

# Xia Jiang

## List of Publications by Year in descending order

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21  
papers

540  
citations

623734

14  
h-index

713466

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g-index

21  
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docs citations

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times ranked

712  
citing authors

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

#	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