems Biology & Bioinformatics, CWRU, Fall 2007, Fall 2008 (Introduced).
4. EECS 340: Algorithms & Data Structures, CWRU, Spring 2008.

Thesis Committees

- (1) Chad W. Seys, (2) Xin Li, (3) Ali Cakmak, (4) Mustafa Kirac, (5) Sulieman Bani-Ahmad, (6) Chris Fietkiewicz, Ph.D., CWRU EECS.

- (7) Vishal Patel, M.D./Ph.D., CWRU Genetics.
- (1) Bret Kraly, (2) Arun Dsouza, (3) Aaron Cederquist, M.S., CWRU EECS.

Other Educational Activities

1. Faculty Advisor, Research at the Interface of Mathematical and Biological Sciences, Case Western Reserve University, 2009-2010.
2. Guest Instructor (Systems Biology and Proteomics), BIOC 460: Introduction to Microarrays, Case Western Reserve University, 2009.
3. Team Coach, Case/CWRU Spartans, ACM International Collegiate Programming Contest (ICPC), 2008.
4. Faculty Advisor, ACM CWRU Chapter, 2007-present.

HONORS AND AWARDS

1. Glennan Fellowship, University Center for Innovation in Teaching and Education (UCITE), Case Western Reserve University, 2009.
2. Theodore and Dana Schroeder Endowed Assistant Professorship in Computer Science & Engineering, Case Western Reserve University, October 2007 – June 2010.
3. Learning Fellowship, University Center for Innovation in Teaching and Education (UCITE), Case Western Reserve University, 2008.
4. European Union 6th Framework Programme travel fellowship for 15th Intl. Conf. on Intelligent Systems for Molecular Biology, Vienna, Austria, July 22-August 26, 2007.
5. Computing Research Association (CRA) scholarship for CRA Academic Careers Workshop, Washington, DC, February 27-28, 2006.
6. RECOMB'05 travel fellowship for 9th Annual Intl. Conf. on Research in Computational Molecular Biology, Boston, MA, May 14-18, 2005.
7. ISCB travel fellowship for 12th Intl. Conf. on Intelligent Systems for Molecular Biology, Glasgow, UK, July 31-August 4, 2004.
8. AAAI and SIGMOD Student Travel Award for 9th ACM Intl. Conf. on Knowledge Discovery and Data Mining, Washington, DC, August 23-27, 2003.
9. Full undergraduate student scholarship, Bilkent University, 1993-1998.
10. Undergraduate fellowship awarded by Asil Gıda Sanayi A.Ş., 1993-1998.

SOFTWARE SYSTEMS

1. NARADA, an open source web applet for functional annotation of regulatory pathways, 2007.
2. SIDES, an open source software for identification of significantly dense subgraphs in molecular interaction networks, 2006.
3. MAWISH, an open source software for pairwise alignment of protein-protein interaction networks, 2005.
4. MULE, an open source software for identification of frequent subgraphs in biological networks, 2004.
5. PROXIMUS, an open source library for non-orthogonal decomposition of binary matrices in C, 2003.

6. A Windows application for identification of relative protein bands on PAGE images in C++, 1998.