

# Gunnar RÃ¶tsch

## List of Publications by Year in descending order

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Version: 2024-02-01

142  
papers

31,559  
citations

36691

53  
h-index

18400

124  
g-index

179  
all docs

179  
docs citations

179  
times ranked

52312  
citing authors

#	ARTICLE	IF	CITATIONS
1	Lossless Indexing with Counting de Bruijn Graphs. Lecture Notes in Computer Science, 2022, , 374-376.	1.0	2
2	Lossless indexing with counting de Bruijn graphs. Genome Research, 2022, 32, 1754-1764.	2.4	5
3	Targeting eIF4A-Dependent Translation of KRAS Signaling Molecules. Cancer Research, 2021, 81, 2002-2014.	0.4	17
4	Identification of HIF-dependent alternative splicing in gastrointestinal cancers and characterization of a long, coding isoform of SLC35A3. Genomics, 2021, 113, 515-529.	1.3	4
5	The Tumor Profiler Study: integrated, multi-omic, functional tumor profiling for clinical decision support. Cancer Cell, 2021, 39, 288-293.	7.7	71
6	A global metagenomic map of urban microbiomes and antimicrobial resistance. Cell, 2021, 184, 3376-3393.e17.	13.5	164
7	Topology-based sparsification of graph annotations. Bioinformatics, 2021, 37, i169-i176.	1.8	4
8	Boosting Variational Inference With Locally Adaptive Step-Sizes. , 2021, , .		1
9	Sparse Gaussian Processes on Discrete Domains. IEEE Access, 2021, 9, 76750-76758.	2.6	1
10	Reconstructing tumor evolutionary histories and clone trees in polynomial-time with SubMARine. PLoS Computational Biology, 2021, 17, e1008400.	1.5	7
11	Communication-Efficient Jaccard similarity for High-Performance Distributed Genome Comparisons. , 2020, , .		34
12	Building an international consortium for tracking coronavirus health status. Nature Medicine, 2020, 26, 1161-1165.	15.2	23
13	Sparse Binary Relation Representations for Genome Graph Annotation. Journal of Computational Biology, 2020, 27, 626-639.	0.8	9
14	Early prediction of circulatory failure in the intensive care unit using machine learning. Nature Medicine, 2020, 26, 364-373.	15.2	204
15	Genomic basis for RNA alterations in cancer. Nature, 2020, 578, 129-136.	13.7	280
16	SCIM: universal single-cell matching with unpaired feature sets. Bioinformatics, 2020, 36, i919-i927.	1.8	37
17	AStarix: Fast and Optimal Sequence-to-Graph Alignment. Lecture Notes in Computer Science, 2020, , 104-119.	1.0	9
18	SPHN/PHRT: Forming a Swiss-Wide Infrastructure for Data-Driven Sepsis Research. Studies in Health Technology and Informatics, 2020, 270, 1163-1167.	0.2	3

#	ARTICLE	IF	CITATIONS
19	Dynamic compression schemes for graph coloring. <i>Bioinformatics</i> , 2019, 35, 407-414.	1.8	19
20	A Pan-cancer Transcriptome Analysis Reveals Pervasive Regulation through Alternative Promoters. <i>Cell</i> , 2019, 178, 1465-1477.e17.	13.5	144
21	Comparative analysis of mRNA and protein degradation in prostate tissues indicates high stability of proteins. <i>Nature Communications</i> , 2019, 10, 2524.	5.8	35
22	c-MYC regulates mRNA translation efficiency and start-site selection in lymphoma. <i>Journal of Experimental Medicine</i> , 2019, 216, 1509-1524.	4.2	32
23	HBEGF <sup>+</sup> macrophages in rheumatoid arthritis induce fibroblast invasiveness. <i>Science Translational Medicine</i> , 2019, 11, .	5.8	143
24	Sparse Binary Relation Representations for Genome Graph Annotation. <i>Lecture Notes in Computer Science</i> , 2019, , 120-135.	1.0	4
25	<i>EIF1AX</i> and <i>RAS</i> Mutations Cooperate to Drive Thyroid Tumorigenesis through ATF4 and c-MYC. <i>Cancer Discovery</i> , 2019, 9, 264-281.	7.7	57
26	BRCA Challenge: BRCA Exchange as a global resource for variants in BRCA1 and BRCA2. <i>PLoS Genetics</i> , 2018, 14, e1007752.	1.5	148
27	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. <i>Cancer Cell</i> , 2018, 34, 211-224.e6.	7.7	623
28	Registered access: authorizing data access. <i>European Journal of Human Genetics</i> , 2018, 26, 1721-1731.	1.4	33
29	Genomic Rearrangements in <i>Arabidopsis</i> Considered as Quantitative Traits. <i>Genetics</i> , 2017, 205, 1425-1441.	1.2	21
30	Prediction of potent shRNAs with a sequential classification algorithm. <i>Nature Biotechnology</i> , 2017, 35, 350-353.	9.4	129
31	RiboDiff: detecting changes of mRNA translation efficiency from ribosome footprints. <i>Bioinformatics</i> , 2017, 33, 139-141.	1.8	134
32	Chronic inflammation regulates the mRNA stabilome in rheumatoid arthritis fibroblast-like synoviocytes. , 2017, , .		0
33	Tumor Necrosis Factor dynamically regulates the mRNA stabilome in rheumatoid arthritis fibroblast-like synoviocytes. <i>PLoS ONE</i> , 2017, 12, e0179762.	1.1	21
34	Abstract A45: Targeting eIF4A dependent translation as therapeutics in pancreatic cancer. , 2017, , .		0
35	Abstract 389: Integrating diverse transcriptomic alterations to identify cancer-relevant genes. , 2017, , .		0
36	<i>SplAdder</i> : identification, quantification and testing of alternative splicing events from RNA-Seq data. <i>Bioinformatics</i> , 2016, 32, 1840-1847.	1.8	124

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37	MMR: a tool for read multi-mapper resolution. <i>Bioinformatics</i> , 2016, 32, 770-772.	1.8	39
38	Alternative Splicing Substantially Diversifies the Transcriptome during Early Photomorphogenesis and Correlates with the Energy Availability in Arabidopsis. <i>Plant Cell</i> , 2016, 28, 2715-2734.	3.1	97
39	Efficient privacy-preserving string search and an application in genomics. <i>Bioinformatics</i> , 2016, 32, 1652-1661.	1.8	46
40	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
41	Protein translational control and its contribution to oncogenesis revealed by computational methods. <i>BMC Bioinformatics</i> , 2015, 16, .	1.2	3
42	Interferon- $\beta$ regulates cellular metabolism and mRNA translation to potentiate macrophage activation. <i>Nature Immunology</i> , 2015, 16, 838-849.	7.0	239
43	The Molecular Taxonomy of Primary Prostate Cancer. <i>Cell</i> , 2015, 163, 1011-1025.	13.5	2,435
44	Probabilistic clustering of time-evolving distance data. <i>Machine Learning</i> , 2015, 100, 635-654.	3.4	2
45	SVM2Motif"Reconstructing Overlapping DNA Sequence Motifs by Mimicking an SVM Predictor. <i>PLoS ONE</i> , 2015, 10, e0144782.	1.1	5
46	DNA methylation in Arabidopsis has a genetic basis and shows evidence of local adaptation. <i>ELife</i> , 2015, 4, e05255.	2.8	457
47	Abstract B23: The 5 UTR of many oncogenes and transcription factors encodes a targetable dependence on the eIF4A RNA helicase. , 2015, , .		0
48	Integrative genome-wide analysis of the determinants of RNA splicing in kidney renal clear cell carcinoma. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2015, , 44-55.	0.7	5
49	INTEGRATIVE GENOME-WIDE ANALYSIS OF THE DETERMINANTS OF RNA SPLICING IN KIDNEY RENAL CLEAR CELL CARCINOMA. , 2014, , .		3
50	CANCER PANOMICS: COMPUTATIONAL METHODS AND INFRASTRUCTURE FOR INTEGRATIVE ANALYSIS OF CANCER HIGH-THROUGHPUT "OMICS" DATA. , 2014, , .		0
51	Genome-wide analysis of alternative splicing in <i>Volvox carteri</i> . <i>BMC Genomics</i> , 2014, 15, 1117.	1.2	37
52	Oqtans: the RNA-seq workbench in the cloud for complete and reproducible quantitative transcriptome analysis. <i>Bioinformatics</i> , 2014, 30, 1300-1301.	1.8	12
53	Regularization-Based Multitask Learning With Applications to Genome Biology and Biological Imaging. <i>KI - Kunstliche Intelligenz</i> , 2014, 28, 29-33.	2.2	6
54	Species-wide Genetic Incompatibility Analysis Identifies Immune Genes as Hot Spots of Deleterious Epistasis. <i>Cell</i> , 2014, 159, 1341-1351.	13.5	247

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55	Graph-regularized 3D shape reconstruction from highly anisotropic and noisy images. <i>Signal, Image and Video Processing</i> , 2014, 8, 41-48.	1.7	3
56	RNA G-quadruplexes cause eIF4A-dependent oncogene translation in cancer. <i>Nature</i> , 2014, 513, 65-70.	13.7	506
57	Multiplatform Analysis of 12 Cancer Types Reveals Molecular Classification within and across Tissues of Origin. <i>Cell</i> , 2014, 158, 929-944.	13.5	1,242
58	Determination and Inference of Eukaryotic Transcription Factor Sequence Specificity. <i>Cell</i> , 2014, 158, 1431-1443.	13.5	1,515
59	Oqtans: a multifunctional workbench for RNA-seq data analysis. <i>BMC Bioinformatics</i> , 2014, 15, .	1.2	0
60	Assessment of transcript reconstruction methods for RNA-seq. <i>Nature Methods</i> , 2013, 10, 1177-1184.	9.0	679
61	Systematic evaluation of spliced alignment programs for RNA-seq data. <i>Nature Methods</i> , 2013, 10, 1185-1191.	9.0	467
62	The Cancer Genome Atlas Pan-Cancer analysis project. <i>Nature Genetics</i> , 2013, 45, 1113-1120.	9.4	6,265
63	An Empirical Analysis of Topic Modeling for Mining Cancer Clinical Notes. , 2013, , .		20
64	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.	3.1	209
65	Accurate detection of differential RNA processing. <i>Nucleic Acids Research</i> , 2013, 41, 5189-5198.	6.5	39
66	MITIE: Simultaneous RNA-Seq-based transcript identification and quantification in multiple samples. <i>Bioinformatics</i> , 2013, 29, 2529-2538.	1.8	57
67	Ecological Modeling from Time-Series Inference: Insight into Dynamics and Stability of Intestinal Microbiota. <i>PLoS Computational Biology</i> , 2013, 9, e1003388.	1.5	487
68	CANCER PANOMICS: COMPUTATIONAL METHODS AND INFRASTRUCTURE FOR INTEGRATIVE ANALYSIS OF CANCER HIGH-THROUGHPUT "OMICS" DATA- SESSION INTRODUCTION. , 2013, , .		0
69	Multiple insert size paired-end sequencing for deconvolution of complex transcriptomes. <i>RNA Biology</i> , 2012, 9, 596-609.	1.5	2
70	Cohesin Rings Devoid of Scc3 and Pds5 Maintain Their Stable Association with the DNA. <i>PLoS Genetics</i> , 2012, 8, e1002856.	1.5	50
71	Efficient Training of Graph-Regularized Multitask SVMs. <i>Lecture Notes in Computer Science</i> , 2012, , 633-647.	1.0	6
72	Polypyrimidine Tract Binding Protein Homologs from <i>Arabidopsis</i> Are Key Regulators of Alternative Splicing with Implications in Fundamental Developmental Processes. <i>Plant Cell</i> , 2012, 24, 4360-4375.	3.1	84

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73	HnRNP L and L-like cooperate in multiple-exon regulation of CD45 alternative splicing. <i>Nucleic Acids Research</i> , 2012, 40, 5666-5678.	6.5	45
74	A spatial and temporal map of <i>C. elegans</i> gene expression. <i>Genome Research</i> , 2011, 21, 325-341.	2.4	241
75	Persistence and Availability of Web Services in Computational Biology. <i>PLoS ONE</i> , 2011, 6, e24914.	1.1	21
76	RNA-Seq analysis in mutant zebrafish reveals role of U1C protein in alternative splicing regulation. <i>EMBO Journal</i> , 2011, 30, 1965-1976.	3.5	39
77	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.	1.2	21
78	Oqtans: a Galaxy-integrated workflow for quantitative transcriptome analysis from NGS Data. <i>BMC Bioinformatics</i> , 2011, 12, .	1.2	2
79	Receptor-type guanylate cyclase is required for carbon dioxide sensation by <i>Caenorhabditis elegans</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 254-259.	3.3	113
80	Multiple reference genomes and transcriptomes for <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2011, 477, 419-423.	13.7	593
81	Statistical Tests for Detecting Differential RNA-Transcript Expression from Read Counts. <i>Nature Precedings</i> , 2010, , .	0.1	13
82	Next generation genome annotation with mGene.ngs. <i>BMC Bioinformatics</i> , 2010, 11, .	1.2	8
83	Inferring latent task structure for Multitask Learning by Multiple Kernel Learning. <i>BMC Bioinformatics</i> , 2010, 11, S5.	1.2	24
84	Exploiting physico-chemical properties in string kernels. <i>BMC Bioinformatics</i> , 2010, 11, S7.	1.2	17
85	Global effects of the small RNA biogenesis machinery on the <i>Arabidopsis thaliana</i> transcriptome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 17466-17473.	3.3	66
86	Integrative Analysis of the <i>Caenorhabditis elegans</i> Genome by the modENCODE Project. <i>Science</i> , 2010, 330, 1775-1787.	6.0	912
87	RNA-Seq Read Alignments with PALMapper. <i>Current Protocols in Bioinformatics</i> , 2010, 32, Unit 11.6.	25.8	46
88	rQuant.web: a tool for RNA-Seq-based transcript quantitation. <i>Nucleic Acids Research</i> , 2010, 38, W348-W351.	6.5	58
89	Leveraging Sequence Classification by Taxonomy-Based Multitask Learning. <i>Lecture Notes in Computer Science</i> , 2010, , 522-534.	1.0	50
90	Novel Machine Learning Methods for MHC Class I Binding Prediction. <i>Lecture Notes in Computer Science</i> , 2010, , 98-109.	1.0	30

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91	mGene: Accurate SVM-based gene finding with an application to nematode genomes. <i>Genome Research</i> , 2009, 19, 2133-2143.	2.4	79
92	KIRMES: kernel-based identification of regulatory modules in euchromatic sequences. <i>Bioinformatics</i> , 2009, 25, 2126-2133.	1.8	21
93	mGene.web: a web service for accurate computational gene finding. <i>Nucleic Acids Research</i> , 2009, 37, W312-W316.	6.5	23
94	Transcript quantification with RNA-Seq data. <i>BMC Bioinformatics</i> , 2009, 10, .	1.2	10
95	Quantitative RNA expression analysis with Affymetrix Tiling 1.0R arrays identifies new E2F target genes. <i>Plant Journal</i> , 2009, 57, 184-194.	2.8	65
96	Stress-induced changes in the <i>Arabidopsis thaliana</i> transcriptome analyzed using whole-genome tiling arrays. <i>Plant Journal</i> , 2009, 58, 1068-1082.	2.8	273
97	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.	3.3	581
98	Prototype Classification: Insights from Machine Learning. <i>Neural Computation</i> , 2009, 21, 272-300.	1.3	17
99	The Feature Importance Ranking Measure. <i>Lecture Notes in Computer Science</i> , 2009, , 694-709.	1.0	57
100	Optimal spliced alignments of short sequence reads. <i>BMC Bioinformatics</i> , 2008, 9, .	1.2	21
101	Revealing sequence variation patterns in rice with machine learning methods. <i>BMC Bioinformatics</i> , 2008, 9, .	1.2	1
102	At-TAX: a whole genome tiling array resource for developmental expression analysis and transcript identification in <i>Arabidopsis thaliana</i> . <i>Genome Biology</i> , 2008, 9, R112.	13.9	91
103	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.	3.3	378
104	POIMs: positional oligomer importance matrices' understanding support vector machine-based signal detectors. <i>Bioinformatics</i> , 2008, 24, i6-i14.	1.8	51
105	Optimal spliced alignments of short sequence reads. <i>Bioinformatics</i> , 2008, 24, i174-i180.	1.8	86
106	Detecting polymorphic regions in <i>Arabidopsis thaliana</i> with resequencing microarrays. <i>Genome Research</i> , 2008, 18, 918-929.	2.4	50
107	Support Vector Machines and Kernels for Computational Biology. <i>PLoS Computational Biology</i> , 2008, 4, e1000173.	1.5	515
108	Transcript normalization and segmentation of tiling array data. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2008, , 527-38.	0.7	8

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109	Improving the <i>Caenorhabditis elegans</i> Genome Annotation Using Machine Learning. PLoS Computational Biology, 2007, 3, e20.	1.5	57
110	PALMA: mRNA to genome alignments using large margin algorithms. Bioinformatics, 2007, 23, 1892-1900.	1.8	12
111	Common Sequence Polymorphisms Shaping Genetic Diversity in <i>Arabidopsis thaliana</i> . Science, 2007, 317, 338-342.	6.0	689
112	NIPS workshop on New Problems and Methods in Computational Biology. BMC Bioinformatics, 2007, 8, .	1.2	2
113	Accurate splice site prediction using support vector machines. BMC Bioinformatics, 2007, 8, S7.	1.2	135
114	TRANSCRIPT NORMALIZATION AND SEGMENTATION OF TILING ARRAY DATA. , 2007, , .		3
115	ARTS: accurate recognition of transcription starts in human. Bioinformatics, 2006, 22, e472-e480.	1.8	101
116	Learning Interpretable SVMs for Biological Sequence Classification. BMC Bioinformatics, 2006, 7, S9.	1.2	58
117	Totally corrective boosting algorithms that maximize the margin. , 2006, , .		59
118	Graph Based Semi-supervised Learning with Sharper Edges. Lecture Notes in Computer Science, 2006, , 401-412.	1.0	13
119	Solving Semi-infinite Linear Programs Using Boosting-Like Methods. Lecture Notes in Computer Science, 2006, , 10-11.	1.0	0
120	RASE: recognition of alternatively spliced exons in <i>C.elegans</i> . Bioinformatics, 2005, 21, i369-i377.	1.8	109
121	Image reconstruction by linear programming. IEEE Transactions on Image Processing, 2005, 14, 737-744.	6.0	17
122	Classifying 'Drug-likeness' with Kernel-Based Learning Methods. Journal of Chemical Information and Modeling, 2005, 45, 249-253.	2.5	90
123	Large scale genomic sequence SVM classifiers. , 2005, , .		27
124	Active Learning with Support Vector Machines in the Drug Discovery Process. Journal of Chemical Information and Computer Sciences, 2003, 43, 667-673.	2.8	281
125	Constructing descriptive and discriminative nonlinear features: rayleigh coefficients in kernel feature spaces. IEEE Transactions on Pattern Analysis and Machine Intelligence, 2003, 25, 623-628.	9.7	158
126	An Introduction to Boosting and Leveraging. Lecture Notes in Computer Science, 2003, , 118-183.	1.0	206



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127	A New Discriminative Kernel from Probabilistic Models. <i>Neural Computation</i> , 2002, 14, 2397-2414.	1.3	88
128	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.	9.7	197
129	Sparse Regression Ensembles in Infinite and Finite Hypothesis Spaces. <i>Machine Learning</i> , 2002, 48, 189-218.	3.4	26
130	Maximizing the Margin with Boosting. <i>Lecture Notes in Computer Science</i> , 2002, , 334-350.	1.0	15
131	New Methods for Splice Site Recognition. <i>Lecture Notes in Computer Science</i> , 2002, , 329-336.	1.0	28
132	An introduction to kernel-based learning algorithms. <i>IEEE Transactions on Neural Networks</i> , 2001, 12, 181-201.	4.8	2,811
133	Soft Margins for AdaBoost. <i>Machine Learning</i> , 2001, 42, 287-320.	3.4	1,000
134	Learning to Predict the Leave-One-Out Error of Kernel Based Classifiers. <i>Lecture Notes in Computer Science</i> , 2001, , 331-338.	1.0	12
135	An Arcing algorithm with an intuitive learning control parameter. <i>Transactions of the Japanese Society for Artificial Intelligence</i> , 2001, 16, 417-426.	0.1	0
136	Engineering support vector machine kernels that recognize translation initiation sites. <i>Bioinformatics</i> , 2000, 16, 799-807.	1.8	373
137	Robust Ensemble Learning for Data Mining. <i>Lecture Notes in Computer Science</i> , 2000, , 341-344.	1.0	14
138	Input space versus feature space in kernel-based methods. <i>IEEE Transactions on Neural Networks</i> , 1999, 10, 1000-1017.	4.8	953
139	Kernel PCA Pattern Reconstruction via Approximate Pre-Images. <i>Perspectives in Neural Computing</i> , 1998, , 147-152.	0.1	60
140	Fisher discriminant analysis with kernels. , 0, , .		1,381
141	Experimental analysis of support vector machines with different kernels based on non-intrusive monitoring data. , 0, , .		9
142	RNA Instant Quality Check: Alignment-Free RNA-Degradation Detection. <i>Journal of Computational Biology</i> , 0, , .	0.8	1