Sungroh Yoon

List of Publications by Year
in descending order

106 papers	4,028 citations	201674 27 h-index	149698 56 g-index
109 all docs	109 docs citations	109 times ranked	5050 citing authors

#	ARTICLE	IF	CITATIONS
1	PixelSteganalysis: Pixel-Wise Hidden Information Removal With Low Visual Degradation. IEEE Transactions on Dependable and Secure Computing, 2023, 20, 331-342.	5.4	5
2	Imbalanced Data Classification via Cooperative Interaction Between Classifier and Generator. IEEE Transactions on Neural Networks and Learning Systems, 2022, 33, 3343-3356.	11.3	9
3	TargetNet: functional microRNA target prediction with deep neural networks. Bioinformatics, 2022, 38, 671-677.	4.1	12
4	Prediction of clinically significant prostate cancer using polygenic risk models in Asians. Investigative and Clinical Urology, 2022, 63, 42.	2.0	6
5	Flexible Dual-Branched Message-Passing Neural Network for a Molecular Property Prediction. ACS Omega, 2022, 7, 4234-4244.	3.5	7
6	Data Embedding Scheme for Efficient Program Behavior Modeling With Neural Networks. IEEE Transactions on Emerging Topics in Computational Intelligence, 2022, 6, 982-993.	4.9	0
7	65â€2: A Light and Fast Branched Neural Network using Perceptual Optimization for Highâ€Quality Visual Restoration of UDC images. Digest of Technical Papers SID International Symposium, 2022, 53, 861-864.	0.3	1
8	MUGAN: multi-GPU accelerated AmpliconNoise server for rapid microbial diversity assessment. Bioinformatics, 2021, 37, 1562-1570.	4.1	1
9	Single-image deblurring with neural networks: A comparative survey. Computer Vision and Image Understanding, 2021, 203, 103134.	4.7	47
10	Feature Concentration for Supervised and Semisupervised Learning With Unbalanced Datasets in Visual Inspection. IEEE Transactions on Industrial Electronics, 2021, 68, 7620-7630.	7.9	8
11	Predicting the efficiency of prime editing guide RNAs in human cells. Nature Biotechnology, 2021, 39, 198-206.	17.5	160
12	DNA Privacy: Analyzing Malicious DNA Sequences using Deep Neural Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, PP, 1-1.	3.0	4
13	Towards Fast and Accurate Object Detection in Bio-Inspired Spiking Neural Networks Through Bayesian Optimization. IEEE Access, 2021, 9, 2633-2643.	4.2	11
14	Learn2Evade: Learning-Based Generative Model for Evading PDF Malware Classifiers. IEEE Transactions on Artificial Intelligence, 2021, 2, 299-313.	4.7	8
15	Gradient Masking of Label Smoothing in Adversarial Robustness. IEEE Access, 2021, 9, 6453-6464.	4.2	8
16	Memory-Augmented Neural Networks on FPGA for Real-Time and Energy-Efficient Question Answering. IEEE Transactions on Very Large Scale Integration (VLSI) Systems, 2021, 29, 162-175.	3.1	2
17	Pre-Training of Deep Bidirectional Protein Sequence Representations With Structural Information. IEEE Access, 2021, 9, 123912-123926.	4.2	20
18	Recording of elapsed time and temporal information about biological events using Cas9. Cell, 2021, 184, 1047-1063.e23.	28.9	29

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19	Protein transfer learning improves identification of heat shock protein families. PLoS ONE, 2021, 16, e0251865.	2.5	11
20	Learned Embeddings from Deep Learning to Visualize and Predict Protein Sets. Current Protocols, 2021, 1, e113.	2.9	61
21	Compensating Nonuniform OLED Pixel Brightness in a Vertical Blanking Interval by Learning TFT Characteristics. IEEE Transactions on Electron Devices, 2021, 68, 3396-3402.	3.0	2
22	Accelerating Neural Architecture Search via Proxy Data. , 2021, , .		3
23	Generation of a more efficient prime editor 2 by addition of the Rad51 DNA-binding domain. Nature Communications, 2021, 12, 5617.	12.8	47
24	Patch SVDD: Patch-Level SVDD for Anomaly Detection and Segmentation. Lecture Notes in Computer Science, 2021, , 375-390.	1.3	72
25	Deep Learning for Anomaly Detection in Time-Series Data: Review, Analysis, and Guidelines. IEEE Access, 2021, 9, 120043-120065.	4.2	137
26	NASCUP: Nucleic Acid Sequence Classification by Universal Probability. IEEE Access, 2021, 9, 162779-162791.	4.2	0
27	How Generative Adversarial Networks and Their Variants Work. ACM Computing Surveys, 2020, 52, 1-43.	23.0	185
28	Development and Validation of a Next-Generation Sequencing–Based Multigene Assay to Predict the Prognosis of Estrogen Receptor–Positive, HER2-Negative Breast Cancer. Clinical Cancer Research, 2020, 26, 6513-6522.	7.0	6
29	60â€¢2: Selfâ€supervised Perceptual Motion Deblurring using a Conditional Generative Neural Network Guided by Optical Flow. Digest of Technical Papers SID International Symposium, 2020, 51, 893-896.	0.3	0
30	Adversarial Vertex Mixup: Toward Better Adversarially Robust Generalization. , 2020, , .		45
31	T2FSNN: Deep Spiking Neural Networks with Time-to-first-spike Coding. , 2020, , .		51
32	Energy-aware Placement for SRAM-NVM Hybrid FPGAs. , 2020, , .		0
33	Prediction of the sequence-specific cleavage activity of Cas9 variants. Nature Biotechnology, 2020, 38, 1328-1336.	17.5	133
34	The message passing neural networks for chemical property prediction on SMILES. Methods, 2020, 179, 65-72.	3.8	29
35	Sequence-specific prediction of the efficiencies of adenine and cytosine base editors. Nature Biotechnology, 2020, 38, 1037-1043.	17.5	73
36	High-throughput analysis of the activities of xCas9, SpCas9-NG and SpCas9 at matched and mismatched target sequences in human cells. Nature Biomedical Engineering, 2020, 4, 111-124.	22.5	98

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37	Anomaly Detection by Learning Dynamics From a Graph. IEEE Access, 2020, 8, 64356-64365.	4.2	5
38	Interpretation of NLP models through input marginalization. , 2020, , .		14
39	End-to-End Representation Learning for Chemical-Chemical Interaction Prediction. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1436-1447.	3.0	14
40	Pediatric Sleep Stage Classification Using Multi-Domain Hybrid Neural Networks. IEEE Access, 2019, 7, 96495-96505.	4.2	17
41	Energy-Efficient Inference Accelerator for Memory-Augmented Neural Networks on an FPGA. , 2019, , .		4
42	Fast and Efficient Information Transmission with Burst Spikes in Deep Spiking Neural Networks. , 2019, , .		52
43	SpCas9 activity prediction by DeepSpCas9, a deep learning–based model with high generalization performance. Science Advances, 2019, 5, eaax9249.	10.3	130
44	Comprehensive ensemble in QSAR prediction for drug discovery. BMC Bioinformatics, 2019, 20, 521.	2.6	104
45	Learning-Based Instantaneous Drowsiness Detection Using Wired and Wireless Electroencephalography. IEEE Access, 2019, 7, 146390-146402.	4.2	14
46	PuVAE: A Variational Autoencoder to Purify Adversarial Examples. IEEE Access, 2019, 7, 126582-126593.	4.2	36
47	Electroencephalographic Resting-State Functional Connectivity of Benign Epilepsy with		

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55	Deep learning based low-cost high-accuracy diagnostic framework for dementia using comprehensive neuropsychological assessment profiles. BMC Geriatrics, 2018, 18, 234.	2.7	18
56	XGBoost-Based Instantaneous Drowsiness Detection Framework Using Multitaper Spectral Information of Electroencephalography. , 2018, , .		6
57	CloudSocket: Fine-Grained Power Sensing System for Datacenters. IEEE Access, 2018, 6, 49601-49610.	4.2	3
58	LncRNAnet: long non-coding RNA identification using deep learning. Bioinformatics, 2018, 34, 3889-3897.	4.1	80
59	TensorLightning: A Traffic-Efficient Distributed Deep Learning on Commodity Spark Clusters. IEEE Access, 2018, 6, 27671-27680.	4.2	5
60	Deep learning in bioinformatics. Briefings in Bioinformatics, 2017, 18, bbw068.	6.5	865
61	Large-Scale Structured Sparsity via Parallel Fused Lasso on Multiple GPUs. Journal of Computational and Graphical Statistics, 2017, 26, 851-864.	1.7	7
62	An effective pre-store/pre-load method exploiting intra-request idle time of NAND flash-based storage devices. Microprocessors and Microsystems, 2017, 50, 222-236.	2.8	1
63	Machine learning-based identification of endogenous cellular microRNA sponges against viral microRNAs. Methods, 2017, 129, 33-40.	3.8	3
64	NC-link: A New Linkage Method for Efficient Hierarchical Clustering of Large-Scale Data. IEEE Access, 2017, , 1-1.	4.2	9
65	Machine learning methods and systems for data-driven discovery in biomedical informatics. Methods, 2017, 129, 1-2.	3.8	1
66	Prediction of pathologic femoral fractures in patients with lung cancer using machine learning algorithms: Comparison of computed tomography-based radiological features with clinical features versus without clinical features. Journal of Orthopaedic Surgery, 2017, 25, 230949901771624.	1.0	21
67	Large-scale machine learning of media outlets for understanding public reactions to nation-wide viral infection outbreaks. Methods, 2017, 129, 50-59.	3.8	43
68	DeepCCI. , 2017, , .		30
69	Development and External Validation of the Korean Prostate Cancer Risk Calculator for High-Grade Prostate Cancer: Comparison with Two Western Risk Calculators in an Asian Cohort. PLoS ONE, 2017, 12, e0168917.	2.5	7
70	DUDE-Seq: Fast, flexible, and robust denoising for targeted amplicon sequencing. PLoS ONE, 2017, 12, e0181463.	2.5	47
71	Exome-based genome-wide association study and risk assessment using genetic risk score to prostate cancer in the Korean population. Oncotarget, 2017, 8, 43934-43943.	1.8	7
72	Genetic risk score to predict biochemical recurrence after radical prostatectomy in prostate cancer: prospective cohort study. Oncotarget, 2017, 8, 75979-75988.	1.8	6

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73	A genetic variant in SLC28A3, rs56350726, is associated with progression to castration-resistant prostate cancer in a Korean population with metastatic prostate cancer. Oncotarget, 2017, 8, 96893-96902.	1.8	4
74	deepTarget. , 2016, , .		66
75	Biometric Authentication Using Noisy Electrocardiograms Acquired by Mobile Sensors. IEEE Access, 2016, 4, 1266-1273.	4.2	86
76	CloudSocket: Smart grid platform for datacenters. , 2016, , .		2
77	Regularization and Kernelization of the Maximin Correlation Approach. IEEE Access, 2016, 4, 1385-1392.	4.2	5
78	Mining internet media for monitoring changes of public emotions about infectious diseases. , 2016, , .		3
79	Exploiting Compression-Induced Internal Fragmentation for Power-Off Recovery in SSD. IEEE Transactions on Computers, 2016, 65, 1720-1733.	3.4	11
80	NAND Flash Memory With Multiple Page Sizes for High-Performance Storage Devices. IEEE Transactions on Very Large Scale Integration (VLSI) Systems, 2016, 24, 764-768.	3.1	7
81	Methodology for Big Data Analysis Using Data from National Health Insurance Service: Preliminary Methodologic Study and Review about the Relationship between Sinus Surgery and Asthma. Journal of Rhinology, 2015, 22, 28.	0.1	3
82	A clinicogenetic model to predict lymph node invasion by use of genome-based biomarkers from exome arrays in prostate cancer patients. Korean Journal of Urology, 2015, 56, 109.	1.2	3
83	Computational prediction of competitive endogenous RNA. , 2015, , .		0
84	Measuring Large-Scale Dynamic Graph Similarity by RICom: RWR with Intergraph Compression. , 2015, , .		2
85	Multi-Threaded Hierarchical Clustering by Parallel Nearest-Neighbor Chaining. IEEE Transactions on Parallel and Distributed Systems, 2015, 26, 2534-2548.	5.6	13
86	High-Dimensional Fused Lasso Regression Using Majorization–Minimization and Parallel Processing. Journal of Computational and Graphical Statistics, 2015, 24, 121-153.	1.7	21
87	Genome-wide detection of allelic genetic variation to predict biochemical recurrence after radical prostatectomy among prostate cancer patients using an exome SNP chip. Journal of Cancer Research and Clinical Oncology, 2015, 141, 1493-1501.	2.5	1
88	Genome-wide detection of allelic genetic variation to predict advanced-stage prostate cancer after radical prostatectomy using an exome SNP chip. Urologic Oncology: Seminars and Original Investigations, 2015, 33, 385.e7-385.e13.	1.6	0
89	IO Workload Characterization Revisited: A Data-Mining Approach. IEEE Transactions on Computers, 2014, 63, 3026-3038.	3.4	28
90	Ensemble learning can significantly improve human microRNA target prediction. Methods, 2014, 69, 220-229.	3.8	18

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91	Ensemble learning for robust prediction of microRNA-mRNA interactions. , 2014, , .		1
92	Design of a bitmap-based QoS-aware memory controller for a packet memory. IEICE Electronics Express, 2014, 11, 20130983-20130983.	0.8	0
93	CASPER: context-aware scheme for paired-end reads from high-throughput amplicon sequencing. BMC Bioinformatics, 2014, 15, S10.	2.6	56
94	The Use of Exome Genotyping to Predict Pathological Gleason Score Upgrade after Radical Prostatectomy in Low-Risk Prostate Cancer Patients. PLoS ONE, 2014, 9, e104146.	2.5	6
95	GPU-based acceleration of an RNA tertiary structure prediction algorithm. Computers in Biology and Medicine, 2013, 43, 1011-1022.	7.0	10
96	Entropy-Based Analysis and Bioinformatics-Inspired Integration of Global Economic Information Transfer. PLoS ONE, 2013, 8, e51986.	2.5	20
97	Rapid and Robust Denoising of Pyrosequenced Amplicons for Metagenomics. , 2012, , .		1
98	Application-Support Particle Filter for Dynamic Voltage Scaling of Multimedia Applications. IEEE Transactions on Computers, 2012, 61, 1256-1269.	3.4	11
99	Got target?: computational methods for microRNA target prediction and their extension. Experimental and Molecular Medicine, 2010, 42, 233.	7.7	156
100	Clustering protein environments for function prediction: finding PROSITE motifs in 3D. BMC Bioinformatics, 2007, 8, S10.	2.6	29
101	Co-clustering: A Versatile Tool for Data Analysis in Biomedical Informatics. IEEE Transactions on Information Technology in Biomedicine, 2007, 11, 493-494.	3.2	13
102	Computational identification of microRNAs and their targets. Birth Defects Research Part C: Embryo Today Reviews, 2006, 78, 118-128.	3.6	59
103	Exploiting Binary Abstractions in Deciphering Gene Interactions. Annual International Conference of the IEEE Engineering in Medicine and Biology Society, 2006, , .	0.5	0
104	Prediction and Analysis of Human microRNA Regulatory Modules. , 2005, 2005, 4799-802.		6
105	Discovering Coherent Biclusters from Gene Expression Data Using Zero-Suppressed Binary Decision Diagrams. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2005, 2, 339-354.	3.0	50
106	Prediction of regulatory modules comprising microRNAs and target genes. Bioinformatics, 2005, 21, ii93-ii100.	4.1	109