Yung-Keun Kwon

List of Publications by Year
in descending order

32 papers	743 citations	623734 14 h-index	526287 27 g-index
32 all docs	32 docs citations	32 times ranked	649 citing authors

#	Article	IF	Citations
1	Quantitative analysis of robustness and fragility in biological networks based on feedback dynamics. Bioinformatics, 2008, 24, 987-994.	4.1	90
2	Coherent coupling of feedback loops: a design principle of cell signaling networks. Bioinformatics, 2008, 24, 1926-1932.	4.1	59
3	A novel mutual information-based Boolean network inference method from time-series gene expression data. PLoS ONE, 2017, 12, e0171097.	2.5	57
4	Boolean Dynamics of Biological Networks with Multiple Coupled Feedback Loops. Biophysical Journal, 2007, 92, 2975-2981.	0.5	56
5	Reduction of Complex Signaling Networks to a Representative Kernel. Science Signaling, 2011, 4, ra35.	3.6	54
6	GPEC: A Cytoscape plug-in for random walk-based gene prioritization and biomedical evidence collection. Computational Biology and Chemistry, 2012, 37, 17-23.	2.3	50
7	Neighbor-favoring weight reinforcement to improve random walk-based disease gene prioritization. Computational Biology and Chemistry, 2013, 44, 1-8.	2.3	50
8	Analysis of feedback loops and robustness in network evolution based on Boolean models. BMC Bioinformatics, 2007, 8, 430.	2.6	48
9	A coherent feedforward loop design principle to sustain robustness of biological networks. Bioinformatics, 2013, 29, 630-637.	4.1	38
10	The relationship between modularity and robustness in signalling networks. Journal of the Royal Society Interface, 2013, 10, 20130771.	3.4	31
11	NetDS: a Cytoscape plugin to analyze the robustness of dynamics and feedforward/feedback loop structures of biological networks. Bioinformatics, 2011, 27, 2767-2768.	4.1	29
12	PANET: A GPU-Based Tool for Fast Parallel Analysis of Robustness Dynamics and Feed-Forward/Feedback Loop Structures in Large-Scale Biological Networks. PLoS ONE, 2014, 9, e103010.	2.5	28
13	Investigations into the relationship between feedback loops and functional importance of a signal transduction network based on Boolean network modeling. BMC Bioinformatics, 2007, 8, 384.	2.6	19
14	The effects of feedback loops on disease comorbidity in human signaling networks. Bioinformatics, 2011, 27, 1113-1120.	4.1	18
15	Edge-based sensitivity analysis of signaling networks by using Boolean dynamics. Bioinformatics, 2016, 32, i763-i771.	4.1	11
16	A Data-Independent Genetic Algorithm Framework for Fault-Type Classification and Remaining Useful Life Prediction. Applied Sciences (Switzerland), 2020, 10, 368.	2.5	11
17	Dynamical Robustness against Multiple Mutations in Signaling Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2016, 13, 996-1002.	3.0	10
18	A novel constrained genetic algorithm-based Boolean network inference method from steady-state gene expression data. Bioinformatics, 2021, 37, i383-i391.	4.1	10

#	Article	IF	Citations
19	Hierarchical closeness efficiently predicts disease genes in a directed signaling network. Computational Biology and Chemistry, 2014, 53, 191-197.	2.3	9
20	MORO: a Cytoscape app for relationship analysis between modularity and robustness in large-scale biological networks. BMC Systems Biology, 2016, 10, 122.	3.0	8
21	A neuro-evolution approach to infer a Boolean network from time-series gene expressions. Bioinformatics, 2020, 36, i762-i769.	4.1	8
22	Towards the Identification of Disease Associated Protein Complexes. Procedia Computer Science, 2013, 23, 15-23.	2.0	7
23	Effective Boolean dynamics analysis to identify functionally important genes in large-scale signaling networks. BioSystems, 2015, 137, 64-72.	2.0	7
24	A hybrid system integrating a piecewise linear representation and a neural network for stock prediction. , 2011, , .		6
25	An Empirical Investigation on a Multiple Filters-Based Approach for Remaining Useful Life Prediction. Machines, 2018, 6, 35.	2.2	6
26	Properties of Boolean dynamics by node classification using feedback loops in a network. BMC Systems Biology, 2016, 10, 83.	3.0	5
27	Hierarchical closeness-based properties reveal cancer survivability and biomarker genes in molecular signaling networks. PLoS ONE, 2018, 13, e0199109.	2.5	5
28	RMut: R package for a Boolean sensitivity analysis against various types of mutations. PLoS ONE, 2019, 14, e0213736.	2.5	5
29	Construction and analysis of gene-gene dynamics influence networks based on a Boolean model. BMC Systems Biology, 2017, 11, 133.	3.0	4
30	Investigation on changes of modularity and robustness by edge-removal mutations in signaling networks. BMC Systems Biology, 2017, 11, 125.	3.0	3
31	Effects of ordered mutations on dynamics in signaling networks. BMC Medical Genomics, 2020, 13, 13.	1.5	1
32	P3-105: CORRELATION OF NOVEL PROTEOMIC ANALYTES WITH ALZHEIMER'S DISEASE BIOMARKERS IN CEREBROSPINAL FLUID FROM MILD SPORADIC ALZHEIMER'S DISEASE DEMENTIA PATIENTS. , 2014, 10, P666-P667.		0