Hector Corrada Bravo

List of Publications by Year
in descending order

49 papers	10,703 citations	218592 26 h-index	214721 47 g-index
58 all docs	58 docs citations	58 times ranked	21515 citing authors

#	Article	IF	Citations
1	Capturing discrete latent structures: choose LDs over PCs. Biostatistics, 2021, , .	0.9	2
2	A transcriptomic and epigenomic cell atlas of the mouse primary motor cortex. Nature, 2021, 598, 103-110.	13.7	166
3	Comparative cellular analysis of motor cortex in human, marmoset and mouse. Nature, 2021, 598, 111-119.	13.7	361
4	Multivariable association discovery in population-scale meta-omics studies. PLoS Computational Biology, 2021, 17, e1009442.	1.5	691
5	Terminus enables the discovery of data-driven, robust transcript groups from RNA-seq data. Bioinformatics, 2020, 36, i102-i110.	1.8	11
6	A framework for assessing 16S rRNA marker-gene survey data analysis methods using mixtures.. Microbiome, 2020, 8, 35.	4.9	2
7	Epiviz File Server: Query, transform and interactively explore data from indexed genomic files. Bioinformatics, 2020, 36, 4682-4690.	1.8	4
8	Interactive exploratory data analysis of Integrative Human Microbiome Project data using Metaviz. F1000Research, 2020, 9, 601.	0.8	0
9	Interactive exploratory data analysis of Integrative Human Microbiome Project data using Metaviz. F1000Research, 2020, 9, 601.	0.8	1
10	Yanagi: Fast and interpretable segment-based alternative splicing and gene expression analysis. BMC Bioinformatics, 2019, 20, 421.	1.2	3
11	metagenomeFeatures: an R package for working with 16S rRNA reference databases and marker-gene survey feature data. Bioinformatics, 2019, 35, 3870-3872.	1.8	4
12	microbiomeDASim:ÂSimulating longitudinal differential abundance for microbiome data. F1000Research, 2019, 8, 1769.	0.8	3
13	Metaviz: interactive statistical and visual analysis of metagenomic data. Nucleic Acids Research, 2018, 46, 2777-2787.	6.5	29
14	Smooth quantile normalization. Biostatistics, 2018, 19, 185-198.	0.9	78
15	Analysis and correction of compositional bias in sparse sequencing count data. BMC Genomics, 2018, 19, 799.	1.2	85
16	Epiviz Web Components: reusable and extensible component library to visualize functional genomic datasets. F1000Research, 2018, 7, 1096.	0.8	4
17	Individual-specific changes in the human gut microbiota after challenge with enterotoxigenic Escherichia coli and subsequent ciprofloxacin treatment. BMC Genomics, 2016, 17, 440.	1.2	55
18	BatchQC: interactive software for evaluating sample and batch effects in genomic data. Bioinformatics, 2016, 32, 3836-3838.	1.8	50

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19	Distinct genomic and epigenomic features demarcate hypomethylated blocks in colon cancer. BMC Cancer, 2016, 16, 88.	1.1	1
20	Heterogeneity of transcription factor binding specificity models within and across cell lines. Genome Research, 2016, 26, 1110-1123.	2.4	7
21	Dual Transcriptome Profiling ofLeishmania-Infected Human Macrophages Reveals Distinct Reprogramming Signatures. MBio, 2016, 7, .	1.8	111
22	Transcriptome Remodeling in Trypanosoma cruzi and Human Cells during Intracellular Infection. PLoS Pathogens, 2016, 12, e1005511.	2.1	157
23	Epiviz: a view inside the design of an integrated visual analysis software for genomics. BMC Bioinformatics, 2015, 16, S4.	1.2	3
24	Simultaneous transcriptional profiling of Leishmania major and its murine macrophage host cell reveals insights into host-pathogen interactions. BMC Genomics, 2015, 16, 1108.	1.2	105
25	Gene Expression Signatures Based on Variability can Robustly Predict Tumor Progression and Prognosis. Cancer Informatics, 2015, 14, CIN.S23862.	0.9	21
26	Orchestrating high-throughput genomic analysis with Bioconductor. Nature Methods, 2015, 12, 115-121.	9.0	3,070
27	Transcriptomic profiling of gene expression and RNA processing duringLeishmania majordifferentiation. Nucleic Acids Research, 2015, 43, 6799-6813.	6.5	77
28	Shape analysis of high-throughput transcriptomics experiment data. Biostatistics, 2015, 16, 627-640.	0.9	4
29	BlindCall: ultra-fast base-calling of high-throughput sequencing data by blind deconvolution. Bioinformatics, 2014, 30, 1214-1219.	1.8	7
30	Diarrhea in young children from low-income countries leads to large-scale alterations in intestinal microbiota composition. Genome Biology, 2014, 15, R76.	13.9	219
31	Determinants of expression variability. Nucleic Acids Research, 2014, 42, 3503-3514.	6.5	68
32	Reply to: "A fair comparison". Nature Methods, 2014, 11, 359-360.	9.0	14
33	Epiviz: interactive visual analytics for functional genomics data. Nature Methods, 2014, 11, 938-940.	9.0	59
34	Large hypomethylated blocks as a universal defining epigenetic alteration in human solid tumors. Genome Medicine, 2014, 6, 61.	3.6	170
35	Removing batch effects for prediction problems with frozen surrogate variable analysis. PeerJ, 2014, 2, e561.	0.9	50
36	Differential abundance analysis for microbial marker-gene surveys. Nature Methods, 2013, 10, 1200-1202.	9.0	1,921

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37	A Decisionâ€Theory Approach to Interpretable Set Analysis for Highâ€Dimensional Data. Biometrics, 2013, 69, 614-623.	0.8	5
38	Gene expression anti-profiles as a basis for accurate universal cancer signatures. BMC Bioinformatics, 2012, 13, 272.	1.2	41
39	The partitioned LASSO-patternsearch algorithm with application to gene expression data. BMC Bioinformatics, 2012, 13, 98.	1.2	6
40	Increased methylation variation in epigenetic domains across cancer types. Nature Genetics, 2011, 43, 768-775.	9.4	968
41	Effective detection of rare variants in pooled DNA samples using Cross-pool tailcurve analysis. Genome Biology, 2011, 12, R93.	13.9	10
42	A Model for Early Prediction of Facial Nerve Recovery After Vestibular Schwannoma Surgery. Otology and Neurotology, 2011, 32, 826-833.	0.7	58
43	Modelâ€Based Quality Assessment and Baseâ€Calling for Secondâ€Generation Sequencing Data. Biometrics, 2010, 66, 665-674.	0.8	50
44	Intensity normalization improves color calling in SOLiD sequencing. Nature Methods, 2010, 7, 336-337.	9.0	31
45	Tackling the widespread and critical impact of batch effects in high-throughput data. Nature Reviews Genetics, 2010, 11, 733-739.	7.7	1,641
46	Overcoming bias and systematic errors in next generation sequencing data. Genome Medicine, 2010, 2, 87.	3.6	84
47	Examining the relative influence of familial, genetic, and environmental covariate information in flexible risk models. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 8128-8133.	3.3	17
48	A Phylogenetic Mixture Model for the Evolution of Gene Expression. Molecular Biology and Evolution, 2009, 26, 2363-2372.	3.5	13
49	Optimizing mpf queries. , 2007, , .		20