

# Blaz Zupan

## List of Publications by Year in descending order

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Version: 2024-02-01

109  
papers

7,569  
citations

81900

39  
h-index

58581

82  
g-index

115  
all docs

115  
docs citations

115  
times ranked

10057  
citing authors

#	ARTICLE	IF	CITATIONS
1	Embedding to reference t-SNE space addresses batch effects in single-cell classification. Machine Learning, 2023, 112, 721-740.	5.4	10
2	Hands-on training about overfitting. PLoS Computational Biology, 2021, 17, e1008671.	3.2	34
3	Transcriptional milestones in <i>Dictyostelium</i> development. Genome Research, 2021, 31, 1498-1511.	5.5	11
4	Seroprevalence of severe acute respiratory syndrome coronavirus 2 in Slovenia: results of two rounds of a nationwide population study on a probability-based sample, challenges and lessons learned. Clinical Microbiology and Infection, 2021, 27, 1039.e1-1039.e7.	6.0	17
5	RICERCANDO: Data mining toolkit for mobile broadband measurements. Computer Networks, 2020, 177, 107294.	5.1	2
6	scOrange—a tool for hands-on training of concepts from single-cell data analytics. Bioinformatics, 2019, 35, i4-i12.	4.1	8
7	Democratized image analytics by visual programming through integration of deep models and small-scale machine learning. Nature Communications, 2019, 10, 4551.	12.8	44
8	Fast optimization of non-negative matrix tri-factorization. PLoS ONE, 2019, 14, e0217994.	2.5	12
9	Embedding to Reference t-SNE Space Addresses Batch Effects in Single-Cell Classification. Lecture Notes in Computer Science, 2019, , 246-260.	1.3	4
10	Genome Sequence of a Lethal Strain of Xylem-Invading <i>Verticillium nonalfalfae</i> . Genome Announcements, 2018, 6, .	0.8	13
11	From hype to reality: data science enabling personalized medicine. BMC Medicine, 2018, 16, 150.	5.5	278
12	A comprehensive structural, biochemical and biological profiling of the human NUDIX hydrolase family. Nature Communications, 2017, 8, 1541.	12.8	124
13	dictyExpress: a web-based platform for sequence data management and analytics in <i>Dictyostelium</i> and beyond. BMC Bioinformatics, 2017, 18, 291.	2.6	29
14	Scalable non-negative matrix tri-factorization. BioData Mining, 2017, 10, 41.	4.0	7
15	Jumping across biomedical contexts using compressive data fusion. Bioinformatics, 2016, 32, i90-i100.	4.1	24
16	Gene discovery by chemical mutagenesis and whole-genome sequencing in <i>Dictyostelium</i> . Genome Research, 2016, 26, 1268-1276.	5.5	23
17	COLLECTIVE PAIRWISE CLASSIFICATION FOR MULTI-WAY ANALYSIS OF DISEASE AND DRUG DATA. , 2016, , .		13
18	Orthogonal matrix factorization enables integrative analysis of multiple RNA binding proteins. Bioinformatics, 2016, 32, 1527-1535.	4.1	108

#	ARTICLE	IF	CITATIONS
19	COLLECTIVE PAIRWISE CLASSIFICATION FOR MULTI-WAY ANALYSIS OF DISEASE AND DRUG DATA. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2016, 21, 81-92.	0.7	11
20	Concurrent software architectures for exploratory data analysis. Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery, 2015, 5, 165-180.	6.8	1
21	Gene Prioritization by Compressive Data Fusion and Chaining. PLoS Computational Biology, 2015, 11, e1004552.	3.2	22
22	Data Imputation in Epistatic MAPs by Network-Guided Matrix Completion. Journal of Computational Biology, 2015, 22, 595-608.	1.6	11
23	Gene network inference by fusing data from diverse distributions. Bioinformatics, 2015, 31, i230-i239.	4.1	34
24	Leaps and lulls in the developmental transcriptome of Dictyostelium discoideum. BMC Genomics, 2015, 16, 294.	2.8	61
25	Data Fusion by Matrix Factorization. IEEE Transactions on Pattern Analysis and Machine Intelligence, 2015, 37, 41-53.	13.9	166
26	Integrative Clustering by Nonnegative Matrix Factorization Can Reveal Coherent Functional Groups From Gene Profile Data. IEEE Journal of Biomedical and Health Informatics, 2015, 19, 698-708.	6.3	1
27	Matrix factorization-based data fusion for drug-induced liver injury prediction. Systems Biomedicine (Austin, Tex ), 2014, 2, 16-22.	0.7	13
28	Survival regression by data fusion. Systems Biomedicine (Austin, Tex ), 2014, 2, 47-53.	0.7	3
29	Crosslinking-immunoprecipitation (iCLIP) analysis reveals global regulatory roles of hnRNP L. RNA Biology, 2014, 11, 146-155.	3.1	82
30	Gene network inference by probabilistic scoring of relationships from a factorized model of interactions. Bioinformatics, 2014, 30, i246-i254.	4.1	3
31	Assessment of Machine Learning Reliability Methods for Quantifying the Applicability Domain of QSAR Regression Models. Journal of Chemical Information and Modeling, 2014, 54, 431-441.	5.4	46
32	Heterogeneous computing architecture for fast detection of SNP-SNP interactions. BMC Bioinformatics, 2014, 15, 216.	2.6	17
33	Computational models reveal genotype-phenotype associations in <i>Saccharomyces cerevisiae</i> . Yeast, 2014, 31, 265-277.	1.7	20
34	Matrix factorization-based data fusion for gene function prediction in baker's yeast and slime mold. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2014, , 400-11.	0.7	14
35	Discovering disease-disease associations by fusing systems-level molecular data. Scientific Reports, 2013, 3, 3202.	3.3	96
36	Transcriptional Profiling of Dictyostelium with RNA Sequencing. Methods in Molecular Biology, 2013, 983, 139-171.	0.9	17

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37	Bacterial Discrimination by Dictyostelid Amoebae Reveals the Complexity of Ancient Interspecies Interactions. <i>Current Biology</i> , 2013, 23, 862-872.	3.9	69
38	Computational Models for Prediction of Yeast Strain Potential for Winemaking from Phenotypic Profiles. <i>PLoS ONE</i> , 2013, 8, e66523.	2.5	21
39	ABC Transporters in <i>Dictyostelium discoideum</i> Development. <i>PLoS ONE</i> , 2013, 8, e70040.	2.5	14
40	Analysis of CLIP and iCLIP methods for nucleotide-resolution studies of protein-RNA interactions. <i>Genome Biology</i> , 2012, 13, R67.	9.6	195
41	Widespread binding of FUS along nascent RNA regulates alternative splicing in the brain. <i>Scientific Reports</i> , 2012, 2, 603.	3.3	231
42	OCT4 and the acquisition of oocyte developmental competence during folliculogenesis. <i>International Journal of Developmental Biology</i> , 2012, 56, 853-858.	0.6	16
43	Supporting Regenerative Medicine by Integrative Dimensionality Reduction. <i>Methods of Information in Medicine</i> , 2012, 51, 341-347.	1.2	5
44	Knowledge-based bioinformatics for the study of mammalian oocytes. <i>International Journal of Developmental Biology</i> , 2012, 56, 859-866.	0.6	1
45	iCLIP - Transcriptome-wide Mapping of Protein-RNA Interactions with Individual Nucleotide Resolution. <i>Journal of Visualized Experiments</i> , 2011, , .	0.3	168
46	Characterizing the RNA targets and position-dependent splicing regulation by TDP-43. <i>Nature Neuroscience</i> , 2011, 14, 452-458.	14.8	956
47	Bzpf is a CREB-like transcription factor that regulates spore maturation and stability in <i>Dictyostelium</i> . <i>Developmental Biology</i> , 2011, 358, 137-146.	2.0	19
48	miR669a and miR669q prevent skeletal muscle differentiation in postnatal cardiac progenitors. <i>Journal of Cell Biology</i> , 2011, 193, 1197-1212.	5.2	77
49	Stage prediction of embryonic stem cell differentiation from genome-wide expression data. <i>Bioinformatics</i> , 2011, 27, 2546-2553.	4.1	18
50	Analysis of alternative splicing associated with aging and neurodegeneration in the human brain. <i>Genome Research</i> , 2011, 21, 1572-1582.	5.5	199
51	Subgroup discovery in data sets with multi-dimensional responses. <i>Intelligent Data Analysis</i> , 2011, 15, 533-549.	0.9	14
52	SNPsyn: detection and exploration of SNP-SNP interactions. <i>Nucleic Acids Research</i> , 2011, 39, W444-W449.	14.5	35
53	A Data Mining Library for miRNA Annotation and Analysis. <i>Lecture Notes in Computer Science</i> , 2011, , 80-84.	1.3	1
54	Ranking and 1-Dimensional Projection of Cell Development Transcription Profiles. <i>Lecture Notes in Computer Science</i> , 2011, , 85-89.	1.3	1

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55	Similarity of Transcription Profiles for Genes in Gene Sets. Lecture Notes in Computer Science, 2011, , 393-399.	1.3	0
56	New components of the Dictyostelium PKA pathway revealed by Bayesian analysis of expression data. BMC Bioinformatics, 2010, 11, 163.	2.6	10
57	FragViz: visualization of fragmented networks. BMC Bioinformatics, 2010, 11, 475.	2.6	2
58	Does replication groups scoring reduce false positive rate in SNP interaction discovery?. BMC Genomics, 2010, 11, 58.	2.8	4
59	iCLIP reveals the function of hnRNP particles in splicing at individual nucleotide resolution. Nature Structural and Molecular Biology, 2010, 17, 909-915.	8.2	1,026
60	iCLIP Predicts the Dual Splicing Effects of TIA-RNA Interactions. PLoS Biology, 2010, 8, e1000530.	5.6	226
61	Conserved developmental transcriptomes in evolutionarily divergent species. Genome Biology, 2010, 11, R35.	9.6	164
62	Inference of the Molecular Mechanism of Action from Genetic Interaction and Gene Expression Data. OMICS A Journal of Integrative Biology, 2010, 14, 357-367.	2.0	3
63	Textual features for corpus visualization using correspondence analysis. Intelligent Data Analysis, 2009, 13, 795-813.	0.9	9
64	dictyBaseâ€”a Dictyostelium bioinformatics resource update. Nucleic Acids Research, 2009, 37, D515-D519.	14.5	71
65	dictyExpress: a Dictyostelium discoideum gene expression database with an explorative data analysis web-based interface. BMC Bioinformatics, 2009, 10, 265.	2.6	63
66	Polymorphic Members of the lag Gene Family Mediate Kin Discrimination in Dictyostelium. Current Biology, 2009, 19, 567-572.	3.9	204
67	Computational approaches for the genetic and phenotypic characterization of a <i>Saccharomyces cerevisiae</i> wine yeast collection. Yeast, 2009, 26, 675-692.	1.7	25
68	Subgroup Discovery in Data Sets with Multiâ€”dimensional Responses: A Method and a Case Study in Traumatology. Lecture Notes in Computer Science, 2009, , 265-274.	1.3	7
69	On Quality of Different Annotation Sources for Gene Expression Analysis. Lecture Notes in Computer Science, 2009, , 421-425.	1.3	3
70	Data Mining in Medicine. , 2009, , 1111-1136.		23
71	Rule-based Clustering for Gene Promoter Structure Discovery. Methods of Information in Medicine, 2009, 48, 229-235.	1.2	3
72	Data-Driven Revision of Decision Models. , 2009, , 617-623.		0

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73	Modelling impacts of cropping systems: Demands and solutions for DEX methodology. <i>European Journal of Operational Research</i> , 2008, 189, 594-608.	5.7	19
74	Predictive data mining in clinical medicine: Current issues and guidelines. <i>International Journal of Medical Informatics</i> , 2008, 77, 81-97.	3.3	653
75	Open-Source Tools for Data Mining. <i>Clinics in Laboratory Medicine</i> , 2008, 28, 37-54.	1.4	28
76	Bioinformatic approaches for the genetic and phenotypic characterization of a <i>Saccharomyces cerevisiae</i> wine yeast collection. <i>Nature Precedings</i> , 2008, , .	0.1	0
77	Finding Patterns in Class-Labeled Data Using Data Visualization. , 2008, , 106-123.		0
78	Visualization-based cancer microarray data classification analysis. <i>Bioinformatics</i> , 2007, 23, 2147-2154.	4.1	67
79	Predictive Model for Estimating Risk of Crush Syndrome: A Data Mining Approach. <i>Journal of Trauma</i> , 2007, 62, 940-945.	2.3	13
80	FreeVizâ€”An intelligent multivariate visualization approach to explorative analysis of biomedical data. <i>Journal of Biomedical Informatics</i> , 2007, 40, 661-671.	4.3	54
81	Towards knowledge-based gene expression data mining. <i>Journal of Biomedical Informatics</i> , 2007, 40, 787-802.	4.3	70
82	Discovery of Genetic Networks Through Abduction and Qualitative Simulation. <i>Lecture Notes in Computer Science</i> , 2007, , 228-247.	1.3	5
83	proDEX â€” A DSS tool for environmental decision-making. <i>Environmental Modelling and Software</i> , 2006, 21, 1514-1516.	4.5	16
84	VizRank: Data Visualization Guided by Machine Learning. <i>Data Mining and Knowledge Discovery</i> , 2006, 13, 119-136.	3.7	69
85	Knowledge-based data analysis and interpretation. <i>Artificial Intelligence in Medicine</i> , 2006, 37, 163-165.	6.5	16
86	Developmentally Regulated DNA Methylation in <i>Dictyostelium discoideum</i> . <i>Eukaryotic Cell</i> , 2006, 5, 18-25.	3.4	61
87	Data Mining in Medicine. , 2005, , 1107-1137.		9
88	Epistasis analysis with global transcriptional phenotypes. <i>Nature Genetics</i> , 2005, 37, 471-477.	21.4	100
89	TA-clustering: Cluster analysis of gene expression profiles through Temporal Abstractions. <i>International Journal of Medical Informatics</i> , 2005, 74, 505-517.	3.3	22
90	Nomograms for visualizing support vector machines. , 2005, , .		55

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91	Simple and effective visual models for gene expression cancer diagnostics. , 2005, , .		1
92	Microarray data mining with visual programming. <i>Bioinformatics</i> , 2005, 21, 396-398.	4.1	131
93	VizRank: finding informative data projections in functional genomics by machine learning. <i>Bioinformatics</i> , 2005, 21, 413-414.	4.1	58
94	GenePath: from mutations to genetic networks and back. <i>Nucleic Acids Research</i> , 2005, 33, W749-W752.	14.5	15
95	A function-decomposition method for development of hierarchical multi-attribute decision models. <i>Decision Support Systems</i> , 2004, 36, 215-233.	5.9	47
96	Nomograms for Visualization of Naive Bayesian Classifier. <i>Lecture Notes in Computer Science</i> , 2004, , 337-348.	1.3	63
97	Orange: From Experimental Machine Learning to Interactive Data Mining. <i>Lecture Notes in Computer Science</i> , 2004, , 537-539.	1.3	174
98	GenePath: a system for inference of genetic networks and proposal of genetic experiments. <i>Artificial Intelligence in Medicine</i> , 2003, 29, 107-130.	6.5	21
99	GenePath: a system for automated construction of genetic networks from mutant data. <i>Bioinformatics</i> , 2003, 19, 383-389.	4.1	54
100	Feature mining and predictive model construction from severe trauma patient's data. <i>International Journal of Medical Informatics</i> , 2001, 63, 41-50.	3.3	39
101	Predicting patient's long-term clinical status after hip arthroplasty using hierarchical decision modelling and data mining. <i>Methods of Information in Medicine</i> , 2001, 40, 25-31.	1.2	1
102	Applications of qualitative multi-attribute decision models in health care. <i>International Journal of Medical Informatics</i> , 2000, 58-59, 191-205.	3.3	67
103	Machine learning for survival analysis: a case study on recurrence of prostate cancer. <i>Artificial Intelligence in Medicine</i> , 2000, 20, 59-75.	6.5	107
104	Predictive model for survival at the conclusion of a damage control laparotomy. <i>American Journal of Surgery</i> , 2000, 180, 540-545.	1.8	42
105	Learning by discovering concept hierarchies. <i>Artificial Intelligence</i> , 1999, 109, 211-242.	5.8	56
106	Machine Learning for Survival Analysis: A Case Study on Recurrence of Prostate Cancer. <i>Lecture Notes in Computer Science</i> , 1999, , 346-355.	1.3	8
107	Acquiring background knowledge for machine learning using function decomposition: a case study in rheumatology. <i>Artificial Intelligence in Medicine</i> , 1998, 14, 101-117.	6.5	7
108	Relating clinical and neurophysiological assessment of spasticity by machine learning. <i>International Journal of Medical Informatics</i> , 1998, 49, 243-251.	3.3	9

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109	Optimization of rule-based systems using state space graphs. IEEE Transactions on Knowledge and Data Engineering, 1998, 10, 238-254.	5.7	22