

## CONTACT INFORMATION

University of Connecticut  
College of Engineering  
School of Computing  
371 Fairfield Way, Unit 4155  
Storrs, CT 06269-4155  
Tel: 860-486-3784  
Fax: 860-486-4817  
E-mail: [ion@engr.uconn.edu](mailto:ion@engr.uconn.edu)  
<http://dna.engr.uconn.edu/ion/>

---

## 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)
- 

## EMPLOYMENT

### University of Connecticut

- Professor (8/2017–)
- Associate Professor (8/2008–8/2017)
- 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, 2016-2017
- United Technologies Corporation Term Professorship in Engineering Innovation, 2013-2015
- NSF Faculty Early Career Development (CAREER) Award, 2006-2011

---

## PUBLICATIONS

### Edited Books

- [EB1] I.I. Măndoiu and A.Z. Zelikovsky (Eds.). *Computational Methods for Next Generation Sequencing Data Analysis*. Wiley Book Series on Bioinformatics. John Wiley & Sons, xxvi+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] M.S. Bansal, I.I. Măndoiu, M. Moussa, M. Patterson, S. Rajasekaran, P. Skums, and A. Zelikovsky (Eds.). *Proc. 11th International Conference on Computational Advances in Bio and Medical Sciences*, volume Lecture Notes in Bioinformatics vol. 13254. Springer-Verlag, Berlin, 2022.
- [EP2] S.K. Jha, I.I. Măndoiu, S. Rajasekaran, P. Skums, and A. Zelikovsky (Eds.). *Proc. 10th International Conference on Computational Advances in Bio and Medical Sciences*, volume Lecture Notes in Bioinformatics vol. 12686. Springer-Verlag, Berlin, 2021.
- [EP3] Z. Cai, I.I. Măndoiu, G. Narasimhan, P. Skums, and X. Gao (Eds.). *Proc. 16th International Symposium on Bioinformatics Research and Applications*, volume Lecture Notes in Bioinformatics vol. 12304. Springer-Verlag, Berlin, 2020.
- [EP4] I.I. Măndoiu, T. M. Murali, G. Narasimhan, S. Rajasekaran, P. Skums, and A. Zelikovsky. *Proc. 9th International Conference on Computational Advances in Bio and Medical Sciences*, volume Lecture Notes in Bioinformatics vol. 12029. Springer-Verlag, Berlin, 2020.
- [EP5] 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.
- [EP6] 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.
- [EP7] 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.
- [EP8] B. Chen et al. (Eds.). *Workshops Proceedings, 2011 IEEE International Conference on Bioinformatics and Biomedicine*. IEEE Computer Society Press, 2011.
- [EP9] 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.
- [EP10] 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.
- [EP11] I.I. Măndoiu, R. Sunderraman, and A. Zelikovsky (Eds.). *Proc. 4th International Symposium on Bioinformatics Research and Applications*, vol. 4983 of *Lecture Notes in Bioinformatics*. Springer-Verlag, Berlin, 2008.
- [EP12] 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.
- [EP13] 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] I.I. Mandoiu, A. Olshevsky, and A.Z. Zelikovsky. *Handbook of Approximation Algorithms and Metaheuristics, Second Edition. Volume 2: Contemporary and Emerging Applications*, chapter Chapter 23: QoS Multimedia Multicast Routing, pages 441–458. Chapman & Hall/CRC, 2018.
- [BC2] A.B. Kahng, I.I. Mandoiu, and A.Z. Zelikovsky. *Handbook of Approximation Algorithms and Metaheuristics, Second Edition. Volume 1: Methodologies and Traditional Applications*, chapter Chapter 37: Practical Approximations of Steiner Trees in Uniform Orientation Metrics, pages 657–670. Chapman & Hall/CRC, 2018.
- [BC3] E. Nenastjeva, 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.
- [BC4] 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. 301–328, John Wiley & Sons, 2016.
- [BC5] 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.
- [BC6] 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.
- [BC7] 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.
- [BC8] 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.
- [BC9] 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.
- [BC10] 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.
- [BC11] 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.
- [BC12] 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.
- [BC13] 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.
- [BC14] 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.
- [BC15] 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] M.A. Gillig, C.A. Brennick, M.M. George, J.L. Balsbaugh, T.V. Shcheglova, I.I. Măndoiu, T. Rosales, B.M. Baker, P.K. Srivastava, and S.H. Karandikar. CD8+ T cell-dependent anti-tumor activity in vivo of a mass spectrometry-identified, neoepitope despite undetectable CD8+ immunogenicity in vitro. *The Journal of Immunology* 211(12):17831791, 2023.
- [J2] S. Al Seesi, A. Al-okaily, T.V. Shcheglova, E. Sherafat, F.H. Alqahtani, A.T. Hagymasi, A. Kaur, P.K. Srivastava, and I.I. Măndoiu. GeNeo: A Bioinformatics Toolbox for Genomics-Guided Neoepitope Prediction. *J. Comput. Biol.*, 30(4):538–551, 2023.
- [J3] S. Ranjekar, J.E. Duan, K. Srirattana, F. Alqahtani, E. Tulman, I.I. Măndoiu, K. Venkitanarayanan, and X. Tian. Transcriptomic Responses of *Mycoplasma bovis* Upon Treatments of trans-Cinnamaldehyde, Carvacrol, and Eugenol. *Frontiers in Microbiology* 13:888433, 2022.
- [J4] S. Dhar, C. Zhang, I.I. Mandoiu, and M.S. Bansal. TNet: Phylogeny-Based Inference of Disease Transmission Networks Using Within-Host Strain Diversity. *IEEE/ACM Trans. on Computational Biology and Bioinformatics* 19(1):230–242, 2022.
- [J5] H. Ebrahimi-Nik, M. Moussa, R.P. Englander, S. Singhaviranon, J. Michaux, H. Pak, H. Miyadera, W.L. Corwin, G.L.J. Keller, A.T. Hagymasi, T.V. Shcheglova, G. Coukos, B.M. Baker, I.I. Măndoiu, M. Bassani-Sternberg, and P.K. Srivastava. Reversion analysis reveals the in vivo immunogenicity of a poorly MHC I-binding cancer neoepitope. *Nat Commun.* 12(1):6423, 2021.
- [J6] F. Rondel, R. Hosseini, B. Sahoo, S. Knyazev, I. Mandric, F. Stewart, I.I. Mandoiu, B. Pasaniuc, Y.Porozov, and A. Zelikovsky. Pipeline for Analyzing Activity of Metabolic Pathways in Planktonic Communities Using Metatranscriptomic Data. *Journal of Computational Biology* 28(8):842-855, 2021.
- [J7] M. Moussa and I.I. Mandoiu. SC1: A tool for interactive web-based single cell RNA-Seq data analysis. *Journal of Computational Biology* 28(8):820-841, 2021.
- [J8] L.L. Boshans, H. Soh, W.M. Wood, M. William, T.M. Nolan, I.I. Mandoiu, Y. Yanagawa, A.V. Tzingounis, and Akiko A. Nishiyama. Direct reprogramming of oligodendrocyte precursor cells into gabaergic inhibitory neurons by a single homeodomain transcription factor *dlx2*. *Scientific Reports*, 11, 3552, 2021.
- [J9] C.A. Brennick, M.M. George, M.R. Moussa, A.T. Hagymasi, Sahar Al Seesi, T.V. Shcheglova, R.P. Englander, G.L.J. Keller, J.L. Balsbaugh, B.M. Baker, A. Schietinger, I.I. Măndoiu, and P.K. Srivastava. An unbiased approach to defining bona fide cancer neoepitopes that elicit immune-mediated cancer rejection. *J Clin Invest.* 131(3):e142823, 2021.
- [J10] E. Sherafat, J. Force, and I.I. Măndoiu. Semi-supervised learning for somatic variant calling and peptide identification in personalized cancer immunotherapy. *BMC Bioinformatics*, 21, 498, 2020.
- [J11] D.K. Wells et al. Key parameters of tumor epitope immunogenicity revealed through a consortium approach improve neoantigen prediction. *Cell*, 183, pp. 818-834.e13, 2020.
- [J12] F. Alqahtani and I.I. Măndoiu. Statistical mitogenome assembly with repeats. *Journal of Computational Biology*, 27(9):1407–1421, 2020.
- [J13] J.T. Nevin, M. Moussa, L. Corwin W, I.I. Măndoiu, and P.K. Srivastava. Sympathetic nervous tone limits the development of myeloid-derived suppressor cells. *Science Immunology*, 5(51):eaay9368, 2020.
- [J14] F. Alqahtani, D. Duckett, S. Pirro, and I.I. Măndoiu. Complete mitochondrial genome of the water vole, *Microtus richardsoni*(Cricetidae, Rodentia). *Mitochondrial DNA Part B*, 5:3:2498–2499, 2020.
- [J15] D. Lähnemann et al. Eleven grand challenges in single-cell data science. *Genome biology*, 21(1):1–35, 2020.
- [J16] M. Moussa and I.I. Măndoiu. Locality Sensitive Imputation for Single-Cell RNA-Seq Data. *Journal of Computational Biology* 26(8):822-835, 2019.

- [J17] L.L. Boshans, D.C. Factor, V. Singh, J. Liu, C. Zhao, I.I. Măndoiu, Q.R. Lu, P. Casaccia, P.J. Tesar, and A. Nishiyama. The chromatin environment around interneuron genes in oligodendrocyte precursor cells and their potential for interneuron reprogramming. *Frontiers in Neuroscience* 13:829, 2019.
- [J18] H. Ebrahimi-Nik, J. Michaux, W.L. Corwin, G.L.J. Keller, T. Shcheglova, H.S. Pak, G. Coukos, B.M. Baker, I.I. Măndoiu, M. Bassani-Sternberg, and P.K. Srivastava. Mass spectrometry driven exploration reveals nuances of neoepitope-driven tumor rejection. *JCI Insight*, 4(14), 2019.
- [J19] J. Duan, Z. Jiang, F. Alqahtani, I.I. Măndoiu, D. Hong, X. Zheng, S.L. Marjani, J. Chen, and X. Tian. Methylome dynamics of bovine gametes and in vivo early embryos. *Frontiers in Genetics* 10:512, 2019.
- [J20] A.L. Sedlacek, T.P. Younker, Y. Zhou, L. Borghesi, T. Shcheglova, I.I. Măndoiu, and R.J. Binder. Cd91 on dendritic cells governs immunosurveillance of nascent, emerging tumors. *JCI Insight*, 4(7):e127239, 2019.
- [J21] J. Duan, K. Flock, N. Jue, M. Zhang, A. Jones, S. Al Seesi, I.I. Măndoiu, S. Pillai, M. Hoffman, R. O'Neill, S. Zinn, K. Govoni, S. Reed, H. Jiang, Z. Jiang, and X. Tian. Dosage Compensation and Gene Expression of the X Chromosome in Sheep. *G3: Genes, Genomes, Genetics*, 9(1), pp. 305-314, 2019.
- [J22] J. Duan, M. Zhang, Ka. Flock, S. Al Seesi, I.I. Măndoiu, A. Jones, E. Johnson, S. Pillai, M. Hoffman, K. McFadden, H. Jiang, S. Reed, K. Govoni, S. Zinn, Z. Jiang, and X. Tian. Effects of maternal nutrition on the expression of genomic imprinted genes in ovine fetuses. *Epigenetics*, 13(8), pp. 793-807, 2018.
- [J23] H. Ebrahimi-Nik, W.L. Corwin, T. Shcheglova, A. Das Mohapatra, I.I. Măndoiu, and P.K. Srivastava. CD11c<sup>+</sup> MHCII<sup>lo</sup> GM-CSF-bone marrow-derived dendritic cells act as antigen donor cells and as antigen presenting cells in neoepitope-elicited tumor immunity against a mouse fibrosarcoma. *Cancer Immunology, Immunotherapy*, 67(9), pp. 1449-1459, 2018.
- [J24] M. Moussa and I.I. Măndoiu. Single cell RNA-Seq data clustering using TF-IDF based methods. *BMC Genomics*, 19(Suppl 6):4922, 2018.
- [J25] M.S. Muyyarikkandy, F. Alqahtani, I.I. Măndoiu, and M.A. Amalaradjou. Draft Genome Sequence of *Lactobacillus paracasei* DUP 13076, which Exhibits Potent Antipathogenic Effects against *Salmonella enterica* Serovars Enteritidis, Typhimurium, and Heidelberg. *Genome Announcements* 6, pp. e00065-18, 2018.
- [J26] M.S. Muyyarikkandy, F. Alqahtani, I.I. Măndoiu, and M.A. Amalaradjou. Draft Genome Sequence of *Lactobacillus rhamnosus* NRRL B-442, a Potential Probiotic Strain. *Genome Announcements* 6, pp. e00046-18, 2018.
- [J27] I. Mandric, Y.T. Tiagueu, T. Shcheglova, S. Al Seesi, A. Zelikovsky, and I.I. Măndoiu. Fast Bootstrapping-Based Estimation of Confidence Intervals of Expression Levels and Differential Expression from RNA-Seq Data. *Bioinformatics* 33(20):3302-3304, 2017.
- [J28] E. Nenastjeva, A. Zelikovsky, I.I. Măndoiu, and Y. Ionov. Identification of cancer-specific motifs in mimotope profiles of serum antibody repertoire. *BMC Bioinformatics* 18(Suppl 8):33-38, 2017.
- [J29] W.L. Corwin, H. Ebrahimi-Nik, S.M. Floyd, P. Tavousi, I.I. Măndoiu, and P.K. Srivastava. Tumor Control Index as a new tool to assess tumor growth in experimental animals. *Journal of Immunological Methods*, 445:71-76, 2017.
- [J30] S. Al Seesi, A. Das Mohapatra, A. Pawashe, I.I. Măndoiu, and F. Duan. Finding neoepitopes in mouse models of personalized cancer immunotherapy. *Frontiers in Biology*, 11(5):366–375, 2016.
- [J31] 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.
- [J32] 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.

- [J33] 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.
- [J34] 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.
- [J35] 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.
- [J36] 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.
- [J37] 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.
- [J38] 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.
- [J39] 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.
- [J40] 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.
- [J41] J. Lindsay, H. Salooti, I.I. Măndoiu, and A. Zelikovsky. ILP-based maximum likelihood genome scaffolding. *BMC Bioinformatics*, 15(Suppl 9):S9, 2014.
- [J42] 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.
- [J43] Y. Huang, M. Khan, and I.I. Măndoiu. Neuraminidase subtyping of Avian influenza viruses with PrimerHunter-designed primers and quadruplicate primer pools. *PLOS ONE*, Volume 8, Issue 11, e81842, 2013.
- [J44] 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.
- [J45] 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.
- [J46] M. Hamdalla, I.I. Măndoiu, D. Hill, S. Rajasekaran, and D. Grant. BioSM: A metabolomics tool for identifying endogenous mammalian biochemical structures in chemical structure space. *Journal of Chemical Information and Modeling*, 53(3):601–612, 2013.
- [J47] N. Mancuso, B. Tork, P. Skums, L. Ganova-Raeva, I.I. Măndoiu, and A. Zelikovsky. Reconstructing viral quasispecies from NGS amplicon reads. *In Silico Biology*, 11(5):237–249, 2012.
- [J48] S. Mangul, A. Caciula, O. Glebova, I.I. Măndoiu, and A. Zelikovsky. Improved transcriptome quantification and reconstruction from RNA-Seq reads using partial annotations. *In Silico Biology*, 11(5):251–261, 2012.
- [J49] F. Duan, S. Simeone, R. Wu, J. Grady, I.I. Măndoiu, and P.K. Srivastava. Area under the curve as a tool to measure kinetics of tumor growth in experimental animals. *Journal of Immunological Methods*, 382(1-2):224–228, 2012.

- [J50] 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.
- [J51] B. Paşaniuc, R. Garfinkel, I.I. Măndoiu, and A. Zelikovsky. Optimal testing of digital microfluidic biochips. *INFORMS Journal on Computing*, pages 518–529, 2011.
- [J52] 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.
- [J53] I. Astrovskaia, B. Tork, S. Mangul, K. Westbrook, I.I. Măndoiu, P. Balfe, and A. Zelikovsky. Inferring viral quasispecies spectra from 454 pyrosequencing reads. *BMC Bioinformatics*, 12(Suppl 6):S1, 2011.
- [J54] 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.
- [J55] C. Lee, I.I. Măndoiu, and C.E. Nelson. Inferring ethnicity from mitochondrial DNA sequence. *BMC Proceedings*, 5(Suppl 2):S11, 2011.
- [J56] 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.
- [J57] 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.
- [J58] J. Jun, I.I. Măndoiu, and C.E. Nelson. Identification of mammalian orthologs using local synteny. *BMC Genomics*, 10:630, 2009.
- [J59] 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.
- [J60] 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.
- [J61] 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.
- [J62] 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.
- [J63] 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.
- [J64] I.I. Măndoiu and C. Prăjescu. High-throughput SNP genotyping by SBE/SBH. *IEEE Transactions on NanoBioscience*, 6(1):28–35, 2007.
- [J65] 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.
- [J66] I.I. Măndoiu and D. Trincă. Exact and approximation algorithms for DNA tag set design. *Journal of Computational Biology*, 13(3):732–744, 2006.
- [J67] A.B. Kahng, I.I. Măndoiu, S. Reda, X. Xu, and A. Zelikovsky. Computer-aided optimization of DNA array design and manufacturing. *IEEE Transactions on Computer-Aided Design*, 25(2):305–320, 2006.
- [J68] 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.
- [J69] 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.

- [J70] B. DasGupta, K.M. Konwar, I.I. Măndoiu, and A.A. Shvartsman. DNA-BAR: distinguisher selection for DNA barcoding. *Bioinformatics*, 21(16):3424–3426, 2005.
- [J71] I.I. Măndoiu, C. Prăjescu, and D. Trincă. Improved tag set design and multiplexing algorithms for universal arrays. *LNCS Transactions on Computational Systems Biology*, II(LNBI 3680):124–137, 2005.
- [J72] P. Gupta, A.B. Kahng, I.I. Măndoiu, and P. Sharma. Layout-aware scan chain synthesis for improved path delay fault coverage. *IEEE Transactions on Computer-Aided Design*, 24(7):1104–1114, 2005.
- [J73] B. DasGupta, K.M. Konwar, I.I. Măndoiu, and A.A. Shvartsman. Highly scalable algorithms for robust string barcoding. *International Journal of Bioinformatics Research and Applications*, 1(2):145–161, 2005.
- [J74] M. Karpinski, I.I. Măndoiu, A. Olshevsky, and A. Zelikovsky. Improved approximation algorithms for the quality of service multicast tree problem. *Algorithmica*, 42(2):109–120, 2005.
- [J75] H. Chen, C.-K. Cheng, A.B. Kahng, I.I. Măndoiu, Q. Wang, and B. Yao. The Y-architecture for on-chip interconnect: Analysis and methodology. *IEEE Transactions on Computer-Aided Design*, 24(4):588–599, 2005.
- [J76] A.B. Kahng, I.I. Măndoiu, P. Pevzner, S. Reda, and A. Zelikovsky. Scalable heuristics for design of DNA probe arrays. *Journal of Computational Biology*, 11(2–3):429–447, 2004.
- [J77] A.B. Kahng, B. Liu, and I.I. Măndoiu. Non-tree routing for reliability and yield improvement. *IEEE Transactions on Computer-Aided Design*, 23(1):148–157, 2004.
- [J78] 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.
- [J79] C. Albrecht, A.B. Kahng, B. Liu, I.I. Măndoiu, and A.Z. Zelikovsky. On the skew-bounded minimum-buffer routing tree problem. *IEEE Transactions on Computer-Aided Design*, 22(7):937–945, 2003.
- [J80] C. Alpert, A.B. Kahng, B. Liu, I.I. Măndoiu, and A.Z. Zelikovsky. Minimum buffered routing with bounded capacitive load for slew rate and reliability control. *IEEE Transactions on Computer-Aided Design*, 22(3):241–253, 2003.
- [J81] 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.
- [J82] F.F. Drăgan, A.B. Kahng, I.I. Măndoiu, S. Muddu, and A.Z. Zelikovsky. Provably good global buffering by generalized multiterminal multicommodity flow approximation. *IEEE Transactions on Computer-Aided Design*, 21(3):263–274, 2002.
- [J83] A.Z. Zelikovsky and I.I. Măndoiu. Practical approximation algorithms for zero- and bounded-skew trees. *SIAM Journal on Discrete Mathematics*, 15:97–111, 2002.
- [J84] I.I. Măndoiu and A.Z. Zelikovsky. A note on the MST heuristic for bounded edge-length Steiner trees with minimum number of Steiner points. *Information Processing Letters*, 75:165–167, 2000.
- [J85] I.I. Măndoiu, V.V. Vazirani, and J.L. Ganley. A new heuristic for rectilinear Steiner trees. *IEEE Transactions on Computer-Aided Design*, 19(10):1129–1139, 2000.
- [J86] K. Jain, I.I. Măndoiu, and V.V. Vazirani. “The art of trellis decoding” is computationally hard—for large fields. *IEEE Transactions on Information Theory*, 44:1211–1214, 1998.
- [J87] I.I. Măndoiu. Optimum extensions of prefix codes. *Information Processing Letters*, 66:35–40, 1998.
- [J88] I.I. Măndoiu. On a theorem of Gács. *International Journal of Computer Mathematics*, 48:157–169, 1993.
- [J89] I.I. Măndoiu. Kraft-Chaitin’s theorem for free-extensible codes. *Mathematical Reports (Studii și Cercetări Matematice)*, 44:497–501, 1992.



## Articles in Refereed Conference Proceedings

- [C1] M. Moussa and I.I. Mandoiu. Computational cell cycle analysis of single cell RNA-Seq data. In S. Rajasekaran P. Skums S.K. Jha, I.I. Mandoiu and A. Zelikovsky (Eds.), editors, *Proc. 10th International Conference on Computational Advances in Bio and Medical Sciences*, volume 12686 of *Lecture Notes in Computer Science*, pages 67–83. Springer, 2021.
- [C2] S. Sledzieski, C. Zhang, I.I. Mandoiu, and M. Bansal. Treefix-TP: Phylogenetic error-correction for infectious disease transmission network inference. In *Proc. 26th Pacific Symposium on Biocomputing*, pages 119–130. World Scientific Publishing Company, 2021.
- [C3] M. Moussa and I.I. Mandoiu. SC1: A tool for interactive web-based single cell rna-seq data analysis. In G. Narasimhan P. Skums Z. Cai, I.I. Mandoiu and X. Gao (Eds.), editors, *Proc. 16th International Symposium on Bioinformatics Research and Applications*, *Lecture Notes in Computer Science*, pages 389–397. Springer, 2020.
- [C4] F. Rondel, R. Hosseini, B. Sahoo, S. Knyazev, I. Mandric, F. Stewart, I.I. Mandoiu, B. Pasaniuc, and A. Zelikovsky. Estimating enzyme participation in metabolic pathways for microbial communities from RNA-Seq data. In G. Narasimhan P. Skums Z. Cai, I.I. Mandoiu and X. Gao (Eds.), editors, *Proc. 16th International Symposium on Bioinformatics Research and Applications*, *Lecture Notes in Computer Science*, pages 335–343. Springer, 2020.
- [C5] S. Dhar, C. Zhang, I.I. Mandoiu, and M.S. Bansal. TNet: Phylogeny-based inference of disease transmission networks using within-host strain diversity. In G. Narasimhan P. Skums Z. Cai, I.I. Mandoiu and X. Gao (Eds.), editors, *Proc. 16th International Symposium on Bioinformatics Research and Applications*, *Lecture Notes in Computer Science*, pages 203–216. Springer, 2020.
- [C6] F. Alqahtani and I.I. Mandoiu. Mitochondrial haplogroup assignment for high-throughput sequencing data from single individual and mixed dna samples. In G. Narasimhan P. Skums Z. Cai, I.I. Mandoiu and X. Gao (Eds.), editors, *Proc. 16th International Symposium on Bioinformatics Research and Applications*, volume 12304 of *Lecture Notes in Computer Science*, pages 1–12. Springer, 2020.
- [C7] F. Alqahtani and I.I. Mandoiu. SMART2: Multi-library statistical mitogenome assembly with repeats. In G. Narasimhan S. Rajasekaran P. Skums I.I. Mandoiu, T. M. Murali and A. Zelikovsky (eds), editors, *Proc. 9th International Conference on Computational Advances in Bio and Medical Sciences*, volume 12029 of *Lecture Notes in Computer Science*, pages 184–198. Springer, 2020.
- [C8] M. Moussa and I.I. Mandoiu. Locality sensitive imputation for single-cell RNA-Seq data. In P. Skums F. Zhang, Z. Cai and S. Zhang (eds), editors, *Proc. 14th International Symposium on Bioinformatics Research and Applications*, volume 10847 of *Lecture Notes in Computer Science*, pp. 347-360, 2018.
- [C9] I. Mandric, S. Knyazev, C. Padilla, F. Stewart, I.I. Mandoiu, and A. Zelikovsky. Metabolic analysis of meta-transcriptomic data from planktonic communities. In *Proc. 13th International Symposium on Bioinformatics Research and Applications*, volume 10330 of *Lecture Notes in Computer Science*, pp. 396-402, 2017.
- [C10] S. Mangul, A. Caciula, S. Al Seesi, D. Brinza, A. Rouf Banday, R. Kanadia, I.I. Mandoiu, 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.
- [C11] J. Lindsay, H. Salooti, A. Zelikovsky, and I.I. Mandoiu. Scalable genome scaffolding using integer linear programming. In *Proc. ACM Conference on Bioinformatics, Computational Biology and Biomedicine*, pages 377–383, 2012.
- [C12] S. Mangul, A. Caciula, S. Al Seesi, D. Brinza, A. Rouf Banday, R. Kanadia, I.I. Mandoiu, 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, 2012.

- [C13] 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.
- [C14] 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.
- [C15] 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.
- [C16] S. Mangul, I. Astrovskaya, M. Nicolae, B. Tork, I.I. Măndoiu, and A. Zelikovsky. Maximum likelihood estimation of incomplete genomic spectrum from HTS data. In *Proc. 11th Workshop on Algorithms in Bioinformatics*, volume 6833 of *Lecture Notes in Computer Science*, pages 213–224, 2011.
- [C17] M. Nicolae and I.I. Măndoiu. Accurate estimation of gene expression levels from DGE sequencing data. In *Proc. 7th International Symposium on Bioinformatics Research and Applications*, volume 6674 of *Lecture Notes in Computer Science*, pages 392–403, 2011.
- [C18] J. Duitama, P.K. Srivastava, and I.I. Măndoiu. Towards accurate detection and genotyping of expressed variants from whole transcriptome sequencing data. In *Proc. 1st IEEE International Conference on Computational Advances in Bio and Medical Sciences*, pages 87–92, 2011.
- [C19] M. Nicolae, S. Mangul, I.I. Măndoiu, and A. Zelikovsky. Estimation of alternative splicing isoform frequencies from RNA-Seq data. In *Proc. 10th Workshop on Algorithms in Bioinformatics*, volume 6293 of *Lecture Notes in Computer Science*, pages 202–214, 2010.
- [C20] 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.
- [C21] 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.
- [C22] J. Jun, P. Ryvkin, E. Hemphill, I.I. Măndoiu, and C.E. Nelson. Estimating the relative contributions of new genes from retrotransposition and segmental duplication events during mammalian evolution. In *Proc. 6th Annual RECOMB Satellite Workshop on Comparative Genomics*, pages 40–54, 2008.
- [C23] B. Dasgupta, J. Jun, and I.I. Măndoiu. Primer selection methods for detection of genomic inversions and deletions via PAMP. In A. Brazma, S. Miyano, and T. Akutsu, editors, *Proc. 6th Asia-Pacific Bioinformatics Conference (APBC)*, *Advances in Bioinformatics and Computational Biology*, pages 353–362, 2008.
- [C24] J. Kennedy, I.I. Măndoiu, and B. Paşaniuc. Genotype error detection using Hidden Markov Models of haplotype diversity. In *Proc. 7th Workshop on Algorithms in Bioinformatics (WABI)*, *Lecture Notes in Computer Science*, pages 73–84, 2007.
- [C25] B. Paşaniuc and I.I. Măndoiu. Highly scalable genotype phasing by entropy minimization. In *Proc. 28th Annual International Conference of the IEEE Engineering in Medicine and Biology Society*, pages 3482–3486, 2006.
- [C26] I.I. Măndoiu and C. Prăjescu. High-throughput SNP genotyping by SBE/SBH. In *Proc. 6th International Conference on Computational Science (ICCS 2006), Part II*, volume 3992 of *Lecture Notes in Computer Science*, pages 742–749, 2006.
- [C27] M.T. Hajiaghayi, K. Jain, L.C. Lau, I.I. Măndoiu, A.C. Russell, and V.V. Vazirani. The minimum multicolored subgraph problem in haplotyping and PCR primer set selection. In *Proc. 6th International Conference on Computational Science (ICCS 2006), Part II*, volume 3992 of *Lecture Notes in Computer Science*, pages 758–766, 2006.

- [C28] I.I. Măndoiu and D. Trincă. Exact and approximation algorithms for DNA tag set design. In *Proc. 16th Annual Symposium on Combinatorial Pattern Matching (CPM)*, volume 3537 of *Lecture Notes in Computer Science*, pages 383–393, 2005.
- [C29] I.I. Măndoiu, C. Prăjescu, and D. Trincă. Improved tag set design and multiplexing algorithms for universal arrays. In *Proc. 5th International Conference on Computational Science (ICCS), Part II*, volume 3515 of *Lecture Notes in Computer Science*, pages 994–1002, 2005.
- [C30] B. DasGupta, K.M. Konwar, I.I. Măndoiu, and A.A. Shvartsman. Highly scalable algorithms for robust string barcoding. In *Proc. 5th International Conference on Computational Science (ICCS), Part II*, volume 3515 of *Lecture Notes in Computer Science*, pages 1020–1028, 2005.
- [C31] K.M. Konwar, I.I. Măndoiu, A.C. Russell, and A.A. Shvartsman. Improved algorithms for multiplex PCR primer set selection with amplification length constraints. In *Proc. 3rd Asia-Pacific Bioinformatics Conference (APBC)*, pages 41–50, 2005.
- [C32] A.B. Kahng, I.I. Măndoiu, Q. Wang, X. Xu, and A.Z. Zelikovsky. Multi-project reticle floorplanning and wafer dicing. In *Proc. ACM/SIGDA International Symposium on Physical Design*, pages 70–77, 2004.
- [C33] G. Călinescu, C.G. Fernandes, I.I. Măndoiu, A. Olshevsky, K. Yang, and A. Zelikovsky. Primal-dual algorithms for QoS multimedia multicast. In *Proc. IEEE Global Communications Conference (GLOBECOM)*, pages 3631–3635, 2003.
- [C34] P. Gupta, A.B. Kahng, I.I. Măndoiu, and P. Sharma. Layout-aware scan chain synthesis for improved path delay fault coverage. In *Proc. IEEE-ACM International Conference on Computer-Aided Design*, pages 754–759, 2003.
- [C35] A.B. Kahng, I.I. Măndoiu, S. Reda, X. Xu, and A. Zelikovsky. Evaluation of placement techniques for DNA probe array layout. In *Proc. IEEE-ACM International Conference on Computer-Aided Design*, pages 262–269, 2003.
- [C36] H. Chen, C.-K. Cheng, A.B. Kahng, I.I. Măndoiu, Q. Wang, and B. Yao. The Y-architecture for on-chip interconnect: Analysis and methodology. In *Proc. IEEE-ACM International Conference on Computer-Aided Design*, pages 13–19, 2003.
- [C37] I.I. Măndoiu. Recent advances in multicommodity flow algorithms for global routing. In *Proc. 5th International Conference on ASIC (ASICON)*, pages 160–165, 2003.
- [C38] A.B. Kahng, I.I. Măndoiu, S. Reda, X. Xu, and A. Zelikovsky. Design flow enhancements for DNA arrays. In *Proc. IEEE International Conference on Computer Design (ICCD)*, pages 116–123, 2003.
- [C39] M. Karpinski, I.I. Măndoiu, A. Olshevsky, and A. Zelikovsky. Improved approximation algorithms for the Quality of Service Steiner tree problem. In *Proc. 8th International Workshop on Algorithms and Data Structures*, volume 2748 of *Lecture Notes in Computer Science*, pages 401–411, 2003.
- [C40] H. Chen, C.K. Cheng, A.B. Kahng, I.I. Măndoiu, and Q. Wang. Estimation of wirelength reduction for  $\lambda$ -geometry vs. Manhattan placement and routing. In *Proc. ACM International Workshop on System-Level Interconnect Prediction (SLIP)*, pages 71–76, 2003.
- [C41] A.B. Kahng, I.I. Măndoiu, P. Pevzner, S. Reda, and A. Zelikovsky. Engineering a scalable placement heuristic for DNA probe arrays. In *Proc. 7th Annual International Conference on Research in Computational Molecular Biology (RECOMB)*, pages 148–156, 2003.
- [C42] E. Althaus, G. Călinescu, I.I. Măndoiu, S. Prasad, N. Tchervenski, and A.Z. Zelikovsky. Power efficient range assignment in ad-hoc wireless networks. In *Proc. IEEE Wireless Communications and Networking Conference (WCNC)*, pages 1889–1894, 2003.
- [C43] A.B. Kahng, I.I. Măndoiu, and A.Z. Zelikovsky. Highly scalable algorithms for rectilinear and octilinear Steiner trees. In *Proc. Asia and South Pacific Design Automation Conference*, pages 827–833, 2003.

- [C44] A.B. Kahng, B. Liu, and I.I. Măndoiu. Non-tree routing for reliability and yield improvement. In *Proc. IEEE-ACM International Conference on Computer-Aided Design*, pages 260–266, 2002.
- [C45] A.B. Kahng, I. Măndoiu, P. Pevzner, S. Reda, and A. Zelikovsky. Border length minimization in DNA array design. In *Proc. 2nd Workshop on Algorithms in Bioinformatics (WABI)*, volume 2452 of *Lecture Notes in Computer Science*, pages 435–448, 2002.
- [C46] C. Bandela, Y. Chen, A.B. Kahng, I.I. Măndoiu, and A.Z. Zelikovsky. Auctions with buyer preferences. In *Information Systems: The e-Business Challenge – Proc. 17th IFIP World Computer Congress, Stream TC8*, pages 221–238, 2002.
- [C47] G. Călinescu, I.I. Măndoiu, and A.Z. Zelikovsky. Symmetric connectivity with minimum power consumption in radio networks. In *Foundations of information technology in the era of network and mobile computing – Proc. 17th IFIP World Computer Congress, Stream TC1/ 2nd IFIP International Conference on Theoretical Computer Science (TCS)*, pages 119–130, 2002.
- [C48] C. Albrecht, A.B. Kahng, I.I. Măndoiu, and A.Z. Zelikovsky. Floorplan evaluation with timing-driven global wireplanning, pin assignment, and buffer/wire sizing. In *Proc. 7th Asia and South Pacific Design Automation Conference and 15th International Conference on VLSI Design*, pages 580–587, 2002.
- [C49] C. Alpert, A.B. Kahng, B. Liu, I.I. Măndoiu, and A.Z. Zelikovsky. Minimum-buffered routing for slew and reliability control. In *Proc. IEEE-ACM International Conference on Computer-Aided Design*, pages 408–415, 2001.
- [C50] C. Albrecht, A.B. Kahng, B. Liu, I.I. Măndoiu, and A.Z. Zelikovsky. On the skew-bounded minimum-buffer routing tree problem. In *Proc. 10th Workshop on Synthesis and System Integration of Mixed Technologies*, pages 250–256, 2001.
- [C51] F.F. Drăgan, A.B. Kahng, I.I. Măndoiu, S. Muddu, and A.Z. Zelikovsky. Practical approximation algorithms for separable packing linear programs. In *Proc. 7th International Workshop on Algorithms and Data Structures*, volume 2125 of *Lecture Notes in Computer Science*, pages 325–337, 2001.
- [C52] G. Călinescu, I.I. Măndoiu, P.-J. Wan, and A.Z. Zelikovsky. Selecting forwarding neighbors in wireless ad hoc networks. In *Proc. 5th International Workshop on Discrete Algorithms and Methods for Mobile Computing and Communications*, pages 34–43, 2001.
- [C53] F.F. Drăgan, A.B. Kahng, I.I. Măndoiu, S. Muddu, and A.Z. Zelikovsky. Provably good global buffering by multiterminal multicommodity flow approximation. In *Proc. 6th Asia and South Pacific Design Automation Conference*, pages 120–125, 2001.
- [C54] A.Z. Zelikovsky and I.I. Măndoiu. Practical approximation algorithms for zero- and bounded-skew trees. In *Proc. 12th ACM-SIAM Annual Symposium on Discrete Algorithms*, pages 407–416, 2001.
- [C55] F.F. Drăgan, A.B. Kahng, I.I. Măndoiu, S. Muddu, and A.Z. Zelikovsky. Provably good global buffering using an available buffer block plan. In *Proc. IEEE-ACM International Conference on Computer-Aided Design*, pages 104–109, 2000.
- [C56] I.I. Măndoiu, V.V. Vazirani, and J.L. Ganley. A new heuristic for rectilinear Steiner trees. In *Proc. IEEE-ACM International Conference on Computer-Aided Design*, pages 157–162, 1999.
- [C57] K. Jain, I.I. Măndoiu, V.V. Vazirani, and D.P. Williamson. A primal-dual schema based approximation algorithm for the element connectivity problem. In *Proc. 10th ACM-SIAM Annual Symposium on Discrete Algorithms*, pages 484–489, 1999.
- [C58] K. Jain, I.I. Măndoiu, and V.V. Vazirani. “The art of trellis decoding” is computationally hard—for large fields. In *Proc. IEEE International Symp. on Information Theory*, page 13, 1998.

## Unrefereed Conference Articles

- [U1] A.B. Kahng, I.I. Măndoiu, X. Xu, and A. Zelikovsky. Multi-project reticle design and wafer dicing under uncertain demand. In *Proc. 22nd European Mask and Lithography Conference (EMLC 2006)*, pages 45–54, 2006.
- [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.
- [U5] I.I. Măndoiu. Kraft-Chaitin’s theorem for free-extensible codes. In *Proc. SALODAYS Symposium on Logic and Theoretical Computer Science*, Bucharest, Romania, 1993. Hyperion XXI Press.

## Patents

- [P1] Y. Ionov., P.K. Srivastava, I.I. Măndoiu, and A.Z. Zelikovsky. Cancer specific immunotherapeutic targets generated by chemotherapeutic drug treatment. Patent Application WO2020092382A1.
- [P2] P.K. Srivastava, I.I. Măndoiu, C.A. Brennick, M.M. George, and M. Moussa. Unbiased identification of tumor rejection mediating neoepitopes. Patent US 11,920,202, March 2024.
- [P3] I.I. Măndoiu, C.E. Nelson, and J. Lindsay. Method for identifying rare cell types by single cell assisted deconvolution of population gene expression data, Patent Application US20180057859A1.
- [P4] C.E. Nelson, I.I. Măndoiu, and H.L. Aguila. Pipeline for rational design and interpretation of biomarker panels. Patent Application US20150080237A1.
- [P5] P.K. Srivastava, I.I. Măndoiu, and F. Duan. Identification of tumor-protective epitopes for the treatment of cancers. Patent US 10,501,801, Dec. 2019.
- [P6] C. Albrecht, A.B. Kahng, I.I. Măndoiu, and A.Z. Zelikovsky. Floorplan evaluation, global routing, and buffer insertion for integrated circuits. Patent US 7,062,743, June 2006.

---

## SOFTWARE PACKAGES

- S. Al Seesi, A. Al-okaily, T.V. Shcheglova, E. Sherafat, F.H. Alqahtani, A.T. Hagymasi, A. Kaur, P.K. Srivastava, and I.I. Măndoiu. GeNeo: A Bioinformatics Toolbox for Genomics-Guided Neoepitope Prediction. Available at <https://neo.engr.uconn.edu>.
- S. Dhar, C. Zhang, I.I. Măndoiu, and M.S. Bansal. TNet: Transmission network inference using within-host strain diversity and its application to geographical tracking of COVID-19 spread. Available at <https://compbio.engr.uconn.edu/software/TNet/>
- M. Moussa and I.I. Măndoiu. SC1: A web-based single cell RNA-seq analysis pipeline. Available at <https://sc1.engr.uconn.edu>.
- F. Alqatani and I.I. Măndoiu. SMART - Statistical Mitogenome Assembly with Repeats. Available at [https://neo.engr.uconn.edu/?tool\\_id=SMART](https://neo.engr.uconn.edu/?tool_id=SMART).
- M. Moussa and I.I. Măndoiu. LSImpute: Locality Sensitive Imputation for scRNA-Seq data. Available at <http://cnv1.engr.uconn.edu:3838/LSImpute/>.

- S. Al Seesi, I. Mandric, I.I. Măndoiu, and A. Zelikovsky. IsoDE2: Bootstrapping-based differential gene expression analysis for RNA-Seq data with and without replicates. Available at [https://neo.engr.uconn.edu/?tool\\_id=isoDE2](https://neo.engr.uconn.edu/?tool_id=isoDE2).
- S. Al Seesi, I. Mandric, I.I. Măndoiu, and A. Zelikovsky. IsoEM2: Inferring Alternative Splicing Isoform Frequencies from High-Throughput RNA-Seq Data. Available at [https://neo.engr.uconn.edu/?tool\\_id=IsoEM2](https://neo.engr.uconn.edu/?tool_id=IsoEM2).
- M. Hamdalla, S. Rajasekaran, D. Grant, and I.I. Măndoiu. TrackSM: Metabolic pathway prediction based on molecular structure matching. Available at <http://dna.engr.uconn.edu/software/TrackSM/>
- 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/>
- J. Lindsay, H. Salooti, I.I. Măndoiu, and A. Zelikovsky. SILP2: ILP-based maximum likelihood genome scaffolding. Available at <http://dna.engr.uconn.edu/software/SILP2/>
- 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/>
- J. Duitama and I.I. Măndoiu. NGSTools – Java tools for analysis of next generation sequencing (NGS) data. Available at <http://dna.engr.uconn.edu/software/NGSTools/>
- 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/>
- M. Nicolae, S. Mangul, I.I. Măndoiu, and A. Zelikovsky. IsoEM: Inferring alternative splicing isoform frequencies from high-throughput RNA-Seq data. Available at <http://dna.engr.uconn.edu/software/IsoEM/>
- 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/>
- J. Kennedy, I.I. Măndoiu, and B. Paşaniuc. GEDI-ADMX: Genotype error detection and imputation for admixed populations. Available at <http://dna.engr.uconn.edu/software/GEDI-ADMX/>
- J. Kennedy, I.I. Măndoiu, and B. Paşaniuc. GEDI: Genotype error detection and imputation. Available at <http://dna.engr.uconn.edu/software/GEDI/>
- A. Gusev, I.I. Măndoiu, and B. Paşaniuc. ENT: Genotype phasing by entropy minimization. Available at <http://dna.engr.uconn.edu/software/ent/>
- K.M. Konwar, I.I. Măndoiu, A.C. Russell, and A.A. Shvartsman. G-POT and PRIMER-ILP: Software tools for multiplex-PCR primer set selection. Available at <http://dna.engr.uconn.edu/software/G-POT/>
- B. DasGupta, K.M. Konwar, I.I. Măndoiu, and A.A. Shvartsman. DNA-BAR: Distinguisher selection for robust DNA barcoding. Available at <http://dna.engr.uconn.edu/software/DNA-BAR/>
- A.B. Kahng, I.I. Măndoiu, S. Reda, and A. Zelikovsky. CHIP: probe placement and embedding for DNA arrays. Available at <http://vlsicad.ucsd.edu/Downloads/chip.tar.gz>
- 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](http://www.engr.uconn.edu/~ion/FILES/software/mcf_floorplan.tar.gz)

- A.B. Kahng, I.I. Măndoiu, and A. Zelikovsky. FastSteiner: Highly scalable rectilinear and octilinear minimum Steiner tree algorithms. Available at <http://vlsicad.ucsd.edu/GSRC/bookshelf/Slots/RSMT/FastSteiner/>
  - 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

- Computational methods for proteogenomics-guided cancer immunotherapy, 5th Forum in Computational Biology, Universidad de los Andes, Dec. 14, 2020
- SC1: interactive web-based single cell RNA-seq analysis, (tutorial, with M. Moussa), 11th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics, Sept. 21, 2020
- Single Cell RNA-Seq Data Analysis, Invited seminar, UCONN Animal Science Department, Sept. 27, 2019
- Computational Methods for Analysis of Single Cell RNA-Seq Data, Invited colloquium, UCONN Center for Cell Analysis & Modeling, Oct. 25, 2018
- Challenges in Single Cell Sequencing Data Analysis, Invited talk at the Lorentz Center workshop on “Single Cell Data Science: Making Sense of Data from Billions of Single Cells,” Jun. 4-8, 2018
- Computational methods for genomics-guided cancer immunotherapy, UCONN Medical Deans Seminar Series “Interdisciplinary Conversations on Innovations in Informatics,” Farmington, CT, Jan. 25, 2018
- Computational Methods for Analysis of Single Cell RNA-Seq Data, JAX-GM course on Big Genomic Data Skills Training for Graduate Professors, Farmington, CT, May 14-19, 2017
- 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 SelectBio-sciences 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-UCHC 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, München, 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, München, 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 – Principal Investigator

- *Algorithms for scalable inference and phylodynamic analysis of tumor haplotypes using low-coverage single cell sequencing data*, NSF award IIS-2212511, 10/22-09/25 (with Co-PI M. Bansal)
- *Chemo-neoepitopes as novel immunotherapy for triple negative breast cancer*, NIH, 05/2021-04/2023 (with PIs Y. Ionov, P.K. Srivastava, and A. Zelikovsky)
- *Exploring The Impact of Microbiome Diversity on Toxicological Outcomes in Preclinical Species*, Pfizer, 01/2021-07/2024 (with Co-PIs J. Bi, S. Nabavi, and S. Rajasekaran)
- *Algorithmic Techniques for Inferring Transmission Networks from Noisy Sequencing Data*, NSF award CCF-1618347, 8/2016-7/2020 (with Co-PI M. Bansal)
- *Computational framework for inference of metabolic pathway activity from RNA-seq data*, NSF award DBI-1564936, 7/2016-6/2020
- *Novel transcript reconstruction from ION Torrent sequencing reads*, Life Technologies Corporation, Collaborative Research Compacts program, 07/2012-12/2012 (with Co-PI A. Zelikovsky)

- *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, 04/2011-03/2014 (with Co-PIs M.I. Khan and R.J. O'Neill, and A. Zelikovsky)
- *Software for robust transcript discovery and quantification from sequencing data*, Life Technologies Corporation, Collaborative Research Compacts program, 08/2011-02/2012 (with Co-PI A. Zelikovsky)
- *Reconstruction of haplotype spectra from high-throughput sequencing data*, NSF award IIS-0916948, 09/2009-08/2013 (with Co-PI Y. Wu)
- *Combinatorial algorithms for high-throughput collection and analysis of genomic diversity data*, NSF CAREER award IIS-0546457, 01/2006-12/2011
- *Bioinformatics tools enabling large-scale DNA barcoding*, NSF award DBI-0543365, 07/2006-06/2010 (with Co-PIs B. DasGupta and M.I. Khan)

## Extramural Research Grants – Co-Investigator

- *Domain- and protein-selective BET mechanisms in cocaine-seeking behaviors*, NIH award R01DA058700, 08/2023-05/2028 (with PI D.S. Sartor and Co-Investigator A.C. Jackson)
- *Effect of in-ovo Probiotic Supplementation on Energy Status, Yolk Sac Function and Intestinal Development in Broilers*, USDA National Institute of Food and Agriculture award 2023-67015-39666, 06/2023-05/2026 (with PI M.A. Amalaradjou and Co-Investigator E.L. Tako)
- *Regulation of satellite cell development, programming and differentiation by myogenic factors*, NIH award 1R01AR076394, 08/2020-07/2025 (with PI D.J. Goldhamer and Co-Investigators L.J. Core and M. Yamamoto)
- *Effect of in-ovo probiotic supplementation on muscle growth and performance in broilers*, USDA National Institute of Food and Agriculture award 2020-67016-30817, 04/2020-04/2022 (with PI M.A. Amalaradjou and Co-Investigators M.J. Darre and S.A. Reed)
- *Inhibitory cell types and circuits in the lateral hypothalamus*, NIH award 1R01MH112739-01, 04/2017-03/2018 (with PI A.C. Jackson and Co-Investigators C.E. Nelson and P. Robson)
- *A Catalog of Cell Types in the Early Organogenesis Embryo - A Single Cell Lineage Map, Phase 1*, Connecticut Innovations Regenerative Medicine Research Fund (RMRF), 06/2017-06/2021 (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)
- *Homeostatic Regulation of NG2 Cell Dynamics*, NIH award 2R01NS073425-06A1, 02/2017-01/2022 (with PI Nishiyama)
- *Understanding Nutrition Through Biomimics*, Foundation for Food and Agriculture Research, 12/2016-12/2019 (with PI M.A. Amalaradjou and Co-PI D. D'Amico)
- *Genomic-Driven Personalized Immunotherapy of Human Ovarian Cancer*, Connecticut Bioscience Innovation Fund (CBIF), 7/2016-6/2018 (with PI P.K. Srivastava and co-PIs A. Kueck and S. Al Seesi)
- *Investigating the beneficial role of cheese starter cultures in the prevention of IBD*, USDA National Institute of Food and Agriculture award 2016-67018-24415, 11/2015-10/2017 (with PI M.A. Amalaradjou and Co-PI D. D'Amico)
- *Identification and Characterization of the Presomitic Mesoderm Progenitor*, NIH award HD071606-01A1, 7/2012-6/2014 (with PI C.E. Nelson)

## 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) 07/2015–06/2018

- *Probiotic Mediated Epigenomic Programming in the Prophylaxis and Treatment of IBD* UConn Research Excellence Program Grant, **Co-PI** (with PI M.A. Amalaradjou), 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), 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**, 06/2004–05/2005

## Other Grants

- *Graduate Assistance in Areas of National Need (GAANN) in Artificial Intelligence*, Department of Education, **Co-PI** (with PI S. Rajasekaran and Co-PIs J. Bi, B. Wang, Y. Wu, M. Bansal, P. Duggirala, S. Nabavi, and Q. Yang), 10/2018-09/2023
- *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) 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) 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), 12/2013
- UConn/Jackson Laboratory faculty fellowship to attend *53rd Annual Short Course on Medical and Experimental Mammalian Genetics*, **PI**, 7/2012
- *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), 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), 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), 02/2011-01/2012
- *Computational Biomedical Science*, UCONN Honors Interdisciplinary Course Development Grant, **PI** (with PI C.E. Nelson), 06/2006-05/2009

---

## PROFESSIONAL SERVICE

### Editorial Board Member and Guest Editor for Journals

- Associate Editor, *BMC Bioinformatics*, 02/2010-present
- Editorial Board Member, *Genes*, 04/2018-present
- Editorial Board Member, *In Silico Biology*, 06/2011-present
- Editorial Board Member, *International Journal of Bioinformatics Research and Applications*, 06/2006–present
- Guest editor (with Mukul S Bansal, Marmar Moussa, Murray Patterson, Sanguthevar Rajasekaran, Pavel Skums, and Alexander Zelikovsky), *JCB special issue devoted to 11th International Conference on Computational Advances in Bio and medical Sciences*

- Guest editor (with Sumit Kumar Jha, Sanguthevar Rajasekaran, Pavel Skums, and Alexander Zelikovsky), *JCB special issue devoted to 10th International Conference on Computational Advances in Bio and medical Sciences*
- Guest editor (with F. Zhang and X. Guo), *Genes special issue devoted to selected papers from the 16th International Symposium on Bioinformatics Research and Applications*
- Guest editor (with T.M. Murali, Giri Narasimhan, Sanguthevar Rajasekaran, Pavel Skums, and Alexander Zelikovsky), *JCB special issue devoted to 9th International Conference on Computational Advances in Bio and medical Sciences*
- Guest editor (with Yury Khudyakov, P. Skums, and A. Zelikovsky), *BMC Bioinformatics special supplement devoted to 8th Workshop on Computational Advances in Molecular Epidemiology*
- Guest editor (with A. Kalyanaraman, Y.-A. Kim, S. Rajasekaran, P.Skums, and A. Zelikovsky), *BMC Bioinformatics special supplement devoted to 8th IEEE International Conference on Computational Advances in Bio and medical Sciences*
- Guest editor (with F. Zhang and X. Guo), *Genes special issue devoted to selected papers from the 15th International Symposium on Bioinformatics Research and Applications*
- Guest editor (with P. Skums and A. Zelikovsky), *IEEE/ACM Transactions on Computational Biology and Bioinformatics 16(4) July-Aug. 2019, special section devoted to selected papers from 12th International Symposium on Bioinformatics Research and Applications*
- Guest editor (with D. Krizanc, S. Rajasekaran, P.Skums, A. Zelikovsky, and S. Zhang), *BMC Bioinformatics 20 (Suppl 11), BMC Genomics 20 (Suppl 5), and BMC Medical Genomics 12 (Suppl 4), June 2019 special supplements devoted to selected papers from the 7th IEEE International Conference on Computational Advances in Bio and Medical Sciences*
- Guest editor (with A. Zelikovsky, P. Skums, and Y. Khudyakov), *BMC Bioinformatics 19 (Suppl 11) Oct. 2018 special supplements devoted to selected papers from the 6th Workshop on Computational Advances in Molecular Epidemiology*
- Guest editor (with S. Rajasekaran, P. Skums, and A. Zelikovsky), *BMC Bioinformatics 18 (Suppl 15) and BMC Genomics 18 (Suppl 10), Dec. 2017 special supplements devoted to selected papers from the 6th IEEE International Conference on Computational Advances in Bio and Medical Sciences*
- Guest editor (with A. Zelikovsky and P. Skums), *BMC Bioinformatics 18 (Suppl 12) and BMC Genomics 18 (Suppl 7), Oct. 2017 special supplements devoted to selected papers from the 12th International Symposium on Bioinformatics Research and Applications*
- Guest editor (with R.W. Harrison and A. Zelikovsky), *IEEE/ACM Transactions on Computational Biology and Bioinformatics 14(3) May-June 2017, special section devoted to selected papers from the 11th International Symposium on Bioinformatics Research and Applications*
- Guest editor (with S. Rajasekaran and A. Zelikovsky), *BMC Bioinformatics 18 (Suppl 8) and BMC Genomics 18 (Suppl 4), June 2017 special supplements devoted to selected papers from the 5th IEEE International Conference on Computational Advances in Bio and Medical Sciences*
- Guest editor (with A. Zelikovsky, R. Harrison, Y. Li and Y. Khudyakov), *BMC Bioinformatics 17 (Suppl 8) and BMC Genomics 17 (Suppl 5), Aug 2016 special supplements devoted to selected papers from the 11th International Symposium on Bioinformatics Research and Applications*
- Guest editor (with J. Chen, Y. Khudyakov, V. Honavar, S. Rajasekaran and A. Zelikovsky), *BMC Bioinformatics 16 (Suppl 17) and BMC Genomics 16 (Suppl 11), Dec. 2015 special supplements devoted to selected papers from the 4th IEEE International Conference on Computational Advances in Bio and Medical Sciences*

- Guest editor (with V. Filkov, A. Kalyanaraman, Y. Khudyakov, S. Rajeskaran, K. Reinert, and A. Zelikovsky), *BMC Bioinformatics* 15 (Suppl 8) and *BMC Genomics* 15 (Suppl 5), July 2014 special supplements devoted to selected papers from the *3rd IEEE International Conference on Computational Advances in Bio and Medical Sciences*
- Guest editor (with J. Wang and A. Zelikovsky), *IEEE/ACM Transactions on Computational Biology and Bioinformatics* 10(6) November-December 2013, special section devoted to selected papers from the *8th International Symposium on Bioinformatics Research and Applications*
- Guest editor (with M. Pop, S. Rajasekaran, and J. Spouge), *International Journal of Bioinformatics Research and Applications* 10 (No. 4/5), June 2014 special issue devoted to selected papers from the *2nd IEEE International Conference on Computational Advances in Bio and Medical Sciences*
- Guest editor (with M. Pop, S. Rajasekaran, and J. Spouge), *BMC Bioinformatics* 14 (Suppl 18) and *BMC Genomics* 14 (Suppl 7), Nov. 2013 special supplements devoted to selected papers from the *2nd IEEE International Conference on Computational Advances in Bio and Medical Sciences*
- Guest editor (with Y. Khudyakov and A. Zelikovsky), *In Silico Biology* 11(5), Nov. 2012, special issue devoted to the *2011 Workshop on Computational Advances in Molecular Epidemiology*
- Guest editor (with J. Chen, R. Sunderraman, J. Wang, and A. Zelikovsky), *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 (with T. Przytycka and S. Rajasekaran), *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 (with P. Gogarten and A. Zelikovsky), *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 (with G. Narasimhan, Y. Pan, and Y. Zhang), *IEEE/ACM Transactions on Computational Biology and Bioinformatics* 7(4), October-December 2010, special section devoted to *5th International Symposium on Bioinformatics Research and Applications*
- Guest editor (with Y. Pan, R. Sunderraman, and A. Zelikovsky), *IEEE/ACM Transactions on Computational Biology and Bioinformatics* 6(2), April-June 2009, special section devoted to *4th International Symposium on Bioinformatics Research and Applications*
- Guest editor (with Y. Pan and A. Zelikovsky), *IEEE/ACM Transactions on Computational Biology and Bioinformatics* 5(3), July-September 2008, special section devoted to *3rd International Symposium on Bioinformatics Research and Applications*
- Guest editor (with Y. Pan and A. Zelikovsky), *IEEE/ACM Transactions on Computational Biology and Bioinformatics* 4(4), October-December 2007, special section devoted to *2nd International Workshop on Bioinformatics Research and Applications*
- Guest editor (with Y. Li and A. Zelikovsky), *International Journal of Sensor Networks* Vol. 6, No. 1, 2009, special issue devoted to *2nd ACIS Workshop on Self-Assembling Wireless Networks*
- Guest editor (with Y. Pan and A. Zelikovsky), *IEEE Transactions on NanoBioscience* 6(1), March 2007, special section on Computational NanoBioscience
- Guest editor (with G. Călinescu, A. Zelikovsky, and M. Zimand), *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, *12th Workshop on Computational Advances for Next Generation Sequencing*, Norman, OK, Dec 11-13, 2023

- Workshop Co-Chair, *2nd Workshop on Advances in Systems Immunology*, Norman, OK, Dec 11-13, 2023
- Workshop Co-Chair, *11th Workshop on Computational Advances for Next Generation Sequencing*, virtual, Dec 16-18, 2021
- Workshop Co-Chair, *1st Workshop on Advances in Systems Immunology*, virtual, Dec 16-18, 2021
- Workshop Co-Chair, *3rd Workshop on Computational Advances for Single-Cell Omics Data Analysis*, virtual, Dec 10-12, 2020
- Workshop Co-Chair, *10th Workshop on Computational Advances for Next Generation Sequencing*, virtual, Dec 10-12, 2020
- Program Co-Chair, *16th International Symposium on Bioinformatics Research and Applications*, Moscow, Russia, Dec. 1-4, 2020
- Workshop Co-Chair, *9th Workshop on Computational Advances in Molecular Epidemiology*, virtual, Sept. 21, 2020
- Workshop Co-Chair, *2nd Workshop on Computational Advances for Single-Cell Omics Data Analysis*, Miami, Florida, Nov. 15-17, 2019
- Workshop Co-Chair, *9th Workshop on Computational Advances for Next Generation Sequencing*, Miami, Florida, Nov. 15-17, 2019
- Workshop co-chair, *8th Workshop on Computational Advances in Molecular Epidemiology*, Niagara Falls, NY, Sept. 7, 2019
- Workshop co-chair, *1st Workshop on Computational Advances for Single-Cell Omics Data Analysis*, Las Vegas, NV, Oct. 18-20, 2018
- Workshop co-chair, *8th Workshop on Computational Advances for Next Generation Sequencing*, Las Vegas, NV, Oct. 18-20, 2018
- Workshop co-chair, *7th Workshop on Computational Advances in Molecular Epidemiology*, Washington, DC, August 29, 2018
- Workshop co-chair, *7th Workshop on Computational Advances for Next Generation Sequencing*, Orlando, FL, October 19-21, 2017
- Workshop co-chair, *6th Workshop on Computational Advances in Molecular Epidemiology*, Boston, MA, August 20, 2017
- 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

- *16th International Conference on Bioinformatics and Computational Biology*, New Orleans, LA, March 18-19, 2024
- *15th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics*, Shenzhen, China, Nov. 22-25, 2024 (area chair)
- *19th International Symposium on Bioinformatics Research and Applications*, Wrocław, Poland, Oct. 9-12, 2023
- *14th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics*, Houston, TX, Sept. 3-6, 2023 (area chair)
- *15th International Conference on Bioinformatics and Computational Biology*, online, March 20-22, 2023
- *18th International Symposium on Bioinformatics Research and Applications*, Haifa, Israel, Nov. 14-17, 2022
- *13th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics*, Chicago, IL, Aug. 7-10, 2022
- *14th International Conference on Bioinformatics and Computational Biology*, online, March 21-23, 2022
- 11th IEEE International Conference on Computational Advances in Bio and Medical Sciences, virtual, Dec. 16-18, 2021
- *17th International Symposium on Bioinformatics Research and Applications*, Shenzhen, China, Nov. 26-28, 2021
- *12th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics*, virtual, Aug. 1-4, 2021
- *11th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics*, virtual, Sept. 21-24, 2020
- *8th RECOMB Satellite on Computational Methods in Genetics*, virtual, June 25-26, 2020
- *9th IEEE International Conference on Computational Advances in Bio and Medical Sciences*, Miami, Florida, Nov. 15-17, 2019
- *2019 IEEE International Conference on Bioinformatics and Biomedicine*, San Diego, CA, Nov. 18-21, 2019
- *10th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics*, Niagara Falls, New York, Sept. 7-10, 2019
- *15th International Symposium on Bioinformatics Research and Applications*, Barcelona, Spain, June 3-6, 2019
- *7th RECOMB Satellite on Computational Methods in Genetics*, Washington, DC, May 4, 2019
- *11th International Conference on Bioinformatics and Computational Biology*, Las Vegas, NV, March 19-21, 2018
- *9th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics*, Washington, DC, August 29-Sept. 1, 2018
- *14th International Symposium on Bioinformatics Research and Applications*, Beijing, China, June 8-11, 2018
- *6th RECOMB Satellite Workshop on Computational Methods in Genetics*, Paris, France, April 19-20, 2018



- *10th International Conference on Bioinformatics and Computational Biology*, Las Vegas, NV, March 19-21, 2018
- *16th Asia Pacific Bioinformatics Conference*, Yokohama, Japan, January 15-17, 2018
- *17th Workshop on Algorithms in Bioinformatics*, Boston, MA, August 21-23, 2017
- *8th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics*, Boston, MA, August 20-23, 2017
- *5th RECOMB Satellite Workshop on Computational Methods in Genetics*, Los Angeles, CA, July 27-28, 2017
- *25th International Conference on Intelligent System for Computational Biology & 16th European Conference on Computational Biology*, Prague, Czech Republic, July 21-25, 2017
- *13th International Symposium on Bioinformatics Research and Applications*, Honolulu, Hawaii, May 29 - June 1, 2017
- *9th International Conference on Bioinformatics and Computational Biology*, Honolulu, Hawaii, March 20 - 22, 2017
- *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
- Panelist, NSF ABI, BD2K, CAREER, HDR, III, OAC, and SCH programs
- Expert assessor for the *Australian Research Council (ARC)*
- Reviewer for the *Israel Science Foundation*
- Judge for the *Regeneron 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*, *IEEE 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, Computational Biology, and Biomedical Informatics (SIGBio)
- New England Statistical Society (NESS)

## 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 3810/6160 & CSE 3810/6800, *Computational Genomics* (Spring 2007, Spring 2008, Spring 2009, Spring 2013, Spring 2015, Spring 2017, Spring 2019, Spring 2020, Spring 2021, Spring 2022, Spring 2023, Spring 2024)
- 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, Fall 2018, Fall 2019, Fall 2020, Fall 2021, Fall 2022, Fall 2023)

- 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, Fall 2018, Spring 2021, Spring 2022)
- CSE 4095: *Competitive Programming* (Spring 2024)
- 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: Rye Howard-Stone, Gulnaz Sterling
- Elham Sherafat, Ph.D. 12/2022, thesis: “Bioinformatics and AI Methods for Neoepitope Prediction in Personalized Cancer Immunotherapy,” current position: Assistant Professor in Residence, Computer Science & Engineering Department, University of Connecticut
- Fahad Alqahtani, Ph.D. 05/2020, thesis: “Algorithms for Mitochondrial Genome Assembly and Haplogroup Assignment from Low-Coverage Whole-Genome Sequencing Data,” current position: Research Assistant Professor, National Center for Biotechnology, King Abdulaziz City for Science and Technology, Riyadh, Saudi Arabia
- Marmar Moussa, Ph.D. 05/2019, thesis: “Computational Methods for the Analysis of Single-Cell RNA-Seq Data,” current position: Assistant Professor, Computer Science Department, University of Oklahoma
- James Lindsay, Ph.D. 05/2015, thesis: “Scalable Optimization Algorithms for High-throughput Genomic Data,” current position: Associate Director of Knowledge Systems Group, Dana-Farber Cancer Institute, Boston, MA
- Jorge Duitama, Ph.D. 12/2010, thesis: “Bioinformatics Methods for Diagnosis and Treatment of Human Diseases”, current position: Associate 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, 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, Sonalysts, Waterford, CT and
- Bogdan Paşaniuc, Ph.D. 5/2008, thesis: “Scalable Algorithms for Analysis of Genomic Diversity Data”, current position: Professor, Departments of Pathology and Laboratory Medicine, Human Genetics, and Computational Medicine, Laboratory Medicine, Geffen School of Medicine, UCLA

### Major Advisor – M.S. Students

- Jordan Force, M.S. Aug. 2022, thesis: “Using Machine Learning to Improve the Detection of MHC-I Presented Peptides”

- Saurav Dhar, M.S. May 2021, co-advised with Mukul Bansal, thesis: “TNet: transmission network inference using within-host strain diversity and its application to geographical tracking of COVID-19 spread”
- 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”, first position: Ph.D. student at UConn
- 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: Associate Professor, Computer Science Department, Southern Connecticut State University