

# Alexander Schliep

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4097947/publications.pdf>

Version: 2024-02-01

60  
papers

1,840  
citations

361388

20  
h-index

289230

40  
g-index

72  
all docs

72  
docs citations

72  
times ranked

2435  
citing authors

#	ARTICLE	IF	CITATIONS
1	Clustering cancer gene expression data: a comparative study. BMC Bioinformatics, 2008, 9, 497.	2.6	334
2	Using hidden Markov models to analyze gene expression time course data. Bioinformatics, 2003, 19, i255-i263.	4.1	198
3	Embracing heterogeneity: coalescing the Tree of Life and the future of phylogenomics. PeerJ, 2019, 7, e6399.	2.0	111
4	Selecting signature oligonucleotides to identify organisms using DNA arrays. Bioinformatics, 2002, 18, 1340-1349.	4.1	102
5	CLEVER: clique-enumerating variant finder. Bioinformatics, 2012, 28, 2875-2882.	4.1	101
6	The Global Museum: natural history collections and the future of evolutionary science and public education. PeerJ, 2020, 8, e8225.	2.0	81
7	Optimal robust non-unique probe selection using Integer Linear Programming. Bioinformatics, 2004, 20, i186-i193.	4.1	75
8	Blood Glucose Prediction with Variance Estimation Using Recurrent Neural Networks. Journal of Healthcare Informatics Research, 2020, 4, 1-18.	7.6	71
9	Cognitive and brain development is independently influenced by socioeconomic status and polygenic scores for educational attainment. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 12411-12418.	7.1	66
10	Analyzing Gene Expression Time-Courses. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2005, 2, 179-193.	3.0	65
11	Single cell genome analysis of an uncultured heterotrophic stramenopile. Scientific Reports, 2014, 4, 4780.	3.3	59
12	Turtle: Identifying frequent k-mers with cache-efficient algorithms. Bioinformatics, 2014, 30, 1950-1957.	4.1	57
13	Ranking and selecting clustering algorithms using a meta-learning approach. , 2008, , .		53
14	The discriminant power of RNA features for pre-miRNA recognition. BMC Bioinformatics, 2014, 15, 124.	2.6	40
15	Constrained mixture estimation for analysis and robust classification of clinical time series. Bioinformatics, 2009, 25, i6-i14.	4.1	30
16	AI-assisted synthesis prediction. Drug Discovery Today: Technologies, 2019, 32-33, 65-72.	4.0	29
17	Comparative study on normalization procedures for cluster analysis of gene expression datasets. , 2008, , .		25
18	Robust inference of groups in gene expression time-courses using mixtures of HMMs. Bioinformatics, 2004, 20, i283-i289.	4.1	23

#	ARTICLE	IF	CITATIONS
19	The Graphical Query Language: a tool for analysis of gene expression time-courses. <i>Bioinformatics</i> , 2005, 21, 2544-2545.	4.1	23
20	Context-specific independence mixture modeling for positional weight matrices. <i>Bioinformatics</i> , 2006, 22, e166-e173.	4.1	23
21	Integer linear programming approaches for non-unique probe selection. <i>Discrete Applied Mathematics</i> , 2007, 155, 840-856.	0.9	22
22	PyMix - The Python mixture package - a tool for clustering of heterogeneous biological data. <i>BMC Bioinformatics</i> , 2010, 11, 9.	2.6	20
23	Inferring differentiation pathways from gene expression. <i>Bioinformatics</i> , 2008, 24, i156-i164.	4.1	16
24	Semi-supervised learning for the identification of syn-expressed genes from fused microarray and in situ image data. <i>BMC Bioinformatics</i> , 2007, 8, S3.	2.6	15
25	Identifying protein complexes directly from high-throughput TAP data with Markov random fields. <i>BMC Bioinformatics</i> , 2007, 8, 482.	2.6	14
26	Classifying short gene expression time-courses with Bayesian estimation of piecewise constant functions. <i>Bioinformatics</i> , 2011, 27, 946-952.	4.1	14
27	Exploiting prior knowledge and gene distances in the analysis of tumor expression profiles with extended Hidden Markov Models. <i>Bioinformatics</i> , 2011, 27, 1645-1652.	4.1	14
28	Clustering Vehicle Maneuver Trajectories Using Mixtures of Hidden Markov Models. , 2018, , .		11
29	Predicting progression and cognitive decline in amyloid-positive patients with Alzheimer's disease. <i>Alzheimer's Research and Therapy</i> , 2021, 13, 151.	6.2	9
30	Decoding non-unique oligonucleotide hybridization experiments of targets related by a phylogenetic tree. <i>Bioinformatics</i> , 2006, 22, e424-e430.	4.1	8
31	Fast MCMC sampling for hidden markov models to determine copy number variations. <i>BMC Bioinformatics</i> , 2011, 12, 428.	2.6	8
32	SLIQ: Simple Linear Inequalities for Efficient Contig Scaffolding. <i>Journal of Computational Biology</i> , 2012, 19, 1162-1175.	1.6	8
33	Partially-supervised protein subclass discovery with simultaneous annotation of functional residues. <i>BMC Structural Biology</i> , 2009, 9, 68.	2.3	7
34	Gene expression trees in lymphoid development. <i>BMC Immunology</i> , 2007, 8, 25.	2.2	6
35	Efficient Algorithms for the Computational Design of Optimal Tiling Arrays. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2008, 5, 557-567.	3.0	6
36	Automatic learning of pre-miRNAs from different species. <i>BMC Bioinformatics</i> , 2016, 17, 224.	2.6	6

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37	Statistical Sensor Modelling for Autonomous Driving Using Autoregressive Input-Output HMMs. , 2018, , .		6
38	Deep Learning for Deep Waters: An Expert-in-the-Loop Machine Learning Framework for Marine Sciences. Journal of Marine Science and Engineering, 2021, 9, 169.	2.6	6
39	Developing Gato and CATBox with Python: Teaching Graph Algorithms through Visualization and Experimentation. Mathematics and Visualization, 2002, , 291-309.	0.6	6
40	Efficient Computational Design of Tiling Arrays Using a Shortest Path Approach. Lecture Notes in Computer Science, 2007, , 383-394.	1.3	5
41	Fast Bayesian Inference of Copy Number Variants using Hidden Markov Models with Wavelet Compression. PLoS Computational Biology, 2016, 12, e1004871.	3.2	5
42	Using Active Learning to Develop Machine Learning Models for Reaction Yield Prediction. Molecular Informatics, 2022, 41, .	2.5	5
43	Effects of network topology on the performance of consensus and distributed learning of SVMs using ADMM. PeerJ Computer Science, 2021, 7, e397.	4.5	4
44	An Indicator for the Number of Clusters: Using a Linear Map to Simplex Structure. , 2006, , 103-110.		4
45	New, Improved, and Practical k-Stem Sequence Similarity Measures for Probe Design. Journal of Computational Biology, 2008, 15, 525-534.	1.6	3
46	Selecting Oligonucleotide Probes for Whole-Genome Tiling Arrays with a Cross-Hybridization Potential. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 1642-1652.	3.0	3
47	Indel-tolerant read mapping with trinucleotide frequencies using cache-oblivious kd-trees. Bioinformatics, 2012, 28, i325-i332.	4.1	3
48	Effect of Network Topology on the Performance of ADMM-Based SVMs. , 2018, , .		3
49	pGQL: A probabilistic graphical query language for gene expression time courses. BioData Mining, 2011, 4, 9.	4.0	2
50	Context-Specific Independence Mixture Modelling for Protein Families. Lecture Notes in Computer Science, 2007, , 79-90.	1.3	2
51	Strongly Connected Components can Predict Protein Structure. Electronic Notes in Discrete Mathematics, 2001, 8, 10-13.	0.4	1
52	An Optimization Problem Related to Bloom Filters with Bit Patterns. Lecture Notes in Computer Science, 2018, , 525-538.	1.3	1
53	Using HaMMLET for Bayesian Segmentation of WGS Read-Depth Data. Methods in Molecular Biology, 2018, 1833, 83-93.	0.9	1
54	Fast parallel construction of variable-length Markov chains. BMC Bioinformatics, 2021, 22, 487.	2.6	1

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55	A new Algorithm for Accelerating Pair-Wise Computations of Melting Temperature. <i>Electronic Notes in Discrete Mathematics</i> , 2001, 8, 46-49.	0.4	0
56	Bayesian localization of CNV candidates in WGS data within minutes. <i>Algorithms for Molecular Biology</i> , 2019, 14, 20.	1.2	0
57	Validating Gene Clusterings by Selecting Informative Gene Ontology Terms with Mutual Information. <i>Lecture Notes in Computer Science</i> , 2007, , 81-92.	1.3	0
58	Mixture Model Based Group Inference in Fused Genotype and Phenotype Data. <i>Studies in Classification, Data Analysis, and Knowledge Organization</i> , 2008, , 119-126.	0.2	0
59	A Modeling Approach for Bioinformatics Workflows. <i>Lecture Notes in Business Information Processing</i> , 2019, , 167-183.	1.0	0
60	On External Indices for Mixtures: Validating Mixtures of Genes. , 2006, , 662-669.		0