

Edoardo M Airoidi

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

70
papers

4,076
citations

26
h-index

63
g-index

78
ext. papers

5,096
ext. citations

7.2
avg, IF

5.67
L-index

#	Paper	IF	Citations
70	Analysis and design of RNA sequencing experiments for identifying isoform regulation. <i>Nature Methods</i> , 2010 , 7, 1009-15	21.6	934
69	Mixed Membership Stochastic Blockmodels. <i>Journal of Machine Learning Research</i> , 2008 , 9, 1981-2014	28.6	424
68	Coordination of growth rate, cell cycle, stress response, and metabolic activity in yeast. <i>Molecular Biology of the Cell</i> , 2008 , 19, 352-67	3.5	405
67	Reversible, Specific, Active Aggregates of Endogenous Proteins Assemble upon Heat Stress. <i>Cell</i> , 2015 , 162, 1286-98	56.2	264
66	Systems-level dynamic analyses of fate change in murine embryonic stem cells. <i>Nature</i> , 2009 , 462, 358-63	30.4	237
65	A Model of Text for Experimentation in the Social Sciences. <i>Journal of the American Statistical Association</i> , 2016 , 111, 988-1003	2.8	225
64	Differential Stoichiometry among Core Ribosomal Proteins. <i>Cell Reports</i> , 2015 , 13, 865-73	10.6	127
63	Accounting for experimental noise reveals that mRNA levels, amplified by post-transcriptional processes, largely determine steady-state protein levels in yeast. <i>PLoS Genetics</i> , 2015 , 11, e1005206	6	107
62	Quantitative visualization of alternative exon expression from RNA-seq data. <i>Bioinformatics</i> , 2015 , 31, 2400-2	7.2	99
61	Defining the Essential Function of Yeast Hsf1 Reveals a Compact Transcriptional Program for Maintaining Eukaryotic Proteostasis. <i>Molecular Cell</i> , 2016 , 63, 60-71	17.6	92
60	Post-transcriptional regulation across human tissues. <i>PLoS Computational Biology</i> , 2017 , 13, e1005535	5	86
59	Predicting cellular growth from gene expression signatures. <i>PLoS Computational Biology</i> , 2009 , 5, e1000357	3.57	78
58	Musashi proteins are post-transcriptional regulators of the epithelial-luminal cell state. <i>ELife</i> , 2014 , 3, e03915	8.9	63
57	The Structure of Negative Social Ties in Rural Village Networks. <i>Sociological Science</i> , 2019 , 6, 197-218	18	62
56	A natural experiment of social network formation and dynamics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 6595-600	11.5	60
55	Constant growth rate can be supported by decreasing energy flux and increasing aerobic glycolysis. <i>Cell Reports</i> , 2014 , 7, 705-14	10.6	56
54	Predicting traffic volumes and estimating the effects of shocks in massive transportation systems. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 5643-8	11.5	52

53	Integrating Utility into Face De-identification. <i>Lecture Notes in Computer Science</i> , 2006 , 227-242	0.9	47
52	Improving and Evaluating Topic Models and Other Models of Text. <i>Journal of the American Statistical Association</i> , 2016 , 111, 1381-1403	2.8	39
51	Assessing the Impact of Granular Privacy Controls on Content Sharing and Disclosure on Facebook. <i>Information Systems Research</i> , 2016 , 27, 848-879	3.8	37
50	A Network Analysis Model for Disambiguation of Names in Lists. <i>Computational and Mathematical Organization Theory</i> , 2005 , 11, 119-139	2.1	33
49	Sampling algorithms for pure network topologies. <i>SIGKDD Explorations: Newsletter of the Special Interest Group (SIG) on Knowledge Discovery & Data Mining</i> , 2005 , 7, 13-22	4.6	32
48	A conserved cell growth cycle can account for the environmental stress responses of divergent eukaryotes. <i>Molecular Biology of the Cell</i> , 2012 , 23, 1986-97	3.5	31
47	Getting started in probabilistic graphical models. <i>PLoS Computational Biology</i> , 2007 , 3, e252	5	30
46	Generalized species sampling priors with latent Beta reinforcements. <i>Journal of the American Statistical Association</i> , 2014 , 109, 1466-1480	2.8	27
45	Stacking models for nearly optimal link prediction in complex networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 23393-23400	11.5	27
44	Estimating selection on synonymous codon usage from noisy experimental data. <i>Molecular Biology and Evolution</i> , 2013 , 30, 1438-53	8.3	26
43	Network Sampling and Classification: An Investigation of Network Model Representations. <i>Decision Support Systems</i> , 2011 , 51, 506-518	5.6	25
42	Who wrote Ronald Reagan's radio addresses?. <i>Bayesian Analysis</i> , 2006 , 1, 289	2.3	24
41	Asymptotic and finite-sample properties of estimators based on stochastic gradients. <i>Annals of Statistics</i> , 2017 , 45,	3.2	23
40	Steady-state and dynamic gene expression programs in <i>Saccharomyces cerevisiae</i> in response to variation in environmental nitrogen. <i>Molecular Biology of the Cell</i> , 2016 , 27, 1383-96	3.5	22
39	Mapping dynamic histone acetylation patterns to gene expression in nanog-depleted murine embryonic stem cells. <i>PLoS Computational Biology</i> , 2010 , 6, e1001034	5	20
38	Estimating Latent Processes on a Network From Indirect Measurements. <i>Journal of the American Statistical Association</i> , 2013 , 108, 149-164	2.8	18
37	A latent mixed membership model for relational data 2005 ,		18
36	Scalable estimation strategies based on stochastic approximations: Classical results and new insights. <i>Statistics and Computing</i> , 2015 , 25, 781-795	1.8	14

35	Reconceptualizing the classification of PNAS articles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 20899-904	11.5	14
34	Quantifying Homologous Proteins and Proteoforms. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 162-168	6	13
33	Model-assisted design of experiments in the presence of network-correlated outcomes. <i>Biometrika</i> , 2018 , 105, 849-858	2	12
32	Markov Blankets and Meta-heuristics Search: Sentiment Extraction from Unstructured Texts. <i>Lecture Notes in Computer Science</i> , 2006 , 167-187	0.9	12
31	Estimating a structured covariance matrix from multi-lab measurements in high-throughput biology. <i>Journal of the American Statistical Association</i> , 2015 , 110, 27-44	2.8	11
30	An Entropy Approach to Disclosure Risk Assessment: Lessons from Real Applications and Simulated Domains. <i>Decision Support Systems</i> , 2011 , 51, 10-20	5.6	11
29	Intersection of the Web-Based Vaping Narrative With COVID-19: Topic Modeling Study. <i>Journal of Medical Internet Research</i> , 2020 , 22, e21743	7.6	11
28	A computational approach to map nucleosome positions and alternative chromatin states with base pair resolution. <i>ELife</i> , 2016 , 5,	8.9	11
27	Identification and Estimation of Treatment and Interference Effects in Observational Studies on Networks. <i>Journal of the American Statistical Association</i> , 2021 , 116, 901-918	2.8	11
26	Cyclic motifs in the Sardex monetary network. <i>Nature Human Behaviour</i> , 2018 , 2, 822-829	12.8	10
25	SLANTS: Sequential Adaptive Nonlinear Modeling of Time Series. <i>IEEE Transactions on Signal Processing</i> , 2017 , 65, 4994-5005	4.8	9
24	Confidence sets for network structure. <i>Statistical Analysis and Data Mining</i> , 2011 , 4, 461-469	1.4	9
23	Combining Stochastic Block Models and Mixed Membership for Statistical Network Analysis 2006 , 57-74		8
22	Limitations of Design-based Causal Inference and A/B Testing under Arbitrary and Network Interference. <i>Sociological Methodology</i> , 2018 , 48, 136-151	2.6	7
21	Whose Ideas? Whose Words? Authorship of Ronald Reagan's Radio Addresses. <i>PS - Political Science and Politics</i> , 2007 , 40, 501-506	0.4	7
20	A Coevolution Model of Network Structure and User Behavior: The Case of Content Generation in Online Social Networks. <i>Information Systems Research</i> , 2019 , 30, 117-132	3.8	5
19	A Multivariate Computational Method to Analyze High-Content RNAi Screening Data. <i>Journal of Biomolecular Screening</i> , 2015 , 20, 985-97		5
18	The Effects of Location Access Behavior on Re-identification Risk in a Distributed Environment. <i>Lecture Notes in Computer Science</i> , 2006 , 413-429	0.9	5

17	MULTI-WAY BLOCKMODELS FOR ANALYZING COORDINATED HIGH-DIMENSIONAL RESPONSES. <i>Annals of Applied Statistics</i> , 2013 , 7, 2431-2457	2.1	4
16	Recovering latent time-series from their observed sums 2004 ,		4
15	Quantifying condition-dependent intracellular protein levels enables high-precision fitness estimates. <i>PLoS ONE</i> , 2013 , 8, e75320	3.7	4
14	Geometric Representations of Random Hypergraphs. <i>Journal of the American Statistical Association</i> , 2017 , 112, 363-383	2.8	3
13	Investigating the Impact of Network Effects on Content Generation: Evidence from a Large Online Student Network. <i>SSRN Electronic Journal</i> , 2015 ,	1	3
12	Discovery of Latent Patterns with Hierarchical Bayesian Mixed-Membership Models and the Issue of Model Choice 2008 , 240-275		3
11	Quantifying homologous proteins and proteoforms		3
10	Nonstandard conditionally specified models for nonignorable missing data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 19045-19053	11.5	3
9	RANKING RELATIONS USING ANALOGIES IN BIOLOGICAL AND INFORMATION NETWORKS. <i>Annals of Applied Statistics</i> , 2010 , 4, 615-644	2.1	2
8	Network Analysis of Wikipedia ⁸¹⁻¹⁰²		2
7	Hybrid Mixed-Membership Blockmodel for Inference on Realistic Network Interactions. <i>IEEE Transactions on Network Science and Engineering</i> , 2019 , 6, 336-350	4.9	2
6	Template-Based Models for Genome-Wide Analysis of Next-Generation Sequencing Data at Base-Pair Resolution. <i>Journal of the American Statistical Association</i> , 2016 , 111, 967-987	2.8	1
5	Species Sampling Priors for Modeling Dependence: An Application to the Detection of Chromosomal Aberrations 2015 , 97-114		1
4	Post-transcriptional regulation across human tissues		1
3	The proximal Robbins-Monro method. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2021 , 83, 188-212	3.9	0
2	Stephen E. Fienberg's Contributions to Categorical Data Analysis and the Social Sciences. <i>Chance</i> , 2013 , 26, 12-14	1	
1	Small sets of interacting proteins suggest functional linkage mechanisms via Bayesian analogical reasoning. <i>Bioinformatics</i> , 2011 , 27, i374-82	7.2	