Ka-Chun Wong

List of Publications by Year
in descending order

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141 papers	2,609 citations	236925 25 h-index	243625 44 g-index
144 all docs	144 docs citations	144 times ranked	2676 citing authors

#	Article	IF	Citations
1	Particle Swarm Optimization With a Balanceable Fitness Estimation for Many-Objective Optimization Problems. IEEE Transactions on Evolutionary Computation, 2018, 22, 32-46.	10.0	202
2	Collective Human Mobility Pattern from Taxi Trips in Urban Area. PLoS ONE, 2012, 7, e34487.	2.5	150
3	Off-target predictions in CRISPR-Cas9 gene editing using deep learning. Bioinformatics, 2018, 34, i656-i663.	4.1	121
4	An External Archive-Guided Multiobjective Particle Swarm Optimization Algorithm. IEEE Transactions on Cybernetics, 2017, 47, 2794-2808.	9.5	96
5	A Clustering-Based Evolutionary Algorithm for Many-Objective Optimization Problems. IEEE Transactions on Evolutionary Computation, 2019, 23, 391-405.	10.0	91
6	Adaptive multiple-elites-guided composite differential evolution algorithm with a shift mechanism. Information Sciences, 2018, 422, 122-143.	6.9	87
7	Mirsynergy: detecting synergistic miRNA regulatory modules by overlapping neighbourhood expansion. Bioinformatics, 2014, 30, 2627-2635.	4.1	79
8	A novel artificial bee colony algorithm with an adaptive population size for numerical function optimization. Information Sciences, 2017, 414, 53-67.	6.9	70
9	Evolutionary multimodal optimization using the principle of locality. Information Sciences, 2012, 194, 138-170.	6.9	57
10	SNPdryad: predicting deleterious non-synonymous human SNPs using only orthologous protein sequences. Bioinformatics, 2014, 30, 1112-1119.	4.1	57
11	Inferring probabilistic miRNAâ€“mRNA interaction signatures in cancers: a role-switch approach. Nucleic Acids Research, 2014, 42, e76-e76.	14.5	55
12	DNA motif elucidation using belief propagation. Nucleic Acids Research, 2013, 41, e153-e153.	14.5	53
13	An adaptive immune-inspired multi-objective algorithm with multiple differential evolution strategies. Information Sciences, 2018, 430-431, 46-64.	6.9	53
14	Discovering proteinâ€“DNA binding sequence patterns using association rule mining. Nucleic Acids Research, 2010, 38, 6324-6337.	14.5	49
15	Evolutionary Multiobjective Clustering and Its Applications to Patient Stratification. IEEE Transactions on Cybernetics, 2019, 49, 1680-1693.	9.5	49
16	iCircRBP-DHN: identification of circRNA-RBP interaction sites using deep hierarchical network. Briefings in Bioinformatics, 2021, 22, .	6.5	45
17	CRISPRâ€Net: A Recurrent Convolutional Network Quantifies CRISPR Offâ€Target Activities with Mismatches and Indels. Advanced Science, 2020, 7, 1903562.	11.2	43
18	Verbal aggression detection on Twitter comments: convolutional neural network for short-text sentiment analysis. Neural Computing and Applications, 2020, 32, 10809-10818.	5.6	40

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19	SignalSpider: probabilistic pattern discovery on multiple normalized ChIP-Seq signal profiles. Bioinformatics, 2015, 31, 17-24.	4.1	39
20	Protein structure prediction on a lattice model via multimodal optimization techniques. , 2010, , .		38
21	A self-adaptive weighted differential evolution approach for large-scale feature selection. Knowledge-Based Systems, 2022, 235, 107633.	7.1	38
22	A probabilistic approach to explore human miRNA targetome by integrating miRNA-overexpression data and sequence information. Bioinformatics, 2014, 30, 621-628.	4.1	37
23	Intrusion detection using multi-objective evolutionary convolutional neural network for Internet of Things in Fog computing. Knowledge-Based Systems, 2022, 244, 108505.	7.1	37
24	Zinc-finger protein 471 suppresses gastric cancer through transcriptionally repressing downstream oncogenic PLS3 and TFAP2A. Oncogene, 2018, 37, 3601-3616.	5.9	35
25	A Diversity-Enhanced Resource Allocation Strategy for Decomposition-Based Multiobjective Evolutionary Algorithm. IEEE Transactions on Cybernetics, 2018, 48, 2388-2401.	9.5	35
26	Herd Clustering: A synergistic data clustering approach using collective intelligence. Applied Soft Computing Journal, 2014, 23, 61-75.	7.2	29
27	Machine Learning Protocols in Early Cancer Detection Based on Liquid Biopsy: A Survey. Life, 2021, 11, 638.	2.4	28
28	A Short Survey on Data Clustering Algorithms. , 2015, , .		27
29	A novel multi-objective evolutionary algorithm with dynamic decomposition strategy. Swarm and Evolutionary Computation, 2019, 48, 182-200.	8.1	26
30	An Effective Ensemble Framework for Multiobjective Optimization. IEEE Transactions on Evolutionary Computation, 2019, 23, 645-659.	10.0	26
31	Generalizing and learning protein-DNA binding sequence representations by an evolutionary algorithm. Soft Computing, 2011, 15, 1631-1642.	3.6	25
32	Synergizing CRISPR/Cas9 off-target predictions for ensemble insights and practical applications. Bioinformatics, 2019, 35, 1108-1115.	4.1	25
33	A Self-Guided Reference Vector Strategy for Many-Objective Optimization. IEEE Transactions on Cybernetics, 2022, 52, 1164-1178.	9.5	25
34	Computational learning on specificity-determining residue-nucleotide interactions. Nucleic Acids Research, 2015, 43, gkv1134.	14.5	20
35	MotifHyades: expectation maximization for de novo DNA motif pair discovery on paired sequences. Bioinformatics, 2017, 33, 3028-3035.	4.1	20
36	Early Cancer Detection from Multianalyte Blood Test Results. IScience, 2019, 15, 332-341.	4.1	20

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37	A novel surrogate-assisted evolutionary algorithm with an uncertainty grouping based infill criterion. Swarm and Evolutionary Computation, 2021, 60, 100787.	8.1	20
38	Single-cell RNA-seq interpretations using evolutionary multiobjective ensemble pruning. Bioinformatics, 2019, 35, 2809-2817.	4.1	19
39	An evolutionary algorithm with species-specific explosion for multimodal optimization. , 2009, , .		17
40	Nature-Inspired Multiobjective Epistasis Elucidation from Genome-Wide Association Studies. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 17, 1-1.	3.0	17
41	Context awareness and embedding for biomedical event extraction. Bioinformatics, 2020, 36, 637-643.	4.1	17
42	Discovering approximate-associated sequence patterns for proteinâ€“DNA interactions. Bioinformatics, 2011, 27, 471-478.	4.1	16
43	A Comparison Study for DNA Motif Modeling on Protein Binding Microarray. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2016, 13, 261-271.	3.0	16
44	Increased expression of GATA zinc finger domain containing 1 through gene amplification promotes liver cancer by directly inducing phosphatase of regenerating liver 3. Hepatology, 2018, 67, 2302-2319.	7.3	16
45	Evolutionary Large-Scale Multiobjective Optimization: Benchmarks and Algorithms. IEEE Transactions on Evolutionary Computation, 2023, 27, 401-415.	10.0	16
46	Effect of Spatial Locality on an Evolutionary Algorithm for Multimodal Optimization. Lecture Notes in Computer Science, 2010, , 481-490.	1.3	16
47	Leveraging Multi-source knowledge for Chinese clinical named entity recognition via relational graph convolutional network. Journal of Biomedical Informatics, 2022, 128, 104035.	4.3	16
48	Nature-Inspired Multiobjective Cancer Subtype Diagnosis. IEEE Journal of Translational Engineering in Health and Medicine, 2019, 7, 1-12.	3.7	15
49	SECOM: A Novel Hash Seed and Community Detection Based-Approach for Genome-Scale Protein Domain Identification. PLoS ONE, 2012, 7, e39475.	2.5	15
50	Multiple source transfer learning for dynamic multiobjective optimization. Information Sciences, 2022, 607, 739-757.	6.9	15
51	New Tricks for â€œOldâ€•Domains: How Novel Architectures and Promiscuous Hubs Contributed to the Organization and Evolution of the ECM. Genome Biology and Evolution, 2014, 6, 2897-2917.	2.5	14
52	Noninvasive early diagnosis of intestinal diseases based on artificial intelligence in genomics and microbiome. Journal of Gastroenterology and Hepatology (Australia), 2021, 36, 823-831.	2.8	13
53	HCRNet: high-throughput circRNA-binding event identification from CLIP-seq data using deep temporal convolutional network. Briefings in Bioinformatics, 2022, 23, .	6.5	13
54	Mini-review: Recent advances in post-translational modification site prediction based on deep learning. Computational and Structural Biotechnology Journal, 2022, 20, 3522-3532.	4.1	13

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55	A novel semi-supervised model for miRNA-disease association prediction based on $$ell_{1}$$ â„“ 1 -norm graph. Journal of Translational Medicine, 2018, 16, 357.	4.4	12
56	Big data challenges in genome informatics. Biophysical Reviews, 2019, 11, 51-54.	3.2	12
57	Transmission trend of the COVID-19 pandemic predicted by dendritic neural regression. Applied Soft Computing Journal, 2021, 111, 107683.	7.2	12
58	Decomposition-based multiobjective optimization with bicriteria assisted adaptive operator selection. Swarm and Evolutionary Computation, 2021, 60, 100790.	8.1	11
59	Human host status inference from temporal microbiome changes via recurrent neural networks. Briefings in Bioinformatics, 2021, 22, .	6.5	11
60	Evolutionary Multitasking for Large-Scale Multiobjective Optimization. IEEE Transactions on Evolutionary Computation, 2023, 27, 863-877.	10.0	11
61	scEFSC: Accurate single-cell RNA-seq data analysis via ensemble consensus clustering based on multiple feature selections. Computational and Structural Biotechnology Journal, 2022, 20, 2181-2197.	4.1	11
62	Identification of coupling DNA motif pairs on long-range chromatin interactions in human K562 cells. Bioinformatics, 2016, 32, 321-324.	4.1	10
63	Multiobjective Patient Stratification Using Evolutionary Multiobjective Optimization. IEEE Journal of Biomedical and Health Informatics, 2018, 22, 1619-1629.	6.3	10
64	Identification of pan-cancer Ras pathway activation with deep learning. Briefings in Bioinformatics, 2021, 22, .	6.5	10
65	Early cancer detection from genome-wide cell-free DNA fragmentation via shuffled frog leaping algorithm and support vector machine. Bioinformatics, 2021, 37, 3099-3105.	4.1	10
66	Evolutionary Multiobjective Clustering Algorithms With Ensemble for Patient Stratification. IEEE Transactions on Cybernetics, 2022, 52, 11027-11040.	9.5	10
67	Implication of Light Absorption Enhancement and Mixing State of Black Carbon (BC) by Coatings in Hong Kong. Aerosol and Air Quality Research, 2018, 18, 2753-2763.	2.1	10
68	Human disease prediction from microbiome data by multiple feature fusion and deep learning. IScience, 2022, 25, 104081.	4.1	10
69	Uncovering the key dimensions of high-throughput biomolecular data using deep learning. Nucleic Acids Research, 2020, 48, e56-e56.	14.5	9
70	A novel web-based system for tropical cyclone analysis and prediction. International Journal of Geographical Information Science, 2012, 26, 75-97.	4.8	8
71	An Improved Neural Network Cascade for Face Detection in Large Scene Surveillance. Applied Sciences (Switzerland), 2018, 8, 2222.	2.5	8
72	DNA Sequencing Technologies. ACM Computing Surveys, 2020, 52, 1-30.	23.0	8

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73	Single-Cell RNA Sequencing Data Interpretation by Evolutionary Multiobjective Clustering. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 17, 1-1.	3.0	8
74	Nature-inspired multiobjective patient stratification from cancer gene expression data. Information Sciences, 2020, 526, 245-262.	6.9	8
75	iDeepSubMito: identification of protein submitochondrial localization with deep learning. Briefings in Bioinformatics, 2021, 22, .	6.5	8
76	EDCNN: identification of genome-wide RNA-binding proteins using evolutionary deep convolutional neural network. Bioinformatics, 2022, 38, 678-686.	4.1	8
77	Evolving Spatial Clusters of Genomic Regions From High-Throughput Chromatin Conformation Capture Data. IEEE Transactions on Nanobioscience, 2017, 16, 400-407.	3.3	7
78	DNA Motif Recognition Modeling from Protein Sequences. IScience, 2018, 7, 198-211.	4.1	7
79	Elucidating Genome-Wide Protein-RNA Interactions Using Differential Evolution. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 272-282.	3.0	7
80	Deep embedded clustering with multiple objectives on scRNA-seq data. Briefings in Bioinformatics, 2021, 22, .	6.5	7
81	High-throughput single-cell RNA-seq data imputation and characterization with surrogate-assisted automated deep learning. Briefings in Bioinformatics, 2022, 23, .	6.5	7
82	EGFI: drugâ€“drug interaction extraction and generation with fusion of enriched entity and sentence information. Briefings in Bioinformatics, 2022, 23, .	6.5	7
83	Evolving Transcription Factor Binding Site Models From Protein Binding Microarray Data. IEEE Transactions on Cybernetics, 2017, 47, 415-424.	9.5	6
84	NSSRF: global network similarity search with subgraph signatures and its applications. Bioinformatics, 2017, 33, 1696-1702.	4.1	6
85	Deep Learning Resolves Representative Movement Patterns in a Marine Predator Species. Applied Sciences (Switzerland), 2019, 9, 2935.	2.5	6
86	Future DNA computing device and accompanied tool stack: Towards high-throughput computation. Future Generation Computer Systems, 2021, 117, 111-124.	7.5	6
87	A selfâ€organizing weighted optimization based framework for largeâ€scale multiâ€objective optimization. Swarm and Evolutionary Computation, 2022, 72, 101084.	8.1	6
88	A scalable community detection algorithm for large graphs using stochastic block models. Intelligent Data Analysis, 2017, 21, 1463-1485.	0.9	5
89	PathEmb: Random Walk Based Document Embedding for Global Pathway Similarity Search. IEEE Journal of Biomedical and Health Informatics, 2019, 23, 1329-1335.	6.3	5
90	Heterodimeric DNA motif synthesis and validations. Nucleic Acids Research, 2019, 47, 1628-1636.	14.5	5

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91	Multiobjective Genome-Wide RNA-Binding Event Identification From CLIP-Seq Data. IEEE Transactions on Cybernetics, 2021, 51, 5811-5824.	9.5	5
92	Elucidating transcriptomic profiles from single-cell RNA sequencing data using nature-inspired compressed sensing. Briefings in Bioinformatics, 2021, 22, .	6.5	5
93	The comprehensive and systematic identification of BLCA-specific SF-regulated, survival-related AS events. Gene, 2022, 835, 146657.	2.2	5
94	Probabilistic Inference on Multiple Normalized Signal Profiles from Next Generation Sequencing: Transcription Factor Binding Sites. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 1416-1428.	3.0	4
95	Unsupervised Learning in Genome Informatics. , 2016, , 405-448.		4
96	Elucidating high-dimensional cancer hallmark annotation via enriched ontology. Journal of Biomedical Informatics, 2017, 73, 84-94.	4.3	4
97	A Comparative Study for Identifying the Chromosome-Wide Spatial Clusters from High-Throughput Chromatin Conformation Capture Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 774-787.	3.0	4
98	ToBio: Global Pathway Similarity Search Based on Topological and Biological Features. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 336-349.	3.0	4
99	Deleterious Non-Synonymous Single Nucleotide Polymorphism Predictions on Human Transcription Factors. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 327-333.	3.0	4
100	GESgnExt: Gene Expression Signature Extraction and Meta-Analysis on Gene Expression Omnibus. IEEE Journal of Biomedical and Health Informatics, 2020, 24, 311-318.	6.3	4
101	Nature-Inspired Compressed Sensing for Transcriptomic Profiling From Random Composite Measurements. IEEE Transactions on Cybernetics, 2021, 51, 4476-4487.	9.5	4
102	Evolving Multiobjective Cancer Subtype Diagnosis From Cancer Gene Expression Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2431-2444.	3.0	4
103	Multiplicative Algorithms for Constrained Non-negative Matrix Factorization. , 2012, , .		3
104	A cone order sequence based multi-objective evolutionary algorithm. , 2016, , .		3
105	Categorical Matrix Completion With Active Learning for High-Throughput Screening. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2261-2270.	3.0	3
106	Protocol for Epistasis Detection with Machine Learning Using GenEpi Package. Methods in Molecular Biology, 2021, 2212, 291-305.	0.9	3
107	Reducing healthcare disparities using multiple multiethnic data distributions with fine-tuning of transfer learning. Briefings in Bioinformatics, 2022, 23, .	6.5	3
108	A dynamic multi-objective evolutionary algorithm based on polynomial regression and adaptive clustering. Swarm and Evolutionary Computation, 2022, 71, 101075.	8.1	3

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109	Active Learning Based on Single-Hidden Layer Feed-Forward Neural Network. , 2015, , .		2
110	A Novel Approach to Predict Core Residues on Cancer-Related DNA-Binding Domains. Cancer Informatics, 2016, 15s2, CIN.S39366.	1.9	2
111	Multiobjective Deep Clustering and its Applications in Single-cell RNA-seq Data. IEEE Transactions on Systems, Man, and Cybernetics: Systems, 2022, 52, 5016-5027.	9.3	2
112	CancerEMC: frontline non-invasive cancer screening from circulating protein biomarkers and mutations in cell-free DNA. Bioinformatics, 2021, 37, 3319-3327.	4.1	2
113	Evolutionary Algorithms. , 0, , 111-137.		2
114	Exploring high-throughput biomolecular data with multiobjective robust continuous clustering. Information Sciences, 2022, 583, 239-265.	6.9	2
115	GMHCC: high-throughput analysis of biomolecular data using graph-based multiple hierarchical consensus clustering. Bioinformatics, 2022, 38, 3020-3028.	4.1	2
116	Colorectal cancer subtype identification from differential gene expression levels using minimalist deep learning. BioData Mining, 2022, 15, 12.	4.0	2
117	Aggressivity Detection on Social Network Comments. , 2017, , .		1
118	Evolving Transcriptomic Profiles from Single-cell RNA-seq Data using Nature-Inspired Multiobjective Optimization. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 18, 1-1.	3.0	1
119	RNCE: network integration with reciprocal neighbors contextual encoding for multi-modal drug community study on cancer targets. Briefings in Bioinformatics, 2021, 22, .	6.5	1
120	Particle Swarm Optimized Gaussian Process Classifier for Treatment Discontinuation Prediction in Multicohort Metastatic Castration-Resistant Prostate Cancer Patients. IEEE Journal of Biomedical and Health Informatics, 2022, 26, 1309-1317.	6.3	1
121	Epistasis Analysis: Classification Through Machine Learning Methods. Methods in Molecular Biology, 2021, 2212, 337-345.	0.9	1
122	Feature Selection and Feature Extraction: Highlights. , 2021, , .		1
123	Accurate Sequence-Based Prediction of Deleterious nsSNPs with Multiple Sequence Profiles and Putative Binding Residues. Biomolecules, 2021, 11, 1337.	4.0	1
124	Evolutionary Algorithms. Advances in Computational Intelligence and Robotics Book Series, 2016, , 190-215.	0.4	1
125	An Artificial Intelligence Approach for Gene Editing Off-Target Quantification: Convolutional Self-attention Neural Network Designs and Considerations. Statistics in Biosciences, 0, , .	1.2	1
126	Exploring Mixed Membership Stochastic Block Models via Non-negative Matrix Factorization. , 2014, , .		0

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127	Data Analytics for Protein-DNA Binding Interactions. , 2015, , .		0
128	Probabilistic Inference on Multiple Normalized Genome-Wide Signal Profiles With Model Regularization. IEEE Transactions on Nanobioscience, 2017, 16, 43-50.	3.3	0
129	Zinc-Finger Protein 471 Functions as a Tumor Suppressor in Gastric Cancer through Transcriptionally Repressing TFAP2A and PLS3. Gastroenterology, 2017, 152, S801-S802.	1.3	0
130	GATAD1 Promotes Hepatocellular Carcinogenesis through Directly Inducing PTP4A3 and Activating Akt Pathway. Gastroenterology, 2017, 152, S1182.	1.3	0
131	A scalable community detection algorithm for large graphs using stochastic block models. Intelligent Data Analysis, 2018, 22, 239.	0.9	0
132	EDITORIAL: Special Issue of 2018 India International Congress on Computational Intelligence. Neural Computing and Applications, 2020, 32, 15427-15428.	5.6	0
133	Special issue of 2017 India International Congress on Computational Intelligence. Neural Computing and Applications, 2020, 32, 10797-10798.	5.6	0
134	Identification of haploinsufficient genes from epigenomic data using deep forest. Briefings in Bioinformatics, 2021, 22, .	6.5	0
135	Analyzing High-Order Epistasis from Genotype-Phenotype Maps Using â€˜Epistasisâ€™ Package. Methods in Molecular Biology, 2021, 2212, 265-275.	0.9	0
136	Epistasis Detection Based on Epi-GTBN. Methods in Molecular Biology, 2021, 2212, 325-335.	0.9	0
137	DeepMotifSyn: a deep learning approach to synthesize heterodimeric DNA motifs. Briefings in Bioinformatics, 2022, 23, .	6.5	0
138	Finding coreâ€“periphery structures in large networks. Physica A: Statistical Mechanics and Its Applications, 2021, 581, 126224.	2.6	0
139	A Belief Degreeâ€“Associated Fuzzy Multifactor Dimensionality Reduction Framework for Epistasis Detection. Methods in Molecular Biology, 2021, 2212, 307-323.	0.9	0
140	Reactionsâ€™ Descriptors Selection and Yield Estimation Using Metaheuristic Algorithms and Voting Ensemble. Computers, Materials and Continua, 2022, 70, 4745-4762.	1.9	0
141	Metric Learning Based Vision Transformer forÂProduct Matching. Lecture Notes in Computer Science, 2021, , 3-13.	1.3	0