

Yung-Keun Kwon

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/421167/publications.pdf>

Version: 2024-02-01

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	A novel constrained genetic algorithm-based Boolean network inference method from steady-state gene expression data. <i>Bioinformatics</i> , 2021, 37, i383-i391.	4.1	10
2	A Data-Independent Genetic Algorithm Framework for Fault-Type Classification and Remaining Useful Life Prediction. <i>Applied Sciences (Switzerland)</i> , 2020, 10, 368.	2.5	11
3	Effects of ordered mutations on dynamics in signaling networks. <i>BMC Medical Genomics</i> , 2020, 13, 13.	1.5	1
4	A neuro-evolution approach to infer a Boolean network from time-series gene expressions. <i>Bioinformatics</i> , 2020, 36, i762-i769.	4.1	8
5	RMut: R package for a Boolean sensitivity analysis against various types of mutations. <i>PLoS ONE</i> , 2019, 14, e0213736.	2.5	5
6	An Empirical Investigation on a Multiple Filters-Based Approach for Remaining Useful Life Prediction. <i>Machines</i> , 2018, 6, 35.	2.2	6
7	Hierarchical closeness-based properties reveal cancer survivability and biomarker genes in molecular signaling networks. <i>PLoS ONE</i> , 2018, 13, e0199109.	2.5	5
8	A novel mutual information-based Boolean network inference method from time-series gene expression data. <i>PLoS ONE</i> , 2017, 12, e0171097.	2.5	57
9	Construction and analysis of gene-gene dynamics influence networks based on a Boolean model. <i>BMC Systems Biology</i> , 2017, 11, 133.	3.0	4
10	Investigation on changes of modularity and robustness by edge-removal mutations in signaling networks. <i>BMC Systems Biology</i> , 2017, 11, 125.	3.0	3
11	Edge-based sensitivity analysis of signaling networks by using Boolean dynamics. <i>Bioinformatics</i> , 2016, 32, i763-i771.	4.1	11
12	Properties of Boolean dynamics by node classification using feedback loops in a network. <i>BMC Systems Biology</i> , 2016, 10, 83.	3.0	5
13	MORO: a Cytoscape app for relationship analysis between modularity and robustness in large-scale biological networks. <i>BMC Systems Biology</i> , 2016, 10, 122.	3.0	8
14	Dynamical Robustness against Multiple Mutations in Signaling Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2016, 13, 996-1002.	3.0	10
15	Effective Boolean dynamics analysis to identify functionally important genes in large-scale signaling networks. <i>BioSystems</i> , 2015, 137, 64-72.	2.0	7
16	PANET: A GPU-Based Tool for Fast Parallel Analysis of Robustness Dynamics and Feed-Forward/Feedback Loop Structures in Large-Scale Biological Networks. <i>PLoS ONE</i> , 2014, 9, e103010.	2.5	28
17	Hierarchical closeness efficiently predicts disease genes in a directed signaling network. <i>Computational Biology and Chemistry</i> , 2014, 53, 191-197.	2.3	9
18	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

#	ARTICLE	IF	CITATIONS
19	Neighbor-favoring weight reinforcement to improve random walk-based disease gene prioritization. Computational Biology and Chemistry, 2013, 44, 1-8.	2.3	50
20	Towards the Identification of Disease Associated Protein Complexes. Procedia Computer Science, 2013, 23, 15-23.	2.0	7
21	A coherent feedforward loop design principle to sustain robustness of biological networks. Bioinformatics, 2013, 29, 630-637.	4.1	38
22	The relationship between modularity and robustness in signalling networks. Journal of the Royal Society Interface, 2013, 10, 20130771.	3.4	31
23	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
24	A hybrid system integrating a piecewise linear representation and a neural network for stock prediction. , 2011, , .		6
25	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
26	Reduction of Complex Signaling Networks to a Representative Kernel. Science Signaling, 2011, 4, ra35.	3.6	54
27	The effects of feedback loops on disease comorbidity in human signaling networks. Bioinformatics, 2011, 27, 1113-1120.	4.1	18
28	Coherent coupling of feedback loops: a design principle of cell signaling networks. Bioinformatics, 2008, 24, 1926-1932.	4.1	59
29	Quantitative analysis of robustness and fragility in biological networks based on feedback dynamics. Bioinformatics, 2008, 24, 987-994.	4.1	90
30	Boolean Dynamics of Biological Networks with Multiple Coupled Feedback Loops. Biophysical Journal, 2007, 92, 2975-2981.	0.5	56
31	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
32	Analysis of feedback loops and robustness in network evolution based on Boolean models. BMC Bioinformatics, 2007, 8, 430.	2.6	48