Gail L Rosen

List of Publications by Year
in descending order

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	Opportunities and obstacles for deep learning in biology and medicine. Journal of the Royal Society Interface, 2018, 15, 20170387.	3.4	1,282
2	Environmental and ecological factors that shape the gut bacterial communities of fish: a meta‐analysis. Molecular Ecology, 2012, 21, 3363-3378.	3.9	814
3	Comprehensive benchmarking and ensemble approaches for metagenomic classifiers. Genome Biology, 2017, 18, 182.	8.8	260
4	NBC: the NaÃ¯ve Bayes Classification tool webserver for taxonomic classification of metagenomic reads. Bioinformatics, 2011, 27, 127-129.	4.1	196
5	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
6	Critical Assessment of Metagenome Interpretation: the second round of challenges. Nature Methods, 2022, 19, 429-440.	19.0	133
7	Emerging Priorities for Microbiome Research. Frontiers in Microbiology, 2020, 11, 136.	3.5	113
8	Metagenome Fragment Classification Using -Mer Frequency Profiles. Advances in Bioinformatics, 2008, 2008, 1-12.	5.7	85
9	Prokaryotic Nucleotide Composition Is Shaped by Both Phylogeny and the Environment. Genome Biology and Evolution, 2015, 7, 1380-1389.	2.5	82
10	Multi-Layer and Recursive Neural Networks for Metagenomic Classification. IEEE Transactions on Nanobioscience, 2015, 14, 608-616.	3.3	78
11	Nanopore sequencing in microgravity. Npj Microgravity, 2016, 2, 16035.	3.7	76
12	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
13	Combining gene prediction methods to improve metagenomic gene annotation. BMC Bioinformatics, 2011, 12, 20.	2.6	46
14	Selecting age-related functional characteristics in the human gut microbiome. Microbiome, 2013, 1, 2.	11.1	45
15	Probabilistic topic modeling for genomic data interpretation. , 2010, , .		40
16	Fizzy: feature subset selection for metagenomics. BMC Bioinformatics, 2015, 16, 358.	2.6	40
17	Quikr: a method for rapid reconstruction of bacterial communities via compressive sensing. Bioinformatics, 2013, 29, 2096-2102.	4.1	39
18	Genetic grouping of SARS-CoV-2 coronavirus sequences using informative subtype markers for pandemic spread visualization. PLoS Computational Biology, 2020, 16, e1008269.	3.2	38

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19	Examining coding structure and redundancy in DNA. IEEE Engineering in Medicine and Biology Magazine, 2006, 25, 62-68.	0.8	36
20	WGSQuikr: Fast Whole-Genome Shotgun Metagenomic Classification. PLoS ONE, 2014, 9, e91784.	2.5	36
21	Metagenomic characterization of ambulances across the USA. Microbiome, 2017, 5, 125.	11.1	32
22	16S rRNA sequence embeddings: Meaningful numeric feature representations of nucleotide sequences that are convenient for downstream analyses. PLoS Computational Biology, 2019, 15, e1006721.	3.2	27
23	Signal Processing for Metagenomics: Extracting Information from the Soup. Current Genomics, 2009, 10, 493-510.	1.6	26
24	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
25	Extensions to Online Feature Selection Using Bagging and Boosting. IEEE Transactions on Neural Networks and Learning Systems, 2018, 29, 4504-4509.	11.3	24
26	POGO-DB—a database of pairwise-comparisons of genomes and conserved orthologous genes. Nucleic Acids Research, 2014, 42, D625-D632.	14.5	22
27	Validating models of bacterial chemotaxis by simulating the random motility coefficient. , 2008, , .		21
28	Amino Acid k-mer Feature Extraction for Quantitative Antimicrobial Resistance (AMR) Prediction by Machine Learning and Model Interpretation for Biological Insights. Biology, 2020, 9, 365.	2.8	21
29	Information-theoretic approaches to SVM feature selection for metagenome read classification. Computational Biology and Chemistry, 2011, 35, 199-209.	2.3	19
30	Establishing a relationship between bacteria in the human gut and Complex Regional Pain Syndrome. Brain, Behavior, and Immunity, 2013, 29, 62-69.	4.1	18
31	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
32	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
33	Exploring thematic structure and predicted functionality of 16S rRNA amplicon data. PLoS ONE, 2019, 14, e0219235.	2.5	17
34	An introduction to machine learning for students in secondary education. , 2011, , .		15
35	Keeping up with the genomes: efficient learning of our increasing knowledge of the tree of life. BMC Bioinformatics, 2020, 21, 412.	2.6	14
36	Learning, visualizing and exploring 16S rRNA structure using an attention-based deep neural network. PLoS Computational Biology, 2021, 17, e1009345.	3.2	13

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37	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
38	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
39	Domain adaptation bounds for multiple expert systems under concept drift. , 2014, , .		11
40	Incremental Author Name Disambiguation for Scientific Citation Data. , 2017, , .		10
41	Connecting Artistically-Inclined K-12 Students to Physics and Math Through Image Processing Examples. , 2009, , .		9
42	RRM2B Is Frequently Amplified Across Multiple Tumor Types: Implications for DNA Repair, Cellular Survival, and Cancer Therapy. Frontiers in Genetics, 2021, 12, 628758.	2.3	9
43	Discounted expert weighting for concept drift. , 2013, , .		8
44	A probabilistic topic-connection model for automatic image annotation. , 2010, , .		7
45	Information theoretic feature selection for high dimensional metagenomic data. , 2012, , .		7
46	Incremental learning of new classes from unbalanced data. , 2013, , .		7
47	Advances in Machine Learning for Processing and Comparison of Metagenomic Data. , 2014, , 295-329.		7
48	Healthcare Shift Workersâ€™ Temporal Habits for Eating, Sleeping, and Light Exposure: A Multi-Instrument Pilot Study. Journal of Circadian Rhythms, 2020, 18, 6.	1.3	7
49	Comparison of Statistical Methods to Classify Environmental Genomic Fragments. IEEE Transactions on Nanobioscience, 2010, 9, 310-316.	3.3	6
50	NBC update: The addition of viral and fungal databases to the NaÃ¯ve Bayes classification tool. BMC Research Notes, 2012, 5, 81.	1.4	6
51	Comparison of Autoregressive Measures for DNA Sequence Similarity. , 2007, , .		5
52	Forensic identification with environmental samples. , 2012, , .		5
53	Inquiry-Based Learning Through Image Processing [dsp Education]. IEEE Signal Processing Magazine, 2012, 29, 164-169.	5.6	5
54	Transductive learning algorithms for nonstationary environments. , 2012, , .		5

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55	Mapping Data to Deep Understanding: Making the Most of the Deluge of SARS-CoV-2 Genome Sequences. MSystems, 2022, 7, e0003522.	3.8	5
56	A text-mining approach for classification of genomic fragments. , 2008, , .		4
57	Benchmarking of gene prediction programs for metagenomic data. , 2010, 2010, 6190-3.		4
58	Neural network-based taxonomic clustering for metagenomics. , 2010, , .		4
59	An information theoretic method of microarray probe design for genome classification. , 2008, 2008, 3779-82.		3
60	Implementation of a Hebbian chemoreceptor model for diffusive source localization. BioSystems, 2009, 96, 223-236.	2.0	3
61	Visualizing and Annotating Protein Sequences using A Deep Neural Network. , 2020, , .		3
62	Incremental and Semi-Supervised Learning of 16S-rRNA Genes For Taxonomic Classification. , 2021, , .		3
63	An iterative approach to probe-design for compressive sensing microarrays. , 2008, , .		2
64	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
65	Teaching Microbiome Analysis: From Design to Computation Through Inquiry. Frontiers in Microbiology, 2020, 11, 528051.	3.5	2
66	Examining Cultural Structures and Functions in Biology. Integrative and Comparative Biology, 2021, , .	2.0	2
67	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. Applied Sciences (Switzerland), 2022, 12, 3656.	2.5	2
68	BENCHMARKING BLAST ACCURACY OF GENUS/PHYLA CLASSIFICATION OF METAGENOMIC READS. , 2009, , 10-20.		1
69	The Effect of Sequence Error and Partial Training Data on BLAST Accuracy. , 2010, , .		1
70	Ordering samples along environmental gradients using particle swarm optimization. , 2011, 2011, 4382-5.		1
71	Applications in Digital Image Processing. The Mathematics Teacher, 2013, 107, 46-53.	0.1	1
72	Scaling a neyman-pearson subset selection approach via heuristics for mining massive data. , 2014, , .		1

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73	Feature subset selection for inferring relative importance of taxonomy. , 2014, , .		1
74	Analysis Methods for Shotgun Metagenomics. Computational Biology, 2018, , 71-112.	0.2	1
75	A Toolkit for ARB to Integrate Custom Databases and Externally Built Phylogenies. PLoS ONE, 2015, 10, e0109277.	2.5	1
76	Spatiotemporal Tracking of SARS-CoV-2 Variants using informative subtype markers and association graphs. , 2020, , .		1
77	Incremental & Semi-Supervised Learning for Functional Analysis of Protein Sequences. , 2021, , .		1
78	How Scalable Are Clade-Specific Marker K-Mer Based Hash Methods for Metagenomic Taxonomic Classification?. Frontiers in Signal Processing, 0, 2, .	1.7	1
79	Automatic loudspeaker directivity control for sound field reconstruction. , 2002, , .		0
80	The effects of C-G content and mutations on the Fourier transform method for periodicity. , 2008, , .		0
81	Comparison of Gene Prediction Programs for Metagenomic Data. , 2010, , .		0
82	Determining significance in metagenomic samples. , 2012, , .		0
83	Characterizing the Empirical Distribution of Prokaryotic Genome n-mers in the Presence of Nullomers. Journal of Computational Biology, 2014, 21, 732-740.	1.6	0
84	Variable Selection to Improve Classification of Metagenomes. , 2013, , 1-9.		0
85	MetaMutationalSigs: comparison of mutational signature refitting results made easy. Bioinformatics, 2022, 38, 2344-2347.	4.1	0
86	Exploring thematic structure and predicted functionality of 16S rRNA amplicon data. , 2019, 14, e0219235.		0
87	Exploring thematic structure and predicted functionality of 16S rRNA amplicon data. , 2019, 14, e0219235.		0
88	Exploring thematic structure and predicted functionality of 16S rRNA amplicon data. , 2019, 14, e0219235.		0
89	Exploring thematic structure and predicted functionality of 16S rRNA amplicon data. , 2019, 14, e0219235.		0