Junhee Seok

List of Publications by Year
in descending order

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		933264	414303
51	4,240	10	32
papers	citations	h-index	g-index

52	52	52	7801
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Simulator acceleration and inverse design of fin field-effect transistors using machine learning. Scientific Reports, 2022, 12, 1140.	1.6	10
2	Privacy-preserving collaborative machine learning in biomedical applications. , 2022, , .		4
3	Non-Invasive Diagnosis for Acute Rejection Using Urinary mRNA Signature Reflecting Allograft Status in Kidney Transplantation. Frontiers in Immunology, 2021, 12, 656632.	2.2	6
4	Keyword Extraction in Economics Literatures using Natural Language Processing. , 2021, , .		4
5	Estimation with Uncertainty via Conditional Generative Adversarial Networks. Sensors, 2021, 21, 6194.	2.1	9
6	Urinary mRNA Signatures as Predictors of Renal Function Decline in Patients With Biopsy-Proven Diabetic Kidney Disease. Frontiers in Endocrinology, 2021, 12, 774436.	1.5	4
7	Portfolio management via two-stage deep learning with a joint cost. Expert Systems With Applications, 2020, 143, 113041.	4.4	27
8	Validation of deep learning natural language processing algorithm for keyword extraction from pathology reports in electronic health records. Scientific Reports, 2020, 10, 20265.	1.6	23
9	Long Term Traffic Prediction in Highway Using Parallel CNN. , 2020, , .		2
10	Phenotype and molecular signature of CD8+ÂT cell subsets in T cell- mediated rejections after kidney transplantation. PLoS ONE, 2020, 15, e0234323.	1.1	5
11	Improved recurrent generative adversarial networks with regularization techniques and a controllable framework. Information Sciences, 2020, 538, 428-443.	4.0	7
12	Simulation acceleration for transmittance of electromagnetic waves in 2D slit arrays using deep learning. Scientific Reports, 2020, 10, 10535.	1.6	7
13	A Survey of Missing Data Imputation Using Generative Adversarial Networks. , 2020, , .		23
14	Serum biomarkers from cell-based assays for AhRL and MIS strongly predicted the future development of diabetes in a large community-based prospective study in Korea. Scientific Reports, 2020, 10, 6339.	1.6	9
15	Network estimation for censored time-to-event data for multiple events based on multivariate survival analysis. PLoS ONE, 2020, 15, e0239760.	1.1	4
16	Clinical Implication of Concordant or Discordant Genomic Profiling between Primary and Matched Metastatic Tissues in Patients with Colorectal Cancer. Cancer Research and Treatment, 2020, 52, 764-778.	1.3	6
17	Title is missing!. , 2020, 15, e0234323.		0
18	Title is missing!. , 2020, 15, e0234323.		0

#	Article	IF	Citations
19	Title is missing!. , 2020, 15, e0234323.		0
20	Title is missing!. , 2020, 15, e0234323.		0
21	The Properties of mode prediction using mean root error for regularization. , 2019, , .		2
22	Stock Price Prediction Through the Sentimental Analysis of News Articles. , 2019, , .		15
23	Controllable Generative Adversarial Network. IEEE Access, 2019, 7, 28158-28169.	2.6	45
24	Prediction of survival risks with adjusted gene expression through risk-gene networks. Bioinformatics, 2019, 35, 4898-4906.	1.8	1
25	Stock Prices Prediction using the Title of Newspaper Articles with Korean Natural Language Processing. , 2019, , .		17
26	Vocabulary Domain Prediction for Pathological Report Analysis Using ICD-O3. , 2019, , .		1
27	Experimental Evaluation of Source Location Privacy Routing Schemes and Energy Consumption Performance. , 2019, , .		0
28	Regression-Based Network Estimation for High-Dimensional Genetic Data. Journal of Computational Biology, 2019, 26, 336-349.	0.8	1
29	GAIT: Gene expression Analysis for Interval Time. Bioinformatics, 2018, 34, 2305-2307.	1.8	5
30	Coordinate-RNN for error correction on numerical weather prediction. , 2018, , .		2
31	The estimation of probability distribution for factor variables with many categorical values. PLoS ONE, 2018, 13, e0202547.	1.1	2
32	Rank Prediction for Portfolio Management Using Artificial Neural Networks. , 2018, , .		0
33	Indoor Semantic Segmentation for Robot Navigating on Mobile. , 2018, , .		28
34	A Comparison of Two-Stage Approaches Based on Penalized Regression for Estimating Gene Networks. Journal of Computational Biology, 2017, 24, 709-720.	0.8	2
35	Estimation of directed subnetworks in ultra-high dimensional data for gene network problems. Statistics and Its Interface, 2017, 10, 657-676.	0.2	1
36	Prediction of information propagation in a drone network by using machine learning. , 2016, , .		9

#	Article	IF	Citations
37	Information propagation modeling in a drone network using disease epidemic models. , 2016, , .		1
38	Mutual Information between Discrete Variables with Many Categories using Recursive Adaptive Partitioning. Scientific Reports, 2015, 5, 10981.	1.6	8
39	A Hybrid Approach of Gene Sets and Single Genes for the Prediction of Survival Risks with Gene Expression Data. PLoS ONE, 2015, 10, e0122103.	1.1	3
40	RASA: Robust Alternative Splicing Analysis for Human Transcriptome Arrays. Scientific Reports, 2015, 5, 11917.	1.6	10
41	Mice are not men. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E345.	3.3	102
42	Evidence-Based Translation for the Genomic Responses of Murine Models for the Study of Human Immunity. PLoS ONE, 2015, 10, e0118017.	1.1	10
43	Density estimation on multivariate censored data with optional Polya tree. Biostatistics, 2014, 15, 182-195.	0.9	7
44	Genomic responses in mouse models poorly mimic human inflammatory diseases. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 3507-3512.	3.3	2,518
45	Coding SNPs as intrinsic markers for sample tracking in large-scale transcriptome studies. BioTechniques, 2012, 52, 386-8.	0.8	3
46	Knowledge-Based Reconstruction of mRNA Transcripts with Short Sequencing Reads for Transcriptome Research. PLoS ONE, 2012, 7, e31440.	1.1	7
47	Distinctive Responsiveness to Stromal Signaling Accompanies Histologic Grade Programming of Cancer Cells. PLoS ONE, 2011, 6, e20016.	1.1	10
48	A genomic storm in critically injured humans. Journal of Experimental Medicine, 2011, 208, 2581-2590.	4.2	1,040
49	Human transcriptome array for high-throughput clinical studies. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 3707-3712.	3.3	122
50	Using high-density exon arrays to profile gene expression in closely related species. Nucleic Acids Research, 2009, 37, e90-e90.	6.5	17
51	Bisphenol A Induces a Profile of Tumor Aggressiveness in High-Risk Cells from Breast Cancer Patients. Cancer Research, 2008, 68, 2076-2080.	0.4	101