## Tapio Salakoski

List of Publications by Year in descending order

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361413 182427 3,070 67 20 51 citations h-index g-index papers 70 70 70 3679 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	A large-scale evaluation of computational protein function prediction. Nature Methods, 2013, 10, 221-227.	19.0	789
2	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. Genome Biology, 2016, 17, 184.	8.8	308
3	BioInfer: a corpus for information extraction in the biomedical domain. BMC Bioinformatics, 2007, 8, 50.	2.6	288
4	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. Genome Biology, 2019, 20, 244.	8.8	261
5	All-paths graph kernel for protein-protein interaction extraction with evaluation of cross-corpus learning. BMC Bioinformatics, 2008, 9, S2.	2.6	193
6	Regularized Machine Learning in the Genetic Prediction of Complex Traits. PLoS Genetics, 2014, 10, e1004754.	3.5	122
7	An experimental comparison of cross-validation techniques for estimating the area under the ROC curve. Computational Statistics and Data Analysis, 2011, 55, 1828-1844.	1.2	116
8	What about a simple language? Analyzing the difficulties in learning to program. Computer Science Education, 2006, 16, 211-227.	3.7	88
9	Large-Scale Event Extraction from Literature with Multi-Level Gene Normalization. PLoS ONE, 2013, 8, e55814.	2.5	83
10	Artificial intelligence in nursing: Priorities and opportunities from an international invitational thinkâ€ŧank of the Nursing and Artificial Intelligence Leadership Collaborative. Journal of Advanced Nursing, 2021, 77, 3707-3717.	3.3	67
11	Selection of a representative set of structures from brookhaven protein data bank. Proteins: Structure, Function and Bioinformatics, 1992, 14, 265-276.	2.6	55
12	University of Turku in the BioNLP'11 Shared Task. BMC Bioinformatics, 2012, 13, S4.	2.6	49
13	Comparison of automatic summarisation methods for clinical free text notes. Artificial Intelligence in Medicine, 2016, 67, 25-37.	6.5	42
14	EXTRACTING CONTEXTUALIZED COMPLEX BIOLOGICAL EVENTS WITH RICH GRAPH-BASED FEATURE SETS. Computational Intelligence, 2011, 27, 541-557.	3.2	38
15	Exploring Biomolecular Literature with EVEX: Connecting Genes through Events, Homology, and Indirect Associations. Advances in Bioinformatics, 2012, 2012, 1-12.	5.7	35
16	Lexical adaptation of link grammar to the biomedical sublanguage: a comparative evaluation of three approaches. BMC Bioinformatics, 2006, 7, S2.	2.6	34
17	Predicting patient acuity from electronic patient records. Journal of Biomedical Informatics, 2014, 51, 35-40.	4.3	31
18	Learning intransitive reciprocal relations with kernel methods. European Journal of Operational Research, 2010, 206, 676-685.	5 <b>.</b> 7	28

#	Article	IF	Citations
19	Wrapper-based selection of genetic features in genome-wide association studies through fast matrix operations. Algorithms for Molecular Biology, 2012, $7,11.$	1.2	28
20	On study habits on an introductory course on programming. Computer Science Education, 2015, 25, 276-291.	3.7	26
21	General formulation and evaluation of agglomerative clustering methods with metric and non-metric distances. Pattern Recognition, 1993, 26, 1395-1406.	8.1	23
22	Multi-Perspective Study of Novice Learners Adopting the Visual Algorithm Simulation Exercise System TRAKLA2. Informatics in Education, 2005, 4, 49-68.	2.2	22
23	Evaluation of two dependency parsers on biomedical corpus targeted at protein–protein interactions. International Journal of Medical Informatics, 2006, 75, 430-442.	3.3	21
24	Multi-label learning under feature extraction budgets. Pattern Recognition Letters, 2014, 40, 56-65.	4.2	20
25	Combining hidden Markov models and latent semantic analysis for topic segmentation and labeling: Method and clinical application. International Journal of Medical Informatics, 2009, 78, e1-e6.	3.3	19
26	Programming Misconceptions in an Introductory Level Programming Course Exam., 2016,,.		19
27	Training linear ranking SVMs in linearithmic time using red–black trees. Pattern Recognition Letters, 2011, 32, 1328-1336.	4.2	18
28	Accurate prediction of protein secondary structural class with fuzzy structural vectors. Protein Engineering, Design and Selection, 1995, 8, 505-512.	2.1	16
29	A Kernel-Based Framework for Learning Graded Relations From Data. IEEE Transactions on Fuzzy Systems, 2012, 20, 1090-1101.	9.8	16
30	Wide-scope biomedical named entity recognition and normalization with CRFs, fuzzy matching and character level modeling. Database: the Journal of Biological Databases and Curation, 2018, 2018, 1-10.	3.0	14
31	Analysis of link grammar on biomedical dependency corpus targeted at protein-protein interactions. , 2004, , .		14
32	Contextual weighting for Support Vector Machines in literature mining: an application to gene versus protein name disambiguation. BMC Bioinformatics, 2005, 6, 157.	2.6	13
33	Speeding Up Greedy Forward Selection for Regularized Least-Squares. , 2010, , .		13
34	Applying language technology to nursing documents: Pros and cons with a focus on ethics. International Journal of Medical Informatics, 2007, 76, S293-S301.	3.3	11
35	Neural Network and Random Forest Models in Protein Function Prediction. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 1772-1781.	3.0	11
36	Representative selection of proteins based on nuclear families. Protein Engineering, Design and Selection, 1995, 8, 501-503.	2.1	10

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37	U-Compare bio-event meta-service: compatible BioNLP event extraction services. BMC Bioinformatics, 2011, 12, 481.	2.6	10
38	Conditional Ranking on Relational Data. Lecture Notes in Computer Science, 2010, , 499-514.	1.3	10
39	Matrix representations, linear transformations, andÂkernels for disambiguation in natural language. Machine Learning, 2009, 74, 133-158.	5.4	9
40	Define and Visualize Your First Programming Language. , 2008, , .		8
41	Towards automated processing of clinical Finnish: Sublanguage analysis and a rule-based parser. International Journal of Medical Informatics, 2009, 78, e7-e12.	3.3	8
42	Comparing the collaborative and independent viewing of program visualizations. , $2011, \ldots$		8
43	Supporting the use of standardized nursing terminologies with automatic subject heading prediction: a comparison of sentence-level text classification methods. Journal of the American Medical Informatics Association: JAMIA, 2020, 27, 81-88.	4.4	8
44	Supporting Communication and Decision Making in Finnish Intensive Care with Language Technology. Journal of Healthcare Engineering, 2010, 1, 595-613.	1.9	7
45	Application of the EVEX resource to event extraction and network construction: Shared Task entry and result analysis. BMC Bioinformatics, 2015, 16, S3.	2.6	7
46	Assisting nurses in care documentation: from automated sentence classification to coherent document structures with subject headings. Journal of Biomedical Semantics, 2020, 11, 10.	1.6	7
47	How does collaboration affect algorithm learning? A case study using TRAKLA2 algorithm visualization tool. , 2010, , .		6
48	On Learning and Cross-Validation with Decomposed Nyström Approximation of Kernel Matrix. Neural Processing Letters, 2011, 33, 17-30.	3.2	4
49	Locality-Convolution Kernel and Its Application to Dependency Parse Ranking. Lecture Notes in Computer Science, 2006, , 610-618.	1.3	4
50	Assessment of metal ion concentration in water with structured feature selection. Chemosphere, 2017, 185, 1063-1071.	8.2	3
51	Efficient Hold-Out for Subset of Regressors. Lecture Notes in Computer Science, 2009, , 350-359.	1.3	3
52	An Improved Training Algorithm for the Linear Ranking Support Vector Machine. Lecture Notes in Computer Science, 2011, , 134-141.	1.3	3
53	Feature selection for regularized least-squares: New computational short-cuts and fast algorithmic implementations. , 2010, , .		2
54	Representative noise-free complete-link classification with application to protein structures. Pattern Recognition, 1997, 30, 467-482.	8.1	1

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55	Locality kernels for sequential data and their applications to parse ranking. Applied Intelligence, 2009, 31, 81-88.	5.3	1
56	Applying Permutation Tests for Assessing the Statistical Significance of Wrapper Based Feature Selection. , 2010, , .		1
57	Fast and parallelized greedy forward selection of genetic variants in Genome-wide association studies., 2011,,.		1
58	Secondary use of electronic health records: Availability aspects in two Nordic countries. Health Information Management Journal, 2019, 48, 144-151.	1.2	1
59	Incorporating External Information in Bayesian Classifiers Via Linear Feature Transformations. Lecture Notes in Computer Science, 2006, , 399-410.	1.3	1
60	Text Classification Model Explainability for Keyword Extraction – Towards Keyword-Based Summarization of Nursing Care Episodes. Studies in Health Technology and Informatics, 2022, , .	0.3	1
61	Evaluation of Protein Hydropathy Scales. , 2007, , .		0
62	Greedy Regularized Least-Squares for Multi-task Learning. , 2011, , .		0
63	Learning Valued Relations from Data. Advances in Intelligent and Soft Computing, 2011, , 257-268.	0.2	O
64	Avoiding Hazards – What Can Health Care Learn from Aviation?. Communications in Computer and Information Science, 2012, , 119-127.	0.5	0
65	Properties of Object-Level Cross-Validation Schemes for Symmetric Pair-Input Data. Lecture Notes in Computer Science, 2014, , 384-393.	1.3	0
66	Learning Low Cost Multi-target Models by Enforcing Sparsity. Lecture Notes in Computer Science, 2015, , 252-261.	1.3	0
67	Clustering Nursing Sentences – Comparing Three Sentence Embedding Methods. Studies in Health Technology and Informatics, 2022, , .	0.3	O