

Rafael A Irizarry

List of Publications by Year in descending order

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Version: 2024-02-01

53
papers

32,248
citations

94269

37
h-index

161609

54
g-index

78
all docs

78
docs citations

78
times ranked

55650
citing authors

#	ARTICLE	IF	CITATIONS
1	Robust decomposition of cell type mixtures in spatial transcriptomics. <i>Nature Biotechnology</i> , 2022, 40, 517-526.	9.4	376
2	Effectiveness estimates of three COVID-19 vaccines based on observational data from Puerto Rico. <i>The Lancet Regional Health Americas</i> , 2022, 9, 100212.	1.5	17
3	Excess deaths associated with covid-19 pandemic in 2020: age and sex disaggregated time series analysis in 29 high income countries. <i>BMJ, The</i> , 2021, 373, n1137.	3.0	281
4	Progressive immune dysfunction with advancing disease stage in renal cell carcinoma. <i>Cancer Cell</i> , 2021, 39, 632-648.e8.	7.7	230
5	Vaginal microbiome topic modeling of laboring Ugandan women with and without fever. <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 75.	2.9	5
6	Capturing discrete latent structures: choose LDs over PCs. <i>Biostatistics</i> , 2021, , .	0.9	2
7	Characterizing batch effects and binding site-specific variability in ChIP-seq data. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab098.	1.5	3
8	Stem-like intestinal Th17 cells give rise to pathogenic effector T _H cells during autoimmunity. <i>Cell</i> , 2021, 184, 6281-6298.e23.	13.5	99
9	Large-Scale Topological Changes Restrain Malignant Progression in Colorectal Cancer. <i>Cell</i> , 2020, 182, 1474-1489.e23.	13.5	126
10	Quantile normalization of single-cell RNA-seq read counts without unique molecular identifiers. <i>Genome Biology</i> , 2020, 21, 160.	3.8	25
11	Quantifying the dynamics of migration after Hurricane Maria in Puerto Rico. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 32772-32778.	3.3	32
12	methyLCC: technology-independent estimation of cell type composition using differentially methylated regions. <i>Genome Biology</i> , 2019, 20, 261.	3.8	13
13	Feature selection and dimension reduction for single-cell RNA-Seq based on a multinomial model. <i>Genome Biology</i> , 2019, 20, 295.	3.8	288
14	Selection-Corrected Statistical Inference for Region Detection With High-Throughput Assays. <i>Journal of the American Statistical Association</i> , 2019, 114, 1351-1365.	1.8	2
15	Detection and accurate false discovery rate control of differentially methylated regions from whole genome bisulfite sequencing. <i>Biostatistics</i> , 2019, 20, 367-383.	0.9	118
16	High-throughput identification of <i>scRNA</i> nuclear enrichment sequences. <i>EMBO Journal</i> , 2018, 37, .	3.5	99
17	Missing data and technical variability in single-cell RNA-sequencing experiments. <i>Biostatistics</i> , 2018, 19, 562-578.	0.9	388
18	Smooth quantile normalization. <i>Biostatistics</i> , 2018, 19, 185-198.	0.9	78

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19	A Guide to Teaching Data Science. <i>American Statistician</i> , 2018, 72, 382-391.	0.9	52
20	Mortality in Puerto Rico after Hurricane Maria. <i>New England Journal of Medicine</i> , 2018, 379, 162-170.	13.9	462
21	Correcting for cell-type heterogeneity in epigenome-wide association studies: revisiting previous analyses. <i>Nature Methods</i> , 2017, 14, 216-217.	9.0	59
22	Salmon provides fast and bias-aware quantification of transcript expression. <i>Nature Methods</i> , 2017, 14, 417-419.	9.0	7,460
23	Bisulfite-independent analysis of CpG island methylation enables genome-scale stratification of single cells. <i>Nucleic Acids Research</i> , 2017, 45, gkx026.	6.5	31
24	SMARCB1 is required for widespread BAF complex-mediated activation of enhancers and bivalent promoters. <i>Nature Genetics</i> , 2017, 49, 1613-1623.	9.4	207
25	Accounting for GC-content bias reduces systematic errors and batch effects in ChIP-seq data. <i>Genome Research</i> , 2017, 27, 1930-1938.	2.4	29
26	Challenges and emerging directions in single-cell analysis. <i>Genome Biology</i> , 2017, 18, 84.	3.8	258
27	Flexible expressed region analysis for RNA-seq with <code>derfinder</code> . <i>Nucleic Acids Research</i> , 2017, 45, e9-e9.	6.5	54
28	Meta-analysis of gut microbiome studies identifies disease-specific and shared responses. <i>Nature Communications</i> , 2017, 8, 1784.	5.8	714
29	A benchmark for RNA-seq quantification pipelines. <i>Genome Biology</i> , 2016, 17, 74.	3.8	160
30	Modeling of RNA-seq fragment sequence bias reduces systematic errors in transcript abundance estimation. <i>Nature Biotechnology</i> , 2016, 34, 1287-1291.	9.4	159
31	A multi-omic analysis of human na ^ï ve CD4 ⁺ T cells. <i>BMC Systems Biology</i> , 2015, 9, 75.	3.0	43
32	quantro: a data-driven approach to guide the choice of an appropriate normalization method. <i>Genome Biology</i> , 2015, 16, 117.	13.9	76
33	Orchestrating high-throughput genomic analysis with Bioconductor. <i>Nature Methods</i> , 2015, 12, 115-121.	9.0	3,070
34	Age and sun exposure-related widespread genomic blocks of hypomethylation in nonmalignant skin. <i>Genome Biology</i> , 2015, 16, 80.	3.8	111
35	Visualization and probability-based scoring of structural variants within repetitive sequences. <i>Bioinformatics</i> , 2014, 30, 1514-1521.	1.8	5
36	Accounting for cellular heterogeneity is critical in epigenome-wide association studies. <i>Genome Biology</i> , 2014, 15, R31.	13.9	880

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37	Genome-wide methylation profiling reveals Zinc finger protein 516 (ZNF516) and FK-506-binding protein 6 (FKBP6) promoters frequently methylated in cervical neoplasia, associated with HPV status and ethnicity in a Chilean population. <i>Epigenetics</i> , 2014, 9, 308-317.	1.3	28
38	Minfi: a flexible and comprehensive Bioconductor package for the analysis of Infinium DNA methylation microarrays. <i>Bioinformatics</i> , 2014, 30, 1363-1369.	1.8	3,192
39	Large hypomethylated blocks as a universal defining epigenetic alteration in human solid tumors. <i>Genome Medicine</i> , 2014, 6, 61.	3.6	170
40	Removing technical variability in RNA-seq data using conditional quantile normalization. <i>Biostatistics</i> , 2012, 13, 204-216.	0.9	532
41	BSmooth: from whole genome bisulfite sequencing reads to differentially methylated regions. <i>Genome Biology</i> , 2012, 13, R83.	13.9	650
42	Bump hunting to identify differentially methylated regions in epigenetic epidemiology studies. <i>International Journal of Epidemiology</i> , 2012, 41, 200-209.	0.9	567
43	Increased methylation variation in epigenetic domains across cancer types. <i>Nature Genetics</i> , 2011, 43, 768-775.	9.4	968
44	Tackling the widespread and critical impact of batch effects in high-throughput data. <i>Nature Reviews Genetics</i> , 2010, 11, 733-739.	7.7	1,641
45	A species-generalized probabilistic model-based definition of CpG islands. <i>Mammalian Genome</i> , 2009, 20, 674-80.	1.0	52
46	The human colon cancer methylome shows similar hypo- and hypermethylation at conserved tissue-specific CpG island shores. <i>Nature Genetics</i> , 2009, 41, 178-186.	9.4	1,977
47	Gene set enrichment analysis made simple. <i>Statistical Methods in Medical Research</i> , 2009, 18, 565-575.	0.7	166
48	Promoter Hypermethylation in MLL-r Leukemia: Biology and Therapeutic Targeting.. <i>Blood</i> , 2009, 114, 3472-3472.	0.6	0
49	Comprehensive high-throughput arrays for relative methylation (CHARM). <i>Genome Research</i> , 2008, 18, 780-790.	2.4	379
50	Multiple-laboratory comparison of microarray platforms. <i>Nature Methods</i> , 2005, 2, 345-350.	9.0	814
51	affy-analysis of Affymetrix GeneChip data at the probe level. <i>Bioinformatics</i> , 2004, 20, 307-315.	1.8	4,830
52	The Role of Academia in Data Science Education. , 0, , .		22
53	A probabilistic gene expression barcode for annotation of cell types from single-cell RNA-seq data. <i>Biostatistics</i> , 0, , .	0.9	11