

Tapio Salakoski

List of Publications by Year in descending order

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Version: 2024-02-01

67
papers

3,070
citations

361413

20
h-index

182427

51
g-index

70
all docs

70
docs citations

70
times ranked

3679
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Clustering Nursing Sentences – Comparing Three Sentence Embedding Methods. Studies in Health Technology and Informatics, 2022, , .	0.3	0
3	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
4	Artificial intelligence in nursing: Priorities and opportunities from an international invitational think-tank of the Nursing and Artificial Intelligence Leadership Collaborative. Journal of Advanced Nursing, 2021, 77, 3707-3717.	3.3	67
5	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
6	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
7	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
8	Secondary use of electronic health records: Availability aspects in two Nordic countries. Health Information Management Journal, 2019, 48, 144-151.	1.2	1
9	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
10	Assessment of metal ion concentration in water with structured feature selection. Chemosphere, 2017, 185, 1063-1071.	8.2	3
11	Programming Misconceptions in an Introductory Level Programming Course Exam. , 2016, , .		19
12	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. Genome Biology, 2016, 17, 184.	8.8	308
13	Comparison of automatic summarisation methods for clinical free text notes. Artificial Intelligence in Medicine, 2016, 67, 25-37.	6.5	42
14	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
15	On study habits on an introductory course on programming. Computer Science Education, 2015, 25, 276-291.	3.7	26
16	Learning Low Cost Multi-target Models by Enforcing Sparsity. Lecture Notes in Computer Science, 2015, , 252-261.	1.3	0
17	Regularized Machine Learning in the Genetic Prediction of Complex Traits. PLoS Genetics, 2014, 10, e1004754.	3.5	122
18	Predicting patient acuity from electronic patient records. Journal of Biomedical Informatics, 2014, 51, 35-40.	4.3	31

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19	Multi-label learning under feature extraction budgets. <i>Pattern Recognition Letters</i> , 2014, 40, 56-65.	4.2	20
20	Properties of Object-Level Cross-Validation Schemes for Symmetric Pair-Input Data. <i>Lecture Notes in Computer Science</i> , 2014, , 384-393.	1.3	0
21	A large-scale evaluation of computational protein function prediction. <i>Nature Methods</i> , 2013, 10, 221-227.	19.0	789
22	Large-Scale Event Extraction from Literature with Multi-Level Gene Normalization. <i>PLoS ONE</i> , 2013, 8, e55814.	2.5	83
23	A Kernel-Based Framework for Learning Graded Relations From Data. <i>IEEE Transactions on Fuzzy Systems</i> , 2012, 20, 1090-1101.	9.8	16
24	Wrapper-based selection of genetic features in genome-wide association studies through fast matrix operations. <i>Algorithms for Molecular Biology</i> , 2012, 7, 11.	1.2	28
25	Exploring Biomolecular Literature with EVEX: Connecting Genes through Events, Homology, and Indirect Associations. <i>Advances in Bioinformatics</i> , 2012, 2012, 1-12.	5.7	35
26	University of Turku in the BioNLP'11 Shared Task. <i>BMC Bioinformatics</i> , 2012, 13, S4.	2.6	49
27	Avoiding Hazards – What Can Health Care Learn from Aviation?. <i>Communications in Computer and Information Science</i> , 2012, , 119-127.	0.5	0
28	Comparing the collaborative and independent viewing of program visualizations. , 2011, , .		8
29	Fast and parallelized greedy forward selection of genetic variants in Genome-wide association studies. , 2011, , .		1
30	Greedy Regularized Least-Squares for Multi-task Learning. , 2011, , .		0
31	EXTRACTING CONTEXTUALIZED COMPLEX BIOLOGICAL EVENTS WITH RICH GRAPH-BASED FEATURE SETS. <i>Computational Intelligence</i> , 2011, 27, 541-557.	3.2	38
32	U-Compare bio-event meta-service: compatible BioNLP event extraction services. <i>BMC Bioinformatics</i> , 2011, 12, 481.	2.6	10
33	On Learning and Cross-Validation with Decomposed Nyström Approximation of Kernel Matrix. <i>Neural Processing Letters</i> , 2011, 33, 17-30.	3.2	4
34	An experimental comparison of cross-validation techniques for estimating the area under the ROC curve. <i>Computational Statistics and Data Analysis</i> , 2011, 55, 1828-1844.	1.2	116
35	Training linear ranking SVMs in linearithmic time using red –black trees. <i>Pattern Recognition Letters</i> , 2011, 32, 1328-1336.	4.2	18
36	An Improved Training Algorithm for the Linear Ranking Support Vector Machine. <i>Lecture Notes in Computer Science</i> , 2011, , 134-141.	1.3	3

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37	Learning Valued Relations from Data. <i>Advances in Intelligent and Soft Computing</i> , 2011, , 257-268.	0.2	0
38	How does collaboration affect algorithm learning? A case study using TRAKLA2 algorithm visualization tool. , 2010, , .		6
39	Learning intransitive reciprocal relations with kernel methods. <i>European Journal of Operational Research</i> , 2010, 206, 676-685.	5.7	28
40	Supporting Communication and Decision Making in Finnish Intensive Care with Language Technology. <i>Journal of Healthcare Engineering</i> , 2010, 1, 595-613.	1.9	7
41	Feature selection for regularized least-squares: New computational short-cuts and fast algorithmic implementations. , 2010, , .		2
42	Applying Permutation Tests for Assessing the Statistical Significance of Wrapper Based Feature Selection. , 2010, , .		1
43	Speeding Up Greedy Forward Selection for Regularized Least-Squares. , 2010, , .		13
44	Conditional Ranking on Relational Data. <i>Lecture Notes in Computer Science</i> , 2010, , 499-514.	1.3	10
45	Combining hidden Markov models and latent semantic analysis for topic segmentation and labeling: Method and clinical application. <i>International Journal of Medical Informatics</i> , 2009, 78, e1-e6.	3.3	19
46	Towards automated processing of clinical Finnish: Sublanguage analysis and a rule-based parser. <i>International Journal of Medical Informatics</i> , 2009, 78, e7-e12.	3.3	8
47	Locality kernels for sequential data and their applications to parse ranking. <i>Applied Intelligence</i> , 2009, 31, 81-88.	5.3	1
48	Matrix representations, linear transformations, and kernels for disambiguation in natural language. <i>Machine Learning</i> , 2009, 74, 133-158.	5.4	9
49	Efficient Hold-Out for Subset of Regressors. <i>Lecture Notes in Computer Science</i> , 2009, , 350-359.	1.3	3
50	All-paths graph kernel for protein-protein interaction extraction with evaluation of cross-corpus learning. <i>BMC Bioinformatics</i> , 2008, 9, S2.	2.6	193
51	Define and Visualize Your First Programming Language. , 2008, , .		8
52	Evaluation of Protein Hydropathy Scales. , 2007, , .		0
53	BiolNfer: a corpus for information extraction in the biomedical domain. <i>BMC Bioinformatics</i> , 2007, 8, 50.	2.6	288
54	Applying language technology to nursing documents: Pros and cons with a focus on ethics. <i>International Journal of Medical Informatics</i> , 2007, 76, S293-S301.	3.3	11

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55	What about a simple language? Analyzing the difficulties in learning to program. Computer Science Education, 2006, 16, 211-227.	3.7	88
56	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
57	Lexical adaptation of link grammar to the biomedical sublanguage: a comparative evaluation of three approaches. BMC Bioinformatics, 2006, 7, S2.	2.6	34
58	Locality-Convolution Kernel and Its Application to Dependency Parse Ranking. Lecture Notes in Computer Science, 2006, , 610-618.	1.3	4
59	Incorporating External Information in Bayesian Classifiers Via Linear Feature Transformations. Lecture Notes in Computer Science, 2006, , 399-410.	1.3	1
60	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
61	Multi-Perspective Study of Novice Learners Adopting the Visual Algorithm Simulation Exercise System TRAKLA2. Informatics in Education, 2005, 4, 49-68.	2.2	22
62	Analysis of link grammar on biomedical dependency corpus targeted at protein-protein interactions. , 2004, , .		14
63	Representative noise-free complete-link classification with application to protein structures. Pattern Recognition, 1997, 30, 467-482.	8.1	1
64	Representative selection of proteins based on nuclear families. Protein Engineering, Design and Selection, 1995, 8, 501-503.	2.1	10
65	Accurate prediction of protein secondary structural class with fuzzy structural vectors. Protein Engineering, Design and Selection, 1995, 8, 505-512.	2.1	16
66	General formulation and evaluation of agglomerative clustering methods with metric and non-metric distances. Pattern Recognition, 1993, 26, 1395-1406.	8.1	23
67	Selection of a representative set of structures from brookhaven protein data bank. Proteins: Structure, Function and Bioinformatics, 1992, 14, 265-276.	2.6	55