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EDUCATION

- Ph.D. in Computer Science, Georgia Institute of Technology (12/2000)
 - M.S. in Computer Science, University of Bucharest (6/1992, B.S. included)
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EMPLOYMENT

University of Connecticut

- Associate Professor (8/2008–present)
- Assistant Professor (8/2003–8/2008)

University of California at San Diego

- Assistant Research Scientist (5/2002–8/2003)
- Visiting Postgraduate Researcher (8/2001–4/2002)

University of California at Los Angeles

- Postdoctoral Researcher (8/2000–7/2001)

Georgia Institute of Technology

- Part-time Instructor (8/2000–5/2001)
- Graduate Research/Teaching Assistant (1/1995–7/2000)

University of Bucharest

- Research Assistant (10/1992–12/1994)
-

HONORS

- Castleman Term Professorship in Engineering Innovation, 2016-19
- United Technologies Corporation Term Professorship in Engineering Innovation, 2013-15
- NSF Faculty Early Career Development (CAREER) Award, 2006-2011

PUBLICATIONS

Edited Books

- [EB1] I.I. Mandoiu and A.Z. Zelikovsky (Eds.). *Computational Methods for Next Generation Sequencing Data Analysis*. Wiley Book Series on Bioinformatics. John Wiley & Sons, xxv+430 pages, 2016.
- [EB2] I.I. Măndoiu and A.Z. Zelikovsky (Eds.). *Bioinformatics Algorithms: Techniques and Applications*. Wiley Book Series on Bioinformatics. John Wiley & Sons, xiv+500 pages, 2008.

Edited Proceedings

- [EP1] R. Harrison, Y. Li, and I.I. Mandoiu (Eds.). *Proc. 11th International Symposium on Bioinformatics Research and Applications*, volume Lecture Notes in Bioinformatics vol. 9096. Springer-Verlag, Berlin, 2015.
- [EP2] L. Bleris, I.I. Mandoiu, R. Schwartz, and J. Wang (Eds.). *Proc. 8th International Symposium on Bioinformatics Research and Applications*, volume Lecture Notes in Bioinformatics vol. 7292. Springer-Verlag, Berlin, 2012.
- [EP3] S. Istrail, I.I. Mandoiu, M. Pop, S. Rajasekaran, and J. Spouge (Eds.). *Proc. 2nd IEEE International Conference on Computational Advances in Bio and Medical Sciences*. IEEE, 2012.
- [EP4] B. Chen et al. (Eds.). *Workshops Proceedings, 2011 IEEE International Conference on Bioinformatics and Biomedicine*. IEEE Computer Society Press, 2011.
- [EP5] I.I. Mandoiu, S. Miyano, T. Przytycka, and S. Rajasekaran (Eds.). *Proc. 1st IEEE International Conference on Computational Advances in Bio and Medical Sciences*. IEEE Computer Society Press, 2011.
- [EP6] I.I. Măndoiu, Giri Narasimhan, and Yanqing Zhang (Eds.). *Proc. 5th International Symposium on Bioinformatics Research and Applications*, volume 5542 of *Lecture Notes in Bioinformatics*. Springer-Verlag, Berlin, 2009.
- [EP7] I.I. Măndoiu and A.Z. Zelikovsky (Eds.). *Proc. 3rd International Symposium on Bioinformatics Research and Applications*, volume 4463 of *Lecture Notes in Bioinformatics*. Springer-Verlag, Berlin, 2007.
- [EP8] X. Hu, I.I. Măndoiu, Z. Obradovic, and J. Xia (Eds.). *Proc. 2007 IEEE International Conference on Bioinformatics and Biomedicine*. IEEE Computer Society Press, 2007.

Book Chapters

- [BC1] E. Nenasteva, B. Tork, A. Artyomenko, N. Mancuso, M.I. Khan, R. O'Neill, I.I. Măndoiu, and A. Zelikovsky. Reconstruction of Infectious Bronchitis Virus Quasispecies from NGS Data. In I.I. Măndoiu and A.Z. Zelikovsky, editors, *Computational Methods for Next Generation Sequencing Data Analysis*, pp. 383–400, John Wiley & Sons, 2016.
- [BC2] O. Glebova, Y. Temate-Tiagueu, A. Caciula, S. Al Seesi, A. Artyomenko, S. Mangul, J. Lindsay, I.I. Măndoiu, and A. Zelikovsky. Transcriptome Quantification and Differential Expression from NGS Data. In I.I. Măndoiu and A.Z. Zelikovsky, editors, *Computational Methods for Next Generation Sequencing Data Analysis*, pp. 301–327, John Wiley & Sons, 2016.
- [BC3] I. Mandric, J. Lindsay, I.I. Măndoiu, and A. Zelikovsky. Scaffolding Algorithms. In I.I. Măndoiu and A.Z. Zelikovsky, editors, *Computational Methods for Next Generation Sequencing Data Analysis*, pp. 105–131, John Wiley & Sons, 2016.
- [BC4] P. Skums, A. Artyomenko, O. Glebova, S. Ramachandran, D.S. Campo, Z. Dimitrova, I.I. Măndoiu, A. Zelikovsky, and Y. Khudyakov. Pooling Strategy for Massive Viral Sequencing. In I.I. Măndoiu and A.Z. Zelikovsky, editors, *Computational Methods for Next Generation Sequencing Data Analysis*, pp. 57–83, John Wiley & Sons, 2016.
- [BC5] S. Al Seesi, F. Duan, I.I. Măndoiu, P.K. Srivastava, and A. Kueck. Genomics-guided immunotherapy of human epithelial ovarian cancer. In A. Rodriguez-Oquendo, editor, *Translational Cardiometabolic Genomic Medicine*, pp. 237–250, Academic Press, 2015.

- [BC6] I. Astrovskaia, N. Mancuso, B. Tork, S. Mangul, A. Artyomenko, P. Skums, L. Ganova-Raeva, I.I. Măndoiu, and A. Zelikovsky. Inferring Viral Quasispecies Spectra from Shotgun and Amplicon Next-Generation Sequencing Reads. In M. Poptsova, editor, *Genome Analysis: Current Procedures and Applications*, pp. 231–262, Caister Academic Press, 2014.
- [BC7] S. Al Seesi, S. Mangul, A. Caciula, A. Zelikovsky, and I.I. Măndoiu. Transcriptome reconstruction and quantification from RNA sequencing data. In M. Poptsova, editor, *Genome Analysis: Current Procedures and Applications*, pp. 39–60, Caister Academic Press, 2014.
- [BC8] B. DasGupta, M.-Y. Kao, and I.I. Măndoiu. Algorithmic issues in DNA barcoding problems. In M. Elloumi and A. Zomaya, editors, *Algorithms in Computational Molecular Biology: Techniques, Approaches and Applications*, pp. 129–142, Wiley, 2011.
- [BC9] K. Konwar, I.I. Măndoiu, A. Russell, and A. Shvartsman. Exact and approximation algorithms for multiplex PCR primer set selection with amplification length constraints. In I.I. Măndoiu and A.Z. Zelikovsky, editors, *Bioinformatics Algorithms: Techniques and Applications*, pp. 241–258, Wiley, 2008.
- [BC10] A.B. Kahng, I.I. Măndoiu, and A.Z. Zelikovsky. Practical approximations of Steiner trees in uniform orientation metrics. In T.E. Gonzalez, editor, *Approximation Algorithms and Metaheuristics*, Chapman & Hall/CRC, 2007.
- [BC11] I.I. Măndoiu, A. Olshevsky, and A.Z. Zelikovsky. QoS multimedia multicast routing. In T.E. Gonzalez, editor, *Approximation Algorithms and Metaheuristics*, Chapman & Hall/CRC, 2007.
- [BC12] C. Albrecht, A.B. Kahng, I.I. Măndoiu, and A.Z. Zelikovsky. Multicommodity flow algorithms for buffered global routing. In T.E. Gonzalez, editor, *Approximation Algorithms and Metaheuristics*, Chapman & Hall/CRC, 2007.
- [BC13] A.B. Kahng, I.I. Măndoiu, S. Reda, X. Xu, and A.Z. Zelikovsky. Computer-aided optimization of DNA array design and manufacturing. In K. Chakrabarty and J. Zeng, editors, *Design Automation Methods and Tools for Microfluidics-Based Biochips*, pp 235–269, Springer Verlag, 2006.

Articles in Refereed Journals

- [J1] Y. Temate-Tiagueu, S. Al Seesi, M. Mathew, I. Mandric, A. Rodriguez, K. Bean, Q. Cheng, O. Glebova, I.I. Măndoiu, N.B. Lopanik, and A. Zelikovsky. Inferring metabolic pathway activity levels from rna-seq data. *BMC Genomics*, 17(Suppl 5):493–503, 2016.
- [J2] D.K.P. Karunakaran, S. Al Seesi, A.R. Banday, M. Baumgartner, A. Olthof, C. Lemoine, I.I. Măndoiu, and R.N. Kanadia. Network-based bioinformatics analysis of spatio-temporal rna-seq data reveals transcriptional programs underpinning normal and aberrant retinal development. *BMC Genomics*, 17(Suppl 5):477–492, 2016.
- [J3] M. Mathew, K.I. Bean, Y.T. Tiagueu, A. Caciula, I.I. Măndoiu, A. Zelikovsky, and N.B. Lopanik. Influence of symbiont-produced bioactive natural product on holobiont fitness in the marine bryozoan, *Bugula neritina* via protein kinase C (PKC). *Marine Biology*, 163:44, 2016.
- [J4] M. Baumgartner, C. Lemoine, S. Al Seesi, D.K.P. Karunakaran, N. Sturrock, A. Rouf Banday, A.M. Kilcollins, I.I. Măndoiu, and R.N. Kanadia. Minor splicing snRNAs are enriched in the developing mouse CNS and are crucial for survival of differentiating retinal neurons. *Developmental Neurobiology*, 75(9):895–907, 2015.
- [J5] M. Hamdalla, S. Rajasekaran, D. Grant, and I.I. Măndoiu. Metabolic pathway predictions for metabolomics: a molecular structure matching approach. *Journal of Chemical Information and Modeling*, 55(5):709–718, 2015.
- [J6] P. Skums, A. Artyomenko, O. Glebova, S. Ramachandran, I.I. Măndoiu, D.S. Campo, Z. Dimitrova, A. Zelikovsky, and Y. Khudyakov. Computational framework for next-generation sequencing of heterogeneous viral populations using combinatorial pooling. *Bioinformatics*, 31(5):682–690, 2015.
- [J7] A. Rouf Banday, M. Baumgartner, S. Al Seesi, D.K.P. Karunakaran, A. Venkatesh, S. Venkatesh, C. Lemoine, A.M. Kilcollins, I.I. Măndoiu, C. Punzo, and R.N. Kanadia. Replication-dependent histone genes are actively transcribed in differentiating and aging retinal neurons. *Cell Cycle*, 13(16):2526–2541, 2014.
- [J8] F. Duan, J. Duitama, S. Al Seesi, C. Ayres, S. Corcelli, A. Pawashe, T. Blanchard, D. McMahon, J. Sidney, A. Sette, B. Baker, I.I. Măndoiu, and P.K. Srivastava. Genomic and bioinformatic profiling of mutational neo-epitopes reveals new rules to predict anti-cancer immunogenicity. *Journal of Experimental Medicine*, 211(11):2231–2248, 2014.

- [J9] S. Al Seesi, Y.T. Tiagueu, A. Zelikovsky, and I.I. Măndoiu. Bootstrap-based differential gene expression analysis for RNA-Seq data without replicates. *BMC Genomics*, 15(Suppl 8):S2, 2014.
- [J10] E. Hemphill, J. Lindsay, C. Lee, I.I. Măndoiu, and C.E. Nelson. Feature selection and classifier performance on diverse biological datasets. *BMC Bioinformatics*, 15(Suppl 13):S4, 2014.
- [J11] J. Lindsay, H. Salooti, I.I. Măndoiu, and A. Zelikovsky. ILP-based maximum likelihood genome scaffolding. *BMC Bioinformatics*, 15(Suppl 9):S9, 2014.
- [J12] S. Mangul, A. Caciula, S. Al Seesi, D. Brinza, I.I. Măndoiu, and A. Zelikovsky. Transcriptome assembly and quantification from Ion Torrent RNA-Seq data. *BMC Genomics*, 15(Suppl 5):S7, 2014.
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- [J14] L. Menikarachchi, D. Hill, M. Hamdalla, I.I. Măndoiu, and D. Grant. In silico enzymatic synthesis of a 400,000 compound biochemical database for non-targeted metabolomics. *Journal of Chemical Information and Modeling*, 53(9):2483–2492, 2013.
- [J15] P. Skums, N. Mancuso, A. Artyomenko, B. Tork, I.I. Măndoiu, Y. Khudyakov, and A. Zelikovsky. Reconstruction of viral population structure from next-generation sequencing data using multicommodity flows. *BMC Bioinformatics*, 14(Suppl 9):S2, 2013.
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- [J20] J. Duitama, P.K. Srivastava, and I.I. Măndoiu. Towards accurate detection and genotyping of expressed variants from whole transcriptome sequencing data. *BMC Genomics*, 13(Suppl 2):S6, 2012.
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- [J22] M.B. Renfree et al. Genome sequence of an Australian kangaroo, *Macropus eugenii*, provides insight into the evolution of mammalian reproduction and development. *Genome Biology*, 12:R81, 2011.
- [J23] I. Astrovskaya, B. Tork, S. Mangul, K. Westbrooks, I.I. Măndoiu, P. Balfe, and A. Zelikovsky. Inferring viral quasispecies spectra from 454 pyrosequencing reads. *BMC Bioinformatics*, 12(Suppl 6):S1, 2011.
- [J24] M. Nicolae, S. Mangul, I.I. Măndoiu, and A. Zelikovsky. Estimation of alternative splicing isoform frequencies from RNA-Seq data. *Algorithms for Molecular Biology*, 6:9, 2011.
- [J25] C. Lee, I.I. Măndoiu, and C.E. Nelson. Inferring ethnicity from mitochondrial DNA sequence. *BMC Proceedings*, 5(Suppl 2):S11, 2011.
- [J26] J. Duitama, J. Kennedy, S. Dinakar, Y. Hernandez, Y. Wu, and I.I. Măndoiu. Linkage disequilibrium based genotype calling from low-coverage shotgun sequencing reads. *BMC Bioinformatics*, 12(Suppl 1):S53, 2011.
- [J27] J. Duitama, D.M. Kumar, E. Hemphill, M. Khan, I.I. Măndoiu, and C.E. Nelson. PrimerHunter: A primer design tool for PCR-based virus subtype identification. *Nucleic Acids Research*, 37(8):2483–2492, 2009.
- [J28] J. Jun, I.I. Măndoiu, and C.E. Nelson. Identification of mammalian orthologs using local synteny. *BMC Genomics*, 10:630, 2009.
- [J29] J. Jun, P. Ryvkin, E. Hemphill, I.I. Măndoiu, and C.E. Nelson. The birth of new genes by RNA- and DNA-mediated duplication during mammalian evolution. *Journal of Computational Biology*, 16(10):1429–1444, 2009.

- [J30] K. Apichonbancha, B. Dasgupta, J. Jun, I.I. Măndoiu, and E. Mendonca. A review of the primer approximation multiplex PCR (PAMP) technique for detecting large scale cancer genomic lesions. *Current Bioinformatics*, 4(1):1–7, 2009.
- [J31] J. Kennedy, I.I. Măndoiu, and B. Paşaniuc. Genotype Error Detection Using Hidden Markov Models of Haplotype Diversity. *Journal of Computational Biology*, 15(9):1155–1171, 2008.
- [J32] A. Gusev, I.I. Măndoiu, and B. Paşaniuc. Highly scalable genotype phasing by entropy minimization. *IEEE/ACM Trans. on Computational Biology and Bioinformatics*, 5(2):252–261, 2008.
- [J33] S. Balla, S. Rajasekaran, and I.I. Măndoiu. Efficient algorithms for degenerate primer search. *International Journal of Foundations of Computer Science*, 18(4):899–910, 2007.
- [J34] I.I. Măndoiu and C. Prăjescu. High-throughput SNP genotyping by SBE/SBH. *IEEE Transactions on NanoBioscience*, 6(1):28–35, 2007.
- [J35] A.B. Kahng, I.I. Măndoiu, X. Xu, and A. Zelikovsky. Enhanced design flow and optimizations for multi-project wafers. *IEEE Transactions on Computer-Aided Design*, 26(2):301–311, 2007.
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- [J38] E. Althaus, G. Călinescu, I.I. Măndoiu, S. Prasad, N. Tchervenski, and A.Z. Zelikovsky. Power efficient range assignment for symmetric connectivity in static ad hoc wireless networks. *Wireless Networks*, 12(3):287–299, 2006.
- [J39] S.V. Babin, A.B. Kahng, I.I. Măndoiu, and S. Muddu. Improving CD accuracy and throughput by subfield scheduling in electron beam mask writing. *Journal of Vacuum Science & Technology B: Microelectronics and Nanometer Structures*, 23(6):3094–3100, 2005.
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- [J48] G. Călinescu, I.I. Măndoiu, P.-J. Wan, and A.Z. Zelikovsky. Selecting forwarding neighbors in wireless ad hoc networks. *ACM Mobile Networks and Applications*, 9(2):101–111, 2004.
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- [J51] K. Jain, I.I. Măndoiu, V.V. Vazirani, and D.P. Williamson. A primal-dual schema based approximation algorithm for the element connectivity problem. *Journal of Algorithms*, 45:1–15, 2002.
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Articles in Refereed Conference Proceedings

- [C1] S. Mangul, A. Caciula, S. Al Seesi, D. Brinza, A. Rouf Banday, R. Kanadia, I.I. Măndoiu, and A. Zelikovsky. Flexible approach for novel transcript reconstruction from RNA-Seq data using maximum likelihood integer programming. In *Proc. 5th International Conference on Bioinformatics and Computational Biology*, 2013.
- [C2] J. Lindsay, H. Salooti, A. Zelikovsky, and I.I. Măndoiu. Scalable genome scaffolding using integer linear programming. In *Proc. ACM Conference on Bioinformatics, Computational Biology and Biomedicine*, pages 377–383, Oct. 7-10, 2012 2012.
- [C3] S. Mangul, A. Caciula, S. Al Seesi, D. Brinza, A. Rouf Banday, R. Kanadia, I.I. Măndoiu, and A. Zelikovsky. An integer programming approach to novel transcript reconstruction from paired-end RNA-Seq reads. In *Proc. ACM Conference on Bioinformatics, Computational Biology and Biomedicine*, pages 369–376, Oct. 7-10, 2012 2012.
- [C4] M. Hamdalla, D. Grant, I.I. Măndoiu, D. Hill, S. Rajasekaran, and R. Ammar. The use of graph matching algorithms to identify biochemical substructures in synthetic chemical compounds: Application to metabolomics. In *Proc. 2nd IEEE International Conference on Computational Advances in Bio and Medical Sciences*, pages 1–6, 2012.
- [C5] N. Mancuso, B. Tork, I.I. Măndoiu, A. Zelikovsky, and P. Skums. Viral quasispecies reconstruction from amplicon 454 pyrosequencing reads. In *Proc. 1st Workshop on Computational Advances in Molecular Epidemiology*, pages 94–101, 2011.
- [C6] S. Mangul, A. Caciula, I.I. Măndoiu, and A. Zelikovsky. RNA-Seq based discovery and reconstruction of unannotated transcripts in partially annotated genomes. In *Proc. 1st Workshop on Computational Advances in Molecular Epidemiology*, pages 118–123, 2011.
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- [C11] B. Pasaniuc, J. Kennedy, and I.I. Măndoiu. Imputation-based local ancestry inference in admixed populations. In *Proc. 5th International Symposium on Bioinformatics Research and Applications/2nd Workshop on Computational Issues in Genetic Epidemiology*, volume 5542 of *Lecture Notes in Computer Science*, pages 221–233, 2009.
- [C12] S. Balla, S. Rajasekaran, and I.I. Măndoiu. Faster greedy algorithms for multiple degenerate primer selection. In *Proc. 8th IEEE International Conference on Bioinformatics and Bioengineering*, pages 1–4, 2008.
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Unrefereed Conference Articles

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- [U2] A.B. Kahng, I.I. Măndoiu, X. Xu, and A. Zelikovsky. Yield-driven multi-project reticle design and wafer dicing. In *Proc. 25th Annual BACUS Symposium on Photomask Technology*, volume 5992 of *Proceedings of SPIE*, pages 1247–1257, 2005.
- [U3] S.V. Babin, A.B. Kahng, I.I. Măndoiu, and S. Muddu. Resist heating dependence on subfield scheduling in 50kV electron beam maskmaking. In *Photomask and Next-Generation Lithography Mask Technology X*, volume 5130 of *Proceedings of SPIE*, pages 718–726, 2003.
- [U4] S.V. Babin, A.B. Kahng, I.I. Măndoiu, and S. Muddu. Subfield scheduling for throughput maximization in electron-beam photomask fabrication. In *Emerging Lithographic Technologies VII*, volume 5037 of *Proceedings of SPIE*, pages 934–942, 2003.
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Patents

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- [P2] C.E. Nelson, I.I. Măndoiu, and H.L. Aguila. Pipeline for rational design and interpretation of biomarker panels. *US Patent Application 2015/0080237 A1*, 2015.
- [P3] P.K. Srivastava, I.I. Măndoiu, and F. Duan. Identification of tumor-protective epitopes for the treatment of cancers. *World Patent Application WO2014052707 A3*, 2015.
- [P4] C. Albrecht, A.B. Kahng, I.I. Măndoiu, and A.Z. Zelikovsky. Floorplan evaluation, global routing, and buffer insertion for integrated circuits. *US Patent #7,062,743*, 2006.

SOFTWARE PACKAGES

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- F. Duan, J. Duitama, S. Al Seesi, P.K. Srivastava, and I.I. Măndoiu. Epi-Seq: Bioinformatics pipeline for predicting cancer specific epitopes from RNA-Seq data. Available at <http://dna.engr.uconn.edu/software/Epi-Seq/>.

- S. Al Seesi, Y.T. Tiagueu, A. Zelikovsky, and I.I. Măndoiu. IsoDE: Bootstrap-based differential gene expression analysis for RNA-Seq data. Available at <http://dna.engr.uconn.edu/software/IsoDE/>.
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- M. Hamdalla, I.I. Măndoiu, D. Hill, S. Rajasekaran, and D. Grant. BioSM: A metabolomics tool for identifying endogenous mammalian biochemical structures. Available at <http://dna.engr.uconn.edu/software/BioSM/>.
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- M. Nicolae and I.I. Măndoiu. DGE-EM: Estimation of gene expression levels from DGE/SAGE-Seq sequencing data. Available at <http://dna.engr.uconn.edu/software/DGE-EM/>.
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- S. Dinakar, J. Duitama, Y. Hernández, J. Kennedy, I.I. Măndoiu, and Y. Wu. GeneSeq: LD-based SNP genotype calling from shotgun sequencing reads. Available at <http://dna.engr.uconn.edu/software/GeneSeq/>.
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- C. Albrecht, A.B. Kahng, I.I. Măndoiu, and A. Zelikovsky. MCF: Multicommodity flow based congestion- and timing-driven global routing and buffer insertion. Available at http://www.engr.uconn.edu/~ion/FILES/software/mcf_floorplan.tar.gz.
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- A.B. Kahng and I.I. Măndoiu. RMST-Pack: rectilinear minimum spanning tree algorithms. Available at <http://vlsicad.ucsd.edu/GSRC/bookshelf/Slots/RSMT/RMST/>.

INVITED TALKS AND COLLOQUIA

- Challenges and opportunities in single cell genomics, *keynote talk*, 12th International Symposium on Bioinformatics Research and Applications, Minsk, Belarus, June 5-8, 2016
- Single cell RNA-Seq analysis, Jax-GM course on Big Genomic Data Skills Training for Professors, Farmington, CT, May 23-27, 2016
- Cancer Vaccine Design, CICATS Science Cafe, Oct. 9, 2015
- Computational methods for genomics-guided immunotherapy, *invited talk*, 5th IEEE International Conference on Computational Advances in Bio and Medical Sciences, Miami, FL, October 15-17, 2015

- Computational Methods for Analysis of Single Cell RNA-Seq Data, CSHL course on Advanced Techniques in Molecular Neuroscience, June 30 -July 16, 2015
- Computational methods for genomics-guided immunotherapy, (mini-tutorial, with S. Al Seesi), 11th International Symposium on Bioinformatics Research and Applications, Norfolk, VA, June 7-10, 2015
- Scalable Algorithms for Next-Generation Sequencing Data Analysis, JAX-UCONN/BECAT/UCHC Workshop on Bioinformatics and Computational Biology, Sept. 4, 2013
- Reconstruction of Haplotype Spectra from NGS Data, IPDPS Workshop on Future Computing Platforms to Accelerate Next-Gen Sequencing Applications, May 19, 2013
- Scalable Algorithms for Next-Generation Sequencing Data Analysis, Booth Engineering Center for Advanced Technology Workshop on HPC, May 16, 2013
- Bioinformatics Tools for Viral Quasispecies Reconstruction from Next-Generation Sequencing Data and Vaccine Optimization, USDA NIFA Agriculture and Food Research Initiative - Animal Breeding, Genetics and Genomics Project Director Meeting, Jan. 11, 2013
- Panel: Bigdata in Biosciences: Challenges and Opportunities, ACM Conference on Bioinformatics, Computational Biology and Biomedicine, Orlando, FL, Oct. 7-10, 2012
- Towards Personalized Genomics-Guided Cancer Immunotherapy, UConn/JAX Genomics Symposium, Storrs, CT, Sept. 6-7, 2012
- Inferring Viral Quasispecies Spectra from NGS Reads, Brown University Center for Computational Molecular Biology, Feb. 1, 2012
- Reconstruction of infectious bronchitis virus quasispecies from 454 pyrosequencing reads, 1st Workshop on Computational Advances in Molecular Epidemiology, Nov. 13, 2011
- Bioinformatics Pipelines for RNA-Seq Data Analysis, (tutorial, with S. Al Seesi), 5th IEEE International Conference on Bioinformatics and Biomedicine, Atlanta GA, Nov. 12-15, 2011
- Computational Advances for Next Generation Sequencing (training course, with A. Zelikovsky), 1st SelectBiosciences Next-Gen Sequencing Congress, Boston, MA , April 28, 2011
- Next-Generation Sequencing: Challenges and Opportunities, Department of Physiology and Neurobiology, University of Connecticut, Storrs, March 16, 2011
- Bioinformatics Tools for Personalized Cancer Immunotherapy, UCONN Working Group on Multiscale Computational Science and Engineering , Feb. 25, 2011
- Estimation of Alternative Splicing Isoform Frequencies From RNA-Seq Data, INFORMS Annual Meeting, Austin, TX, Nov. 7-10, 2010
- Estimation of Alternative Splicing Isoform Frequencies from RNA-Seq Data, Max Planck Institute for Molecular Genetics, July 19, 2010
- Estimation of Alternative Splicing Isoform Frequencies from RNA-Seq Data, Dagstuhl seminar on Structure Discovery in Biology: Motifs, Networks & Phylogenies, June 6-11, 2010
- Imputation-Based Local Ancestry Inference in Admixed Populations, DIMACS Workshop on Algorithmics in Human Population-Genomics, DIMACS Center, Rutgers University, Apr. 27-29, 2009
- Genotype and Haplotype Reconstruction from Low-Coverage Short Sequencing Reads, 1st International Conference on Bioinformatics and Computational Biology (BICoB 2009), New Orleans, LA, Apr. 8-10, 2009
- Algorithms for Genotype and Haplotype Inference from Low-Coverage Short Sequencing Reads, 11th INFORMS Computing Society Conference, Charleston, SC, Jan. 11-13, 2009
- LD-Based Genotype and Haplotype Inference from Low-Coverage Short Sequencing Reads, UCLA bioinformatics seminar series, Nov. 3, 2008
- Linkage Disequilibrium Based SNP Genotype Calling from Short Sequencing Reads, SoE-UCHC Bioengineering Research Forum, UCONN Health Center, Farmington, CT, Oct. 29, 2008

- Hidden Markov Models of Haplotype Diversity and Applications in Genetic Epidemiology, INFORMS Annual Meeting, Oct. 12-15, 2008
- Computational Challenges in Whole-Genome Association Studies, SoE-UHC Bioengineering Research Forum, University of Connecticut, Storrs, CT, April 22, 2008
- Rational DNA Sequence Design for Molecular Nanotechnology, SoE Nanotechnology Research Forum, University of Connecticut, Storrs, CT, March 5, 2008
- Algorithms for Biochip Design and Optimization, Cadence Berkeley Labs, Berkeley, CA, Nov. 01, 2007
- Scalable Algorithms for Genotype and Haplotype Analysis, tutorial, 3rd International Symposium on Bioinformatics Research and Applications (ISBRA), Atlanta, Georgia, May 7-10, 2007
- Genotype Error Detection using Hidden Markov Models of Haplotype Diversity, 21st New England Statistics Symposium, University of Connecticut (NESS), Storrs, CT, April 21, 2007
- Algorithms for SNP Data Collection and Analysis, Department of Computer Science, University of Rhode Island, Nov. 10, 2006
- Design and Optimization of Universal DNA Arrays, Affymetrix Inc., Santa Clara, CA, July 26, 2006
- Combinatorial Algorithms for Maximum Likelihood Tag SNP Selection and Haplotype Inference, *3rd International Workshop on Applied Probability (IWAP)*, Storrs, CT, May 15-18, 2006
- Panel: What Should be the Technology Platform of Choice for Biochips and is this the Right Time to Talk About CAD for Biochips? IEEE/ACM Design, Automation and Test in Europe (DATE) Workshop on Emerging CAD Challenges for Biochip Design, Munich, Germany, March 10, 2006
- Design and Optimization of Universal DNA Arrays, IEEE/ACM Design, Automation and Test in Europe (DATE) Workshop on Emerging CAD Challenges for Biochip Design, Munich, Germany, March 10, 2006
- Multi-Project Reticle Design and Wafer Dicing under Uncertain Demand, 22nd European Mask and Lithography Conference (EMLC), Dresden, Germany, Jan. 24, 2006
- Design and Optimization of Universal DNA Arrays, 2nd SECABC Fall Workshop on Biocomputing, Atlanta, GA, Oct. 27, 2005
- Algorithms for Universal DNA Tag Array Design and Optimization, Computer Science Colloquium, Kent State University, Kent, Feb. 25, 2005
- Greedy Approximation Algorithms for Covering Problems in Computational Biology, Operations and Information Management Department, University of Connecticut, Storrs, Oct. 22, 2004
- Combinatorial Optimization Methods for Reliable Genomic-Based Pathogen Detection Systems, Comparative Pathology Seminar, Department of Pathobiology and Veterinary Science, University of Connecticut, Storrs, Sept. 30, 2004
- Minimum PCR Primer Set Selection with Amplification Length and Uniqueness Constraints, 2nd Georgia State Biotech Symposium, Atlanta, GA, May 25, 2004
- Combinatorial Optimization Problems in Computational Biology, Mathematics Department Colloquium, University of Connecticut, Storrs, Apr. 22, 2004
- Non-tree Routing for Reliability and Yield Improvement, Fujitsu Laboratories, Kawasaki, Japan, Jan. 20, 2003.

FUNDING

Extramural Research Grants

- *Understanding Nutrition Through Biomics*, Foundation for Food and Agriculture Research Animal Science, **co-PI** (with PI M.A. Amalaradjou and Co-PI D. D'Amico) \$360k, recommended for funding
- *A Catalog of Cell Types in the Early Organogenesis Embryo - A Single Cell Lineage Map, Phase 1*, Connecticut Innovations Regenerative Medicine Research Fund (RMRF) award, **co-PI** (with PI C.E. Nelson and co-PIs J.D. Gibson, D.J. Goldhamer, O. Harel, H.Y. Bar, K. Chen, D. Pejril, and M.S. Bansal), \$675k, recommended for funding

- *Genomic-Driven Personalized Immunotherapy of Human Ovarian Cancer*, Connecticut Bioscience Innovation Fund (CBIF) award, **co-PI** (with PI P.K. Srivastava and co-PIs A. Kueck and S. Al Seesi), \$500k, recommended for funding
- *Algorithmic Techniques for Inferring Transmission Networks from Noisy Sequencing Data*, NSF award CCF-1618347, **PI** (with Co-PI M. Bansal), \$200k, 8/2016–7/2019
- *Computational framework for inference of metabolic pathway activity from RNA-seq data*, NSF award DBI-1564936, **PI**, \$300k, 7/1/2016–6/30/2019
- *Investigating the beneficial role of cheese starter cultures in the prevention of IBD*, USDA National Institute of Food and Agriculture award 2016-67018-24415, **Co-PI** (with PI M.A. Amalaradjou and Co-PI D. D'Amico) \$150k, 11/2015–10/2017
- *Identification and Characterization of the Presomitic Mesoderm Progenitor*, NIH R21 award HD071606-01A1, **Co-PI** (with PI C.E. Nelson), \$406k, 7/2012-6/2014
- *Novel transcript reconstruction from ION Torrent sequencing reads*, Life Technologies Corporation, Collaborative Research Compacts program, **PI** (with Co-PI A. Zelikovsky), \$30k, 07/2012-12/2012
- *Bioinformatics tools for viral quasispecies reconstruction from next-generation sequencing data and vaccine optimization*, USDA National Institute of Food and Agriculture award 2011-67016-30331, **PI** (with Co-PIs M.I. Khan and R.J. O'Neill, and A. Zelikovsky), \$420k, 04/2011-03/2014
- *Software for robust transcript discovery and quantification from sequencing data*, Life Technologies Corporation, Collaborative Research Compacts program, **PI** (with Co-PI A. Zelikovsky), \$30k, 08/2011-02/2012
- *Reconstruction of haplotype spectra from high-throughput sequencing data*, NSF award IIS-0916948, **PI** (with Co-PI Y. Wu), \$275k, 09/2009-08/2013
- *Combinatorial algorithms for high-throughput collection and analysis of genomic diversity data*, NSF CAREER award IIS-0546457, **PI**, \$570k, 01/2006–12/2011
- *Bioinformatics tools enabling large-scale DNA barcoding*, NSF award DBI-0543365, **PI** (with Co-PIs B. Dasgupta and M.I. Khan), \$400k, 07/2006–06/2010

Intramural Research Grants

- *Single Cell Lineage Map*, UConn Academic Vision Program Grant, **Co-PI** (with PI C.E. Nelson and Co-PIs O. Harel, T. Hunter, and I. Moraru) \$100k, 07/2015–06/2016
- *Probiotic Mediated Epigenomic Programming in the Prophylaxis and Treatment of IBD* UConn Research Excellence Program Grant, **Co-PI** (with PI M.A. Amalaradjou), \$25k, 03/2015–03/2016
- *The mechanism of phenotypic drift in hES cells*, UCHC/Storrs and Regional Campus Incentive Grants ("UCIG") Award, **co-PI** (with PI R. O'Neill and co-PIs B. Graveley, T. Rasmussen, and Y. Wu), \$50k, 9/2009–8/2010
- *Primer selection algorithms for cost-effective DNA amplification by multiplex PCR*, University of Connecticut Research Foundation, Large Faculty Research Grant Program, **PI**, \$18k, 06/2004–05/2005

Other Grants

- *Travel Support: 12th International Symposium on Bioinformatics Research and Applications*, National Science Foundation award IIS-1639612 **Co-PI** (with PI A. Zelikovsky and Co-PIs Z. Cai, Y. Pan, and R. Sunderraman) \$20k, 06/2016-05/2017
- *Travel Support: 11th International Symposium on Bioinformatics Research and Applications*, National Science Foundation award IIS-1542617, **Co-PI** (with PI A. Zelikovsky and Co-PIs Y. Li, Y. Pan, and R. Sunderraman) \$20k, 05/2015-04/2016
- *Oncoimmune, a tumor-specific immunotherapy for the treatment of stage III/IV ovarian cancer*, UCHC Spark grant for early stage commercialization and development, **co-PI** (with PI P.K. Srivastava and co-PIs A. Kueck, F. Duan, and S. Al Seesi), \$30k, 12/2013
- UConn/Jackson Laboratory faculty fellowship to attend *53rd Annual Short Course on Medical and Experimental Mammalian Genetics*, **PI**, \$3.5k, 7/15/2012–7/27/2012

- *Travel Support: 8th International Symposium on Bioinformatics Research and Applications*, National Science Foundation award IIS-1237310, **co-PI** (with PI R. Sunderraman and co-PIs A. Zelikovsky and O. Daescu), \$20k, 06/2012-05/2013
 - *Travel Support: 7th International Symposium on Bioinformatics Research and Applications*, National Science Foundation award IIS-1116001, **co-PI** (with PI A. Zelikovsky and co-PI Y. Pan), \$20k, 04/2011-03/2012
 - *First International IEEE Conference on Computational Advances in Bio and Medical Sciences (ICCABS) – Travel Awards*, National Science Foundation award IIS-1112395, **co-PI** (with PI S. Rajasekaran), \$20k, 02/2011-01/2012
 - *Computational Biomedical Science*, UCONN Honors Interdisciplinary Course Development Grant, **PI** (with PI C.E. Nelson), \$8k, 06/2006–05/2009
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- Guest editor, *BMC Bioinformatics* 17 (Suppl 8) and *BMC Genomics* 17 (Suppl 5), special supplements devoted to selected papers from the *11th International Symposium on Bioinformatics Research and Applications*
- Guest editor, *BMC Bioinformatics* 16 (Suppl 17) and *BMC Genomics* 16 (Suppl 11), special supplements devoted to selected papers from the *4th IEEE International Conference on Computational Advances in Bio and Medical Sciences*
- Guest editor, *BMC Bioinformatics* 15 (Suppl 8) and *BMC Genomics* 15 (Suppl 5), special supplements devoted to selected papers from the *3rd IEEE International Conference on Computational Advances in Bio and Medical Sciences*
- Guest editor, *IEEE/ACM Transaction on Computational Biology and Bioinformatics* 10(6) November-December 2013, special section devoted to *8th International Symposium on Bioinformatics Research and Applications*
- Guest editor, *BMC Bioinformatics* 14 (Suppl 18), *BMC Genomics* 14 (Suppl 7), and *International Journal of Bioinformatics Research and Applications* 10 (No. 4/5) special supplements devoted to selected papers from the *2nd IEEE International Conference on Computational Advances in Bio and Medical Sciences*
- Guest editor, *In Silico Biology* 11(5), Nov. 2012, special issue devoted to the *2011 Workshop on Computational Advances in Molecular Epidemiology*
- Guest editor, *BMC Bioinformatics* 13(Suppl 10), June 2012, special supplement devoted to selected papers from the *7th International Symposium on Bioinformatics Research and Applications*
- Guest editor, *BMC Bioinformatics* 13(Suppl 5) and *BMC Genomics* 13(Suppl 2), April 2012, special supplements devoted to selected papers from the *1st IEEE International Conference on Computational Advances in Bio and Medical Sciences*
- Guest editor, *BMC Proceedings* 5(Suppl 2), April 2011, special supplement devoted to selected papers from the *6th International Symposium on Bioinformatics Research and Applications*
- Guest editor, *IEEE/ACM Transaction on Computational Biology and Bioinformatics* 7(4), October-December 2010, special section devoted to *5th International Symposium on Bioinformatics Research and Applications*
- Guest editor, *IEEE/ACM Transaction on Computational Biology and Bioinformatics* 6(2), April-June 2009, special section devoted to *4th International Symposium on Bioinformatics Research and Applications*
- Guest editor, *IEEE/ACM Transaction on Computational Biology and Bioinformatics* 5(3), July-September 2008, special section devoted to *3rd International Symposium on Bioinformatics Research and Applications*
- Guest editor, *IEEE/ACM Transaction on Computational Biology and Bioinformatics* 4(4), October-December 2007, special section devoted to *2nd International Workshop on Bioinformatics Research and Applications*

- Guest editor, *International Journal of Sensor Networks* Vol. 6, No. 1, 2009, special issue devoted to *2nd ACIS Workshop on Self-Assembling Wireless Networks*
- Guest editor, *IEEE Transactions on NanoBioscience* 6(1), March 2007, special section on Computational NanoBioscience
- Guest editor, *Journal of Universal Computer Science* 13(1), March 2007, special issue devoted to *1st ACIS Workshop on Self-Assembling Wireless Networks*

Chair of International Workshops and Conferences

- Workshop co-chair, *6th Workshop on Computational Advances for Next Generation Sequencing*, Atlanta, GA, October 13-15, 2016.
- Workshop co-chair, *5th Workshop on Computational Advances in Molecular Epidemiology*, Atlanta, GA, October 13-15, 2016.
- Workshop co-chair, *5th Workshop on Computational Advances for Next Generation Sequencing*, Miami, Florida, Oct 16, 2015
- Workshop co-chair, *4rd Workshop on Computational Advances in Molecular Epidemiology*, Norfolk, Virginia, June 9, 2015.
- Program Co-Chair, *11th International Symposium on Bioinformatics Research and Applications*, Norfolk, Virginia, June 7-10, 2015.
- Workshop co-chair, *4th Workshop on Computational Advances for Next Generation Sequencing*, Miami Beach, Florida, June 2-3, 2014
- Workshop co-chair, *3rd Workshop on Computational Advances in Molecular Epidemiology*, Miami Beach, Florida, June 3, 2014
- Workshop co-chair, *3rd Workshop on Computational Advances for Next Generation Sequencing*, New Orleans, LA, June 12-13, 2013
- Workshop co-chair, *2nd Workshop on Computational Advances in Molecular Epidemiology*, New Orleans, LA, June 13, 2013
- Program committee co-chair, *8th International Symposium on Bioinformatics Research and Applications*, Dallas, Texas, May 21-23, 2012
- Workshop co-chair, *2nd Workshop on Computational Advances for Next Generation Sequencing*, Las Vegas, Nevada, Feb. 24-25, 2012
- Program committee co-chair, *2nd IEEE International Conference on Computational Advances in Bio and Medical Sciences*, Las Vegas, Nevada, Feb. 23-25, 2012
- Workshop co-chair, *1st Workshop on Computational Advances in Molecular Epidemiology*, Atlanta, GA, Nov. 12, 2011
- Publicity co-chair, *7th International Symposium on Bioinformatics Research and Applications*, Changsha, Hunan, China, May 27-29, 2011
- Workshop co-chair, *1st Workshop on Computational Advances for Next Generation Sequencing*, Orlando, Florida, Feb. 4, 2011
- Program committee co-chair, *1st IEEE International Conference on Computational Advances in Bio and Medical Sciences*, Orlando, Florida, Feb. 3-5, 2011
- General co-chair, *6th International Symposium on Bioinformatics Research and Applications*, Storrs, CT, May 23-26, 2010
- Program committee co-chair, *5th International Symposium on Bioinformatics Research and Applications*, Ft. Lauderdale, FL, May 13-16, 2009
- Program committee co-chair, *4th International Symposium on Bioinformatics Research and Applications*, Atlanta, GA, May 6-8, 2008

- Chair, *10th International Workshop on System Level Interconnect Prediction*, Newcastle, UK, April 5-6, 2008
- Program committee co-chair, *2007 IEEE International Conference on Bioinformatics and Biomedicine*, San Jose, CA, Nov. 2-4, 2007
- Co-chair, *3rd ACIS International Workshop on Self-Assembling Wireless Networks*, Qingdao, China, July 30-Aug 1, 2007
- Program committee co-chair, *3rd International Symposium on Bioinformatics Research and Applications*, Atlanta, GA, May 7-10, 2007
- Program committee chair, *9th International Workshop on System Level Interconnect Prediction*, Austin, TX, March 17-18, 2007
- Publicity chair, *9th SIGDA Ph.D. Forum at the Design Automation Conference*, San Francisco, CA, July 25, 2006
- Co-chair, *2nd ACIS International Workshop on Self-Assembling Wireless Networks*, Las Vegas, June 20, 2006
- Program committee chair, *2nd International Workshop on Bioinformatics Research and Applications*, Reading, UK, May 28-31, 2006
- Publicity chair, *8th International Workshop on System Level Interconnect Prediction*, Munich, Germany, March 4-5, 2006
- Publicity chair, *8th SIGDA Ph.D. Forum at the Design Automation Conference*, Anaheim, CA, June 14, 2005
- Co-chair, *1st ACIS International Workshop on Self-Assembling Wireless Networks*, Towson, MD, May 24, 2005
- Publicity chair, *7th International Workshop on System Level Interconnect Prediction*, San Francisco, CA, April 2-3, 2005
- Publicity chair, *6th International Workshop on System Level Interconnect Prediction*, Paris, France, Feb. 14-15, 2004

Member of Program Committees

- *15th Asia Pacific Bioinformatics Conference*, Shenzhen, China, Jan. 16-18, 2017
- *24th International Conference on Intelligent System for Computational Biology*, Orlando, Florida, July 8 - 12, 2016
- *12th International Symposium on Bioinformatics Research and Applications*, Minsk, Belarus, June 5-8, 2016
- *6th RECOMB Satellite Workshop on Massively Parallel Sequencing*, Los Angeles, CA, April 16-17, 2016
- *4th RECOMB Satellite on Computational Methods in Genetics*, Los Angeles, CA, April 16-17, 2016
- *14th Asia Pacific Bioinformatics Conference*, San Francisco, CA, Jan. 11-13, 2016
- *23rd International Conference on Intelligent System for Computational Biology and 14th European Conference on Computational Biology*, Dublin, Ireland, July 10-14, 2015
- *12th RECOMB Satellite Workshop on Comparative Genomics*, Cold Spring Harbor, NY, Oct. 19-22, 2014
- *14th Workshop on Algorithms in Bioinformatics*, Wroclaw, Poland, Sept. 08-10, 2014
- *22nd Annual International Conference on Intelligent Systems in Molecular Biology*, Boston, MA, July 11-15, 2014
- *10th International Symposium on Bioinformatics Research and Applications*, Zhangjiajie, China, June 28-30, 2014
- *4th IEEE International Conference on Computational Advances in Bio and Medical Sciences*, Miami Beach, Florida, June 2-4, 2014
- *13th Workshop on Algorithms in Bioinformatics*, Sophia Antipolis, France, Sept. 2-4, 2013

- *21st International Conference on Intelligent System for Computational Biology and 12th European Conference on Computational Biology*, Berlin, Germany, July 19 - 23, 2013
- *9th International Symposium on Bioinformatics Research and Applications*, Charlotte, NC, May 20-22, 2013
- *12th Workshop on Algorithms in Bioinformatics*, Ljubljana, Slovenia, Sept. 10-12, 2012
- *2012 Brazilian Symposium on Bioinformatics*, Campo Grande, Brazil, Aug. 15-17, 2012
- *20th International Conference on Intelligent System for Computational Biology*, Long Beach, CA, July 15-17, 2012
- *2nd Annual RECOMB Satellite Workshop on Massively Parallel Sequencing*, Barcelona, Spain, April 19-20, 2012
- *5th IEEE International Conference on Bioinformatics and Biomedicine*, Atlanta, GA, Nov. 12-15, 2011
- *11th IEEE International Symposium on Bioinformatics and Bio Engineering*, Taichung, Taiwan, Oct. 24-26, 2011
- *11th Workshop on Algorithms in Bioinformatics*, Saarbrücken, Germany, Sept. 5-7, 2011
- *2011 Brazilian Symposium on Bioinformatics*, Brasília, Brazil, Aug. 10-12, 2011
- *2nd ACM Conference on Bioinformatics, Computational Biology and Biomedicine*, Chicago, IL, August 1-3, 2011
- *19th International Conference on Intelligent System for Computational Biology & 10th European Conference on Computational Biology*, Vienna, Austria, July 17-19, 2011
- *Bioinformatics 2011*, Rome, Italy, Jan. 26-29, 2011
- *Advances in the Theory of Computing*, special section of *12th International Symposium on Symbolic and Numeric Algorithms for Scientific Computing*, Timisoara, Romania, Sept. 23-26, 2010
- *10th Workshop on Algorithms in Bioinformatics*, Liverpool, UK, Sept. 6-8, 2010
- *2010 Brazilian Symposium on Bioinformatics*, Rio de Janeiro, Brazil, Aug. 30 - September 3, 2010
- *18th Annual International Conference on Intelligent Systems for Molecular Biology*, Boston, MA, July 11- 13, 2010
- *21st Annual Symposium on Combinatorial Pattern Matching*, New York, NY, June 21-23, 2010
- *1st International Workshop on Bio-Design Automation*, San Francisco, CA, July 27, 2009
- *2009 Brazilian Symposium on Bioinformatics*, Porto Alegre, RS, Brazil, July 29-31, 2009
- *17th Annual International Conference on Intelligent Systems for Molecular Biology & 8th European Conference on Computational Biology*, Stockholm, Sweden, June 27 - July 2, 2009
- *9th IEEE International Symposium on Bioinformatics & Bioengineering*, Taichung, Taiwan, June 22-24, 2009
- *1st International Conference on Bioinformatics and Computational Biology*, New Orleans, LA, Apr. 8-10, 2009
- *International Conference on Wireless Algorithms, Systems and Applications*, Dallas, TX, Oct. 26-28, 2008
- *3rd International Multi-Conference on Computing in the Global Information Technology*, Athens, Greece, July 27 - August 1, 2008
- *7th IEEE International Symposium on Bioinformatics & Bioengineering*, Boston, MA, Oct. 14-17, 2007
- *2nd VLDB Workshop on Data Mining in Bioinformatics*, Vienna, Austria, Sept. 23, 2007
- *10th SIGDA Ph.D. Forum at the Design Automation Conference*, San Diego, CA, June 5, 2007
- *2nd International Conference on Computing in the Global Information Technology*, Guadeloupe, French Caribbean, March 4-9, 2007
- *1st International Conference on Computing in the Global Information Technology*, Bucharest, Romania, August 1-3, 2006

- 7th ACIS International Conference on Software Engineering, Artificial Intelligence, Networking, and Parallel/Distributed Computing, Las Vegas, June 19-20, 2006
- 8th Int. Conf. on Computer Science and Informatics, Salt Lake City, Utah, July 21-26, 2005
- 6th ACIS International Conference on Software Engineering, Artificial Intelligence, Networking, and Parallel/Distributed Computing, Towson, MD, May 23-25, 2005
- 1st International Workshop on Bioinformatics Research and Applications, Atlanta, GA, May 22-25, 2005
- 7th SIGDA Ph.D. Forum at the Design Automation Conference, San Diego, CA, June 8, 2004
- 5th International Workshop on Approximation Algorithms for Combinatorial Optimization Problems, Rome, Italy, Sept. 17-21, 2002

Referee

- Panelist, NCI Omnibus R03 & R21 (1 panel)
- Panelist, NSF III (7 panels), BD2K (2 panels), CAREER (1 panel), SCH (1 panel), and ABI (1 panel)
- Expert assessor for the *Australian Research Council (ARC)*
- Reviewer for the *Israel Science Foundation*
- Judge for the *Intel Science Talent Search (STS)* competition
- Reviewer for *Computing Reviews*
- Technical referee for *ACM Transactions on Design Automation of Electronic Systems, Advances in Bioinformatics, Algorithmica, BMC Bioinformatics, BMC Genome Medicine, Bioinformatics, Combinatorica, Discrete Applied Mathematics, Genetics, IEEE Transactions on Computational Biology and Bioinformatics, IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems, IEEE Transactions on Computers, IEE Proceedings - Circuits, Devices and Systems, Information Processing Letters, Integration, the VLSI Journal, International Journal of Sensor Networks, International Journal of Bioinformatics Research and Applications, Journal of Bioinformatics and Computational Biology, Journal of Computational Biology, Journal of Combinatorial Optimization, SIAM Journal on Computing, Theoretical Computer Science, ACM-IEEE Design Automation Conference (DAC), European Symposium on Algorithms (ESA), ACM-SIAM Symposium on Discrete Algorithms (SODA), ACM/IEEE International Workshop on Timing Issues in the Specification and Synthesis of Digital Systems, Asia and South Pacific Design Automation Conference (ASP-DAC), IEEE-ACM International Conference on Computer-Aided Design (ICCAD), International Conference on Intelligent Systems for Molecular Biology (ISMB), International Conference on Research in Computational Molecular Biology (RECOMB)*

Professional Societies

- Association for Computing Machinery (ACM)
- ACM Special Interest Group on Algorithms and Computation Theory (SIGACT)
- ACM Special Interest Group on Bioinformatics (SIGBioinformatics)

TEACHING AND ADVISING

Courses Taught

University of Connecticut

- BME1401/CSE1401/MCB1401, *Honors Core: Computational Molecular Biology* (Fall 2007, Fall 2008, Spring 2009, Fall 2010, Spring 2011, Fall 2011, Spring 2012, Fall 2013, Spring 2014)
- BME 4985/6160 & CSE 4095/6800, *Computational Genomics* (Spring 2007, Spring 2008, Spring 2009, Spring 2013, Spring 2015)

- BME4800 & CSE3800/5800, *Bioinformatics* (Spring 2005, Spring 2006, Fall 2006, Fall 2007, Fall 2008, Fall 2010, Fall 2011, Fall 2012, Fall 2013, Fall 2015, Fall 2016)
- BME 295/300 & CSE 298/300: *Computational Molecular Biology* (Fall 2005)
- CSE2100: *Data Structures and Introduction to Algorithms* (Spring 2006, Fall 2006, Spring 2008, Spring 2011, Spring 2012, Spring 2013, Spring 2014, Spring 2015, Spring 2016)
- CSE243: *Computer Architecture and Hardware/Software Interface* (Spring 2004, Fall 2004)
- CSE300: *Algorithms in Bioinformatics* (Fall 2003)
- CSE3100, *Systems Programming* (Fall 2014, Fall 2015, Fall 2016)
- INTD198: *Freshman Honors Seminar – Bioinformatics and Molecular Evolution* (Fall 2006)

Georgia Institute of Technology

- CS1050: *Understanding and constructing proofs* (Spring 2001)
- CS3500: *Theory I* (Spring 2000, Fall 2000)
- CS1155: *Understanding and constructing proofs* (Summer 1999)
- CS3156: *Introduction to automata theory* (Fall 1998)

Major Advisor – Ph.D. Students

- Current advisees: Fahad Alqahtani, Mohammad Alsulami, Paramik Dasgupta, Elham Sherafat
- James Lindsay, Ph.D. 05/2015, thesis: “Scalable Optimization Algorithms for High-throughput Genomic Data”, current position: Senior Bioinformatics Engineer at Dana-Farber Cancer Institute, Boston, MA
- Jorge Duitama, Ph.D. 12/2010, thesis: “Bioinformatics Methods for Diagnosis and Treatment of Human Diseases”, current position: Assistant Professor, Universidad de los Andes, Bogotá, Colombia
- Jin Jun, Ph.D. 5/2010, co-advised with C.E. Nelson, thesis: “Reconstruction and Analysis of Gene Family Evolution in Mammals”, first position: post-doctoral scholar at the Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany
- Justin Kennedy, Ph.D. 12/2009, thesis: “Efficient Algorithms for SNP Genotype Data Analysis using Hidden Markov Models of Haplotype Diversity”, current position: Senior Software Engineer at Sonalysts, Waterford, CT and
- Bogdan Paşaniuc, Ph.D. 5/2008, thesis: “Scalable Algorithms for Analysis of Genomic Diversity Data”, current position: Assistant Professor, Institute for Molecular Medicine, David Geffen School of Medicine, UCLA

Major Advisor – M.S. Students

- Gabriel Ilie, M.S. 12/2013, thesis: “Algorithms for Multisample Read Binning”, current position: Software Developer, Mysis Corp.
- Pankaj Ghimire, M.S. 12/2012, co-advised with Y. Wu, thesis: “Detection of Genomic Inversion from Single End Reads”, current position: Senior Software Development Consultant at TechDigital Corporation
- Marius Nicolae, M.S. 12/2011, thesis: “Accurate Estimation of Isoform and Gene Expression Levels from Next Generation Sequencing Data”, current position: Software Developer Engineer, Amazon Web Services
- Claudia Prajescu, M.S. 12/2005, thesis: “Multiplexing Algorithms for High-Throughput Genomic Based Assays”, first position: Software Developer with Siemens VDO Automotive
- Dragos Trinca, M.S. 12/2005, thesis: “Exact and Approximation Algorithms for DNA Tag Set Design”, first position: Ph.D. student at UConn

Mentor – Post-Doctoral Fellows

- Bassam Tork (2013-2014, co-mentored with P.K. Srivastava), current position: Information and Communication Technology Research & Development Unit, Al-Quds Open University
- Sahar Al Seesi (2010-2013, co-mentored with P.K. Srivastava), current position: Assistant Professor in Residence, Computer Science & Engineering Department, University of Connecticut