

# Haris Vikalo

## List of Publications by Year in descending order

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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	Greedy sensor selection: Leveraging submodularity. , 2010, , .		197
2	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
3	On noise processes and limits of performance in biosensors. Journal of Applied Physics, 2007, 102, .	2.5	76
4	SDhaP: haplotype assembly for diploids and polyploids via semi-definite programming. BMC Genomics, 2015, 16, 260.	2.8	69
5	Multiplexed identification, quantification and genotyping of infectious agents using a semiconductor biochip. Nature Biotechnology, 2018, 36, 738-745.	17.5	59
6	Real-Time Radio Technology and Modulation Classification via an LSTM Auto-Encoder. IEEE Transactions on Wireless Communications, 2022, 21, 370-382.	9.2	46
7	Real-time DNA microarray analysis. Nucleic Acids Research, 2009, 37, e132-e132.	14.5	34
8	Distributed Algorithms for Spectrum Access in Cognitive Radio Relay Networks. IEEE Journal on Selected Areas in Communications, 2012, 30, 1947-1957.	14.0	34
9	Randomized Greedy Sensor Selection: Leveraging Weak Submodularity. IEEE Transactions on Automatic Control, 2021, 66, 199-212.	5.7	27
10	On robust signal reconstruction in noisy filter banks. Signal Processing, 2005, 85, 1-14.	3.7	26
11	On scaling laws of biosensors: A stochastic approach. Journal of Applied Physics, 2009, 105, .	2.5	26
12	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
13	Performance of sphere decoding of block codes. IEEE Transactions on Communications, 2009, 57, 2940-2950.	7.8	25
14	Semi-Supervised Affinity Propagation with Soft Instance-Level Constraints. IEEE Transactions on Pattern Analysis and Machine Intelligence, 2015, 37, 1041-1052.	13.9	24
15	Viral quasispecies reconstruction via tensor factorization with successive read removal. Bioinformatics, 2018, 34, i23-i31.	4.1	24
16	OnlineCall: fast online parameter estimation and base calling for illumina's next-generation sequencing. Bioinformatics, 2012, 28, 1677-1683.	4.1	22
17	Sparse Tensor Decomposition for Haplotype Assembly of Diploids and Polyploids. BMC Genomics, 2018, 19, 191.	2.8	22
18	Sparsity-Aware Sphere Decoding: Algorithms and Complexity Analysis. IEEE Transactions on Signal Processing, 2014, 62, 2212-2225.	5.3	21

#	ARTICLE	IF	CITATIONS
19	aBayesQR: A Bayesian Method for Reconstruction of Viral Populations Characterized by Low Diversity. <i>Journal of Computational Biology</i> , 2018, 25, 637-648.	1.6	21
20	Decoding Genetic Variations: Communications-Inspired Haplotype Assembly. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2016, 13, 518-530.	3.0	20
21	Structured Low-Rank Matrix Factorization for Haplotype Assembly. <i>IEEE Journal on Selected Topics in Signal Processing</i> , 2016, 10, 647-657.	10.8	19
22	QSdpR: Viral quasispecies reconstruction via correlation clustering. <i>Genomics</i> , 2018, 110, 375-381.	2.9	18
23	A Randomized Greedy Algorithm for Near-Optimal Sensor Scheduling in Large-Scale Sensor Networks. , 2018, , .		18
24	Federating recommendations using differentially private prototypes. <i>Pattern Recognition</i> , 2022, 129, 108746.	8.1	18
25	Maximum-likelihood decoding and integer least-squares: The expected complexity. <i>DIMACS Series in Discrete Mathematics and Theoretical Computer Science</i> , 2003, , 161-191.	0.0	17
26	Greedy Sensor Selection under Channel Uncertainty. <i>IEEE Wireless Communications Letters</i> , 2012, 1, 376-379.	5.0	16
27	Bayesian Active Learning for Drug Combinations. <i>IEEE Transactions on Biomedical Engineering</i> , 2013, 60, 3248-3255.	4.2	15
28	Online Topology Inference from Streaming Stationary Graph Signals. , 2019, , .		13
29	Modeling and Estimation for Real-Time Microarrays. <i>IEEE Journal on Selected Topics in Signal Processing</i> , 2008, 2, 286-296.	10.8	12
30	Designing optimal mortality risk prediction scores that preserve clinical knowledge. <i>Journal of Biomedical Informatics</i> , 2015, 56, 145-156.	4.3	11
31	Sparse linear regression via generalized orthogonal least-squares. , 2016, , .		11
32	Evolutionary Self-Expressive Models for Subspace Clustering. <i>IEEE Journal on Selected Topics in Signal Processing</i> , 2018, 12, 1534-1546.	10.8	11
33	Message-Passing Algorithms for Coordinated Spectrum Sensing in Cognitive Radio Networks. <i>IEEE Communications Letters</i> , 2013, 17, 812-815.	4.1	10
34	Accelerated orthogonal least-squares for large-scale sparse reconstruction. , 2018, 82, 91-105.		9
35	aBayesQR: A Bayesian Method for Reconstruction of Viral Populations Characterized by Low Diversity. <i>Lecture Notes in Computer Science</i> , 2017, , 353-369.	1.3	8
36	Graphical Models and Inference on Graphs in Genomics: Challenges of high-throughput data analysis. <i>IEEE Signal Processing Magazine</i> , 2012, 29, 51-65.	5.6	7

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37	Information-Theoretic Analysis of Haplotype Assembly. IEEE Transactions on Information Theory, 2017, 63, 3468-3479.	2.4	7
38	ComHapDet: a spatial community detection algorithm for haplotype assembly. BMC Genomics, 2020, 21, 586.	2.8	7
39	Joint haplotype assembly and genotype calling via sequential Monte Carlo algorithm. BMC Bioinformatics, 2015, 16, 223.	2.6	6
40	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
41	Limits of Performance of Quantitative Polymerase Chain Reaction Systems. IEEE Transactions on Information Theory, 2010, 56, 688-695.	2.4	4
42	Base-calling for Illumina's next-generation DNA sequencing systems via Viterbi algorithm. , 2011, , .		4
43	Evolutionary Clustering via Message Passing. IEEE Transactions on Knowledge and Data Engineering, 2021, 33, 2452-2466.	5.7	4
44	Communication-Efficient Variance-Reduced Decentralized Stochastic Optimization Over Time-Varying Directed Graphs. IEEE Transactions on Automatic Control, 2022, 67, 6583-6594.	5.7	4
45	Estimating Time-Varying Sparse Signals Under Communication Constraints. IEEE Transactions on Signal Processing, 2011, 59, 2961-2964.	5.3	3
46	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
47	Evolutionary affinity propagation. , 2017, , .		3
48	Sampling and Reconstruction of Graph Signals via Weak Submodularity and Semidefinite Relaxation. , 2018, , .		3
49	Towards Accelerated Greedy Sampling and Reconstruction of Bandlimited Graph Signals. Signal Processing, 2022, , 108505.	3.7	3
50	On the Performance of Sphere Decoding of Block Codes. , 2006, , .		2
51	Joint Parameter Estimation and Base-Calling for Pyrosequencing Systems. IEEE Transactions on Signal Processing, 2012, 60, 4376-4386.	5.3	2
52	End-to-End Optimization of High-Throughput DNA Sequencing. Journal of Computational Biology, 2016, 23, 789-800.	1.6	2
53	Recovery of sparse signals via Branch and Bound Least-Squares. , 2017, , .		2
54	Cyclic block coordinate minimization algorithms for DOA estimation in co-prime arrays. Signal Processing, 2018, 145, 272-284.	3.7	2

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55	On Submodularity of Quadratic Observation Selection in Constrained Networked Sensing Systems. , 2019, , .		2
56	Stochastic modeling of reaction kinetics in biosensors using the Fokker Planck equation. , 2009, , .		1
57	Model-based sequential base calling for Illumina sequencing. , 2010, , .		1
58	Distributed routing in networks using affinity propagation. , 2011, , .		1
59	A message-passing algorithm for spectrum access in cognitive radio relay networks. , 2011, , .		1
60	Adaptive experimental design for drug combinations. , 2012, , .		1
61	A message passing algorithm for reference-guided sequence assembly from high-throughput sequencing data. , 2012, , .		1
62	Estimating Parameters of Sampled Diffusion Processes in Affinity Biosensors. IEEE Transactions on Signal Processing, 2012, 60, 3228-3239.	5.3	1
63	Expected complexity of sphere decoding for sparse integer least-square problems. , 2013, , .		1
64	A message passing algorithm for haplotype assembly. , 2013, , .		1
65	Nonnegative gridless compressive sensing for co-prime arrays. , 2016, , .		1
66	Binary matrix completion with performance guarantees for single individual haplotyping. , 2017, , .		1
67	Matrix Completion and Performance Guarantees for Single Individual Haplotyping. IEEE Transactions on Signal Processing, 2019, 67, 4782-4794.	5.3	1
68	Evolutionary Subspace Clustering: Discovering Structure in Self-expressive Time-series Data. , 2019, , .		1
69	A Map Framework for Support Recovery of Sparse Signals Using Orthogonal Least Squares. , 2019, , .		1
70	Weighted Subset Selection for Fast SVM Training. , 2019, , .		1
71	PEP analysis of SDP-based non-coherent signal detection. , 2007, , .		0
72	Further results on message-passing algorithms for motif finding. , 2010, , .		0

#	ARTICLE	IF	CITATIONS
73	Inferring parameters of gene regulatory networks via particle filtering. , 2010, , .		0
74	Optimal estimation in DNA microarrays via global optimization. , 2010, , .		0
75	Message-passing for base-calling in sequencing-by-synthesis systems. , 2011, , .		0
76	Sequential Monte Carlo method for parameter estimation in diffusion models of affinity-based biosensors. , 2011, , .		0
77	An MCMC algorithm for base calling in sequencing-by-synthesis. , 2011, , .		0
78	A sequential Monte Carlo base-calling method for next-generation dna sequencing. , 2011, , .		0
79	Base calling error rates in next-generation DNA sequencing. , 2012, , .		0
80	Deterministic sequential Monte Carlo for haplotype inference. , 2013, , .		0
81	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
82	Distributed self localization of sensors with poisson deployment using extended Kalman filter. , 2015, , .		0
83	Structurally-constrained gradient descent for matrix factorization in haplotype assembly problems. , 2016, , .		0
84	Sparse Tensor Decomposition for Haplotype Assembly of Diploids and Polyploids. , 2017, , .		0
85	A NOVEL SCHEME FOR SUPPORT IDENTIFICATION AND ITERATIVE SAMPLING OF BANDLIMITED GRAPH SIGNALS. , 2018, , .		0