

Gunnar RÃ¶tsch

List of Publications by Year in descending order

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Version: 2024-02-01

142
papers

31,559
citations

31976

53
h-index

16183

124
g-index

179
all docs

179
docs citations

179
times ranked

46976
citing authors

#	ARTICLE	IF	CITATIONS
1	The Cancer Genome Atlas Pan-Cancer analysis project. <i>Nature Genetics</i> , 2013, 45, 1113-1120.	21.4	6,265
2	An introduction to kernel-based learning algorithms. <i>IEEE Transactions on Neural Networks</i> , 2001, 12, 181-201.	4.2	2,811
3	The Molecular Taxonomy of Primary Prostate Cancer. <i>Cell</i> , 2015, 163, 1011-1025.	28.9	2,435
4	Determination and Inference of Eukaryotic Transcription Factor Sequence Specificity. <i>Cell</i> , 2014, 158, 1431-1443.	28.9	1,515
5	Fisher discriminant analysis with kernels. , 0, , .		1,381
6	Multiplatform Analysis of 12 Cancer Types Reveals Molecular Classification within and across Tissues of Origin. <i>Cell</i> , 2014, 158, 929-944.	28.9	1,242
7	Soft Margins for AdaBoost. <i>Machine Learning</i> , 2001, 42, 287-320.	5.4	1,000
8	Input space versus feature space in kernel-based methods. <i>IEEE Transactions on Neural Networks</i> , 1999, 10, 1000-1017.	4.2	953
9	Integrative Analysis of the <i>Caenorhabditis elegans</i> Genome by the modENCODE Project. <i>Science</i> , 2010, 330, 1775-1787.	12.6	912
10	Common Sequence Polymorphisms Shaping Genetic Diversity in <i>Arabidopsis thaliana</i> . <i>Science</i> , 2007, 317, 338-342.	12.6	689
11	Assessment of transcript reconstruction methods for RNA-seq. <i>Nature Methods</i> , 2013, 10, 1177-1184.	19.0	679
12	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. <i>Cancer Cell</i> , 2018, 34, 211-224.e6.	16.8	623
13	Multiple reference genomes and transcriptomes for <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2011, 477, 419-423.	27.8	593
14	Genomewide SNP variation reveals relationships among landraces and modern varieties of rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 12273-12278.	7.1	581
15	Support Vector Machines and Kernels for Computational Biology. <i>PLoS Computational Biology</i> , 2008, 4, e1000173.	3.2	515
16	RNA G-quadruplexes cause eIF4A-dependent oncogene translation in cancer. <i>Nature</i> , 2014, 513, 65-70.	27.8	506
17	Ecological Modeling from Time-Series Inference: Insight into Dynamics and Stability of Intestinal Microbiota. <i>PLoS Computational Biology</i> , 2013, 9, e1003388.	3.2	487
18	Systematic evaluation of spliced alignment programs for RNA-seq data. <i>Nature Methods</i> , 2013, 10, 1185-1191.	19.0	467

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19	DNA methylation in <i>Arabidopsis</i> has a genetic basis and shows evidence of local adaptation. <i>ELife</i> , 2015, 4, e05255.	6.0	457
20	Dual roles of the nuclear cap-binding complex and SERRATE in pre-mRNA splicing and microRNA processing in <i>Arabidopsis thaliana</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 8795-8800.	7.1	378
21	Engineering support vector machine kernels that recognize translation initiation sites. <i>Bioinformatics</i> , 2000, 16, 799-807.	4.1	373
22	Active Learning with Support Vector Machines in the Drug Discovery Process. <i>Journal of Chemical Information and Computer Sciences</i> , 2003, 43, 667-673.	2.8	281
23	Genomic basis for RNA alterations in cancer. <i>Nature</i> , 2020, 578, 129-136.	27.8	280
24	Stress-induced changes in the <i>Arabidopsis thaliana</i> transcriptome analyzed using whole-genome tiling arrays. <i>Plant Journal</i> , 2009, 58, 1068-1082.	5.7	273
25	Species-wide Genetic Incompatibility Analysis Identifies Immune Genes as Hot Spots of Deleterious Epistasis. <i>Cell</i> , 2014, 159, 1341-1351.	28.9	247
26	A spatial and temporal map of <i>C. elegans</i> gene expression. <i>Genome Research</i> , 2011, 21, 325-341.	5.5	241
27	Interferon- β regulates cellular metabolism and mRNA translation to potentiate macrophage activation. <i>Nature Immunology</i> , 2015, 16, 838-849.	14.5	239
28	Nonsense-Mediated Decay of Alternative Precursor mRNA Splicing Variants Is a Major Determinant of the <i>Arabidopsis</i> Steady State Transcriptome. <i>Plant Cell</i> , 2013, 25, 3726-3742.	6.6	209
29	An Introduction to Boosting and Leveraging. <i>Lecture Notes in Computer Science</i> , 2003, , 118-183.	1.3	206
30	Early prediction of circulatory failure in the intensive care unit using machine learning. <i>Nature Medicine</i> , 2020, 26, 364-373.	30.7	204
31	Constructing boosting algorithms from SVMs: an application to one-class classification. <i>IEEE Transactions on Pattern Analysis and Machine Intelligence</i> , 2002, 24, 1184-1199.	13.9	197
32	A global metagenomic map of urban microbiomes and antimicrobial resistance. <i>Cell</i> , 2021, 184, 3376-3393.e17.	28.9	164
33	Constructing descriptive and discriminative nonlinear features: rayleigh coefficients in kernel feature spaces. <i>IEEE Transactions on Pattern Analysis and Machine Intelligence</i> , 2003, 25, 623-628.	13.9	158
34	BRCA Challenge: BRCA Exchange as a global resource for variants in BRCA1 and BRCA2. <i>PLoS Genetics</i> , 2018, 14, e1007752.	3.5	148
35	A Pan-cancer Transcriptome Analysis Reveals Pervasive Regulation through Alternative Promoters. <i>Cell</i> , 2019, 178, 1465-1477.e17.	28.9	144
36	HBEGF ⁺ macrophages in rheumatoid arthritis induce fibroblast invasiveness. <i>Science Translational Medicine</i> , 2019, 11, .	12.4	143

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37	Accurate splice site prediction using support vector machines. BMC Bioinformatics, 2007, 8, S7.	2.6	135
38	RiboDiff: detecting changes of mRNA translation efficiency from ribosome footprints. Bioinformatics, 2017, 33, 139-141.	4.1	134
39	Prediction of potent shRNAs with a sequential classification algorithm. Nature Biotechnology, 2017, 35, 350-353.	17.5	129
40	<i>SplAdder</i>: identification, quantification and testing of alternative splicing events from RNA-Seq data. Bioinformatics, 2016, 32, 1840-1847.	4.1	124
41	Receptor-type guanylate cyclase is required for carbon dioxide sensation by <i>Caenorhabditis elegans</i>. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 254-259.	7.1	113
42	RASE: recognition of alternatively spliced exons in C.elegans. Bioinformatics, 2005, 21, i369-i377.	4.1	109
43	ARTS: accurate recognition of transcription starts in human. Bioinformatics, 2006, 22, e472-e480.	4.1	101
44	Alternative Splicing Substantially Diversifies the Transcriptome during Early Photomorphogenesis and Correlates with the Energy Availability in Arabidopsis. Plant Cell, 2016, 28, 2715-2734.	6.6	97
45	At-TAX: a whole genome tiling array resource for developmental expression analysis and transcript identification in Arabidopsis thaliana. Genome Biology, 2008, 9, R112.	9.6	91
46	Classifying 'Drug-likeness' with Kernel-Based Learning Methods. Journal of Chemical Information and Modeling, 2005, 45, 249-253.	5.4	90
47	A New Discriminative Kernel from Probabilistic Models. Neural Computation, 2002, 14, 2397-2414.	2.2	88
48	Optimal spliced alignments of short sequence reads. Bioinformatics, 2008, 24, i174-i180.	4.1	86
49	Polypyrimidine Tract Binding Protein Homologs from <i>Arabidopsis</i> Are Key Regulators of Alternative Splicing with Implications in Fundamental Developmental Processes. Plant Cell, 2012, 24, 4360-4375.	6.6	84
50	mGene: Accurate SVM-based gene finding with an application to nematode genomes. Genome Research, 2009, 19, 2133-2143.	5.5	79
51	The Tumor Profiler Study: integrated, multi-omic, functional tumor profiling for clinical decision support. Cancer Cell, 2021, 39, 288-293.	16.8	71
52	Global effects of the small RNA biogenesis machinery on the <i>Arabidopsis thaliana</i> transcriptome. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 17466-17473.	7.1	66
53	Quantitative RNA expression analysis with Affymetrix Tiling 1.0R arrays identifies new E2F target genes. Plant Journal, 2009, 57, 184-194.	5.7	65
54	Kernel PCA Pattern Reconstruction via Approximate Pre-Images. Perspectives in Neural Computing, 1998, , 147-152.	0.1	60

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55	Totally corrective boosting algorithms that maximize the margin. , 2006, , .		59
56	Learning Interpretable SVMs for Biological Sequence Classification. BMC Bioinformatics, 2006, 7, S9.	2.6	58
57	rQuant.web: a tool for RNA-Seq-based transcript quantitation. Nucleic Acids Research, 2010, 38, W348-W351.	14.5	58
58	Improving the <i>Caenorhabditis elegans</i> Genome Annotation Using Machine Learning. PLoS Computational Biology, 2007, 3, e20.	3.2	57
59	MITIE: Simultaneous RNA-Seq-based transcript identification and quantification in multiple samples. Bioinformatics, 2013, 29, 2529-2538.	4.1	57
60	<i>EIF1AX</i> and <i>RAS</i> Mutations Cooperate to Drive Thyroid Tumorigenesis through ATF4 and c-MYC. Cancer Discovery, 2019, 9, 264-281.	9.4	57
61	The Feature Importance Ranking Measure. Lecture Notes in Computer Science, 2009, , 694-709.	1.3	57
62	POIMs: positional oligomer importance matrices—understanding support vector machine-based signal detectors. Bioinformatics, 2008, 24, i6-i14.	4.1	51
63	Detecting polymorphic regions in <i>Arabidopsis thaliana</i> with resequencing microarrays. Genome Research, 2008, 18, 918-929.	5.5	50
64	Cohesin Rings Devoid of Scc3 and Pds5 Maintain Their Stable Association with the DNA. PLoS Genetics, 2012, 8, e1002856.	3.5	50
65	Leveraging Sequence Classification by Taxonomy-Based Multitask Learning. Lecture Notes in Computer Science, 2010, , 522-534.	1.3	50
66	RNA-Seq Read Alignments with PALMapper. Current Protocols in Bioinformatics, 2010, 32, Unit 11.6.	25.8	46
67	Efficient privacy-preserving string search and an application in genomics. Bioinformatics, 2016, 32, 1652-1661.	4.1	46
68	HnRNP L and L-like cooperate in multiple-exon regulation of CD45 alternative splicing. Nucleic Acids Research, 2012, 40, 5666-5678.	14.5	45
69	RNA-Seq analysis in mutant zebrafish reveals role of U1C protein in alternative splicing regulation. EMBO Journal, 2011, 30, 1965-1976.	7.8	39
70	Accurate detection of differential RNA processing. Nucleic Acids Research, 2013, 41, 5189-5198.	14.5	39
71	MMR: a tool for read multi-mapper resolution. Bioinformatics, 2016, 32, 770-772.	4.1	39
72	Genome-wide analysis of alternative splicing in <i>Volvox carteri</i> . BMC Genomics, 2014, 15, 1117.	2.8	37

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73	SCIM: universal single-cell matching with unpaired feature sets. <i>Bioinformatics</i> , 2020, 36, i919-i927.	4.1	37
74	Comparative analysis of mRNA and protein degradation in prostate tissues indicates high stability of proteins. <i>Nature Communications</i> , 2019, 10, 2524.	12.8	35
75	Communication-Efficient Jaccard similarity for High-Performance Distributed Genome Comparisons. , 2020, , .		34
76	Registered access: authorizing data access. <i>European Journal of Human Genetics</i> , 2018, 26, 1721-1731.	2.8	33
77	c-MYC regulates mRNA translation efficiency and start-site selection in lymphoma. <i>Journal of Experimental Medicine</i> , 2019, 216, 1509-1524.	8.5	32
78	Novel Machine Learning Methods for MHC Class I Binding Prediction. <i>Lecture Notes in Computer Science</i> , 2010, , 98-109.	1.3	30
79	New Methods for Splice Site Recognition. <i>Lecture Notes in Computer Science</i> , 2002, , 329-336.	1.3	28
80	Large scale genomic sequence SVM classifiers. , 2005, , .		27
81	Sparse Regression Ensembles in Infinite and Finite Hypothesis Spaces. <i>Machine Learning</i> , 2002, 48, 189-218.	5.4	26
82	Inferring latent task structure for Multitask Learning by Multiple Kernel Learning. <i>BMC Bioinformatics</i> , 2010, 11, S5.	2.6	24
83	mGene.web: a web service for accurate computational gene finding. <i>Nucleic Acids Research</i> , 2009, 37, W312-W316.	14.5	23
84	Building an international consortium for tracking coronavirus health status. <i>Nature Medicine</i> , 2020, 26, 1161-1165.	30.7	23
85	Optimal spliced alignments of short sequence reads. <i>BMC Bioinformatics</i> , 2008, 9, .	2.6	21
86	KIRMES: kernel-based identification of regulatory modules in euchromatic sequences. <i>Bioinformatics</i> , 2009, 25, 2126-2133.	4.1	21
87	Persistence and Availability of Web Services in Computational Biology. <i>PLoS ONE</i> , 2011, 6, e24914.	2.5	21
88	Support vector machines-based identification of alternative splicing in <i>Arabidopsis thaliana</i> from whole-genome tiling arrays. <i>BMC Bioinformatics</i> , 2011, 12, 55.	2.6	21
89	Genomic Rearrangements in <i>Arabidopsis</i> Considered as Quantitative Traits. <i>Genetics</i> , 2017, 205, 1425-1441.	2.9	21
90	Tumor Necrosis Factor dynamically regulates the mRNA stabilome in rheumatoid arthritis fibroblast-like synoviocytes. <i>PLoS ONE</i> , 2017, 12, e0179762.	2.5	21

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91	An Empirical Analysis of Topic Modeling for Mining Cancer Clinical Notes. , 2013, , .		20
92	Dynamic compression schemes for graph coloring. Bioinformatics, 2019, 35, 407-414.	4.1	19
93	Image reconstruction by linear programming. IEEE Transactions on Image Processing, 2005, 14, 737-744.	9.8	17
94	Prototype Classification: Insights from Machine Learning. Neural Computation, 2009, 21, 272-300.	2.2	17
95	Exploiting physico-chemical properties in string kernels. BMC Bioinformatics, 2010, 11, S7.	2.6	17
96	Targeting eIF4A-Dependent Translation of KRAS Signaling Molecules. Cancer Research, 2021, 81, 2002-2014.	0.9	17
97	Maximizing the Margin with Boosting. Lecture Notes in Computer Science, 2002, , 334-350.	1.3	15
98	Robust Ensemble Learning for Data Mining. Lecture Notes in Computer Science, 2000, , 341-344.	1.3	14
99	Statistical Tests for Detecting Differential RNA-Transcript Expression from Read Counts. Nature Precedings, 2010, , .	0.1	13
100	Graph Based Semi-supervised Learning with Sharper Edges. Lecture Notes in Computer Science, 2006, , 401-412.	1.3	13
101	PALMA: mRNA to genome alignments using large margin algorithms. Bioinformatics, 2007, 23, 1892-1900.	4.1	12
102	Oqtans: the RNA-seq workbench in the cloud for complete and reproducible quantitative transcriptome analysis. Bioinformatics, 2014, 30, 1300-1301.	4.1	12
103	Learning to Predict the Leave-One-Out Error of Kernel Based Classifiers. Lecture Notes in Computer Science, 2001, , 331-338.	1.3	12
104	Transcript quantification with RNA-Seq data. BMC Bioinformatics, 2009, 10, .	2.6	10
105	Experimental analysis of support vector machines with different kernels based on non-intrusive monitoring data. , 0, , .		9
106	Sparse Binary Relation Representations for Genome Graph Annotation. Journal of Computational Biology, 2020, 27, 626-639.	1.6	9
107	AStarix: Fast and Optimal Sequence-to-Graph Alignment. Lecture Notes in Computer Science, 2020, , 104-119.	1.3	9
108	Next generation genome annotation with mGene.ngs. BMC Bioinformatics, 2010, 11, .	2.6	8

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109	Transcript normalization and segmentation of tiling array data. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2008, , 527-38.	0.7	8
110	Reconstructing tumor evolutionary histories and clone trees in polynomial-time with SubMARine. PLoS Computational Biology, 2021, 17, e1008400.	3.2	7
111	Efficient Training of Graph-Regularized Multitask SVMs. Lecture Notes in Computer Science, 2012, , 633-647.	1.3	6
112	Regularization-Based Multitask Learning With Applications to Genome Biology and Biological Imaging. KI - Kunstliche Intelligenz, 2014, 28, 29-33.	3.2	6
113	SVM2Motif"Reconstructing Overlapping DNA Sequence Motifs by Mimicking an SVM Predictor. PLoS ONE, 2015, 10, e0144782.	2.5	5
114	Integrative genome-wide analysis of the determinants of RNA splicing in kidney renal clear cell carcinoma. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2015, , 44-55.	0.7	5
115	Lossless indexing with counting de Bruijn graphs. Genome Research, 2022, 32, 1754-1764.	5.5	5
116	Sparse Binary Relation Representations for Genome Graph Annotation. Lecture Notes in Computer Science, 2019, , 120-135.	1.3	4
117	Identification of HIF-dependent alternative splicing in gastrointestinal cancers and characterization of a long, coding isoform of SLC35A3. Genomics, 2021, 113, 515-529.	2.9	4
118	Topology-based sparsification of graph annotations. Bioinformatics, 2021, 37, i169-i176.	4.1	4
119	INTEGRATIVE GENOME-WIDE ANALYSIS OF THE DETERMINANTS OF RNA SPLICING IN KIDNEY RENAL CLEAR CELL CARCINOMA. , 2014, , .		3
120	Graph-regularized 3D shape reconstruction from highly anisotropic and noisy images. Signal, Image and Video Processing, 2014, 8, 41-48.	2.7	3
121	Protein translational control and its contribution to oncogenesis revealed by computational methods. BMC Bioinformatics, 2015, 16, .	2.6	3
122	TRANSCRIPT NORMALIZATION AND SEGMENTATION OF TILING ARRAY DATA. , 2007, , .		3
123	SPHN/PHRT: Forming a Swiss-Wide Infrastructure for Data-Driven Sepsis Research. Studies in Health Technology and Informatics, 2020, 270, 1163-1167.	0.3	3
124	NIPS workshop on New Problems and Methods in Computational Biology. BMC Bioinformatics, 2007, 8, .	2.6	2
125	Oqtans: a Galaxy-integrated workflow for quantitative transcriptome analysis from NGS Data. BMC Bioinformatics, 2011, 12, .	2.6	2
126	Multiple insert size paired-end sequencing for deconvolution of complex transcriptomes. RNA Biology, 2012, 9, 596-609.	3.1	2

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127	Probabilistic clustering of time-evolving distance data. Machine Learning, 2015, 100, 635-654.	5.4	2
128	Lossless Indexing with Counting de Bruijn Graphs. Lecture Notes in Computer Science, 2022, , 374-376.	1.3	2
129	Revealing sequence variation patterns in rice with machine learning methods. BMC Bioinformatics, 2008, 9, .	2.6	1
130	Boosting Variational Inference With Locally Adaptive Step-Sizes. , 2021, , .		1
131	Sparse Gaussian Processes on Discrete Domains. IEEE Access, 2021, 9, 76750-76758.	4.2	1
132	RNA Instant Quality Check: Alignment-Free RNA-Degradation Detection. Journal of Computational Biology, 0, , .	1.6	1
133	CANCER PANOMICS: COMPUTATIONAL METHODS AND INFRASTRUCTURE FOR INTEGRATIVE ANALYSIS OF CANCER HIGH-THROUGHPUT "OMICS" DATA. , 2014, , .		0
134	Oqtans: a multifunctional workbench for RNA-seq data analysis. BMC Bioinformatics, 2014, 15, .	2.6	0
135	04.10"Chronic inflammation regulates the mrna stabilome in rheumatoid arthritis fibroblast-like synoviocytes. , 2017, , .		0
136	An Arcing algorithm with an intuitive learning control parameter. Transactions of the Japanese Society for Artificial Intelligence, 2001, 16, 417-426.	0.1	0
137	Solving Semi-infinite Linear Programs Using Boosting-Like Methods. Lecture Notes in Computer Science, 2006, , 10-11.	1.3	0
138	CANCER PANOMICS: COMPUTATIONAL METHODS AND INFRASTRUCTURE FOR INTEGRATIVE ANALYSIS OF CANCER HIGH-THROUGHPUT "OMICS" DATA- SESSION INTRODUCTION. , 2013, , .		0
139	Abstract B23: The 5 UTR of many oncogenes and transcription factors encodes a targetable dependence on the eIF4A RNA helicase. , 2015, , .		0
140	Abstract 892: Functional characterization of EIF1AX mutations in thyroid cancer predicts for gain of function by increasing translational rate with concomitant derepression of upstream inputs from mTOR. , 2016, , .		0
141	Abstract A45: Targeting eIF4A dependent translation as therapeutics in pancreatic cancer. , 2017, , .		0
142	Abstract 389: Integrating diverse transcriptomic alterations to identify cancer-relevant genes. , 2017, , .		0