Xuejun Liu

List of Publications by Year in descending order

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XIIFUIN LUI

#	Article	IF	CITATIONS
1	A generative deep learning framework for airfoil flow field prediction with sparse data. Chinese Journal of Aeronautics, 2022, 35, 470-484.	5.3	16
2	Numerical investigation on keyhole collapsing and rebuilding behavior during pulsed laser beam welding of Ti6Al4V titanium alloy under various pulse frequencies. Applied Physics A: Materials Science and Processing, 2022, 128, 1.	2.3	7
3	A data-driven deep learning approach for predicting separation-induced transition of submarines. Physics of Fluids, 2022, 34, .	4.0	5
4	Numerical investigation on keyhole stability and weld pool dynamics during quasi-continuous laser beam welding of Ti6Al4V plate using constant and modulated high-frequency pulsed heat input. International Journal of Advanced Manufacturing Technology, 2022, 121, 229-247.	3.0	2
5	DAE-TPGM: A deep autoencoder network based on a two-part-gamma model for analyzing single-cell RNA-seq data. Computers in Biology and Medicine, 2022, 146, 105578.	7.0	1
6	Predicting pressure coefficients of wing surface based on the transfer of spatial dependency. AIP Advances, 2022, 12, 055225.	1.3	0
7	Detecting differential transcript usage across multiple conditions for RNA-seq data based on the smoothed LDA model. Frontiers of Computer Science, 2021, 15, 1.	2.4	2
8	Mapping RNA-seq reads to transcriptomes efficiently based on learning to hash method. Computers in Biology and Medicine, 2020, 116, 103539.	7.0	8
9	A deep learning approach for efficiently and accurately evaluating the flow field of supercritical airfoils. Computers and Fluids, 2020, 198, 104393.	2.5	76
10	Highâ€Voltage Chargingâ€Induced Strain, Heterogeneity, and Microâ€Cracks in Secondary Particles of a Nickelâ€Rich Layered Cathode Material. Advanced Functional Materials, 2019, 29, 1900247.	14.9	219
11	PBSeq: Modeling base-level bias to estimate gene and isoform expression for RNA-seq data. International Journal of Machine Learning and Cybernetics, 2017, 8, 1247-1258.	3.6	2
12	Improving RNA-Seq expression estimation by modeling isoform- and exon-specific read sequencing rate. BMC Bioinformatics, 2015, 16, 332.	2.6	14
13	Modeling Exon-Specific Bias Distribution Improves the Analysis of RNA-Seq Data. PLoS ONE, 2015, 10, e0140032.	2.5	1
14	Detecting differential expression from RNA-seq data with expression measurement uncertainty. Frontiers of Computer Science, 2015, 9, 652-663.	2.4	1
15	puma 3.0: improved uncertainty propagation methods for gene and transcript expression analysis. BMC Bioinformatics, 2013, 14, 39.	2.6	6
16	Including Probe-Level Measurement Error in Robust Mixture Clustering of Replicated Microarray Gene Expression. Statistical Applications in Genetics and Molecular Biology, 2010, 9, Article42.	0.6	3
17	puma: a Bioconductor package for propagating uncertainty in microarray analysis. BMC Bioinformatics, 2009, 10, 211.	2.6	66
18	An Improved Probabilistic Model for Finding Differential Gene Expression. , 2009, , .		0

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19	Including probe-level uncertainty in model-based gene expression clustering. BMC Bioinformatics, 2007, 8, 98.	2.6	16
20	Probe-level measurement error improves accuracy in detecting differential gene expression. Bioinformatics, 2006, 22, 2107-2113.	4.1	68
21	A tractable probabilistic model for Affymetrix probe-level analysis across multiple chips. Bioinformatics, 2005, 21, 3637-3644.	4.1	66