

# Maria De Iorio

## List of Publications by Year in descending order

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85  
papers

4,430  
citations

159358

30  
h-index

110170

64  
g-index

89  
all docs

89  
docs citations

89  
times ranked

7019  
citing authors

#	ARTICLE	IF	CITATIONS
1	Human metabolic phenotype diversity and its association with diet and blood pressure. <i>Nature</i> , 2008, 453, 396-400.	13.7	966
2	Simultaneous Analysis of All SNPs in Genome-Wide and Re-Sequencing Association Studies. <i>PLoS Genetics</i> , 2008, 4, e1000130.	1.5	298
3	An ANOVA Model for Dependent Random Measures. <i>Journal of the American Statistical Association</i> , 2004, 99, 205-215.	1.8	228
4	Review and evaluation of penalised regression methods for risk prediction in low-dimensional data with few events. <i>Statistics in Medicine</i> , 2016, 35, 1159-1177.	0.8	227
5	Genome-wide significance for dense SNP and resequencing data. <i>Genetic Epidemiology</i> , 2008, 32, 179-185.	0.6	187
6	Bayesian deconvolution and quantification of metabolites in complex 1D NMR spectra using BATMAN. <i>Nature Protocols</i> , 2014, 9, 1416-1427.	5.5	167
7	BATMAN—an R package for the automated quantification of metabolites from nuclear magnetic resonance spectra using a Bayesian model. <i>Bioinformatics</i> , 2012, 28, 2088-2090.	1.8	142
8	Optimal Bayesian Design by Inhomogeneous Markov Chain Simulation. <i>Journal of the American Statistical Association</i> , 2004, 99, 788-798.	1.8	129
9	Opening up the "Black Box": Metabolic phenotyping and metabolome-wide association studies in epidemiology. <i>Journal of Clinical Epidemiology</i> , 2010, 63, 970-979.	2.4	125
10	Metabolic Profiling and the Metabolome-Wide Association Study: Significance Level For Biomarker Identification. <i>Journal of Proteome Research</i> , 2010, 9, 4620-4627.	1.8	123
11	Metabolome-Wide Association Study Identifies Multiple Biomarkers that Discriminate North and South Chinese Populations at Differing Risks of Cardiovascular Disease: INTERMAP Study. <i>Journal of Proteome Research</i> , 2010, 9, 6647-6654.	1.8	116
12	Meeting-in-the-middle using metabolic profiling—a strategy for the identification of intermediate biomarkers in cohort studies. <i>Biomarkers</i> , 2011, 16, 83-88.	0.9	113
13	Bayesian Nonparametric Nonproportional Hazards Survival Modeling. <i>Biometrics</i> , 2009, 65, 762-771.	0.8	111
14	Sequence-Level Population Simulations Over Large Genomic Regions. <i>Genetics</i> , 2007, 177, 1725-1731.	1.2	99
15	Conserved Mosquito/Parasite Interactions Affect Development of <i>Plasmodium falciparum</i> in Africa. <i>PLoS Pathogens</i> , 2008, 4, e1000069.	2.1	93
16	Significance testing in ridge regression for genetic data. <i>BMC Bioinformatics</i> , 2011, 12, 372.	1.2	84
17	Ridge Regression in Prediction Problems: Automatic Choice of the Ridge Parameter. <i>Genetic Epidemiology</i> , 2013, 37, 704-714.	0.6	84
18	Subset Optimization by Reference Matching (STORM): An Optimized Statistical Approach for Recovery of Metabolic Biomarker Structural Information from <sup>1</sup> H NMR Spectra of Biofluids. <i>Analytical Chemistry</i> , 2012, 84, 10694-10701.	3.2	75

#	ARTICLE	IF	CITATIONS
19	Importance sampling on coalescent histories. I. <i>Advances in Applied Probability</i> , 2004, 36, 417-433.	0.4	73
20	Metabolic profiling of polycystic ovary syndrome reveals interactions with abdominal obesity. <i>International Journal of Obesity</i> , 2017, 41, 1331-1340.	1.6	64
21	Importance sampling on coalescent histories. II: Subdivided population models. <i>Advances in Applied Probability</i> , 2004, 36, 434-454.	0.4	59
22	Fregene: Simulation of realistic sequence-level data in populations and ascertained samples. <i>BMC Bioinformatics</i> , 2008, 9, 364.	1.2	57
23	Genome-wide data reveal novel genes for methotrexate response in a large cohort of juvenile idiopathic arthritis cases. <i>Pharmacogenomics Journal</i> , 2014, 14, 356-364.	0.9	52
24	Bayesian semiparametric inference for multivariate doubly-interval-censored data. <i>Annals of Applied Statistics</i> , 2010, 4, .	0.5	50
25	Modelling the acid/base 1H NMR chemical shift limits of metabolites in human urine. <i>Metabolomics</i> , 2016, 12, 152.	1.4	47
26	Stepwise mutation likelihood computation by sequential importance sampling in subdivided population models. <i>Theoretical Population Biology</i> , 2005, 68, 41-53.	0.5	41
27	A Bayesian Model of NMR Spectra for the Deconvolution and Quantification of Metabolites in Complex Biological Mixtures. <i>Journal of the American Statistical Association</i> , 2012, 107, 1259-1271.	1.8	41
28	Proximal Femoral Allograft in Revision Hip Surgery With Severe Femoral Bone Loss. <i>Journal of Arthroplasty</i> , 2012, 27, 829-836.e1.	1.5	34
29	A genome-wide association study and biological pathway analysis of epilepsy prognosis in a prospective cohort of newly treated epilepsy. <i>Human Molecular Genetics</i> , 2014, 23, 247-258.	1.4	33
30	A Differential Network Approach to Exploring Differences between Biological States: An Application to Prediabetes. <i>PLoS ONE</i> , 2011, 6, e24702.	1.1	33
31	Genetic Association Mapping via Evolution-Based Clustering of Haplotypes. <i>PLoS Genetics</i> , 2007, 3, e111.	1.5	31
32	Urinary ATP as an indicator of infection and inflammation of the urinary tract in patients with lower urinary tract symptoms. <i>BMC Urology</i> , 2015, 15, 7.	0.6	25
33	Dietary and Urinary Metabonomic Factors Possibly Accounting for Higher Blood Pressure of Black Compared With White Americans. <i>Hypertension</i> , 2013, 62, 1074-1080.	1.3	24
34	Bayesian inference for multiple Gaussian graphical models with application to metabolic association networks. <i>Annals of Applied Statistics</i> , 2017, 11, .	0.5	23
35	Importance sampling on coalescent histories. II: Subdivided population models. <i>Advances in Applied Probability</i> , 2004, 36, 434-454.	0.4	22
36	Genome metabolome integrated network analysis to uncover connections between genetic variants and complex traits: an application to obesity. <i>Journal of the Royal Society Interface</i> , 2014, 11, 20130908.	1.5	20

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37	Recalcitrant chronic bladder pain and recurrent cystitis but negative urinalysis: What should we do?. International Urogynecology Journal, 2018, 29, 1035-1043.	0.7	20
38	Bayesian logistic regression using a perfect phylogeny. Biostatistics, 2007, 8, 32-52.	0.9	19
39	MetAssimulo:Simulation of Realistic NMR Metabolic Profiles. BMC Bioinformatics, 2010, 11, 496.	1.2	17
40	Finding Associations in Dense Genetic Maps: A Genetic Algorithm Approach. Human Heredity, 2005, 60, 97-108.	0.4	15
41	Comparison of the Utility and Validity of Three Scoring Tools to Measure Skin Involvement in Patients With Juvenile Dermatomyositis. Arthritis Care and Research, 2016, 68, 1514-1521.	1.5	15
42	Lower urinary tract symptoms that predict microscopic pyuria. International Urogynecology Journal, 2018, 29, 1019-1028.	0.7	15
43	Statistical Techniques in Metabolic Profiling. , 2008, , 347-373.		13
44	Variable selection in covariate dependent random partition models: an application to urinary tract infection. Statistics in Medicine, 2016, 35, 1373-1389.	0.8	13
45	Bayesian estimation of the number of protonation sites for urinary metabolites from NMR spectroscopic data. Metabolomics, 2018, 14, 56.	1.4	13
46	A nonparametric Bayesian model for inference in related longitudinal studies. Journal of the Royal Statistical Society Series C: Applied Statistics, 2005, 54, 611-626.	0.5	12
47	A comparative review of variable selection techniques for covariate dependent Dirichlet process mixture models. Canadian Journal of Statistics, 2017, 45, 254-273.	0.6	12
48	Joint modeling of recurrent events and survival: a Bayesian non-parametric approach. Biostatistics, 2018, 21, 1-14.	0.9	12
49	Importance sampling on coalescent histories. I. Advances in Applied Probability, 2004, 36, 417-433.	0.4	11
50	Dynamics of the Risk of Smoking-Induced Lung Cancer. Epidemiology, 2014, 25, 28-34.	1.2	9
51	Bayesian Inference for Duplication-Mutation with Complementarity Network Models. Journal of Computational Biology, 2015, 22, 1025-1033.	0.8	8
52	Clinical signs and symptoms in a joint model of four disease activity parameters in juvenile dermatomyositis: a prospective, longitudinal, multicenter cohort study. Arthritis Research and Therapy, 2018, 20, 180.	1.6	8
53	Computational Methods for a Class of Network Models. Journal of Computational Biology, 2014, 21, 141-161.	0.8	7
54	An Evolutionary Algorithm to Find Associations in Dense Genetic Maps. IEEE Transactions on Evolutionary Computation, 2008, 12, 297-306.	7.5	6

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55	Bridging trees for posterior inference on ancestral recombination graphs. <i>Proceedings of the Royal Society A: Mathematical, Physical and Engineering Sciences</i> , 2018, 474, 20180568.	1.0	6
56	Dependent generalized Dirichlet process priors for the analysis of acute lymphoblastic leukemia. <i>Biostatistics</i> , 2018, 19, 342-358.	0.9	6
57	Modelling disease activity in juvenile dermatomyositis: A Bayesian approach. <i>Statistical Methods in Medical Research</i> , 2019, 28, 35-49.	0.7	6
58	The $G$ -Wishart Weighted Proposal Algorithm: Efficient Posterior Computation for Gaussian Graphical Models. <i>Journal of Computational and Graphical Statistics</i> , 2022, 31, 1215-1224.	0.9	6
59	Unbiased approximation of posteriors via coupled particle Markov chain Monte Carlo. <i>Statistics and Computing</i> , 2022, 32, 1.	0.8	6
60	Recombination hotspots as a point process. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2005, 360, 1597-1603.	1.8	5
61	Bayesian semiparametric meta-analysis for genetic association studies. <i>Genetic Epidemiology</i> , 2011, 35, 333-340.	0.6	5
62	Bayesian splines versus fractional polynomials in network meta-analysis. <i>BMC Medical Research Methodology</i> , 2020, 20, 261.	1.4	5
63	Monte Carlo co-ordinate ascent variational inference. <i>Statistics and Computing</i> , 2020, 30, 887-905.	0.8	5
64	A spatial probit model for fine-scale mapping of disease genes. <i>Genetic Epidemiology</i> , 2007, 31, 252-260.	0.6	4
65	Bayesian survival analysis in genetic association studies. <i>Bioinformatics</i> , 2008, 24, 2030-2036.	1.8	4
66	The time machine: a simulation approach for stochastic trees. <i>Proceedings of the Royal Society A: Mathematical, Physical and Engineering Sciences</i> , 2011, 467, 2350-2368.	1.0	4
67	Variance and covariance heterogeneity analysis for detection of metabolites associated with cadmium exposure. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2014, 13, 191-201.	0.2	4
68	A Bayesian semiparametric Markov regression model for juvenile dermatomyositis. <i>Statistics in Medicine</i> , 2018, 37, 1711-1731.	0.8	4
69	A comparative review of network meta-analysis models in longitudinal randomized controlled trial. <i>Statistics in Medicine</i> , 2019, 38, 3053-3072.	0.8	4
70	Modeling Population Structure Under Hierarchical Dirichlet Processes. <i>Bayesian Analysis</i> , 2019, 14, .	1.6	4
71	Integrating dynamic mixed-effect modelling and penalized regression to explore genetic association with pharmacokinetics. <i>Pharmacogenetics and Genomics</i> , 2015, 25, 231-238.	0.7	3
72	Bayesian Autoregressive Frailty Models for Inference in Recurrent Events. <i>International Journal of Biostatistics</i> , 2020, 16, .	0.4	3

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73	Bayesian Deconvolution and Quantification of Metabolites from J-Resolved NMR Spectroscopy. Bayesian Analysis, 2021, 16, .	1.6	3
74	Bayesian variable selection for survival regression in genetics. Genetic Epidemiology, 2010, 34, 689-701.	0.6	2
75	A Simulation Approach for Change-Points on Phylogenetic Trees. Journal of Computational Biology, 2015, 22, 10-24.	0.8	2
76	Modelling correlated binary variables: an application to lower urinary tract symptoms. Journal of the Royal Statistical Society Series C: Applied Statistics, 2018, 67, 1083-1100.	0.5	2
77	Dynamic degree-corrected blockmodels for social networks: A nonparametric approach. Statistical Modelling, 2019, 19, 386-411.	0.5	2
78	A Bayesian nonparametric approach to dynamic itemâ€response modeling: An application to the GUSTO cohort study. Statistics in Medicine, 2021, 40, 6021-6037.	0.8	2
79	Modelling ethnic differences in the distribution of insulin resistance via Bayesian nonparametric processes: an application to the SABRE cohort study. International Journal of Biostatistics, 2021, 17, 153-164.	0.4	2
80	Bayesian inference on the number of recurrent events: A joint model of recurrence and survival. Statistical Methods in Medical Research, 2022, 31, 139-153.	0.7	2
81	Intrinsic autoregressions at multiple resolutions. Journal of Statistical Planning and Inference, 2005, 134, 102-115.	0.4	1
82	Application of the Optimal Discovery Procedure to Genetic Case-Control Studies: Comparison with p Values and Asymptotic Bayes Factors. Human Heredity, 2011, 71, 37-49.	0.4	1
83	Bayesian Inference on Population Structure: From Parametric to Nonparametric Modeling., 2015, , 135-151.		1
84	A Bayesian nonparametric model for white blood cells in patients with lower urinary tract symptoms. Electronic Journal of Statistics, 2016, 10, .	0.4	1
85	Bayesian Nonparametric Modelling of Multiple Graphs with an Application to Ethnic Metabolic Differences. Journal of the Royal Statistical Society Series C: Applied Statistics, 2022, 71, 1181-1204.	0.5	1