Rafael A Irizarry

List of Publications by Year in Descending Order

Source: https://exaly.com/author-pdf/4284257/rafael-a-irizarry-publications-by-year.pdf
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64 papers	20,400 citations	34 h-index	78 g-index
78 ext. papers	27,831 ext. citations	16.8 avg, IF	7.05 L-index

#	Paper	IF	Citations
64	Effectiveness estimates of three COVID-19 vaccines based on observational data from Puerto Rico.. *The Lancet Regional Health Americas*, **2022**, 9, 100212		3
63	Stem-like intestinal Th17 cells give rise to pathogenic effector T cells during autoimmunity. *Cell*, **2021**,	56.2	13
62	Characterizing batch effects and binding site-specific variability in ChIP-seq data. *NAR Genomics and Bioinformatics*, **2021**, 3, lqab098	3.7	2
61	Excess deaths associated with covid-19 pandemic in 2020: age and sex disaggregated time series analysis in 29 high income countries. *BMJ, The*, **2021**, 373, n1137	5.9	101
60	Progressive immune dysfunction with advancing disease stage in renal cell carcinoma. *Cancer Cell*, **2021**, 39, 632-648.e8	24.3	42
59	Robust decomposition of cell type mixtures in spatial transcriptomics. *Nature Biotechnology*, **2021**,	44.5	64
58	Vaginal microbiome topic modeling of laboring Ugandan women with and without fever. *Npj Biofilms and Microbiomes*, **2021**, 7, 75	8.2	0
57	Quantile normalization of single-cell RNA-seq read counts without unique molecular identifiers. *Genome Biology*, **2020**, 21, 160	18.3	6
56	Quantifying the dynamics of migration after Hurricane Maria in Puerto Rico. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 32772-32778	11.5	10
55	Large-Scale Topological Changes Restrain Malignant Progression in Colorectal Cancer. *Cell*, **2020**, 182, 1474-1489.e23	56.2	41
54	methylCC: technology-independent estimation of cell type composition using differentially methylated regions. *Genome Biology*, **2019**, 20, 261	18.3	6
53	Feature selection and dimension reduction for single-cell RNA-Seq based on a multinomial model. *Genome Biology*, **2019**, 20, 295	18.3	122
52	Selection-Corrected Statistical Inference for Region Detection With High-Throughput Assays. *Journal of the American Statistical Association*, **2019**, 114, 1351-1365	2.8	1
51	Detection and accurate false discovery rate control of differentially methylated regions from whole genome bisulfite sequencing. *Biostatistics*, **2019**, 20, 367-383	3.7	51
50	High-throughput identification of RNA nuclear enrichment sequences. *EMBO Journal*, **2018**, 37,	13	64
49	Missing data and technical variability in single-cell RNA-sequencing experiments. *Biostatistics*, **2018**, 19, 562-578	3.7	223
48	Smooth quantile normalization. *Biostatistics*, **2018**, 19, 185-198	3.7	37

47	A Guide to Teaching Data Science. *American Statistician*, **2018**, 72, 382-391	5	34
46	Mortality in Puerto Rico after Hurricane Maria. *New England Journal of Medicine*, **2018**, 379, 162-170	59.2	308
45	Correcting for cell-type heterogeneity in epigenome-wide association studies: revisiting previous analyses. *Nature Methods*, **2017**, 14, 216-217	21.6	47
44	Salmon provides fast and bias-aware quantification of transcript expression. *Nature Methods*, **2017**, 14, 417-419	21.6	3249
43	Bisulfite-independent analysis of CpG island methylation enables genome-scale stratification of single cells. *Nucleic Acids Research*, **2017**, 45, e77	20.1	24
42	SMARCB1 is required for widespread BAF complex-mediated activation of enhancers and bivalent promoters. *Nature Genetics*, **2017**, 49, 1613-1623	36.3	121
41	Accounting for GC-content bias reduces systematic errors and batch effects in ChIP-seq data. *Genome Research*, **2017**, 27, 1930-1938	9.7	18
40	Meta-analysis of gut microbiome studies identifies disease-specific and shared responses. *Nature Communications*, **2017**, 8, 1784	17.4	425
39	Challenges and emerging directions in single-cell analysis. *Genome Biology*, **2017**, 18, 84	18.3	166
38	Flexible expressed region analysis for RNA-seq with derfinder. *Nucleic Acids Research*, **2017**, 45, e9	20.1	32
37	A benchmark for RNA-seq quantification pipelines. *Genome Biology*, **2016**, 17, 74	18.3	117
36	Modeling of RNA-seq fragment sequence bias reduces systematic errors in transcript abundance estimation. *Nature Biotechnology*, **2016**, 34, 1287-1291	44.5	91
35	Age and sun exposure-related widespread genomic blocks of hypomethylation in nonmalignant skin. *Genome Biology*, **2015**, 16, 80	18.3	83
34	A multi-omic analysis of human naïve CD4+ T cells. *BMC Systems Biology*, **2015**, 9, 75	3.5	30
33	quantro: a data-driven approach to guide the choice of an appropriate normalization method. *Genome Biology*, **2015**, 16, 117	18.3	54
32	Orchestrating high-throughput genomic analysis with Bioconductor. *Nature Methods*, **2015**, 12, 115-21	21.6	1949
31	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. *Epigenetics*, **2014**, 9, 308-17	5.7	21
30	Minfi: a flexible and comprehensive Bioconductor package for the analysis of Infinium DNA methylation microarrays. *Bioinformatics*, **2014**, 30, 1363-9	7.2	1941

29	Large hypomethylated blocks as a universal defining epigenetic alteration in human solid tumors. *Genome Medicine*, **2014**, 6, 61	14.4	120
28	Visualization and probability-based scoring of structural variants within repetitive sequences. *Bioinformatics*, **2014**, 30, 1514-21	7.2	4
27	Accounting for cellular heterogeneity is critical in epigenome-wide association studies. *Genome Biology*, **2014**, 15, R31	18.3	660
26	BSmooth: from whole genome bisulfite sequencing reads to differentially methylated regions. *Genome Biology*, **2012**, 13, R83	18.3	445
25	Bump hunting to identify differentially methylated regions in epigenetic epidemiology studies. *International Journal of Epidemiology*, **2012**, 41, 200-9	7.8	430
24	Removing technical variability in RNA-seq data using conditional quantile normalization. *Biostatistics*, **2012**, 13, 204-16	3.7	378
23	Increased methylation variation in epigenetic domains across cancer types. *Nature Genetics*, **2011**, 43, 768-75	36.3	825
22	Tackling the widespread and critical impact of batch effects in high-throughput data. *Nature Reviews Genetics*, **2010**, 11, 733-9	30.1	1232
21	A species-generalized probabilistic model-based definition of CpG islands. *Mammalian Genome*, **2009**, 20, 674-80	3.2	47
20	The human colon cancer methylome shows similar hypo- and hypermethylation at conserved tissue-specific CpG island shores. *Nature Genetics*, **2009**, 41, 178-186	36.3	1681
19	Gene set enrichment analysis made simple. *Statistical Methods in Medical Research*, **2009**, 18, 565-75	2.3	134
18	Promoter Hypermethylation in MLL-r Leukemia: Biology and Therapeutic Targeting.. *Blood*, **2009**, 114, 3472-3472	2.2	
17	Comprehensive high-throughput arrays for relative methylation (CHARM). *Genome Research*, **2008**, 18, 780-90	9.7	350
16	Multiple-laboratory comparison of microarray platforms. *Nature Methods*, **2005**, 2, 345-50	21.6	716
15	affy--analysis of Affymetrix GeneChip data at the probe level. *Bioinformatics*, **2004**, 20, 307-15	7.2	3733
14	Effectiveness of different booster regimens for preventing infection and adverse outcomes in Puerto Rico		1
13	The Role of Academia in Data Science Education		9
12	Time-Varying Effectiveness of Three Covid-19 Vaccines in Puerto Rico		2

List of Publications

11	Quantifying the Dynamics of Migration after a Disaster: Impact of Hurricane Maria in Puerto Rico	1
10	Missing Data and Technical Variability in Single-Cell RNA- Sequencing Experiments	33
9	Smooth Quantile Normalization	6
8	Varying-Censoring Aware Matrix Factorization for Single Cell RNA-Sequencing	4
7	A probabilistic gene expression barcode for annotation of cell-types from single cell RNA-seq data	2
6	Robust decomposition of cell type mixtures in spatial transcriptomics	16
5	Monitoring Health Systems by Estimating Excess Mortality	7
4	Genome-wide repressive capacity of promoter DNA methylation is revealed through epigenomic manipulation	7
3	Feature Selection and Dimension Reduction for Single Cell RNA-Seq based on a Multinomial Model	24
2	Quantile normalization of single-cell RNA-seq read counts without unique molecular identifiers	1
1	All-cause excess mortality in the State of Gujarat, India, during the COVID-19 pandemic (March 2020-April 2021)	2