## Jyotishka Datta

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/474471/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	The Genetic Basis of Hepatosplenic T-cell Lymphoma. Cancer Discovery, 2017, 7, 369-379.	9.4	163
2	Enteropathy-associated T cell lymphoma subtypes are characterized by loss of function of SETD2. Journal of Experimental Medicine, 2017, 214, 1371-1386.	8.5	144
3	The Horseshoe+ Estimator of Ultra-Sparse Signals. Bayesian Analysis, 2017, 12, .	3.0	76
4	Lasso Meets Horseshoe: A Survey. Statistical Science, 2019, 34, .	2.8	70
5	Age-Related Changes in the Relationship Between Auditory Brainstem Responses and Envelope-Following Responses. JARO - Journal of the Association for Research in Otolaryngology, 2014, 15, 649-661.	1.8	56
6	Asymptotic Properties of Bayes Risk for the Horseshoe Prior. Bayesian Analysis, 2013, 8, .	3.0	53
7	GNA13 loss in germinal center B cells leads to impaired apoptosis and promotes lymphoma in vivo. Blood, 2016, 127, 2723-2731.	1.4	52
8	Default Bayesian analysis with global-local shrinkage priors. Biometrika, 2016, 103, 955-969.	2.4	30
9	Geomorphons: Landform and property predictions in a glacial moraine in Indiana landscapes. Catena, 2016, 142, 66-76.	5.0	27
10	Extending the susceptibleâ€exposedâ€infectedâ€removed (SEIR) model to handle the false negative rate and symptomâ€based administration of COVIDâ€19 diagnostic tests: <i>SEIRâ€fansy</i> . Statistics in Medicine, 2022, 41, 2317-2337.	1.6	16
11	Bayesian inference on quasi-sparse count data. Biometrika, 2016, 103, 971-983.	2.4	12
12	Horseshoe Regularisation for Machine Learning in Complex and Deep Models <sup>1</sup> . International Statistical Review, 2020, 88, 302-320.	1.9	10
13	The Horseshoe-Like Regularization for Feature Subset Selection. Sankhya B, 2021, 83, 185-214.	0.9	9
14	Bootstrap—An exploration. Statistical Methodology, 2014, 20, 63-72.	0.5	7
15	A Meta-Analysis of the Protein Components in Rattlesnake Venom. Toxins, 2021, 13, 372.	3.4	7
16	Integrative Genetic and Clinical Analysis through Whole Exome Sequencing in 1001 Diffuse Large B Cell Lymphoma (DLBCL) Patients Reveals Novel Disease Drivers and Risk Groups. Blood, 2016, 128, 1087-1087.	1.4	4
17	Some Remarks on Pseudo Panel Data. Springer Proceedings in Mathematics and Statistics, 2015, , 25-34.	0.2	3
18	Evaluation of malnutrition as a predictor of adverse outcomes in febrile neutropenia associated with paediatric haematological malignancies. Journal of Paediatrics and Child Health, 2016, 52, 704-709.	0.8	3

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19	Joint mean–covariance estimation via the horseshoe. Journal of Multivariate Analysis, 2021, 183, 104716.	1.0	3
20	Correlation of ATP7B gene mutations with clinical phenotype and radiological features in Indian Wilson disease patients. Acta Neurologica Belgica, 2022, 122, 181-190.	1.1	3
21	Understanding racial disparities in severe maternal morbidity using Bayesian network analysis. PLoS ONE, 2021, 16, e0259258.	2.5	2
22	Discussion on "Regression Models for Understanding COVID-19 Epidemic Dynamics With Incomplete Data― Journal of the American Statistical Association, 2021, 116, 1583-1586.	3.1	1
23	Global-Local Mixtures: A Unifying Framework. Sankhya A, 2020, 82, 426-447.	0.8	0
24	Improving Spatial Visualization Abilities Using 3D Printed Blocks. , 0, , .		0