

Donald Geman

List of Publications by Year in descending order

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Version: 2024-02-01

33
papers

18,296
citations

516215

16
h-index

500791

28
g-index

33
all docs

33
docs citations

33
times ranked

14216
citing authors

#	ARTICLE	IF	CITATIONS
1	Stochastic Relaxation, Gibbs Distributions, and the Bayesian Restoration of Images. IEEE Transactions on Pattern Analysis and Machine Intelligence, 1984, PAMI-6, 721-741.	9.7	13,839
2	Tackling the widespread and critical impact of batch effects in high-throughput data. Nature Reviews Genetics, 2010, 11, 733-739.	7.7	1,641
3	Shape Quantization and Recognition with Randomized Trees. Neural Computation, 1997, 9, 1545-1588.	1.3	953
4	Stochastic relaxation, Gibbs distributions and the Bayesian restoration of images*. Journal of Applied Statistics, 1993, 20, 25-62.	0.6	325
5	Classifying Gene Expression Profiles from Pairwise mRNA Comparisons. Statistical Applications in Genetics and Molecular Biology, 2004, 3, 1-19.	0.2	297
6	Coarse-to-Fine Face Detection. , 2001, 41, 85-107.		199
7	Visual Turing test for computer vision systems. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 3618-3623.	3.3	178
8	Computational Medicine: Translating Models to Clinical Care. Science Translational Medicine, 2012, 4, 158rv11.	5.8	171
9	A Computational Model for Visual Selection. Neural Computation, 1999, 11, 1691-1715.	1.3	124
10	A coarse-to-fine strategy for multiclass shape detection. IEEE Transactions on Pattern Analysis and Machine Intelligence, 2004, 26, 1606-1621.	9.7	106
11	Identifying Tightly Regulated and Variably Expressed Networks by Differential Rank Conservation (DIRAC). PLoS Computational Biology, 2010, 6, e1000792.	1.5	73
12	Hierarchical testing designs for pattern recognition. Annals of Statistics, 2005, 33, 1155.	1.4	51
13	Revisiting the tumorigenesis timeline with a data-driven generative model. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 857-864.	3.3	44
14	switchBox: an R package for kâ€“Top Scoring Pairs classifier development. Bioinformatics, 2015, 31, 273-274.	1.8	40
15	Science in the age of selfies. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 9384-9387.	3.3	38
16	Learning Dysregulated Pathways in Cancers from Differential Variability Analysis. Cancer Informatics, 2014, 13s5, CiN.S14066.	0.9	37
17	High resolution time-course mapping of early transcriptomic, molecular and cellular phenotypes in Huntingtonâ€™s disease CAG knock-in mice across multiple genetic backgrounds. Human Molecular Genetics, 2017, 26, 913-922.	1.4	37
18	Digitizing omics profiles by divergence from a baseline. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 4545-4552.	3.3	23

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19	Efficient Focusing and Face Detection. , 1998, , 157-173.		19
20	Measuring the Effect of Inter-Study Variability on Estimating Prediction Error. PLoS ONE, 2014, 9, e110840.	1.1	19
21	Multi-study Integration of Brain Cancer Transcriptomes Reveals Organ-Level Molecular Signatures. PLoS Computational Biology, 2013, 9, e1003148.	1.5	16
22	A Comprehensive Statistical Model for Cell Signaling. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 592-606.	1.9	12
23	Tracking Cross-Validated Estimates of Prediction Error as Studies Accumulate. Journal of the American Statistical Association, 2015, 110, 1239-1247.	1.8	11
24	Splice Expression Variation Analysis (SEVA) for inter-tumor heterogeneity of gene isoform usage in cancer. Bioinformatics, 2018, 34, 1859-1867.	1.8	11
25	An argument for mechanism-based statistical inference in cancer. Human Genetics, 2015, 134, 479-495.	1.8	9
26	Identifying Personalized Metabolic Signatures in Breast Cancer. Metabolites, 2021, 11, 20.	1.3	7
27	Identification of direction in gene networks from expression and methylation. BMC Systems Biology, 2013, 7, 118.	3.0	6
28	Attribute Prototype Learning for Interactive Face Retrieval. IEEE Transactions on Information Forensics and Security, 2021, 16, 2593-2607.	4.5	5
29	An R package for divergence analysis of omics data. PLoS ONE, 2021, 16, e0249002.	1.1	2
30	Efficient representations of tumor diversity with paired DNA-RNA aberrations. PLoS Computational Biology, 2021, 17, e1008944.	1.5	2
31	Coarse-to-Fine Classification and Scene Labeling. Lecture Notes in Statistics, 2003, , 31-48.	0.1	1
32	In Search of a Unifying Theory for Image Interpretation. , 2006, , .		0
33	Robust determination of differential abundance in shotgun proteomics using nonparametric statistics. Molecular Omics, 2018, 14, 424-436.	1.4	0