Haris Vikalo

List of Publications by Year
in descending order

85 papers	**1,249** citations	516710 **16** h-index	477307 **29** g-index
90 all docs	**90** docs citations	**90** times ranked	**1261** citing authors

#	Article	IF	Citations
1	Real-Time Radio Technology and Modulation Classification via an LSTM Auto-Encoder. IEEE Transactions on Wireless Communications, 2022, 21, 370-382.	9.2	46
2	Communication-Efficient Variance-Reduced Decentralized Stochastic Optimization Over Time-Varying Directed Graphs. IEEE Transactions on Automatic Control, 2022, 67, 6583-6594.	5.7	4
3	Towards Accelerated Greedy Sampling and Reconstruction of Bandlimited Graph Signals. Signal Processing, 2022, , 108505.	3.7	3
4	Federating recommendations using differentially private prototypes. Pattern Recognition, 2022, 129, 108746.	8.1	18
5	Randomized Greedy Sensor Selection: Leveraging Weak Submodularity. IEEE Transactions on Automatic Control, 2021, 66, 199-212.	5.7	27
6	Evolutionary Clustering via Message Passing. IEEE Transactions on Knowledge and Data Engineering, 2021, 33, 2452-2466.	5.7	4
7	ComHapDet: a spatial community detection algorithm for haplotype assembly. BMC Genomics, 2020, 21, 586.	2.8	7
8	A Graph Auto-Encoder for Haplotype Assembly and Viral Quasispecies Reconstruction. Proceedings of the AAAI Conference on Artificial Intelligence, 2020, 34, 719-726.	4.9	6
9	Online Topology Inference from Streaming Stationary Graph Signals. , 2019, , .		13
10	Matrix Completion and Performance Guarantees for Single Individual Haplotyping. IEEE Transactions on Signal Processing, 2019, 67, 4782-4794.	5.3	1
11	Evolutionary Subspace Clustering: Discovering Structure in Self-expressive Time-series Data. , 2019, , .		1
12	A Map Framework for Support Recovery of Sparse Signals Using Orthogonal Least Squares. , 2019, , .		1
13	Weighted Subset Selection for Fast SVM Training. , 2019, , .		1
14	On Submodularity of Quadratic Observation Selection in Constrained Networked Sensing Systems. , 2019, , .		2
15	QSdpR: Viral quasispecies reconstruction via correlation clustering. Genomics, 2018, 110, 375-381.	2.9	18
16	Cyclic block coordinate minimization algorithms for DOA estimation in co-prime arrays. Signal Processing, 2018, 145, 272-284.	3.7	2
17	Sparse Tensor Decomposition for Haplotype Assembly of Diploids and Polyploids. BMC Genomics, 2018, 19, 191.	2.8	22
18	aBayesQR: A Bayesian Method for Reconstruction of Viral Populations Characterized by Low Diversity. Journal of Computational Biology, 2018, 25, 637-648.	1.6	21

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19	A NOVEL SCHEME FOR SUPPORT IDENTIFICATION AND ITERATIVE SAMPLING OF BANDLIMITED GRAPH SIGNALS. , 2018, , .		0
20	A Randomized Greedy Algorithm for Near-Optimal Sensor Scheduling in Large-Scale Sensor Networks. , 2018, , .		18
21	Evolutionary Self-Expressive Models for Subspace Clustering. IEEE Journal on Selected Topics in Signal Processing, 2018, 12, 1534-1546.	10.8	11
22	Sampling and Reconstruction of Graph Signals via Weak Submodularity and Semidefinite Relaxation. , 2018, , .		3
23	Viral quasispecies reconstruction via tensor factorization with successive read removal. Bioinformatics, 2018, 34, i23-i31.	4.1	24
24	Accelerated orthogonal least-squares for large-scale sparse reconstruction. , 2018, 82, 91-105.		9
25	Multiplexed identification, quantification and genotyping of infectious agents using a semiconductor biochip. Nature Biotechnology, 2018, 36, 738-745.	17.5	59
26	Information-Theoretic Analysis of Haplotype Assembly. IEEE Transactions on Information Theory, 2017, 63, 3468-3479.	2.4	7
27	Optimal Haplotype Assembly via a Branch-and-Bound Algorithm. IEEE Transactions on Molecular, Biological, and Multi-Scale Communications, 2017, 3, 1-12.	2.1	3
28	Sparse Tensor Decomposition for Haplotype Assembly of Diploids and Polyploids. , 2017, , .		0
29	Binary matrix completion with performance guarantees for single individual haplotyping. , 2017, , .		1
30	Recovery of sparse signals via Branch and Bound Least-Squares. , 2017, , .		2
31	Evolutionary affinity propagation. , 2017, , .		3
32	aBayesQR: A Bayesian Method for Reconstruction of Viral Populations Characterized by Low Diversity. Lecture Notes in Computer Science, 2017, , 353-369.	1.3	8
33	Sparse linear regression via generalized orthogonal least-squares. , 2016, , .		11
34	Structurally-constrained gradient descent for matrix factorization in haplotype assembly problems. , 2016, , .		0
35	Nonnegative gridless compressive sensing for co-prime arrays. , 2016, , .		1
36	Structured Low-Rank Matrix Factorization for Haplotype Assembly. IEEE Journal on Selected Topics in Signal Processing, 2016, 10, 647-657.	10.8	19

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37	Decoding Genetic Variations: Communications-Inspired Haplotype Assembly. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2016, 13, 518-530.	3.0	20
38	End-to-End Optimization of High-Throughput DNA Sequencing. Journal of Computational Biology, 2016, 23, 789-800.	1.6	2
39	Joint haplotype assembly and genotype calling via sequential Monte Carlo algorithm. BMC Bioinformatics, 2015, 16, 223.	2.6	6
40	Semi-Supervised Affinity Propagation with Soft Instance-Level Constraints. IEEE Transactions on Pattern Analysis and Machine Intelligence, 2015, 37, 1041-1052.	13.9	24
41	SDhaP: haplotype assembly for diploids and polyploids via semi-definite programming. BMC Genomics, 2015, 16, 260.	2.8	69
42	Designing optimal mortality risk prediction scores that preserve clinical knowledge. Journal of Biomedical Informatics, 2015, 56, 145-156.	4.3	11
43	Distributed self localization of sensors with poisson deployment using extended Kalman filter. , 2015, , .		0
44	Iterative Learning for Reference-Guided DNA Sequence Assembly From Short Reads: Algorithms and Limits of Performance. IEEE Transactions on Signal Processing, 2014, 62, 4425-4435.	5.3	0
45	Sparsity-Aware Sphere Decoding: Algorithms and Complexity Analysis. IEEE Transactions on Signal Processing, 2014, 62, 2212-2225.	5.3	21
46	Message-Passing Algorithms for Coordinated Spectrum Sensing in Cognitive Radio Networks. IEEE Communications Letters, 2013, 17, 812-815.	4.1	10
47	Deterministic sequential Monte Carlo for haplotype inference. , 2013, , .		0
48	Bayesian Active Learning for Drug Combinations. IEEE Transactions on Biomedical Engineering, 2013, 60, 3248-3255.	4.2	15
49	Expected complexity of sphere decoding for sparse integer least-square problems. , 2013, , .		1
50	A message passing algorithm for haplotype assembly. , 2013, , .		1
51	Base calling error rates in next-generation DNA sequencing. , 2012, , .		0
52	Adaptive experimental design for drug combinations. , 2012, , .		1
53	Greedy Sensor Selection under Channel Uncertainty. IEEE Wireless Communications Letters, 2012, 1, 376-379.	5.0	16
54	Joint Parameter Estimation and Base-Calling for Pyrosequencing Systems. IEEE Transactions on Signal Processing, 2012, 60, 4376-4386.	5.3	2

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55	A message passing algorithm for reference-guided sequence assembly from high-throughput sequencing data. , 2012, , .		1
56	Estimating Parameters of Sampled Diffusion Processes in Affinity Biosensors. IEEE Transactions on Signal Processing, 2012, 60, 3228-3239.	5.3	1
57	Distributed Algorithms for Spectrum Access in Cognitive Radio Relay Networks. IEEE Journal on Selected Areas in Communications, 2012, 30, 1947-1957.	14.0	34
58	Graphical Models and Inference on Graphs in Genomics: Challenges of high-throughput data analysis. IEEE Signal Processing Magazine, 2012, 29, 51-65.	5.6	7
59	OnlineCall: fast online parameter estimation and base calling for illumina's next-generation sequencing. Bioinformatics, 2012, 28, 1677-1683.	4.1	22
60	Distributed routing in networks using affinity propagation. , 2011, , .		1
61	Message-passing for base-calling in sequencing-by-synthesis systems. , 2011, , .		0
62	Sequential Monte Carlo method for parameter estimation in diffusion models of affinity-based biosensors. , 2011, , .		0
63	A message-passing algorithm for spectrum access in cognitive radio relay networks. , 2011, , .		1
64	An MCMC algorithm for base calling in sequencing-by-synthesis. , 2011, , .		0
65	A sequential Monte Carlo base-calling method for next-generation dna sequencing. , 2011, , .		0
66	Estimating Time-Varying Sparse Signals Under Communication Constraints. IEEE Transactions on Signal Processing, 2011, 59, 2961-2964.	5.3	3
67	Base-calling for Illumina's next-generation DNA sequencing systems via Viterbi algorithm. , 2011, , .		4
68	Limits of Performance of Quantitative Polymerase Chain Reaction Systems. IEEE Transactions on Information Theory, 2010, 56, 688-695.	2.4	4
69	Further results on message-passing algorithms for motif finding. , 2010, , .		0
70	Inferring parameters of gene regulatory networks via particle filtering. , 2010, , .		0
71	Optimal estimation in DNA microarrays via global optimization. , 2010, , .		0
72	Model-based sequential base calling for Illumina sequencing. , 2010, , .		1

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73	Greedy sensor selection: Leveraging submodularity. , 2010, , .		197
74	On scaling laws of biosensors: A stochastic approach. Journal of Applied Physics, 2009, 105, .	2.5	26
75	Real-time DNA microarray analysis. Nucleic Acids Research, 2009, 37, e132-e132.	14.5	34
76	Performance of sphere decoding of block codes. IEEE Transactions on Communications, 2009, 57, 2940-2950.	7.8	25
77	Stochastic modeling of reaction kinetics in biosensors using the Fokker Planck equation. , 2009, , .		1
78	Modeling and Estimation for Real-Time Microarrays. IEEE Journal on Selected Topics in Signal Processing, 2008, 2, 286-296.	10.8	12
79	Recovering Sparse Signals Using Sparse Measurement Matrices in Compressed DNA Microarrays. IEEE Journal on Selected Topics in Signal Processing, 2008, 2, 275-285.	10.8	148
80	Speeding up the Sphere Decoder With $H^{\infty }$ and SDP Inspired Lower Bounds. IEEE Transactions on Signal Processing, 2008, 56, 712-726.	5.3	25
81	PEP analysis of SDP-based non-coherent signal detection. , 2007, , .		0
82	On noise processes and limits of performance in biosensors. Journal of Applied Physics, 2007, 102, .	2.5	76
83	On the Performance of Sphere Decoding of Block Codes. , 2006, , .		2
84	On robust signal reconstruction in noisy filter banks. Signal Processing, 2005, 85, 1-14.	3.7	26
85	Maximum-likelihood decoding and integer least-squares: The expected complexity. DIMACS Series in Discrete Mathematics and Theoretical Computer Science, 2003, , 161-191.	0.0	17