

Byung-Jun Yoon

List of Publications by Year in descending order

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Version: 2024-02-01

113
papers

1,707
citations

361413

20
h-index

330143

37
g-index

120
all docs

120
docs citations

120
times ranked

1596
citing authors

#	ARTICLE	IF	CITATIONS
1	Deep graph representations embed network information for robust disease marker identification. <i>Bioinformatics</i> , 2022, 38, 1075-1086.	4.1	5
2	Robust importance sampling for error estimation in the context of optimal Bayesian transfer learning. <i>Patterns</i> , 2022, 3, 100428.	5.9	2
3	Protocol for condition-dependent metabolite yield prediction using the TRIMER pipeline. <i>STAR Protocols</i> , 2022, 3, 101184.	1.2	2
4	Synthetic data for design and evaluation of binary classifiers in the context of Bayesian transfer learning. <i>Data in Brief</i> , 2022, 42, 108113.	1.0	1
5	AI-enabled, implantable, multichannel wireless telemetry for photodynamic therapy. <i>Nature Communications</i> , 2022, 13, 2178.	12.8	14
6	MONACO: accurate biological network alignment through optimal neighborhood matching between focal nodes. <i>Bioinformatics</i> , 2021, 37, 1401-1410.	4.1	6
7	Optimal Experimental Design for Uncertain Systems Based on Coupled Differential Equations. <i>IEEE Access</i> , 2021, 9, 53804-53810.	4.2	6
8	Quantifying the Multi-Objective Cost of Uncertainty. <i>IEEE Access</i> , 2021, 9, 80351-80359.	4.2	5
9	Co-design Center for Exascale Machine Learning Technologies (ExaLearn). <i>International Journal of High Performance Computing Applications</i> , 2021, 35, 598-616.	3.7	6
10	TRIMER: Transcription Regulation Integrated with Metabolic Regulation. <i>IScience</i> , 2021, 24, 103218.	4.1	7
11	Accelerating Optimal Experimental Design for Robust Synchronization of Uncertain Kuramoto Oscillator Model Using Machine Learning. <i>IEEE Transactions on Signal Processing</i> , 2021, 69, 6473-6487.	5.3	3
12	AI-Enabled High-Throughput Wireless Telemetry for Effective Photodynamic Therapy. , 2021, , .		0
13	ClusterM: a scalable algorithm for computational prediction of conserved protein complexes across multiple protein interaction networks. <i>BMC Genomics</i> , 2020, 21, 615.	2.8	4
14	Model-Based Robust Filtering and Experimental Design for Stochastic Differential Equation Systems. <i>IEEE Transactions on Signal Processing</i> , 2020, 68, 3849-3859.	5.3	13
15	Selected Research Articles from the 2019 International Workshop on Computational Network Biology: Modeling, Analysis, and Control (CNB-MAC). <i>BMC Genomics</i> , 2020, 21, 584.	2.8	0
16	NAPAbench 2: A network synthesis algorithm for generating realistic protein-protein interaction (PPI) network families. <i>PLoS ONE</i> , 2020, 15, e0227598.	2.5	5
17	Machine Learning Enabled Adaptive Wireless Power Transmission System for Neuroscience Study. , 2020, , .		3
18	Network-Based RNA Structural Alignment Through Optimal Local Neighborhood Matching. , 2020, , .		0

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19	Selected research articles from the 2018 International Workshop on Computational Network Biology: Modeling, Analysis, and Control (CNB-MAC). BMC Bioinformatics, 2019, 20, 316.	2.6	1
20	RNAdetect: efficient computational detection of novel non-coding RNAs. Bioinformatics, 2019, 35, 1133-1141.	4.1	7
21	TOPAS: network-based structural alignment of RNA sequences. Bioinformatics, 2019, 35, 2941-2948.	4.1	7
22	Examining De Novo Transcriptome Assemblies via a Quality Assessment Pipeline. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 494-505.	3.0	4
23	Computational Prediction of Pathogenic Network Modules in <i>Fusarium verticillioides</i> . IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 506-515.	3.0	18
24	Comprehensive Updates in Network Synthesis Models to Create An Improved Benchmark for Network Alignment Algorithms. , 2018, , .		0
25	Characterizing co-expression networks underpinning maize stalk rot virulence in <i>Fusarium verticillioides</i> through computational subnetwork module analyses. Scientific Reports, 2018, 8, 8310.	3.3	14
26	Selected research articles from the 2017 International Workshop on Computational Network Biology: Modeling, Analysis, and Control (CNB-MAC). BMC Bioinformatics, 2018, 19, 69.	2.6	1
27	Optimal hybrid sequencing and assembly: Feasibility conditions for accurate genome reconstruction and cost minimization strategy. Computational Biology and Chemistry, 2017, 69, 153-163.	2.3	3
28	SEQUOIA: significance enhanced network querying through context-sensitive random walk and minimization of network conductance. BMC Systems Biology, 2017, 11, 20.	3.0	6
29	Selected research articles from the 2016 International Workshop on Computational Network Biology: Modeling, Analysis, and Control (CNB-MAC). BMC Bioinformatics, 2017, 18, 159.	2.6	2
30	CUFID-query: accurate network querying through random walk based network flow estimation. BMC Bioinformatics, 2017, 18, 500.	2.6	1
31	CNB-MAC'17. , 2017, , .		0
32	Effective computational detection of piRNAs using n-gram models and support vector machine. BMC Bioinformatics, 2017, 18, 517.	2.6	7
33	SEQUOIA. , 2016, , .		0
34	Co-segmentation of multiple images through random walk on graphs. , 2016, , .		2
35	Incorporating topological information for predicting robust cancer subnetwork markers in human protein-protein interaction network. BMC Bioinformatics, 2016, 17, 351.	2.6	15
36	Effective comparative analysis of protein-protein interaction networks by measuring the steady-state network flow using a Markov model. BMC Bioinformatics, 2016, 17, 395.	2.6	14

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37	Computational identification of genetic subnetwork modules associated with maize defense response to <i>Fusarium verticillioides</i> . <i>BMC Bioinformatics</i> , 2015, 16, S12.	2.6	13
38	Efficient experimental design for uncertainty reduction in gene regulatory networks. <i>BMC Bioinformatics</i> , 2015, 16, S2.	2.6	24
39	Effective Estimation of Node-to-Node Correspondence Between Different Graphs. <i>IEEE Signal Processing Letters</i> , 2015, 22, 661-665.	3.6	7
40	Optimal Experimental Design for Gene Regulatory Networks in the Presence of Uncertainty. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015, 12, 938-950.	3.0	53
41	Accurate multiple network alignment through context-sensitive random walk. <i>BMC Systems Biology</i> , 2015, 9, S7.	3.0	18
42	Discrete optimal Bayesian classification with error-conditioned sequential sampling. <i>Pattern Recognition</i> , 2015, 48, 3766-3782.	8.1	22
43	Simultaneous identification of robust synergistic subnetwork markers for effective cancer prognosis. <i>Eurasip Journal on Bioinformatics and Systems Biology</i> , 2014, 2014, 19.	1.4	2
44	Sequence alignment by passing messages. <i>BMC Genomics</i> , 2014, 15, S14.	2.8	2
45	Computationally efficient experimental design strategy for reducing gene network uncertainty. , 2014, , .		0
46	PicXAA: A Probabilistic Scheme for Finding the Maximum Expected Accuracy Alignment of Multiple Biological Sequences. <i>Methods in Molecular Biology</i> , 2014, 1079, 203-210.	0.9	0
47	Quantifying the Objective Cost of Uncertainty in Complex Dynamical Systems. <i>IEEE Transactions on Signal Processing</i> , 2013, 61, 2256-2266.	5.3	61
48	Finding robust subnetwork markers that improve cross-dataset performance of cancer classification. , 2013, , .		0
49	Designing experiments for optimal reduction of uncertainty in gene regulatory networks. , 2013, , .		1
50	Classifier design given an uncertainty class of feature distributions via regularized maximum likelihood and the incorporation of biological pathway knowledge in steady-state phenotype classification. <i>Pattern Recognition</i> , 2013, 46, 2783-2797.	8.1	9
51	SMETANA: Accurate and Scalable Algorithm for Probabilistic Alignment of Large-Scale Biological Networks. <i>PLoS ONE</i> , 2013, 8, e67995.	2.5	82
52	Identification of Robust Pathway Markers for Cancer through Rank-Based Pathway Activity Inference. <i>Advances in Bioinformatics</i> , 2013, 2013, 1-8.	5.7	17
53	RESQUE: Network reduction using semi-Markov random walk scores for efficient querying of biological networks. <i>Bioinformatics</i> , 2012, 28, 2129-2136.	4.1	20
54	Structural intervention of gene regulatory networks by general rank-k matrix perturbation. , 2012, , .		6

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55	Finding robust pathway markers for cancer classification. , 2012, , .		1
56	Fast DNA barcode generating algorithm using Radix Coding method. , 2012, , .		0
57	Comparative Analysis of Biological Networks: Hidden Markov model and Markov chain-based approach. IEEE Signal Processing Magazine, 2012, 29, 22-34.	5.6	23
58	Adaptive reference update (ARU) algorithm. A stochastic search algorithm for efficient optimization of multi-drug cocktails. BMC Genomics, 2012, 13, S12.	2.8	4
59	A Network Synthesis Model for Generating Protein Interaction Network Families. PLoS ONE, 2012, 7, e41474.	2.5	34
60	A Novel Low-Complexity HMM Similarity Measure. IEEE Signal Processing Letters, 2011, 18, 87-90.	3.6	28
61	Efficient combinatorial drug optimization through stochastic search. , 2011, , .		1
62	Uncertainty-based essentiality in gene regulatory networks. , 2011, , .		0
63	Probabilistic consistency transformation for multiple alignment of biological networks. , 2011, , .		1
64	Genomic Signal Processing. Eurasip Journal on Advances in Signal Processing, 2011, 2010, .	1.7	0
65	Enhanced stochastic optimization algorithm for finding effective multi-target therapeutics. BMC Bioinformatics, 2011, 12, S18.	2.6	23
66	Comparative analysis of protein interaction networks reveals that conserved pathways are susceptible to HIV-1 interception. BMC Bioinformatics, 2011, 12, S19.	2.6	6
67	PicXAA-R: Efficient structural alignment of multiple RNA sequences using a greedy approach. BMC Bioinformatics, 2011, 12, S38.	2.6	15
68	Enhancing the accuracy of HMM-based conserved pathway prediction using global correspondence scores. BMC Bioinformatics, 2011, 12, S6.	2.6	4
69	Probabilistic reconstruction of the tumor progression process in gene regulatory networks in the presence of uncertainty. BMC Bioinformatics, 2011, 12, S9.	2.6	10
70	Finding effective subnetwork markers for cancer by passing messages. , 2011, , .		0
71	Fast network querying algorithm for searching large-scale biological networks. , 2011, , .		8
72	Designing enhanced classifiers using prior process knowledge: Regularized maximum-likelihood. , 2011, , .		0

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73	Contour-based hidden Markov model to segment 2D ultrasound images. , 2011, , .		5
74	PicXAA-Web: a web-based platform for non-progressive maximum expected accuracy alignment of multiple biological sequences. Nucleic Acids Research, 2011, 39, W8-W12.	14.5	10
75	Identification of diagnostic subnetwork markers for cancer in human protein-protein interaction network. BMC Bioinformatics, 2010, 11, S8.	2.6	58
76	PicXAA: greedy probabilistic construction of maximum expected accuracy alignment of multiple sequences. Nucleic Acids Research, 2010, 38, 4917-4928.	14.5	41
77	Shape matching based on graph alignment using hidden Markov models. , 2010, , .		2
78	Identifying reliable subnetwork markers in protein-protein interaction network for classification of breast cancer metastasis. , 2010, , .		1
79	Accurate and Reliable Cancer Classification Based on Probabilistic Inference of Pathway Activity. PLoS ONE, 2009, 4, e8161.	2.5	111
80	Simple alignment constraints for efficient alignment of RNA sequences using family-specific models. , 2009, , .		0
81	Efficient Alignment of RNAs with Pseudoknots Using Sequence Alignment Constraints. Eurasip Journal on Bioinformatics and Systems Biology, 2009, 2009, 1-13.	1.4	3
82	Identification of differentially expressed miRNAs in chicken lung and trachea with avian influenza virus infection by a deep sequencing approach. BMC Genomics, 2009, 10, 512.	2.8	113
83	Querying Pathways in Protein Interaction Networks Based on Hidden Markov Models. Journal of Computational Biology, 2009, 16, 145-157.	1.6	27
84	Hidden Markov Models and their Applications in Biological Sequence Analysis. Current Genomics, 2009, 10, 402-415.	1.6	252
85	Effective Identification of Conserved Pathways in Biological Networks Using Hidden Markov Models. PLoS ONE, 2009, 4, e8070.	2.5	24
86	Structural Alignment of RNAs Using Profile-csHMMs and Its Application to RNA homology Search: Overview and New Results. IEEE Transactions on Circuits and Systems Part 1: Regular Papers, 2009, , .	0.1	0
87	Fast Structural Alignment of RNAs by Optimizing the Adjoining Order of Profile-csHMMs. IEEE Journal on Selected Topics in Signal Processing, 2008, 2, 400-411.	10.8	3
88	Effective annotation of noncoding RNA families using profile context-sensitive HMMs. , 2008, , .		1
89	Structural Alignment of RNAs Using Profile-csHMMs and Its Application to RNA Homology Search: Overview and New Results. IEEE Transactions on Automatic Control, 2008, 53, 10-25.	5.7	12
90	Coding Overcomplete Representations of Audio Using the MCLT. Proceedings of the Data Compression Conference, 2008, , .	0.0	5

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91	A simple method for finding structurally similar RNAs using two-dimensional discrete convolution. , 2008, , .		0
92	Robust Adaptive Beamforming Algorithm using Instantaneous Direction of Arrival with Enhanced Noise Suppression Capability. , 2007, , .		15
93	Fast Search of Sequences with Complex Symbol Correlations using Profile Context-Sensitive HMMS and Pre-Screening Filters. , 2007, , .		6
94	Fast Structural Similarity Search of Noncoding RNAs Based on Matched Filtering of Stem Patterns. Conference Record of the Asilomar Conference on Signals, Systems and Computers, 2007, , .	0.0	3
95	Computational identification and analysis of noncoding RNAs - Unearthing the buried treasures in the genome. IEEE Signal Processing Magazine, 2007, 24, 64-74.	5.6	20
96	Modeling and identification of alternative folding in regulatory RNAs using context-sensitive HMMS. , 2006, , .		1
97	Context-Sensitive Hidden Markov Models for Modeling Long-Range Dependencies in Symbol Sequences. IEEE Transactions on Signal Processing, 2006, 54, 4169-4184.	5.3	21
98	A practical approach for the design of nonuniform lapped transforms. IEEE Signal Processing Letters, 2006, 13, 469-472.	3.6	1
99	An overview of the role of context-sensitive HMMS in the prediction of NCRNA genes. , 2005, , .		2
100	A multirate DSP model for estimation of discrete probability density functions. IEEE Transactions on Signal Processing, 2005, 53, 252-264.	5.3	9
101	The role of signal-processing concepts in genomics and proteomics. Journal of the Franklin Institute, 2004, 341, 111-135.	3.4	135
102	Discrete probability density estimation using multirate DSP models. , 2003, , .		1
103	Digital filters for gene prediction applications. , 2002, , .		64
104	Discrete probability density estimation using multirate DSP models. , 0, , .		4
105	Improved estimation of discrete probability density functions using multirate models. , 0, , .		5
106	Identification of CPG islands using a bank of IIR lowpass filters. , 0, , .		4
107	Discrete pdf estimation in the presence of noise. , 0, , .		2
108	HMM with auxiliary memory: a new tool for modeling RNA secondary structures. , 0, , .		11

#	ARTICLE	IF	CITATIONS
109	RNA secondary structure prediction using context-sensitive hidden markov models. , 0, , .		10
110	Wavelet-based denoising by customized thresholding. , 0, , .		25
111	Optimal Alignment Algorithm for Context-Sensitive Hidden Markov Models. , 0, , .		3
112	Profile Context-Sensitive HMMs for Probabilistic Modeling of Sequences With Complex Correlations. , 0, , .		8
113	Inference of gene regulatory networks: validation and uncertainty. , 0, , 337-364.		0