

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	Bayesian inference on the number of recurrent events: A joint model of recurrence and survival. <i>Statistical Methods in Medical Research</i> , 2022, 31, 139-153.	0.7	2
2	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
3	Unbiased approximation of posteriors via coupled particle Markov chain Monte Carlo. <i>Statistics and Computing</i> , 2022, 32, 1.	0.8	6
4	Bayesian Nonparametric Modelling of Multiple Graphs with an Application to Ethnic Metabolic Differences. <i>Journal of the Royal Statistical Society Series C: Applied Statistics</i> , 2022, 71, 1181-1204.	0.5	1
5	Bayesian Deconvolution and Quantification of Metabolites from J-Resolved NMR Spectroscopy. <i>Bayesian Analysis</i> , 2021, 16, .	1.6	3
6	A Bayesian nonparametric approach to dynamic item response modeling: An application to the GUSTO cohort study. <i>Statistics in Medicine</i> , 2021, 40, 6021-6037.	0.8	2
7	Modelling ethnic differences in the distribution of insulin resistance via Bayesian nonparametric processes: an application to the SABRE cohort study. <i>International Journal of Biostatistics</i> , 2021, 17, 153-164.	0.4	2
8	Bayesian Autoregressive Frailty Models for Inference in Recurrent Events. <i>International Journal of Biostatistics</i> , 2020, 16, .	0.4	3
9	Bayesian splines versus fractional polynomials in network meta-analysis. <i>BMC Medical Research Methodology</i> , 2020, 20, 261.	1.4	5
10	Monte Carlo co-ordinate ascent variational inference. <i>Statistics and Computing</i> , 2020, 30, 887-905.	0.8	5
11	Dynamic degree-corrected blockmodels for social networks: A nonparametric approach. <i>Statistical Modelling</i> , 2019, 19, 386-411.	0.5	2
12	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
13	Modeling Population Structure Under Hierarchical Dirichlet Processes. <i>Bayesian Analysis</i> , 2019, 14, .	1.6	4
14	Modelling disease activity in juvenile dermatomyositis: A Bayesian approach. <i>Statistical Methods in Medical Research</i> , 2019, 28, 35-49.	0.7	6
15	A Bayesian semiparametric Markov regression model for juvenile dermatomyositis. <i>Statistics in Medicine</i> , 2018, 37, 1711-1731.	0.8	4
16	Recalcitrant chronic bladder pain and recurrent cystitis but negative urinalysis: What should we do?. <i>International Urogynecology Journal</i> , 2018, 29, 1035-1043.	0.7	20
17	Modelling correlated binary variables: an application to lower urinary tract symptoms. <i>Journal of the Royal Statistical Society Series C: Applied Statistics</i> , 2018, 67, 1083-1100.	0.5	2
18	Lower urinary tract symptoms that predict microscopic pyuria. <i>International Urogynecology Journal</i> , 2018, 29, 1019-1028.	0.7	15

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19	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
20	Dependent generalized Dirichlet process priors for the analysis of acute lymphoblastic leukemia. <i>Biostatistics</i> , 2018, 19, 342-358.	0.9	6
21	Joint modeling of recurrent events and survival: a Bayesian non-parametric approach. <i>Biostatistics</i> , 2018, 21, 1-14.	0.9	12
22	Bayesian estimation of the number of protonation sites for urinary metabolites from NMR spectroscopic data. <i>Metabolomics</i> , 2018, 14, 56.	1.4	13
23	Clinical signs and symptoms in a joint model of four disease activity parameters in juvenile dermatomyositis: a prospective, longitudinal, multicenter cohort study. <i>Arthritis Research and Therapy</i> , 2018, 20, 180.	1.6	8
24	Metabolic profiling of polycystic ovary syndrome reveals interactions with abdominal obesity. <i>International Journal of Obesity</i> , 2017, 41, 1331-1340.	1.6	64
25	A comparative review of variable selection techniques for covariate dependent Dirichlet process mixture models. <i>Canadian Journal of Statistics</i> , 2017, 45, 254-273.	0.6	12
26	Bayesian inference for multiple Gaussian graphical models with application to metabolic association networks. <i>Annals of Applied Statistics</i> , 2017, 11, .	0.5	23
27	Variable selection in covariate dependent random partition models: an application to urinary tract infection. <i>Statistics in Medicine</i> , 2016, 35, 1373-1389.	0.8	13
28	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
29	Modelling the acid/base ¹ H NMR chemical shift limits of metabolites in human urine. <i>Metabolomics</i> , 2016, 12, 152.	1.4	47
30	Comparison of the Utility and Validity of Three Scoring Tools to Measure Skin Involvement in Patients With Juvenile Dermatomyositis. <i>Arthritis Care and Research</i> , 2016, 68, 1514-1521.	1.5	15
31	A Bayesian nonparametric model for white blood cells in patients with lower urinary tract symptoms. <i>Electronic Journal of Statistics</i> , 2016, 10, .	0.4	1
32	Bayesian Inference for Duplication-Mutation with Complementarity Network Models. <i>Journal of Computational Biology</i> , 2015, 22, 1025-1033.	0.8	8
33	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
34	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
35	Bayesian Inference on Population Structure: From Parametric to Nonparametric Modeling. , 2015, , 135-151.		1
36	A Simulation Approach for Change-Points on Phylogenetic Trees. <i>Journal of Computational Biology</i> , 2015, 22, 10-24.	0.8	2

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37	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
38	Computational Methods for a Class of Network Models. <i>Journal of Computational Biology</i> , 2014, 21, 141-161.	0.8	7
39	Dynamics of the Risk of Smoking-Induced Lung Cancer. <i>Epidemiology</i> , 2014, 25, 28-34.	1.2	9
40	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
41	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
42	Bayesian deconvolution and quantification of metabolites in complex 1D NMR spectra using BATMAN. <i>Nature Protocols</i> , 2014, 9, 1416-1427.	5.5	167
43	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
44	Ridge Regression in Prediction Problems: Automatic Choice of the Ridge Parameter. <i>Genetic Epidemiology</i> , 2013, 37, 704-714.	0.6	84
45	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
46	BATMANâ€”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
47	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
48	Subset Optimization by Reference Matching (STORM): An Optimized Statistical Approach for Recovery of Metabolic Biomarker Structural Information from ¹ H NMR Spectra of Biofluids. <i>Analytical Chemistry</i> , 2012, 84, 10694-10701.	3.2	75
49	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
50	Significance testing in ridge regression for genetic data. <i>BMC Bioinformatics</i> , 2011, 12, 372.	1.2	84
51	Bayesian semiparametric meta-analysis for genetic association studies. <i>Genetic Epidemiology</i> , 2011, 35, 333-340.	0.6	5
52	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
53	Application of the Optimal Discovery Procedure to Genetic Case-Control Studies: Comparison with p Values and Asymptotic Bayes Factors. <i>Human Heredity</i> , 2011, 71, 37-49.	0.4	1
54	Meeting-in-the-middle using metabolic profiling â€” a strategy for the identification of intermediate biomarkers in cohort studies. <i>Biomarkers</i> , 2011, 16, 83-88.	0.9	113

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55	A Differential Network Approach to Exploring Differences between Biological States: An Application to Prediabetes. PLoS ONE, 2011, 6, e24702.	1.1	33
56	Bayesian semiparametric inference for multivariate doubly-interval-censored data. Annals of Applied Statistics, 2010, 4, .	0.5	50
57	Metabolic Profiling and the Metabolome-Wide Association Study: Significance Level For Biomarker Identification. Journal of Proteome Research, 2010, 9, 4620-4627.	1.8	123
58	MetAssimulo:Simulation of Realistic NMR Metabolic Profiles. BMC Bioinformatics, 2010, 11, 496.	1.2	17
59	Bayesian variable selection for survival regression in genetics. Genetic Epidemiology, 2010, 34, 689-701.	0.6	2
60	Metabolome-Wide Association Study Identifies Multiple Biomarkers that Discriminate North and South Chinese Populations at Differing Risks of Cardiovascular Disease: INTERMAP Study. Journal of Proteome Research, 2010, 9, 6647-6654.	1.8	116
61	Opening up the "Black Box": Metabolic phenotyping and metabolome-wide association studies in epidemiology. Journal of Clinical Epidemiology, 2010, 63, 970-979.	2.4	125
62	Bayesian Nonparametric Nonproportional Hazards Survival Modeling. Biometrics, 2009, 65, 762-771.	0.8	111
63	Genome-wide significance for dense SNP and resequencing data. Genetic Epidemiology, 2008, 32, 179-185.	0.6	187
64	Statistical Techniques in Metabolic Profiling. , 2008, , 347-373.		13
65	Human metabolic phenotype diversity and its association with diet and blood pressure. Nature, 2008, 453, 396-400.	13.7	966
66	Fregene: Simulation of realistic sequence-level data in populations and ascertained samples. BMC Bioinformatics, 2008, 9, 364.	1.2	57
67	An Evolutionary Algorithm to Find Associations in Dense Genetic Maps. IEEE Transactions on Evolutionary Computation, 2008, 12, 297-306.	7.5	6
68	Simultaneous Analysis of All SNPs in Genome-Wide and Re-Sequencing Association Studies. PLoS Genetics, 2008, 4, e1000130.	1.5	298
69	Bayesian survival analysis in genetic association studies. Bioinformatics, 2008, 24, 2030-2036.	1.8	4
70	Conserved Mosquito/Parasite Interactions Affect Development of Plasmodium falciparum in Africa. PLoS Pathogens, 2008, 4, e1000069.	2.1	93
71	Sequence-Level Population Simulations Over Large Genomic Regions. Genetics, 2007, 177, 1725-1731.	1.2	99
72	Genetic Association Mapping via Evolution-Based Clustering of Haplotypes. PLoS Genetics, 2007, 3, e111.	1.5	31

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73	Bayesian logistic regression using a perfect phylogeny. <i>Biostatistics</i> , 2007, 8, 32-52.	0.9	19
74	A spatial probit model for fine-scale mapping of disease genes. <i>Genetic Epidemiology</i> , 2007, 31, 252-260.	0.6	4
75	Intrinsic autoregressions at multiple resolutions. <i>Journal of Statistical Planning and Inference</i> , 2005, 134, 102-115.	0.4	1
76	A nonparametric Bayesian model for inference in related longitudinal studies. <i>Journal of the Royal Statistical Society Series C: Applied Statistics</i> , 2005, 54, 611-626.	0.5	12
77	Recombination hotspots as a point process. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2005, 360, 1597-1603.	1.8	5
78	Finding Associations in Dense Genetic Maps: A Genetic Algorithm Approach. <i>Human Heredity</i> , 2005, 60, 97-108.	0.4	15
79	Stepwise mutation likelihood computation by sequential importance sampling in subdivided population models. <i>Theoretical Population Biology</i> , 2005, 68, 41-53.	0.5	41
80	Optimal Bayesian Design by Inhomogeneous Markov Chain Simulation. <i>Journal of the American Statistical Association</i> , 2004, 99, 788-798.	1.8	129
81	An ANOVA Model for Dependent Random Measures. <i>Journal of the American Statistical Association</i> , 2004, 99, 205-215.	1.8	228
82	Importance sampling on coalescent histories. II: Subdivided population models. <i>Advances in Applied Probability</i> , 2004, 36, 434-454.	0.4	22
83	Importance sampling on coalescent histories. I. <i>Advances in Applied Probability</i> , 2004, 36, 417-433.	0.4	11
84	Importance sampling on coalescent histories. I. <i>Advances in Applied Probability</i> , 2004, 36, 417-433.	0.4	73
85	Importance sampling on coalescent histories. II: Subdivided population models. <i>Advances in Applied Probability</i> , 2004, 36, 434-454.	0.4	59