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EDUCATION

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

University of Connecticut

- 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, 2016-17
- United Technologies Corporation Term Professorship in Engineering Innovation, 2013-15
- NSF Faculty Early Career Development (CAREER) Award, 2006-2011

PUBLICATIONS

Edited Books

- [EB1] I.I. Mandoiu and A.Z. Zelikovsky (Eds.). *Computational Methods for Next Generation Sequencing Data Analysis*. Wiley Book Series on Bioinformatics. John Wiley & Sons, 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] R. Harrison, Y. Li, and I.I. Mandoiu (Eds.). *Proc. 11th International Symposium on Bioinformatics Research and Applications*, volume Lecture Notes in Bioinformatics vol. 9096. Springer-Verlag, Berlin, 2015.
- [EP2] L. Bleris, I.I. Mandoiu, R. Schwartz, and J. Wang (Eds.). *Proc. 8th International Symposium on Bioinformatics Research and Applications*, volume Lecture Notes in Bioinformatics vol. 7292. Springer-Verlag, Berlin, 2012.
- [EP3] S. Istrail, I.I. Mandoiu, M. Pop, S. Rajasekaran, and J. Spouge (Eds.). *Proc. 2nd IEEE International Conference on Computational Advances in Bio and Medical Sciences*. IEEE, 2012.
- [EP4] B. Chen et al. (Eds.). *Workshops Proceedings, 2011 IEEE International Conference on Bioinformatics and Biomedicine*. IEEE Computer Society Press, 2011.
- [EP5] I.I. Mandoiu, S. Miyano, T. Przytycka, and S. Rajasekaran (Eds.). *Proc. 1st IEEE International Conference on Computational Advances in Bio and Medical Sciences*. IEEE Computer Society Press, 2011.
- [EP6] I.I. Măndoiu, Giri Narasimhan, and Yanqing Zhang (Eds.). *Proc. 5th International Symposium on Bioinformatics Research and Applications*, volume 5542 of *Lecture Notes in Bioinformatics*. Springer-Verlag, Berlin, 2009.
- [EP7] I.I. Măndoiu, 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.
- [EP8] 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.
- [EP9] 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. Astrovskaya, 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] C. Albrecht, A.B. Kahng, I.I. Măndoiu, and A.Z. Zelikovsky. Multicommodity flow algorithms for buffered global routing. In T.E. Gonzalez, editor, *Approximation Algorithms and Metaheuristics*, Chapman & Hall/CRC, 2007.
- [BC13] A.B. Kahng, I.I. Măndoiu, S. Reda, X. Xu, and A.Z. Zelikovsky. Computer-aided optimization of DNA array design and manufacturing. In K. Chakrabarty and J. Zeng, editors, *Design Automation Methods and Tools for Microfluidics-Based Biochips*, pp 235–269, Springer Verlag, 2006.

Articles in Refereed Journals

- [J1] J. Duan, M. Zhang, Ka. Flock, S. Al Seesi, I.I. Mandoiu, 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*, 2018 (online first).
- [J2] M. Moussa and I.I. Măndoiu. Single cell RNA-Seq data clustering using TF-IDF based methods. *BMC Genomics*, 19(Suppl 6):4922, 2018.
- [J3] H. Ebrahimi-Nik, W.L. Corwin, T. Shcheglova, A. Das Mohapatra, I.I. Măndoiu, and P.K. Srivastava. CD11c⁺ MHCII^{lo} GM-CSF-bone marrow-derived dendritic cells act as antigen donor cells and as antigen presenting cells in neopeptide-elicited tumor immunity against a mouse fibrosarcoma. *Cancer Immunology, Immunotherapy*, 2018 (online first).
- [J4] M.S. Muiyyarikandy, 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.
- [J5] M.S. Muiyyarikandy, 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.
- [J6] 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.
- [J7] 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.
- [J8] 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.

- [J9] 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.
- [J10] 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.
- [J11] 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.
- [J12] 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.
- [J13] 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.
- [J14] 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.
- [J15] 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.
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- [J17] 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.
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- [J19] 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.
- [J20] J. Lindsay, H. Salooti, I.I. Măndoiu, and A. Zelikovsky. ILP-based maximum likelihood genome scaffolding. *BMC Bioinformatics*, 15(Suppl 9):S9, 2014.
- [J21] 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.
- [J22] 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.
- [J23] 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.
- [J24] 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.
- [J25] 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.
- [J26] 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.

- [J27] 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.
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- [J29] 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.
- [J30] B. Pasaniuc, R. Garfinkel, I.I. Măndoiu, and A. Zelikovsky. Optimal testing of digital microfluidic biochips. *INFORMS Journal on Computing*, pages 518–529, 2011.
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- [J32] I. Astrovskaya, B. Tork, S. Mangul, K. Westbrooks, I.I. Măndoiu, P. Balfe, and A. Zelikovsky. Inferring viral quasispecies spectra from 454 pyrosequencing reads. *BMC Bioinformatics*, 12(Suppl 6):S1, 2011.
- [J33] 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.
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- [J35] 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.
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- [J45] I.I. Măndoiu and D. Trincă. Exact and approximation algorithms for DNA tag set design. *Journal of Computational Biology*, 13(3):732–744, 2006.
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Articles in Refereed Conference Proceedings

- [C1] M. Moussa and I.I. Măndoiu. 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.
- [C2] I. Mandric, S. Knyazev, C. Padilla, F. Stewart, I.I. Măndoiu, 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.
- [C3] S. Mangul, A. Caciula, S. Al Seesi, D. Brinza, A. Rouf Banday, R. Kanadia, I.I. Măndoiu, and A. Zelikovsky. Flexible approach for novel transcript reconstruction from RNA-Seq data using maximum likelihood integer programming. In *Proc. 5th International Conference on Bioinformatics and Computational Biology*, 2013.
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Unrefereed Conference Articles

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

- [P1] 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, Provisional Application, 2016.
- [P2] C.E. Nelson, I.I. Măndoiu, and H.L. Aguila. Pipeline for rational design and interpretation of biomarker panels. *US Patent Application 2015/0080237 A1*, 2015.
- [P3] P.K. Srivastava, I.I. Măndoiu, and F. Duan. Identification of tumor-protective epitopes for the treatment of cancers. *World Patent Application WO2014052707 A3*, 2015.
- [P4] C. Albrecht, A.B. Kahng, I.I. Măndoiu, and A.Z. Zelikovsky. Floorplan evaluation, global routing, and buffer insertion for integrated circuits. *US Patent #7,062,743*, 2006.

SOFTWARE PACKAGES

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- F. Duan, J. Duitama, S. Al Seesi, P.K. Srivastava, and I.I. Măndoiu. Epi-Seq: Bioinformatics pipeline for predicting cancer specific epitopes from RNA-Seq data. Available at <http://dna.engr.uconn.edu/software/Epi-Seq/>
- S. Al Seesi, Y.T. Tiagueu, A. Zelikovsky, and I.I. Măndoiu. IsoDE: Bootstrap-based differential gene expression analysis for RNA-Seq data. Available at <http://dna.engr.uconn.edu/software/IsoDE/>
- 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/>

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- 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
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- A.B. Kahng and I.I. Măndoiu. RMST-Pack: rectilinear minimum spanning tree algorithms. Available at <http://vlsicad.ucsd.edu/GSRC/bookshelf/Slots/RSMT/RMST/>

INVITED TALKS AND COLLOQUIA

- 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/UHC 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

- *Algorithmic Techniques for Inferring Transmission Networks from Noisy Sequencing Data*, NSF award CCF-1618347, \$200k, 8/2016–7/2019 (with Co-PI M. Bansal)
- *Computational framework for inference of metabolic pathway activity from RNA-seq data*, NSF award DBI-1564936, \$300k, 7/1/2016–6/30/2019
- *Novel transcript reconstruction from ION Torrent sequencing reads*, Life Technologies Corporation, Collaborative Research Compacts program, \$30k, 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, \$420k, 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, \$30k, 08/2011-02/2012 (with Co-PI A. Zelikovsky)
- *Reconstruction of haplotype spectra from high-throughput sequencing data*, NSF award IIS-0916948, \$275k, 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, \$570k, 01/2006–12/2011
- *Bioinformatics tools enabling large-scale DNA barcoding*, NSF award DBI-0543365, \$400k, 07/2006–06/2010 (with Co-PIs B. DasGupta and M.I. Khan)

Extramural Research Grants – Co-Investigator

- *Inhibitory cell types and circuits in the lateral hypothalamus*, NIH award 1R01MH112739-01, \$2M, 04/2017–03/2022 (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), \$675k, (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, \$339k, 02/2017–01/2018 (with PI Nishiyama)
- *Understanding Nutrition Through Biomics*, Foundation for Food and Agriculture Research, \$360k, 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), \$500k, 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, \$150k, 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, \$406k, 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) \$300k, 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), \$25k, 03/2015–03/2016
- *The mechanism of phenotypic drift in hES cells*, UCHC/Storrs and Regional Campus Incentive Grants ("UCIG") Award, **co-PI** (with PI R. O'Neill and co-PIs B. Graveley, T. Rasmussen, and Y. Wu), \$50k, 9/2009–8/2010
- *Primer selection algorithms for cost-effective DNA amplification by multiplex PCR*, University of Connecticut Research Foundation, Large Faculty Research Grant Program, **PI**, \$18k, 06/2004–05/2005

Other Grants

- *Travel Support: 12th International Symposium on Bioinformatics Research and Applications*, National Science Foundation award IIS-1639612 **Co-PI** (with PI A. Zelikovsky and Co-PIs Z. Cai, Y. Pan, and R. Sunderraman) \$20k, 06/2016–05/2017
- *Travel Support: 11th International Symposium on Bioinformatics Research and Applications*, National Science Foundation award IIS-1542617, **Co-PI** (with PI A. Zelikovsky and Co-PIs Y. Li, Y. Pan, and R. Sunderraman) \$20k, 05/2015–04/2016
- *Oncoimmune, a tumor-specific immunotherapy for the treatment of stage III/IV ovarian cancer*, UCHC Spark grant for early stage commercialization and development, **co-PI** (with PI P.K. Srivastava and co-PIs A. Kueck, F. Duan, and S. Al Seesi), \$30k, 12/2013
- UConn/Jackson Laboratory faculty fellowship to attend *53rd Annual Short Course on Medical and Experimental Mammalian Genetics*, **PI**, \$3.5k, 7/15/2012–7/27/2012
- *Travel Support: 8th International Symposium on Bioinformatics Research and Applications*, National Science Foundation award IIS-1237310, **co-PI** (with PI R. Sunderraman and co-PIs A. Zelikovsky and O. Daescu), \$20k, 06/2012–05/2013

- *Travel Support: 7th International Symposium on Bioinformatics Research and Applications*, National Science Foundation award IIS-1116001, **co-PI** (with PI A. Zelikovsky and co-PI Y. Pan), \$20k, 04/2011-03/2012
 - *First International IEEE Conference on Computational Advances in Bio and Medical Sciences (ICCABS) – Travel Awards*, National Science Foundation award IIS-1112395, **co-PI** (with PI S. Rajasekaran), \$20k, 02/2011-01/2012
 - *Computational Biomedical Science*, UCONN Honors Interdisciplinary Course Development Grant, **PI** (with PI C.E. Nelson), \$8k, 06/2006–05/2009
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PROFESSIONAL SERVICE

Editorial Board Member and Guest Editor for Journals

- Associate Editor, *Genes*, 04/2018-present
- Associate Editor, *BMC Bioinformatics*, 02/2010-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 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 *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 *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, *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

- *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, III, and SCH programs
- Expert assessor for the *Australian Research Council (ARC)*
- Reviewer for the *Israel Science Foundation*
- Judge for the *Intel Science Talent Search (STS)* competition
- Reviewer for *Computing Reviews*
- Technical referee for *ACM Transactions on Design Automation of Electronic Systems*, *Advances in Bioinformatics*, *Algorithmica*, *BMC Bioinformatics*, *BMC Genome Medicine*, *Bioinformatics*, *Combinatorica*, *Discrete Applied Mathematics*, *Genetics*, *IEEE Transactions on Computational Biology and Bioinformatics*, *IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems*, *IEEE Transactions on Computers*, *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 (SIGBioinformatics)

TEACHING AND ADVISING

Courses Taught

University of Connecticut

- BME1401/CSE1401/MCB1401, *Honors Core: Computational Molecular Biology* (Fall 2007, Fall 2008, Spring 2009, Fall 2010, Spring 2011, Fall 2011, Spring 2012, Fall 2013, Spring 2014)
- BME 4985/6160 & CSE 4095/6800, *Computational Genomics* (Spring 2007, Spring 2008, Spring 2009, Spring 2013, Spring 2015, Spring 2017)
- 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)
- 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)
- INTD198: *Freshman Honors Seminar – Bioinformatics and Molecular Evolution* (Fall 2006)

Georgia Institute of Technology

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

Major Advisor – Ph.D. Students

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

Major Advisor – M.S. Students

- Gabriel Ilie, M.S. 12/2013, thesis: “Algorithms for Multisample Read Binning”, current position: Software Developer, Mysis Corp.

- Pankaj Ghimire, M.S. 12/2012, co-advised with Y. Wu, thesis: “Detection of Genomic Inversion from Single End Reads”, current position: Senior Software Development Consultant at TechDigital Corporation
- Marius Nicolae, M.S. 12/2011, thesis: “Accurate Estimation of Isoform and Gene Expression Levels from Next Generation Sequencing Data”, 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: Lecturer, Computer Science Department, Smith College