Sepp Hochreiter

List of Publications by Year
in descending order

71	67,952	109321 35	98798 67
papers	citations	h-index	g-index

93	93	93	57315
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Long Short-Term Memory. Neural Computation, 1997, 9, 1735-1780.	2.2	58,553
2	The Vanishing Gradient Problem During Learning Recurrent Neural Nets and Problem Solutions. International Journal of Uncertainty, Fuzziness and Knowlege-Based Systems, 1998, 06, 107-116.	1.9	1,725
3	A comprehensive assessment of RNA-seq accuracy, reproducibility and information content by the Sequencing Quality Control Consortium. Nature Biotechnology, 2014, 32, 903-914.	17.5	883
4	DeepTox: Toxicity Prediction using Deep Learning. Frontiers in Environmental Science, 2016, 3, .	3.3	593
5	msa: an R package for multiple sequence alignment. Bioinformatics, 2015, 31, 3997-3999.	4.1	458
6	APCluster: an R package for affinity propagation clustering. Bioinformatics, 2011, 27, 2463-2464.	4.1	407
7	cn.MOPS: mixture of Poissons for discovering copy number variations in next-generation sequencing data with a low false discovery rate. Nucleic Acids Research, 2012, 40, e69-e69.	14.5	394
8	Flat Minima. Neural Computation, 1997, 9, 1-42.	2.2	388
9	Large-scale comparison of machine learning methods for drug target prediction on ChEMBL. Chemical Science, 2018, 9, 5441-5451.	7.4	357
10	DeepSynergy: predicting anti-cancer drug synergy with Deep Learning. Bioinformatics, 2018, 34, 1538-1546.	4.1	341
11	Toward Improved Predictions in Ungauged Basins: Exploiting the Power of Machine Learning. Water Resources Research, 2019, 55, 11344-11354.	4.2	279
12	Towards learning universal, regional, and local hydrological behaviors via machine learning applied to large-sample datasets. Hydrology and Earth System Sciences, 2019, 23, 5089-5110.	4.9	276
13	FABIA: factor analysis for bicluster acquisition. Bioinformatics, 2010, 26, 1520-1527.	4.1	258
14	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. Nature Communications, 2019, 10, 2674.	12.8	240
15	A new summarization method for affymetrix probe level data. Bioinformatics, 2006, 22, 943-949.	4.1	229
16	Learning to Learn Using Gradient Descent. Lecture Notes in Computer Science, 2001, , 87-94.	1.3	227
17	Repurposing High-Throughput Image Assays Enables Biological Activity Prediction for Drug Discovery. Cell Chemical Biology, 2018, 25, 611-618.e3.	5.2	176
18	FrÃ©chet ChemNet Distance: A Metric for Generative Models for Molecules in Drug Discovery. Journal of Chemical Information and Modeling, 2018, 58, 1736-1741.	5.4	161

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19	I/NI-calls for the exclusion of non-informative genes: a highly effective filtering tool for microarray data. Bioinformatics, 2007, 23, 2897-2902.	4.1	154
20	Assessing technical performance in differential gene expression experiments with external spike-in RNA control ratio mixtures. Nature Communications, 2014, 5, 5125.	12.8	122
21	Fast model-based protein homology detection without alignment. Bioinformatics, 2007, 23, 1728-1736.	4.1	106
22	Rainfallâ€“runoff prediction at multiple timescales with a single Long Short-Term Memory network. Hydrology and Earth System Sciences, 2021, 25, 2045-2062.	4.9	106
23	Prediction of human population responses to toxic compounds by a collaborative competition. Nature Biotechnology, 2015, 33, 933-940.	17.5	88
24	Using transcriptomics to guide lead optimization in drug discovery projects: Lessons learned from the QSTAR project. Drug Discovery Today, 2015, 20, 505-513.	6.4	80
25	Support Vector Machines for Dyadic Data. Neural Computation, 2006, 18, 1472-1510.	2.2	73
26	panelcn.MOPS: Copy-number detection in targeted NGS panel data for clinical diagnostics. Human Mutation, 2017, 38, 889-897.	2.5	72
27	Accurate Prediction of Biological Assays with High-Throughput Microscopy Images and Convolutional Networks. Journal of Chemical Information and Modeling, 2019, 59, 1163-1171.	5.4	69
28	Interpretable Deep Learning in Drug Discovery. Lecture Notes in Computer Science, 2019, , 331-345.	1.3	62
29	On failure modes in molecule generation and optimization. Drug Discovery Today: Technologies, 2019, 32-33, 55-63.	4.0	59
30	Feature Extraction Through LOCOCODE. Neural Computation, 1999, 11, 679-714.	2.2	55
31	NeuralHydrology â€“ Interpreting LSTMs in Hydrology. Lecture Notes in Computer Science, 2019, , 347-362.	1.3	46
32	KeBABS: an R package for kernel-based analysis of biological sequences. Bioinformatics, 2015, 31, 2574-2576.	4.1	44
33	Explaining and Interpreting LSTMs. Lecture Notes in Computer Science, 2019, , 211-238.	1.3	44
34	Machine Learning in Drug Discovery. Journal of Chemical Information and Modeling, 2019, 59, 945-946.	5.4	43
35	In silico proof of principle of machine learning-based antibody design at unconstrained scale. MAbs, 2022, 14, 2031482.	5.2	40
36	Complex Networks Govern Coiled-Coil Oligomerization â€“ Predicting and Profiling by Means of a Machine Learning Approach. Molecular and Cellular Proteomics, 2011, 10, M110.004994.	3.8	39

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37	Furby: fuzzy force-directed bicluster visualization. BMC Bioinformatics, 2014, 15, S4.	2.6	38
38	Uncertainty estimation with deep learning for rainfallâ€“runoff modeling. Hydrology and Earth System Sciences, 2022, 26, 1673-1693.	4.9	38
39	A note on leveraging synergy in multiple meteorological data sets with deep learning for rainfallâ€“runoff modeling. Hydrology and Earth System Sciences, 2021, 25, 2685-2703.	4.9	35
40	Large-Scale Ligand-Based Virtual Screening for SARS-CoV-2 Inhibitors Using Deep Neural Networks. SSRN Electronic Journal, 0, , .	0.4	35
41	The Promise of AI for DILI Prediction. Frontiers in Artificial Intelligence, 2021, 4, 638410.	3.4	31
42	Improving Few- and Zero-Shot Reaction Template Prediction Using Modern Hopfield Networks. Journal of Chemical Information and Modeling, 2022, 62, 2111-2120.	5.4	30
43	Connecting gene expression data from connectivity map and in silico target predictions for small molecule mechanism-of-action analysis. Molecular BioSystems, 2015, 11, 86-96.	2.9	28
44	An SMO Algorithm for the Potential Support Vector Machine. Neural Computation, 2008, 20, 271-287.	2.2	27
45	DEXUS: identifying differential expression in RNA-Seq studies with unknown conditions. Nucleic Acids Research, 2013, 41, e198-e198.	14.5	26
46	Industry-scale application and evaluation of deep learning for drug target prediction. Journal of Cheminformatics, 2020, 12, 26.	6.1	23
47	Machine learningâ€“based prediction of transfusion. Transfusion, 2020, 60, 1977-1986.	1.6	22
48	Filtering data from high-throughput experiments based on measurement reliability. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, E173-4; author reply E175.	7.1	21
49	HapFABIA: Identification of very short segments of identity by descent characterized by rare variants in large sequencing data. Nucleic Acids Research, 2013, 41, e202-e202.	14.5	21
50	Machine Learning in Drug Discovery. Journal of Chemical Information and Modeling, 2018, 58, 1723-1724.	5.4	21
51	Visual Scene Understanding for Autonomous Driving Using Semantic Segmentation. Lecture Notes in Computer Science, 2019, , 285-296.	1.3	21
52	Artificial neural networks and pathologists recognize basal cell carcinomas based on different histological patterns. Modern Pathology, 2021, 34, 895-903.	5.5	20
53	cn.FARMS: a latent variable model to detect copy number variations in microarray data with a low false discovery rate. Nucleic Acids Research, 2011, 39, e79-e79.	14.5	19
54	Rchemcpp: a web service for structural analoging in ChEMBL, Drugbank and the Connectivity Map. Bioinformatics, 2015, 31, 3392-3394.	4.1	16

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55	Domain Shifts in Machine Learning Based Covid-19 Diagnosis From Blood Tests. Journal of Medical Systems, 2022, 46, 23.	3.6	14
56	Genome-Wide Chromatin Remodeling Identified at GC-Rich Long Nucleosome-Free Regions. PLoS ONE, 2012, 7, e47924.	2.5	13
57	Nonlinear Feature Selection with the Potential Support Vector Machine. Studies in Fuzziness and Soft Computing, 2006, , 419-438.	0.8	11
58	Informative or Noninformative Calls for Gene Expression: A Latent Variable Approach. Statistical Applications in Genetics and Molecular Biology, 2010, 9, Article 4.	0.6	8
59	Rectified factor networks for biclustering of omics data. Bioinformatics, 2017, 33, i59-i66.	4.1	7
60	Quantum Optical Experiments Modeled by Long Short-Term Memory. Photonics, 2021, 8, 535.	2.0	7
61	IBD Sharing between Africans, Neandertals, and Denisovans. Genome Biology and Evolution, 2016, 8, 3406-3416.	2.5	6
62	Unsupervised coding with lococode. Lecture Notes in Computer Science, 1997, , 655-660.	1.3	4
63	LOCOCODE versus PCA and ICA. Perspectives in Neural Computing, 1998, , 669-674.	0.1	3
64	Increasing the discovery power of -omics studies. Systems Biomedicine (Austin, Tex), 2013, 1, 84-93.	0.7	2
65	Cost Optimization at Early Stages of Design Using Deep Reinforcement Learning. , 2020, , .		2
66	Optimal gradient-based learning using importance weights. , 0, , .		1
67	Optimality of LSTD and its Relation to MC. , 2007, , .		1
68	Monaural Speech Separation by Support Vector Machines: Bridging the Divide Between Supervised and Unsupervised Learning Methods. Signals and Communication Technology, 2007, , 411-428.	0.5	1
69	Optimal kernels for unsupervised learning. , 0, , .		0
70	Detection of Nonlinear Effects in Gene Expression Pathways. Nature Precedings, 2010, , .	0.1	0
71	Identifying Copy Number Variations based on Next Generation Sequencing Data by a Mixture of Poisson Model. Nature Precedings, 2010, , .	0.1	0