Mohammad Shahrokh Esfahani

List of Publications by Year
in descending order

26 papers	1,791 citations	687363 13 h-index	752698 20 g-index
26 all docs	26 docs citations	26 times ranked	2780 citing authors

#	Article	IF	Citations
1	Early Detection of Molecular Residual Disease in Localized Lung Cancer by Circulating Tumor DNA Profiling. Cancer Discovery, 2017, 7, 1394-1403.	9.4	701
2	Distinct biological subtypes and patterns of genome evolution in lymphoma revealed by circulating tumor DNA. Science Translational Medicine, 2016, 8, 364ra155.	12.4	348
3	Circulating Tumor DNA Measurements As Early Outcome Predictors in Diffuse Large B-Cell Lymphoma. Journal of Clinical Oncology, 2018, 36, 2845-2853.	1.6	313
4	Effect of separate sampling on classification accuracy. Bioinformatics, 2014, 30, 242-250.	4.1	77
5	Inferring gene expression from cell-free DNA fragmentation profiles. Nature Biotechnology, 2022, 40, 585-597.	17.5	63
6	Intrinsically Bayesian Robust Kalman Filter: An Innovation Process Approach. IEEE Transactions on Signal Processing, 2017, 65, 2531-2546.	5.3	43
7	Incorporation of Biological Pathway Knowledge in the Construction of Priors for Optimal Bayesian Classification. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014, 11, 202-218.	3.0	38
8	Short Diagnosis-to-Treatment Interval Is Associated With Higher Circulating Tumor DNA Levels in Diffuse Large B-Cell Lymphoma. Journal of Clinical Oncology, 2021, 39, 2605-2616.	1.6	37
9	Incorporating biological prior knowledge for Bayesian learning via maximal knowledge-driven information priors. BMC Bioinformatics, 2017, 18, 552.	2.6	32
10	Optimal Bayesian Kalman Filtering With Prior Update. IEEE Transactions on Signal Processing, 2018, 66, 1982-1996.	5.3	26
11	Discrete optimal Bayesian classification with error-conditioned sequential sampling. Pattern Recognition, 2015, 48, 3766-3782.	8.1	22
12	An Optimization-Based Framework for the Transformation of Incomplete Biological Knowledge into a Probabilistic Structure and Its Application to the Utilization of Gene/Protein Signaling Pathways in Discrete Phenotype Classification. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 1304-1321.	3.0	15
13	Profiling of Circulating Tumor DNA for Noninvasive Disease Detection, Risk Stratification, and MRD Monitoring in Patients with CNS Lymphoma. Blood, 2021, 138, 6-6.	1.4	15
14	Circulating DNA for Molecular Response Prediction, Characterization of Resistance Mechanisms and Quantification of CAR T-Cells during Axicabtagene Ciloleucel Therapy. Blood, 2019, 134, 550-550.	1.4	13
15	Probabilistic reconstruction of the tumor progression process in gene regulatory networks in the presence of uncertainty. BMC Bioinformatics, 2011, 12, S9.	2.6	10
16	Classifier design given an uncertainty class of feature distributions via regularized maximum likelihood and the incorporation of biological pathway knowledge in steady-state phenotype classification. Pattern Recognition, 2013, 46, 2783-2797.	8.1	9
17	Towards Non-Invasive Classification of DLBCL Genetic Subtypes By Ctdna Profiling. Blood, 2019, 134, 551-551.	1.4	9
18	Evaluating upfront high-dose consolidation after R-CHOP for follicular lymphoma by clinical and genetic risk models. Blood Advances, 2020, 4, 4451-4462.	5.2	8

#	ARTICLE	IF	CITATIONS
19	An Atlas of Clinically-Distinct Tumor Cellular Ecosystems in Diffuse Large B Cell Lymphoma. Blood, 2019, 134, 655-655.	1.4	4
20	A Bayesian framework for robust Kalman filtering under uncertain noise statistics. , 2016, , .		3
21	An experimental design framework for Markovian gene regulatory networks under stationary control policy. BMC Systems Biology, 2018, 12, 137.	3.0	3
22	Inference of Nonlinear ODE-Based Gene Regulatory Networks via Intrinsically Bayesian Robust Kalman Filtering. , 2016, , .		1
23	Bayesian Kalman filtering in the presence of unknown noise statistics using factor graphs. , 2017, , .		1
24	Designing enhanced classifiers using prior process knowledge: Regularized maximum-likelihood. , 2011, , .		0
25	Short Diagnosis-to-Treatment Interval Is Associated with Higher Levels of Circulating Tumor DNA in Aggressive B-Cell Non-Hodgkin Lymphoma. Blood, 2019, 134, 491-491.	1.4	0
26	Noninvasive Cell-of-Origin Classification of Diffuse Large B-Cell Lymphoma Using Inferred Gene Expression from Cell-Free DNA Sequencing. Blood, 2021, 138, 37-37.	1.4	0