

Haris Vikalo

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Education

- Ph.D. in Electrical Engineering, Stanford University, Stanford, CA, 2003.
- M.Sc. in Electrical Engineering, Lehigh University, Bethlehem, PA, 1997.
- B.Sc. in Electrical Engineering, University of Zagreb, Croatia, 1995.

Current and Previous Academic Positions

- **Associate Professor**, ECE Department, University of Texas at Austin, 09/2013 - present.
Member of the Institute for Cellular and Molecular Biology (ICMB) at UT Austin, 2014 - present.
- **Assistant Professor**, ECE Department, University of Texas at Austin, 09/2007 - 08/2013.
- **Associate Scientist**, EE Department, California Institute of Technology, 07/2003 - 09/2007.
- **Postdoctoral Researcher**, EE Department, California Institute of Technology, 01/2003 - 07/2003.
- **Research Assistant**, EE Department, Stanford University, 09/1997 - 10/2002.
- **Research Assistant**, EECS Department, Lehigh University, PA, 01/1996 - 09/1997.

Other Professional Experience

- **Visiting Professor**, Max F. Perutz Laboratories, Vienna, June 2014 - December 2014.
- **Member of Technical Staff**, Bell Labs, Murray Hill, NJ, 06/1999 - 09/1999.

Teaching in the Last Five Years

- *EE 381K-6 Estimation Theory*, Spring 2016, Fall 2017.
- *EE 351M Digital Signal Processing*, UT Austin, Spring 2015, Fall 2015, Spring 2017, Spring 2018, Spring 2019.
- *EE 381V Genomic Signal Processing*, UT-Austin, Fall 2016, Fall 2018.

Awards, Honors and Professional Memberships

- Jack Kilby/Texas Instruments Endowed Faculty Fellowship in Computer Engineering, 2012-2014, 2017-2018.
- Elevated to the grade of IEEE Senior Member, 2015.
- NSF Career Award, 2009.
- University of Zagreb, Faculty of Electrical Engineering's Award "Josip Loncar" (graduated ranked first in the class of 550 students).

University Committee Assignments

Departmental

- DICE Graduate Area Advisor, 2013-present
- bioECE Graduate Area Admissions Coordinator, 2015-present
- ECE Junior Faculty Recruiting Committee, 2013-2015, 2016-present
- DICE Graduate Admission Committee, 2007-present
- Annual WNCG Open House Coordinator, 2014-present
- DICE Technical Core Area Reform Committee, 2015-2016
- DICE Pre-qual Committee, 2012-present
- Major Sequence Appeals Committee, 2012-2015
- ECE Benchmarking/Directions Committee, 2014
- ECE Recruiting Vision Committee, 2013

College

- Systems Biology Faculty Recruitment Committee, 2011-2012

Community Activities and Professional Service

- Associate Editor, IEEE Transactions on Molecular, Biological and Multi-Scale Communications, 2018 – current.
- Technical Program Committee Member, 2018 IEEE International Symposium on Information Theory (ISIT), Vail, CO, June 2018.
- Technical Program Committee Member, the 4th International Workshop on Computational Network Biology (CNB-MAC), Boston, MA, August 2017.
- Session Chair (?Genome Assembly and DNA Storage Systems?), 2017 Information Theory and Applications Workshop, San Diego, CA.
- NSF Panelist, CCF Program, 2017.
- Technical Program Co-Chair for the “Symposium on Signal Processing and Mathematical Modeling of Biological Processes with Applications to Cyber-Physical Systems for Precise Medicine,” at the IEEE Global Conf. on Signal and Information Processing (GlobalSIP), Orlando, FL, December 2015.
- Technical Program Committee Member, the 2nd International Workshop on Computational Network Biology (CNB-MAC), Atlanta, GA, September 2015.
- NSF Panelist, CCF Program, 2014.
- Technical Program Committee Member, 8th International Symposium on Turbo Codes and Iterative Information Processing (ISTC), Bremen, Germany, August 2014.
- Technical Program Committee Member, International Workshop on Computational Network Biology: Modeling, Analysis, and Control, Newport Beach, CA, September 2014.
- General Chair, IEEE Symposium on Bioinformatics and Systems Biology, IEEE GlobalSIP Workshop, Austin, TX, December 2013.
- Technical Program Chair, XVI International Conference on Information, Communication, and Automation Technologies, Sarajevo, Bosnia and Herzegovina, October 2013.
- Student Paper Award Chair, IEEE Workshop on Genomic Signal Processing and Statistics (GENSIPS), Houston, TX, November 2013.
- Technical Program Committee Member, IEEE Workshop on Genomic Signal Processing and Statistics (GENSIPS), San Antonio, TX, December 2011.

- Technical Chair for the IEEE Asilomar Conference on Signals, Systems and Computers, Pacific Grove, CA, November 7-11, 2011 (Track F: Bio image and signal processing).
- Technical Program Chair for the IEEE International Workshop on Genomic Signal Processing and Statistics (GENSIPS), Cold Spring Harbor, NY, November 10-12, 2010.
- Guest Editor for *EURASIP Journal on Advances in Signal Processing, Special Issue on Genomic Signal Processing*, 2010.
- Tutorial Chair for the IEEE International Workshop on Genomic Signal Processing and Statistics (GENSIPS), Minneapolis, MN, May 2009.
- Technical Program Committee Member, IEEE Workshop on Genomic Signal Processing and Statistics (GENSIPS), Minneapolis, MN, May 2009.
- Co-organized and presented a full-day tutorial on *Bioinformatics and Computational Biology I, II* at the IEEE International Conf. on Acoustic, Speech, and Signal Processing, Las Vegas, NV, April 2008.
- Technical Program Committee Member, IEEE Workshop on Genomic Signal Processing and Statistics (GENSIPS), Tuusula, Finland, June 10-12, 2007.
- Served as a reviewer for the following journals and conferences:
 - IEEE Transactions on Signal Processing; IEEE Transactions on Information Theory; IEEE Transactions on Communications; IEEE Transactions on Wireless Communications; IEEE Transactions on Molecular, Biological, and Multi-Scale Communications; EURASIP Signal Processing; Oxford’s Bioinformatics
 - IEEE Workshop on Genomic Signal Processing and Statistics (GENSIPS); IEEE International Communication Conference; IEEE Globecom Conference; IEEE International Conference on Acoustic, Speech, and Signal Processing; IEEE International Symposium on Information Theory; IEEE Workshop on Statistical Signal Processing

Patents

- “Multiplex QPCR Arrays,” with A. Hassibi and B. Hassibi, U.S. patent no. 9,458,497, October 2016.
- “Method and apparatus for detection, identification, and quantification of single-and multi-analytes in affinity-based sensor arrays,” with B. Hassibi and A. Hassibi, U.S. patent 9,223,929, December 2015.
- “Real-time microarrays,” with A. Hassibi, J.-L. Reichmann, and B. Hassibi, U.S. patent 9,133,504, September 2015.

Grants and Contacts

- Visibility and Interactive Information Sharing in Collaborative Sensing Systems, *National Science Foundation*, \$450,000, 08/15/18-07/31/21 (co-PI).
- Reconstructing Mixtures of DNA Sequences from High-Throughput Sequencing Data, *National Science Foundation*, \$400,000, 09/01/16-08/31/19 (PI).
- Algorithms for Haplotype Assembly from Next-Generation Sequencing Data, *National Science Foundation*, \$400,000, 09/01/2013-05/31/2018 (PI).
- WNCG Industrial Affiliates, \$70k (2012-ongoing).
- RAPID: Methods for Estimating Genetic Diversity of the Ebola Virus, *National Science Foundation*, \$200,000, 12/01/2014-12/01/2016 (PI).
- Algorithms for Base-Calling in Sequencing-By-Synthesis, *National Institute of Health*, \$352,259, 09/01/2011-08/31/2013 (PI).

- Modeling, Estimation, and Coding for Biosensor Arrays, *National Science Foundation CAREER Award*, \$400,000, 01/01/2009-12/31/2013 (PI).
- Next Generation DNA Sequencing: Signal Processing Perspectives, *National Science Foundation*, \$122,500, 09/01/2010-08/31/2011 (PI).

M.S. Supervisions Completed

Wu, Ting (2011) Electrical and Computer Engineering Department, UT-Austin

Das, Shreepriya (2011) (co-advised with A. Hassibi) ECE Department, UT-Austin

Shen, Xiaohu (2010) Electrical and Computer Engineering Department, UT-Austin

Gokdemir, Mahsuni (2010) Electrical and Computer Engineering Department, UT-Austin

Park, Mijung (2010) (co-advised with J. Pillow) ECE Department, UT-Austin

Lee, Juhun (2009) Electrical and Computer Engineering Department, UT-Austin

Ph.D. Supervisions Completed

Ahn, Soyeon, 2018

Barik, Somsubhra, 2017

Arzeno-González, Natalia, 2016

Das, Shreepriya, 2015.

Shen, Xiaohu, 2014.

Shamaiah, Manohar, 2013.

Lee, Sang-Hyun (co-advised with S. Vishwanath), 2012.

Publications

Books and book chapters

1. M. Shamaiah and H. Vikalo, "Estimation of Time-Varying Sparse Signals in Sensor Networks," in *Filtering from Undersampled Data with Introduction to Compressed Sensing*, Springer, 2014.
2. A. Hassibi, H. Vikalo, J. L. Riechmann, and B. Hassibi, "FRET-Based Real-Time DNA microarrays, in *Functional Genomics: Methods and Protocols*, Springer, 2012.
3. S. Das, H. Vikalo, and A. Hassibi, "Affinity-based biosensors: Stochastic modeling and figures of merit," in *Integrated Microsystems: Mechanical, Photonic, and Biological Interfaces*, Taylor and Francis LLC 2011.
4. T. Kailath, H. Vikalo, and B. Hassibi, "MIMO receive algorithms," in *Space-Time Wireless Systems: From Array Processing to MIMO Communications*, Cambridge University Press, 2006.
5. B. Hassibi and H. Vikalo, "Maximum-likelihood decoding and integer least-squares: The expected complexity," in *Multiantenna Channels: Capacity, Coding and Signal Processing*, AMS 2003.

Journal papers (in review)

1. Z. Ke and H. Vikalo, "GAEhaP: Haplotype assembly for diploids and polyploids via graph auto-encoders," submitted.
2. S. Barik and H. Vikalo, "Matrix completion and performance guarantees for single individual haplotyping," submitted (in the 2nd round of review).
3. A. Hashemi, M. Ghasemi, H. Vikalo and U. Topcu, "Randomized greedy sensor selection: Leveraging weak submodularity," submitted.
4. N. M. Arzeno and H. Vikalo, "Evolutionary clustering via message passing," submitted (in the 2nd round of review).
5. A. Hashemi, R. Shafipour, H. Vikalo and G. Mateos, "Accelerated greedy sampling of graph signals: A weak submodular optimization framework," submitted (in the 2nd round of review).

Journal papers (published or accepted)

1. A. Hashemi and H. Vikalo, "Evolutionary self-expressive models for subspace clustering," *IEEE Journal of Selected Topics in Signal Processing, Special Issue on Data Science: Robust Subspace Learning and Tracking*, vol. 12, no. 6, December 2018, pp. 1534-1546.
2. S. Barik, S. Das, and H. Vikalo, "Viral quasispecies reconstruction via correlation clustering," *Genomics*, vol. 110, no. 6, November 2018, pp. 375-381.
3. A. Hashemi and H. Vikalo, "Accelerated orthogonal least-squares for large-scale sparse reconstruction," *Digital Signal Processing*, vol. 82, no. 11, November 2018, pp. 91-105.
4. S. Ahn, Z. Ke and H. Vikalo, "Viral quasispecies reconstruction via tensor factorization with successive removal," *Bioinformatics*, vol. 34, no. 13, July 2018, pp. i23-i31.
5. A. Hassibi, A. Manickam, R. Singh, S. Bolouki, R. Sinha, K. Jirage, M. McDermott, B. Hassibi, H. Vikalo, G. Mazarei, L. Pei, L. Bousse, M. Miller, M. Heshami, M. Savage, M. Taylor, N. Gamini, N. Wood, P. Mantina, P. Grogan, P. Kuimelis, P. Savalia, S. Conradson, Y. Li, R. Meyer, E. Ku, J. Ebert, B. Pinsky, G. Dolganov, T. Van, K. Johnson, P. Naraghi-Arani, R. Kuimelis, G. Schoolnik, "Multiplexed identification, quantification and genotyping of infectious agents using a semiconductor biochip," *Nature Biotechnology*, 36, 2018, pp. 738-745.
6. S. Ahn and H. Vikalo, "aBayesQR: A Bayesian method for reconstruction of viral populations characterized by low diversity," *Journal of Computational Biology*, vol. 25, no. 7, July 2018, pp. 637-648.
7. H. Yang, J. Chun, and H. Vikalo, "Cyclic block coordinate minimization algorithms for DOA estimation in co-prime arrays," *Signal Processing*, vol. 145, no. 4, April 2018, pp. 272-284.
8. A. Hashemi, B. Zhu and H. Vikalo, "Sparse tensor decomposition for haplotype assembly of diploids and polyploids," *BMC Genomics*, 19(Suppl 4):191, March 2018.
9. H. Si, H. Vikalo, and S. Vishwanath, "Information-theoretic analysis of haplotype assembly," *IEEE Transactions on Information Theory*, vol. 63, no. 7, July 2017, pp: 3468-3479.
10. S. Das and H. Vikalo, "Optimal haplotype assembly via a branch-and-bound algorithm," *IEEE Transactions on Molecular, Biological, and Multi-Scale Communications*, vol. 3, no. 1, March 2017, pp: 1-12.

11. E. O'Reilly, F. Baccelli, G. de Veciana, and H. Vikalo, "End-to-end optimization of high-throughput DNA sequencing" *Journal of Computational Biology*, 23(10): 789-800, October 2016.
12. C. Cai, S. Sanghavi, and H. Vikalo, "Structured low-rank matrix factorization for haplotype assembly," *IEEE Journal of Selected Topics in Signal Processing, Special Issue on Structured Matrices in Signal and Data Processing*, vol. 10, no. 4, August 2016, pp: 647-657.
13. Z. Puljiz and H. Vikalo, "Decoding genetic variations: Communications-inspired haplotype assembly," *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, vol. 13, no. 3, June 2016, pp: 518-530.
14. N. M. Arzeno and H. Vikalo, "A novel mortality risk prediction score based on nonlinear feature transformations," *Journal of Biomedical Informatics*, vol. 56, August 2015, pp: 145-156.
15. S. Ahn and H. Vikalo, "Joint haplotype assembly and genotype calling via sequential Monte Carlo algorithm," *BMC Bioinformatics*, 16:223, July 2015, doi:10.1186/s12859-015-0651-8.
16. S. Das and H. Vikalo, "SDhaP: Haplotype assembly for diploids and polyploids via semi-definite programming," *BMC Genomics*, 16:260, April 2015, doi:10.1186/s12864-015-1408-5.
17. N. M. Arzeno and H. Vikalo, "Semi-supervised affinity propagation with soft instance-level constraints," *IEEE Transactions on Pattern Analysis and Machine Intelligence*, vol. 37, no. 5, May 2015, pp: 1041-1052.
18. X. Shen, M. Shamaiah, and H. Vikalo, "Iterative learning of a DNA consensus sequence from high-throughput short reads: Algorithms and limits of performance," *IEEE Transactions on Signal Processing*, vol. 62, no. 17, September 2014, pp: 4425-4435.
19. S. Barik and H. Vikalo, "Sparsity-aware sphere decoding: Algorithms and complexity analysis," *IEEE Transactions on Signal Processing*, vol. 62, no. 9, May 2014, pp: 2212-2225.
20. M. Park, M. Nassar, and H. Vikalo, "Bayesian active learning for drug combinations," *IEEE Transactions on Biomedical Engineering*, 60(11), November 2013, pp: 3248-3255.
21. S. Das and H. Vikalo, "Base calling for high-throughput short-read sequencing: Dynamic programming solutions," *BMC Bioinformatics*, 2013, 14:129 doi:10.1186/1471-2105-14-129.
22. S.-H. Lee, M. Shamaiah, H. Vikalo, and S. Vishwanath, "Message-passing algorithms for coordinated spectrum sensing in cognitive radio networks," *IEEE Communication Letters*, vol. 17, no. 4, April 2013, pp: 812-815.
23. M. Shamaiah, S.-H. Lee, S. Vishwanath, and H. Vikalo, "Distributed algorithms for spectrum access in cognitive radio relay networks," *IEEE Journal on Sel. Areas in Communications - Cognitive Radio Series*, vol. 30, no. 10, November 2012, pp: 1947-1957.
24. T. Wu and H. Vikalo, "Joint parameter estimation and base-calling for pyrosequencing systems," *IEEE Transactions on Signal Processing*, vol. 60, no. 8, August 2012, pp: 4376-4386.
25. M. Shamaiah, S. Banerjee, and H. Vikalo, "Greedy sensor selection under channel uncertainty," *IEEE Wireless Communications Letters*, vol. 1, no. 4, August 2012, pp: 376-379.
26. S. Das and H. Vikalo, "OnlineCall: Fast online parameter estimation and base calling for Illumina's next-generation sequencing," *Bioinformatics*, 2012, doi:10.1093/bioinformatics/bts256.

27. X. Shen and H. Vikalo, "ParticleCall: A particle filter for base calling in next-generation sequencing systems," *BMC Bioinformatics*, vol. 13, no. 160, July 2012.
28. M. Shamaiah, X. Shen, and H. Vikalo, "Estimating parameters of sampled diffusion processes in affinity biosensors," *IEEE Transactions on Signal Processing*, vol. 60, no. 6, June 2012, pp: 3228-3239.
29. M. Shamaiah, S.-H. Lee, and H. Vikalo, "Graphical models and inference on graphs in genomics," *IEEE Signal Processing Magazine*, vol. 29, no. 1, January 2012, pp: 51-65.
30. M. Shamaiah and H. Vikalo, "Estimating time-varying sparse signals under communication constraints," *IEEE Transactions on Signal Processing*, vol. 59, no. 6, June 2011, pp. 2961-2964.
31. H. Vikalo and M. Gokdemir, "An MCMC algorithm for estimation in real-time biosensor arrays," *EURASIP Journal on Advances in Signal Processing, Special Issue on Genomic Signal Processing*, 2010, doi:10.1155/2010/736301.
32. X. Shen and H. Vikalo, "Inferring parameters of gene regulatory networks via particle filtering," *EURASIP Journal on Advances in Signal Processing, Special Issue on Genomic Signal Processing*, 2010, doi:10.1155/2010/204612.
33. H. Vikalo, B. Hassibi, and A. Hassibi, "Limits of performance of quantitative polymerase chain reaction systems," *IEEE Transactions on Information Theory, Special Issue on Molecular Biology and Neuroscience*, vol. 56, no. 2, February 2010, pp: 1-8.
34. M. El-Khamy, H. Vikalo, B. Hassibi, and R. J. McEliece, "Bounds on the performance of sphere decoding of linear block codes," *IEEE Transactions on Communications*, vol. 57, no. 10, October 2009, pp: 2940-2950.
35. A. Hassibi, H. Vikalo, J.-L. Reichmann, and B. Hassibi, "Real-time DNA microarray analysis," *Nucleic Acids Research*, vol. 37, no. 20, 2009, e132:1-12.
36. S. Das, H. Vikalo, and A. Hassibi, "On scaling laws of biosensors," *Journal of Applied Physics*, vol. 105, no. 10, pp. 102021-102021-7, May 2009.
37. H. Vikalo, B. Hassibi, and A. Hassibi, "Modeling and estimation for real-time microarrays," *IEEE Journal of Selected Topics in Signal Processing, Special Issue on Genomic and Proteomic Signal Processing*, vol. 2, no. 3, June 2008, pp: 286-296.
38. F. Parvaresh, H. Vikalo, S. Misra, and B. Hassibi, "Recovering sparse signals using sparse measurement matrices in compressed DNA microarrays," *IEEE Journal of Sel. Topics in Signal Processing, Special Issue on Genomic and Proteomic Signal Processing*, vol. 2, no. 3, June 2008, pp: 275-285.
39. M. Stojnic, H. Vikalo, and B. Hassibi, "An H-infinity design approach to improve the speed of the sphere decoding algorithm," *IEEE Trans. on Sig. Processing*, vol. 56, no. 2, Feb. 2008, pp. 712-726.
40. A. Hassibi, H. Vikalo, and A. Hajimiri, "On noise processes and limits of performance in biosensors," *Journal of Applied Physics*, vol. 102, no. 1, July 2007, pp. 014909-014909-12.
41. H. Vikalo and B. Hassibi, "On joint detection and decoding of linear block codes on Gaussian vector channels," *IEEE Transactions on Signal Processing*, vol. 54, no. 9, September 2006, pp. 3330-3342.
42. M. Stojnic, H. Vikalo, and B. Hassibi, "Maximizing the sum-rate of multi-antenna broadcast channels using linear preprocessing," *IEEE Trans. on Wireless Comm.*, vol. 5, no. 9, Sept. 2006, pp. 2338-42.

43. H. Vikalo, B. Hassibi, and P. Stoica, "Joint ML channel estimation and signal detection," *IEEE Transactions on Wireless Communications*, vol. 5, no. 7, July 2006, pp. 1838-1845.
44. H. Vikalo, B. Hassibi, and U. Mitra, "Sphere-constrained ML detection for frequency-selective channels," *IEEE Transactions on Communications*, vol. 54, no. 7, July 2006, pp. 1179-1183.
45. H. Vikalo, A. Hassibi, and B. Hassibi, "A statistical model for microarrays, optimal estimation algorithms, and limits of performance," *IEEE Transactions on Signal Processing, Special Issue on Genomic Signal Processing*, vol. 54, no. 6, June 2006, pp. 2444-2455.
46. H. Vikalo and B. Hassibi, "On sphere decoding algorithm. II. Generalizations, second-order statistics, and applications to communications," *IEEE Trans. on Sig. Proc.*, vol. 53, no. 8, Aug. 2005, 2819-34.
47. B. Hassibi and H. Vikalo, "On sphere decoding algorithm. I. Expected complexity," *IEEE Transactions on Signal Processing*, vol. 53, no. 8, August 2005, pp. 2806-2818 .
48. H. Vikalo, B. Hassibi, A. Erdogan, and T. Kailath, "On H-infinity design techniques for robust signal reconstruction in noisy filter banks," *EURASIP Signal Processing*, vol. 85, no. 1, Jan. 2005, pp. 1-14.
49. H. Vikalo, B. Hassibi, and T. Kailath, "Iterative decoding for MIMO channels via modified sphere decoder," *IEEE Trans. on Wireless Communications*, vol.3, no. 6, November 2004, pp. 2299-2311.
50. H. Vikalo, B. Hassibi, B. Hochwald, and T. Kailath, "On the capacity of frequency-selective channels in training-based transmission schemes," *IEEE Trans. Sig. Proc.*, vol. 52, no. 9, Sept. 2004, 2572-83.
51. H. Vikalo and B. Hassibi, "On ML sequence detection for multiple antenna systems over dispersive channels," *EURASIP J. Appl. Sig. Proc., Special Issue on Space-Time Coding*, May 2002, pp. 525-31.

Conference and workshop papers

1. M. Ghasemi, A. Hashemi, U. Topcu and H. Vikalo, "On submodularity of quadratic observation selection in constrained networked sensing systems," *The 2019 American Control Conference (ACC)*, Philadelphia, PA, July 10-12, 2019.
2. S. Consul, A. Hashemi and H. Vikalo, "A MAP framework for support recovery of sparse signals using orthogonal least squares," *IEEE International Conference on Acoustics, Speech and Signal Processing (ICASSP)*, Brighton, UK, May 12-17, 2019.
3. A. Hashemi and H. Vikalo, "Evolutionary subspace clustering: Discovering structure in self-expressive time-series data," *IEEE International Conference on Acoustics, Speech and Signal Processing (ICASSP)*, Brighton, UK, May 12-17, 2019.
4. M. Ribero, D. Chizhik, R. A. Valenzuela, R. W. Heath Jr. and H. Vikalo, "Deep learning propagation models over irregular terrain," *IEEE International Conference on Acoustics, Speech and Signal Processing (ICASSP)*, Brighton, UK, May 12-17, 2019.
5. A. Hashemi, O. F. Kilic, and H. Vikalo, "Near-optimal distributed estimation for a network of sensing units operating under communication constraints," *57th IEEE Conference on Decision and Control (CDC)*, Miami Beach, FL, Dec. 17-19, 2018.
6. S. Ahn, Z. Ke and H. Vikalo, "Viral quasispecies reconstruction via tensor factorization with successive removal," *26th Conference on Intelligent Systems for Molecular Biology (ISMB)*, Chicago, IL, July 6-10, 2018. (Acceptance rate: 19.6%).

7. A. Hashemi, M. Ghasemi, H. Vikalo and U. Topcu, "A randomized greedy algorithm for near-optimal sensor scheduling in large-scale sensor networks," *The 2018 American Control Conference (ACC)*, Milwaukee, WI, June 27-29, 2018. (Best student paper award finalist).
8. A. Hashemi, R. Shafipour, H. Vikalo and G. Mateos "Sampling and reconstruction of graph signal via weak submodularity and semidefinite relaxation," *IEEE International Conference on Acoustics, Speech and Signal Processing (ICASSP)*, Calgary, Alberta, Canada, April 15-20, 2018.
9. S. Ahn, Z. Ke and H. Vikalo, "Viral quasispecies reconstruction via tensor factorization," *55th Annual Allerton Conference on Communication, Control, and Computing*, Monticello, IL, October 3-6, 2017 (invited).
10. S. Mourad, A. Tewfik and H. Vikalo, "Data subset selection for efficient SVM training," *The 25th European Signal Processing Conference (EUSIPCO)*, Kos island, Greece, August 28 - September 2, 2017.
11. A. Hashemi, B. Zhu and H. Vikalo, "Sparse tensor decomposition for haplotype assembly of diploids and polyploids," *The 4th International Workshop on Computational Network Biology: Modeling, Analysis, and Control (CNB-MAC)*, Boston, MA, August 20-23, 2017.
12. S. Ahn and H. Vikalo, "aBayesQR: A Bayesian method for reconstruction of viral populations characterized by low diversity," *The 21st Annual International Conference on Research in Computational Molecular Biology (RECOMB)*, Hong Kong, May 3-7, 2017. (Acceptance rate: 21%).
13. X. Zheng, H. Vikalo, S. Song, L. K. John and A. Gerstlauer, "Sampling-based binary-level cross-platform performance estimation," *Design, Estimation and Test in Europe (DATE)*, Lausanne, Switzerland, March 27-31, 2017. (Acceptance rate: 24%).
14. A. Hashemi and H. Vikalo, "Recovery of sparse signals via branch-and-bound least squares," *IEEE International Conference on Acoustics, Speech and Signal Processing (ICASSP)*, New Orleans, LA, March 5-9, 2017.
15. N. M. Arzeno and H. Vikalo, "Evolutionary affinity propagation," *IEEE International Conference on Acoustics, Speech and Signal Processing (ICASSP)*, New Orleans, LA, March 5-9, 2017.
16. S. Barik and H. Vikalo, "Binary matrix completion with performance guarantees for single individual haplotyping," *IEEE International Conference on Acoustics, Speech and Signal Processing (ICASSP)*, New Orleans, LA, March 5-9, 2017.
17. A. Hashemi and H. Vikalo, "Sparse linear regression via generalized orthogonal least-squares," *2016 IEEE GlobalSIP Symposium on Signal Processing of Big Data*, Washington DC, December 2016.
18. H. Yang, H. Vikalo, and J. Chun, "Nonnegative gridless compressive sensing for co-prime arrays," *2016 IEEE GlobalSIP Symposium on Sparse Signal Processing for Communications*, Washington DC, December 2016.
19. V. Va, H. Vikalo, and R. Heath, "Beam tracking for mobile millimeter wave communication systems," *2016 IEEE GlobalSIP Symposium on Transceivers and Signal Processing for 5G Wireless and mm-Wave Systems*, Washington DC, December 2016.
20. C. Cai, S. Sanghavi, and H. Vikalo, "Structurally-constrained gradient descent for matrix factorization in haplotype assembly problems," *IEEE International Conference on Acoustic, Speech and Signal Processing (ICASSP)*, Shanghai, March 2016.

21. T. Goodall, A. C. Bovik, H. Vikalo, and N. G. Paulter Jr., "Non-uniformity correction of IR images using natural scene statistics," *IEEE Global Conference on Signal and Information Processing (GlobalSIP)*, Orlando, FL, December 2015.
22. S. Barik, S. Das and H. Vikalo, "Semi-definite programming methods for viral quasispecies reconstruction," *Intelligent Systems in Molecular Biology (ISMB)*, Dublin, Ireland, July 2015.
23. A. Gupta, S. Barik, and H. Vikalo, "Distributed self localization of sensors with Poisson deployment using extended Kalman filter," *2015 IEEE Wireless Communications and Networking Conference (WCNC)*, New Orleans, LA, March 2015, pp: 1500-1505.
24. S. Das and H. Vikalo, "Optimal haplotype assembly with statistical pruning," *IEEE GlobalSIP14 - Workshop on Genomic Signal Proc. and Statistics*, Atlanta, GA, Dec. 2014.
25. S. Das and H. Vikalo, "Single individual haplotyping with low rank semidefinite programming," *NIPS 2014 Workshop on Machine Learning in Computational Biology (MLCB)*, Montreal, Canada, December 2014.
26. H. Si, H. Vikalo and S. Vishwanath, "Haplotype assembly: An information-theoretic view," *IEEE Information Theory Workshop*, Tasmania, Australia, November 2-5, 2014.
27. Z. Puljiz and H. Vikalo, "Iterative learning of single individual haplotypes from high-throughput DNA sequencing data," *8th International Symposium on Turbo Codes and Iterative Information Processing (ISTC)*, Bremen, Germany, August 2014.
28. S. Ahn and H. Vikalo, "Deterministic sequential Monte Carlo for haplotype inference," *IEEE Global Conference on Signal and Information Processing*, Austin, TX, December 2-4, 2013.
29. Z. Puljiz and H. Vikalo, "Message-passing algorithms for haplotype assembly," *Asilomar Conference on Systems, Signals & Computers*, Asilomar, November 3-6, 2013 (invited).
30. N. Arzeno-Gonzales and H. Vikalo, "Exploiting time series properties for mortality prediction in pediatric brain injury," *Workshop on Role of Machine Learning in Transforming Healthcare, International Conference on Machine Learning*, Atlanta, June 16-21, 2013.
31. X. Shen, M. Shamaiah, and H. Vikalo, "Message passing algorithm for inferring consensus sequence from next-generation sequencing data," *IEEE International Symposium on Information Theory*, Istanbul, Turkey, July 7-12, 2013.
32. S. Barik and H. Vikalo, "Expected complexity of sphere decoding for sparse integer least-square problems," *IEEE Intern'l Conf. on Acoustic, Signal, and Speech Processing*, Vancouver, Canada, May 26-31, 2013.
33. X. Shen and H. Vikalo, "A message-passing algorithm for reference-guided sequence assembly from high-throughput sequencing data," *IEEE International Workshop on Genomic Signal Processing and Statistics (GENSIPS)*, Washington, D.C., TX, December 2012.
34. C. H. Lee, N. M. Arzeno, J. C. Ho, H. Vikalo, and J. Ghosh, "An imputation-enhanced algorithm for ICU mortality prediction," *Computing in Cardiology (CinC)*, Krakow, Poland, September 2012.
35. M. Shamaiah and H. Vikalo, "Base calling error rates in next-generation DNA sequencing," *IEEE Workshop on Statistical Signal Processing*, Ann Arbor, MI, August 2012.

36. M. Park, M. Nassar, B. Evans, and H. Vikalo, "Adaptive experimental design for drug combinations," *IEEE Workshop on Statistical Signal Processing*, Ann Arbor, MI, August 2012.
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Recent Invited Talks

- The Chinese University of Hong Kong, May 2017
"Algorithms for Haplotype Assembly"
- USC, 2015 Molecular, Biological and Multi-Scale Communications Workshop, December 2015
"Algorithms for Haplotype Assembly"
- Caltech, Department of Electrical Engineering, December 2015
"Algorithms for Haplotype Assembly"
- Stanford, 2015 Kailath Lecture and Colloquia, September 2015
"Algorithms for Haplotype Assembly"
- EPFL, School of Computer and Communication Sciences, December 2014
"Decoding genetic variations: Communications-inspired haplotype assembly"
- ETHZ, Department of Information Technology and Electrical Engineering, December 2014
"Decoding genetic variations: Communications-inspired haplotype assembly"
- TU Munich, Department of Electrical Engineering, November 2014
"Decoding genetic variations: Communications-inspired haplotype assembly"
- University of Stuttgart, Department of Electrical Engineering, November 2014
"Decoding genetic variations: Communications-inspired haplotype assembly"
- Max F. Perutz Laboratories, Center for Integrative Bioinformatics, Vienna, October 2014
"Decoding genetic variations: Communications-inspired haplotype assembly"
- Korea Advanced Institute of Science and Technology, Dept. of Electrical Engineering, June 2012
"Signal Processing for Next Generation Biosensing and Sequencing"
- Samsung Advanced Institute of Technology, South Korea, June 2012
"Signal Processing for Next Generation Biosensing and Sequencing"
- Stanford University, Department of Electrical Engineering, May 2012
"How to read your genes: Signal Processing for Next Generation Sequencing and Biosensing"
- University of California Los Angeles, Department of Electrical Engineering, March 2012
"Signal Processing for Next Generation Sequencing and Biosensing"
- MIT, Department of Electrical Engineering and Computer Science, March 2012
"How to Read your Genes: Signal Processing for Next Generation Sequencing and Biosensing"

- University of Illinois at Urbana-Champaign, Dept. of Electrical and Comp. Engineering, March 2012
“How to Read your Genes: Signal Processing for Next Generation Sequencing and Biosensing”
- California Institute of Technology, Department of Electrical Engineering, February 2012
“Signal Processing for Next Generation Sequencing and Biosensing”
- University of Southern California, Department of Electrical Engineering, February 2012
“Signal Processing for Next Generation Sequencing and Biosensing”