Susana Vinga

List of Publications by Year
in descending order

104 papers	3,097 citations	257101 24 h-index	174990 52 g-index
113 all docs	113 docs citations	113 times ranked	3296 citing authors

#	Article	IF	Citations
1	Alignment-free sequence comparison--a review. Bioinformatics, 2003, 19, 513-523.	1.8	700
2	Alignment-free sequence comparison: benefits, applications, and tools. Genome Biology, 2017, 18, 186.	3.8	371
3	Benchmarking of alignment-free sequence comparison methods. Genome Biology, 2019, 20, 144.	3.8	147
4	From physiology to systems metabolic engineering for the production of biochemicals by lactic acid bacteria. Biotechnology Advances, 2013, 31, 764-788.	6.0	139
5	Information theory applications for biological sequence analysis. Briefings in Bioinformatics, 2014, 15, 376-389.	3.2	111
6	Parameter optimization in S-system models. BMC Systems Biology, 2008, 2, 35.	3.0	78
7	Host Glycan Sugar-Specific Pathways in Streptococcus pneumonia: Galactose as a Key Sugar in Colonisation and Infection. PLoS ONE, 2015, 10, e0121042.	1.1	78
8	Arthroscopic Superior Capsular Reconstruction With a Minimally Invasive Harvested Fascia Lata Autograft Produces Good Clinical Results. Orthopaedic Journal of Sports Medicine, 2018, 6, 232596711880824.	0.8	77
9	RÃ©nyi continuous entropy of DNA sequences. Journal of Theoretical Biology, 2004, 231, 377-388.	0.8	70
10	Analysis of the Genetic Variability of Virulence-Related Loci in Epidemic Clones of Methicillin-Resistant Staphylococcus aureus. Antimicrobial Agents and Chemotherapy, 2005, 49, 366-379.	1.4	68
11	Automated smoother for the numerical decoupling of dynamics models. BMC Bioinformatics, 2007, 8, 305.	1.2	64
12	Assessment of allelic variation in the ccrAB locus in methicillin-resistant Staphylococcus aureus clones. Journal of Antimicrobial Chemotherapy, 2006, 58, 23-30.	1.3	63
13	A Review of Recent Machine Learning Advances for Forecasting Harmful Algal Blooms and Shellfish Contamination. Journal of Marine Science and Engineering, 2021, 9, 283.	1.2	57
14	Editorial: Alignment-free methods in computational biology. Briefings in Bioinformatics, 2014, 15, 341-342.	3.2	51
15	A Survey on Methods for Modeling and Analyzing Integrated Biological Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 943-958.	1.9	50
16	Kinetic modeling of cell metabolism for microbial production. Journal of Biotechnology, 2016, 219, 126-141.	1.9	43
17	Universal sequence map (USM) of arbitrary discrete sequences. BMC Bioinformatics, 2002, 3, 6.	1.2	42
18	Transcriptional and metabolic effects of glucose on Streptococcus pneumoniae sugar metabolism. Frontiers in Microbiology, 2015, 6, 1041.	1.5	41

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19	Comparative evaluation of word composition distances for the recognition of SCOP relationships. Bioinformatics, 2004, 20, 206-215.	1.8	39
20	Identification of neutral biochemical network models from time series data. BMC Systems Biology, 2009, 3, 47.	3.0	39
21	Local Renyi entropic profiles of DNA sequences. BMC Bioinformatics, 2007, 8, 393.	1.2	35
22	Pattern matching through Chaos Game Representation: bridging numerical and discrete data structures for biological sequence analysis. Algorithms for Molecular Biology, 2012, 7, 10.	0.3	34
23	Identification of switched ARX models via convex optimization and expectation maximization. Journal of Process Control, 2015, 28, 9-16.	1.7	31
24	A Data Mining Approach for the Detection of High-Risk Breast Cancer Groups. Advances in Intelligent and Soft Computing, 2010, , 43-51.	0.2	27
25	Structured sparsity regularization for analyzing high-dimensional omics data. Briefings in Bioinformatics, 2021, 22, 77-87.	3.2	27
26	A Combinatorial Algorithm for Microbial Consortia Synthetic Design. Scientific Reports, 2016, 6, 29182.	1.6	24
27	Identification of influential observations in high-dimensional cancer survival data through the rank product test. BioData Mining, 2018, 11, 1.	2.2	24
28	Ensemble outlier detection and gene selection in triple-negative breast cancer data. BMC Bioinformatics, 2018, 19, 168.	1.2	23
29	DegreeCox â€" a network-based regularization method for survival analysis. BMC Bioinformatics, 2016, 17, 449.	1.2	22
30	Fractal MapReduce decomposition of sequence alignment. Algorithms for Molecular Biology, 2012, 7, 12.	0.3	21
31	Ki MoSys: a web-based repository of experimental data for KInetic MOdels of biological SYStems. BMC Systems Biology, 2014, 8, 85.	3.0	21
32	Interplay Between Capsule Expression and Uracil Metabolism in Streptococcus pneumoniae D39. Frontiers in Microbiology, 2018, 9, 321.	1.5	20
33	Dynamic modeling of bone metastasis, microenvironment and therapy. Journal of Theoretical Biology, 2016, 391, 1-12.	0.8	19
34	Computational Approach to the Discovery of Phytochemical Molecules with Therapeutic Potential Targets to the PKCZ protein. Letters in Drug Design and Discovery, 2018, 15, 488-499.	0.4	19
35	Biological sequences as pictures â€" a generic two dimensional solution for iterated maps. BMC Bioinformatics, 2009, 10, 100.	1.2	17
36	Robust identification of target genes and outliers in triple-negative breast cancer data. Statistical Methods in Medical Research, 2019, 28, 3042-3056.	0.7	17

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37	Tracking intratumoral heterogeneity in glioblastoma via regularized classification of single-cell RNA-Seq data. BMC Bioinformatics, 2020, 21, 59.	1.2	17
38	ccrB typing tool: an online resource for staphylococci ccrB sequence typing. Journal of Antimicrobial Chemotherapy, 2008, 61, 959-960.	1.3	16
39	An extended dynamic model of Lactococcus lactis metabolism for mannitol and 2,3-butanediol production. Molecular BioSystems, 2014, 10, 628.	2.9	16
40	Subcellular metabolic organization in the context of dynamic energy budget and biochemical systems theories. Philosophical Transactions of the Royal Society B: Biological Sciences, 2010, 365, 3429-3442.	1.8	15
41	An analysis of the positional distribution of DNA motifs in promoter regions and its biological relevance. BMC Bioinformatics, 2008, 9, 89.	1.2	14
42	Computing distribution of scale independent motifs in biological sequences. Algorithms for Molecular Biology, 2006, 1, 18.	0.3	13
43	Entropic Profiler â€" detection of conservation in genomes using information theory. BMC Research Notes, 2009, 2, 72.	0.6	13
44	BGFit: management and automated fitting of biological growth curves. BMC Bioinformatics, 2013, 14, 283.	1.2	13
45	Identifying IIR filter coefficients using particle swarm optimization with application to reconstruction of missing cardiovascular signals. Engineering Applications of Artificial Intelligence, 2014, 34, 193-198.	4.3	13
46	Optimal and receding horizon control of tumor growth in myeloma bone disease. Biomedical Signal Processing and Control, 2016, 24, 128-134.	3.5	13
47	OptPipe - a pipeline for optimizing metabolic engineering targets. BMC Systems Biology, 2017, 11, 143.	3.0	13
48	Global Meta-Analysis of Transcriptomics Studies. PLoS ONE, 2014, 9, e89318.	1.1	13
49	BacHBerry: BACterial Hosts for production of Bioactive phenolics from bERRY fruits. Phytochemistry Reviews, 2018, 17, 291-326.	3.1	12
50	Twiner: correlation-based regularization for identifying common cancer gene signatures. BMC Bioinformatics, 2019, 20, 356.	1.2	12
51	Mechanical bone remodelling: Comparative study of distinct numerical approaches. Engineering Analysis With Boundary Elements, 2019, 100, 125-139.	2.0	12
52	Simplifying biochemical tumorous bone remodeling models through variable order derivatives. Computers and Mathematics With Applications, 2018, 75, 3147-3157.	1.4	10
53	Nonlinear MPC of HIV-1 infection with periodic inputs. , 2011, , .		9
54	Using Information Interaction to Discover Epistatic Effects in Complex Diseases. PLoS ONE, 2013, 8, e76300.	1.1	9

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55	MOMO - multi-objective metabolic mixed integer optimization: application to yeast strain engineering. BMC Bioinformatics, 2020, 21, 69.	1.2	8
56	Outlier Detection in Survival Analysis based on the Concordance C-index. , 2015, , .		8
57	Spatiotemporal Correlation Feature Spaces to Support Anomaly Detection in Water Distribution Networks. Water (Switzerland), 2021, 13, 2551.	1.2	7
58	The Role of Network Science in Glioblastoma. Cancers, 2021, 13, 1045.	1.7	6
59	Predicting Biologic Therapy Outcome of Patients With Spondyloarthritis: Joint Models for Longitudinal and Survival Analysis. JMIR Medical Informatics, 2021, 9, e26823.	1.3	6
60	Online Bayesian Time-varying Parameter Estimation of HIV-1 Time-series. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 2012, 45, 1294-1299.	0.4	5
61	A comprehensive evaluation of binning methods to recover human gut microbial species from a non-redundant reference gene catalog. NAR Genomics and Bioinformatics, 2021, 3, lqab009.	1.5	5
62	Outlier Detection for Multivariate Time Series Using Dynamic Bayesian Networks. Applied Sciences (Switzerland), 2021, 11, 1955.	1.3	5
63	Adenoma incidence decreases under the effect of polypectomy. World Journal of Gastroenterology, 2012, 18, 1243.	1.4	5
64	Models of Bone Metastases and Therapy using Fractional Derivatives. Journal of Applied Nonlinear Dynamics, 2018, 7, 81-94.	0.1	5
65	Fuzzy Clustering for Incomplete Short Time Series Data. Lecture Notes in Computer Science, 2015, , 353-359.	1.0	4
66	Modeling multiple experiments using regularized optimization: A case study on bacterial glucose utilization dynamics. Computers in Biology and Medicine, 2015, 63, 301-309.	3.9	4
67	Improving Protein Expression Prediction Using Extra Features and Ensemble Averaging. PLoS ONE, 2016, 11, e0150369.	1.1	4
68	Identification and automatic segmentation of multiphasic cell growth using a linear hybrid model. Mathematical Biosciences, 2016, 279, 83-89.	0.9	4
69	Variable Order Differential Models of Bone Remodelling * *This work was supported by FCT, through IDMEC, under LAETA, projects UID/EMS/50022/2013, BoneSys, joint Polish-Portuguese project Modelling and controlling cancer evolution using fractional calculus, PERSEIDS (PTDC/EMS-SIS/0642/2014) and IF/00653/2012. IFAC-PapersOnLine, 2017, 50, 8066-8071.	0.5	4
70	AliClu - Temporal sequence alignment for clustering longitudinal clinical data. BMC Medical Informatics and Decision Making, 2019, 19, 289.	1.5	4
71	TCox: Correlation-Based Regularization Applied to Colorectal Cancer Survival Data. Biomedicines, 2020, 8, 488.	1.4	4
72	Exploring the Cellular Objective in Flux Balance Constraint-Based Models. Lecture Notes in Computer Science, 2014, , 211-224.	1.0	4

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73	Outlier Detection in Cox Proportional Hazards Models Based on the Concordance c-Index. Lecture Notes in Computer Science, 2015, , 252-256.	1.0	4
74	Optimization strategies for metabolic networks. BMC Systems Biology, 2010, 4, 113.	3.0	3
75	QUANTITATIVE MODELING OF THE *SACCHAROMYCES CEREVISIAE* FLR1 REGULATORY NETWORK USING AN S-SYSTEM FORMALISM. Journal of Bioinformatics and Computational Biology, 2011, 09, 613-630.	0.3	3
76	Modelling cancer outcomes of bone metastatic patients: combining survival data with N-Telopeptide of type I collagen (NTX) dynamics through joint models. BMC Medical Informatics and Decision Making, 2019, 19, 13.	1.5	3
77	Variable Selection and Outlier Detection in Regularized Survival Models: Application to Melanoma Gene Expression Data. Lecture Notes in Computer Science, 2019, , 431-440.	1.0	3
78	Hybrid identification of time-varying parameter with particle filtering and expectation maximization. , 2013, , .		2
79	Control analysis of the impact of allosteric regulation mechanism in a Escherichia coli kinetic model: Application to serine production. Biochemical Engineering Journal, 2016, 110, 59-70.	1.8	2
80	Unsupervised learning of pharmacokinetic responses. Computational Statistics, 2017, 32, 409-428.	0.8	2
81	Dynamic Biochemical and Cellular Models of Bone Physiology: Integrating Remodeling Processes, Tumor Growth, and Therapy. Lecture Notes in Computational Vision and Biomechanics, 2020, , 95-128.	0.5	2
82	A model for bone remodeling: Cellular dynamics and mechanical loading. , 2017, , .		1
83	Assessing *Escherichia coli* metabolism models and simulation approaches in phenotype predictions: Validation against experimental data. Biotechnology Progress, 2018, 34, 1344-1354.	1.3	1
84	Bridging computer science and bioengineering for the multiscale modeling of biological systems. Annals of Medicine, 2024, 51, 28-28.	1.5	1
85	Studying Bone Remodelling and Tumour Growth for Therapy Predictive Control. Mathematics, 2020, 8, 679.	1.1	1
86	Predictive Medicine Using Interpretable Recurrent Neural Networks. Lecture Notes in Computer Science, 2021, , 187-202.	1.0	1
87	Dynamic modeling of bone remodeling, osteolytic metastasis and PK/PD therapy: introducing variable order derivatives as a simplification technique. Journal of Mathematical Biology, 2021, 83, 39.	0.8	1
88	Variable-order derivatives and bone remodeling in the presence of metastases. , 2019, , 69-94.		1
89	ROSIE: RObust Sparse ensemble for outlIEr detection and gene selection in cancer omics data. Statistical Methods in Medical Research, 2022, , 096228022110724.	0.7	1
90	Quantitative Modeling the Saccharomyces cerevisiae FLR1 Regulatory Network Using an S-System Formalism. , 2011, , .		0

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91	Parameter estimation and identifiability of a HIV-1 model. , 2013, , .		0
92	Bone Remodelling, Tumour Growth, and Fractional Order Therapy Predictive Control. SSRN Electronic Journal, 2018, , .	0.4	0
93	Variable Order Fractional Derivatives and Bone Remodeling in the Presence of Metastases. , 2018, , 1-36.		0
94	Latent Variable Modelling and Variational Inference for scRNA-seq Differential Expression Analysis. Lecture Notes in Computer Science, 2021, , 56-68.	1.0	0
95	Coupling sparse Cox models with clustering of longitudinal transcriptomics data for trauma prognosis. BioData Mining, 2021, 14, 25.	2.2	0
96	Learning Biomedical Networks: Toward Data-Informed Clinical Decision and Therapy. Computational Biology, 2021, , 77-92.	0.1	0
97	On the Role of Hub and Orphan Genes in the Diagnosis of Breast Invasive Carcinoma. Lecture Notes in Computer Science, 2019, , 631-642.	1.0	0
98	Unravelling Breast and Prostate Common Gene Signatures by Bayesian NetworkÂLearning. Lecture Notes in Computer Science, 2020, , 285-292.	1.0	0
99	Identification of Common Gene Signatures in Microarray and RNA-Sequencing Data Using Network-Based Regularization. Lecture Notes in Computer Science, 2020, , 15-26.	1.0	0
100	MSAX: Multivariate Symbolic Aggregate Approximation for Time Series Classification. Lecture Notes in Computer Science, 2020, , 90-97.	1.0	0
101	Variational Inference in Probabilistic Single-cell RNA-seq Models. Lecture Notes in Computer Science, 2020, , 11-18.	1.0	0
102	Sparse Consensus Classification forÂDiscovering Novel Biomarkers inÂRheumatoid Arthritis. Lecture Notes in Computer Science, 2020, , 125-136.	1.0	0
103	Random Sample Consensus for the Robust Identification of Outliers in Cancer Data. Lecture Notes in Computer Science, 2020, , 108-118.	1.0	0
104	Network-Based Variable Selection for Survival Outcomes in Oncological Data. Lecture Notes in Computer Science, 2020, , 550-561.	1.0	0