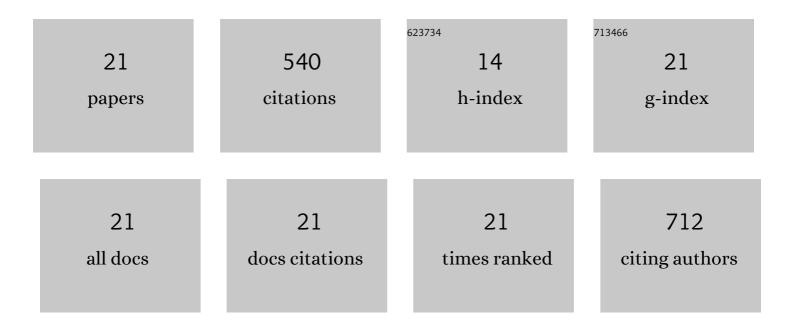
Xia Jiang

List of Publications by Year in descending order

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YIA HANC

#	Article	IF	CITATIONS
1	Machine Learning to Discern Interactive Clusters of Risk Factors for Late Recurrence of Metastatic Breast Cancer. Cancers, 2022, 14, 253.	3.7	3
2	Leveraging Bayesian networks and information theory to learn risk factors for breast cancer metastasis. BMC Bioinformatics, 2020, 21, 298.	2.6	4
3	A clinical decision support system learned from data to personalize treatment recommendations towards preventing breast cancer metastasis. PLoS ONE, 2019, 14, e0213292.	2.5	32
4	Using natural language processing and machine learning to identify breast cancer local recurrence. BMC Bioinformatics, 2018, 19, 498.	2.6	60
5	Conjugated equine estrogen and medroxyprogesterone acetate are associated with decreased risk of breast cancer relative to bioidentical hormone therapy and controls. PLoS ONE, 2018, 13, e0197064.	2.5	7
6	An algorithm for direct causal learning of influences on patient outcomes. Artificial Intelligence in Medicine, 2017, 75, 1-15.	6.5	9
7	Modeling miRNA-mRNA interactions that cause phenotypic abnormality in breast cancer patients. PLoS ONE, 2017, 12, e0182666.	2.5	27
8	Computational methods for ubiquitination site prediction using physicochemical properties of protein sequences. BMC Bioinformatics, 2016, 17, 116.	2.6	20
9	LEAP: Biomarker Inference Through Learning and Evaluating Association Patterns. Genetic Epidemiology, 2015, 39, 173-184.	1.3	11
10	Learning Predictive Interactions Using Information Gain and Bayesian Network Scoring. PLoS ONE, 2015, 10, e0143247.	2.5	18
11	Pan-cancer analysis of TCGA data reveals notable signaling pathways. BMC Cancer, 2015, 15, 516.	2.6	33
12	A novel artificial neural network method for biomedical prediction based on matrix pseudo-inversion. Journal of Biomedical Informatics, 2014, 48, 114-121.	4.3	27
13	Modeling the Altered Expression Levels of Genes on Signaling Pathways in Tumors as Causal Bayesian Networks. Cancer Informatics, 2014, 13, CIN.S13578.	1.9	14
14	Mining Pure, Strict Epistatic Interactions from High-Dimensional Datasets: Ameliorating the Curse of Dimensionality. PLoS ONE, 2012, 7, e46771.	2.5	14
15	Learning genetic epistasis using Bayesian network scoring criteria. BMC Bioinformatics, 2011, 12, 89.	2.6	79
16	A Bayesian Method for Evaluating and Discovering Disease Loci Associations. PLoS ONE, 2011, 6, e22075.	2.5	27
17	A real-time temporal Bayesian architecture for event surveillance and its application to patient-specific multiple disease outbreak detection. Data Mining and Knowledge Discovery, 2010, 20, 328-360.	3.7	14
18	ldentifying genetic interactions in genomeâ€wide data using Bayesian networks. Genetic Epidemiology, 2010, 34, 575-581.	1.3	56

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#	Article	IF	CITATIONS
19	A Bayesian spatio-temporal method for disease outbreak detection. Journal of the American Medical Informatics Association: JAMIA, 2010, 17, 462-471.	4.4	38
20	A fast algorithm for learning epistatic genomic relationships. AMIA Annual Symposium proceedings, 2010, 2010, 341-5.	0.2	19
21	Bayesian prediction of an epidemic curve. Journal of Biomedical Informatics, 2009, 42, 90-99.	4.3	28