

Gail L Rosen

List of Publications by Year in descending order

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Version: 2024-02-01

89
papers

4,257
citations

304743

22
h-index

206112

48
g-index

104
all docs

104
docs citations

104
times ranked

7074
citing authors

#	ARTICLE	IF	CITATIONS
1	MetaMutationalSigs: comparison of mutational signature refitting results made easy. <i>Bioinformatics</i> , 2022, 38, 2344-2347.	4.1	0
2	Mapping Data to Deep Understanding: Making the Most of the Deluge of SARS-CoV-2 Genome Sequences. <i>MSystems</i> , 2022, 7, e0003522.	3.8	5
3	Critical Assessment of Metagenome Interpretation: the second round of challenges. <i>Nature Methods</i> , 2022, 19, 429-440.	19.0	133
4	Predicting Institution Outcomes for Inter Partes Review (IPR) Proceedings at the United States Patent Trial & Appeal Board by Deep Learning of Patent Owner Preliminary Response Briefs. <i>Applied Sciences (Switzerland)</i> , 2022, 12, 3656.	2.5	2
5	RRM2B Is Frequently Amplified Across Multiple Tumor Types: Implications for DNA Repair, Cellular Survival, and Cancer Therapy. <i>Frontiers in Genetics</i> , 2021, 12, 628758.	2.3	9
6	Examining Cultural Structures and Functions in Biology. <i>Integrative and Comparative Biology</i> , 2021, , .	2.0	2
7	Learning, visualizing and exploring 16S rRNA structure using an attention-based deep neural network. <i>PLoS Computational Biology</i> , 2021, 17, e1009345.	3.2	13
8	Incremental and Semi-Supervised Learning of 16S-rRNA Genes For Taxonomic Classification. , 2021, , .		3
9	Incremental & Semi-Supervised Learning for Functional Analysis of Protein Sequences. , 2021, , .		1
10	Keeping up with the genomes: efficient learning of our increasing knowledge of the tree of life. <i>BMC Bioinformatics</i> , 2020, 21, 412.	2.6	14
11	Teaching Microbiome Analysis: From Design to Computation Through Inquiry. <i>Frontiers in Microbiology</i> , 2020, 11, 528051.	3.5	2
12	Genetic grouping of SARS-CoV-2 coronavirus sequences using informative subtype markers for pandemic spread visualization. <i>PLoS Computational Biology</i> , 2020, 16, e1008269.	3.2	38
13	Amino Acid k-mer Feature Extraction for Quantitative Antimicrobial Resistance (AMR) Prediction by Machine Learning and Model Interpretation for Biological Insights. <i>Biology</i> , 2020, 9, 365.	2.8	21
14	Emerging Priorities for Microbiome Research. <i>Frontiers in Microbiology</i> , 2020, 11, 136.	3.5	113
15	Healthcare Shift Workersâ€™ Temporal Habits for Eating, Sleeping, and Light Exposure: A Multi-Instrument Pilot Study. <i>Journal of Circadian Rhythms</i> , 2020, 18, 6.	1.3	7
16	Visualizing and Annotating Protein Sequences using A Deep Neural Network. , 2020, , .		3
17	Spatiotemporal Tracking of SARS-CoV-2 Variants using informative subtype markers and association graphs. , 2020, , .		1
18	16S rRNA sequence embeddings: Meaningful numeric feature representations of nucleotide sequences that are convenient for downstream analyses. <i>PLoS Computational Biology</i> , 2019, 15, e1006721.	3.2	27

#	ARTICLE	IF	CITATIONS
19	Exploring thematic structure and predicted functionality of 16S rRNA amplicon data. PLoS ONE, 2019, 14, e0219235.	2.5	17
20	Exploring thematic structure and predicted functionality of 16S rRNA amplicon data. , 2019, 14, e0219235.		0
21	Exploring thematic structure and predicted functionality of 16S rRNA amplicon data. , 2019, 14, e0219235.		0
22	Exploring thematic structure and predicted functionality of 16S rRNA amplicon data. , 2019, 14, e0219235.		0
23	Exploring thematic structure and predicted functionality of 16S rRNA amplicon data. , 2019, 14, e0219235.		0
24	Opportunities and obstacles for deep learning in biology and medicine. Journal of the Royal Society Interface, 2018, 15, 20170387.	3.4	1,282
25	A Sequential Learning Approach for Scaling Up Filter-Based Feature Subset Selection. IEEE Transactions on Neural Networks and Learning Systems, 2018, 29, 2530-2544.	11.3	18
26	Extensions to Online Feature Selection Using Bagging and Boosting. IEEE Transactions on Neural Networks and Learning Systems, 2018, 29, 4504-4509.	11.3	24
27	Analysis Methods for Shotgun Metagenomics. Computational Biology, 2018, , 71-112.	0.2	1
28	Incremental Author Name Disambiguation for Scientific Citation Data. , 2017, , .		10
29	Comprehensive benchmarking and ensemble approaches for metagenomic classifiers. Genome Biology, 2017, 18, 182.	8.8	260
30	Metagenomic characterization of ambulances across the USA. Microbiome, 2017, 5, 125.	11.1	32
31	Emerging investigators series: untangling the microbial ecosystem and kinetics in a nitrogen removing photosynthetic high density bioreactor. Environmental Science: Water Research and Technology, 2016, 2, 705-716.	2.4	2
32	Engineering Human Microbiota: Influencing Cellular and Community Dynamics for Therapeutic Applications. International Review of Cell and Molecular Biology, 2016, 324, 67-124.	3.2	12
33	Nanopore sequencing in microgravity. Npj Microgravity, 2016, 2, 16035.	3.7	76
34	Marker genes that are less conserved in their sequences are useful for predicting genome-wide similarity levels between closely related prokaryotic strains. Microbiome, 2016, 4, 18.	11.1	58
35	Fizzy: feature subset selection for metagenomics. BMC Bioinformatics, 2015, 16, 358.	2.6	40
36	A Bootstrap Based Neyman-Pearson Test for Identifying Variable Importance. IEEE Transactions on Neural Networks and Learning Systems, 2015, 26, 880-886.	11.3	24

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37	Prokaryotic Nucleotide Composition Is Shaped by Both Phylogeny and the Environment. <i>Genome Biology and Evolution</i> , 2015, 7, 1380-1389.	2.5	82
38	Multi-Layer and Recursive Neural Networks for Metagenomic Classification. <i>IEEE Transactions on Nanobioscience</i> , 2015, 14, 608-616.	3.3	78
39	A Toolkit for ARB to Integrate Custom Databases and Externally Built Phylogenies. <i>PLoS ONE</i> , 2015, 10, e0109277.	2.5	1
40	WGSQuikr: Fast Whole-Genome Shotgun Metagenomic Classification. <i>PLoS ONE</i> , 2014, 9, e91784.	2.5	36
41	Scaling a neyman-pearson subset selection approach via heuristics for mining massive data. , 2014, , .		1
42	Feature subset selection for inferring relative importance of taxonomy. , 2014, , .		1
43	Characterizing the Empirical Distribution of Prokaryotic Genome <i>n</i> -mers in the Presence of Nullomers. <i>Journal of Computational Biology</i> , 2014, 21, 732-740.	1.6	0
44	Domain adaptation bounds for multiple expert systems under concept drift. , 2014, , .		11
45	Advances in Machine Learning for Processing and Comparison of Metagenomic Data. , 2014, , 295-329.		7
46	POGO-DB—a database of pairwise-comparisons of genomes and conserved orthologous genes. <i>Nucleic Acids Research</i> , 2014, 42, D625-D632.	14.5	22
47	Quikr: a method for rapid reconstruction of bacterial communities via compressive sensing. <i>Bioinformatics</i> , 2013, 29, 2096-2102.	4.1	39
48	Establishing a relationship between bacteria in the human gut and Complex Regional Pain Syndrome. <i>Brain, Behavior, and Immunity</i> , 2013, 29, 62-69.	4.1	18
49	Selecting age-related functional characteristics in the human gut microbiome. <i>Microbiome</i> , 2013, 1, 2.	11.1	45
50	Discounted expert weighting for concept drift. , 2013, , .		8
51	Incremental learning of new classes from unbalanced data. , 2013, , .		7
52	Applications in Digital Image Processing. <i>The Mathematics Teacher</i> , 2013, 107, 46-53.	0.1	1
53	Variable Selection to Improve Classification of Metagenomes. , 2013, , 1-9.		0
54	Information theoretic feature selection for high dimensional metagenomic data. , 2012, , .		7

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55	Forensic identification with environmental samples. , 2012, , .		5
56	Determining significance in metagenomic samples. , 2012, , .		0
57	Inquiry-Based Learning Through Image Processing [dsp Education]. IEEE Signal Processing Magazine, 2012, 29, 164-169.	5.6	5
58	Exploiting the Functional and Taxonomic Structure of Genomic Data by Probabilistic Topic Modeling. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 980-991.	3.0	17
59	Transductive learning algorithms for nonstationary environments. , 2012, , .		5
60	Using the RDP Classifier to Predict Taxonomic Novelty and Reduce the Search Space for Finding Novel Organisms. PLoS ONE, 2012, 7, e32491.	2.5	153
61	NBC update: The addition of viral and fungal databases to the Naïve Bayes classification tool. BMC Research Notes, 2012, 5, 81.	1.4	6
62	Environmental and ecological factors that shape the gut bacterial communities of fish: a meta-analysis. Molecular Ecology, 2012, 21, 3363-3378.	3.9	814
63	Combining gene prediction methods to improve metagenomic gene annotation. BMC Bioinformatics, 2011, 12, 20.	2.6	46
64	Information-theoretic approaches to SVM feature selection for metagenome read classification. Computational Biology and Chemistry, 2011, 35, 199-209.	2.3	19
65	NBC: the Naïve Bayes Classification tool webserver for taxonomic classification of metagenomic reads. Bioinformatics, 2011, 27, 127-129.	4.1	196
66	An introduction to machine learning for students in secondary education. , 2011, , .		15
67	Ordering samples along environmental gradients using particle swarm optimization. , 2011, 2011, 4382-5.		1
68	Discovering the Unknown: Improving Detection of Novel Species and Genera from Short Reads. Journal of Biomedicine and Biotechnology, 2011, 2011, 1-11.	3.0	11
69	Benchmarking of gene prediction programs for metagenomic data. , 2010, 2010, 6190-3.		4
70	Neural network-based taxonomic clustering for metagenomics. , 2010, , .		4
71	A probabilistic topic-connection model for automatic image annotation. , 2010, , .		7
72	Comparison of Statistical Methods to Classify Environmental Genomic Fragments. IEEE Transactions on Nanobioscience, 2010, 9, 310-316.	3.3	6

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73	Probabilistic topic modeling for genomic data interpretation. , 2010, , .		40
74	The Effect of Sequence Error and Partial Training Data on BLAST Accuracy. , 2010, , .		1
75	Comparison of Gene Prediction Programs for Metagenomic Data. , 2010, , .		0
76	Connecting Artistically-Inclined K-12 Students to Physics and Math Through Image Processing Examples. , 2009, , .		9
77	Implementation of a Hebbian chemoreceptor model for diffusive source localization. BioSystems, 2009, 96, 223-236.	2.0	3
78	BENCHMARKING BLAST ACCURACY OF GENUS/PHYLA CLASSIFICATION OF METAGENOMIC READS. , 2009, , 10-20.		1
79	Signal Processing for Metagenomics: Extracting Information from the Soup. Current Genomics, 2009, 10, 493-510.	1.6	26
80	A text-mining approach for classification of genomic fragments. , 2008, , .		4
81	An iterative approach to probe-design for compressive sensing microarrays. , 2008, , .		2
82	Validating models of bacterial chemotaxis by simulating the random motility coefficient. , 2008, , .		21
83	An information theoretic method of microarray probe design for genome classification. , 2008, 2008, 3779-82.		3
84	The effects of C-G content and mutations on the Fourier transform method for periodicity. , 2008, , .		0
85	Metagenome Fragment Classification Using -Mer Frequency Profiles. Advances in Bioinformatics, 2008, 2008, 1-12.	5.7	85
86	Comparison of Autoregressive Measures for DNA Sequence Similarity. , 2007, , .		5
87	Examining coding structure and redundancy in DNA. IEEE Engineering in Medicine and Biology Magazine, 2006, 25, 62-68.	0.8	36
88	Automatic loudspeaker directivity control for sound field reconstruction. , 2002, , .		0
89	How Scalable Are Clade-Specific Marker K-Mer Based Hash Methods for Metagenomic Taxonomic Classification?. Frontiers in Signal Processing, 0, 2, .	1.7	1