Swati Biswas

List of Publications by Year in descending order

40 papers	767 citations	623734 14 h-index	526287 27 g-index
40 all docs	40 docs citations	40 times ranked	1214 citing authors

#	Article	IF	Citations
1	Joint risk prediction for hazardous use of alcohol, cannabis, and tobacco among adolescents: A preliminary study using statistical and machine learning. Preventive Medicine Reports, 2022, 25, 101674.	1.8	6
2	A Bayesian learning model to predict the risk for cannabis use disorder. Drug and Alcohol Dependence, 2022, 236, 109476.	3.2	5
3	CBCRisk-Black: a personalized contralateral breast cancer risk prediction model for black women. Breast Cancer Research and Treatment, 2022, 194, 179-186.	2.5	2
4	Detecting rare haplotype association with two correlated phenotypes of binary and continuous types. Statistics in Medicine, 2021, 40, 1877-1900.	1.6	1
5	Comparison of haplotype-based tests for detecting gene–environment interactions with rare variants. Briefings in Bioinformatics, 2020, 21, 851-862.	6.5	3
6	A preliminary risk prediction model for cannabis use disorder. Preventive Medicine Reports, 2020, 20, 101228.	1.8	9
7	Bivariate logistic Bayesian LASSO for detecting rare haplotype association with two correlated phenotypes. Genetic Epidemiology, 2019, 43, 996-1017.	1.3	5
8	A Bayesian Hierarchical Framework for Pathway Analysis in Genome-Wide Association Studies. Human Heredity, 2019, 84, 240-255.	0.8	1
9	Dose-dependent effect of mammographic breast density on the risk of contralateral breast cancer. Breast Cancer Research and Treatment, 2018, 170, 143-148.	2.5	5
10	Validation of a personalized risk prediction model for contralateral breast cancer. Breast Cancer Research and Treatment, 2018, 170, 415-423.	2.5	19
11	A Family-Based Rare Haplotype Association Method for Quantitative Traits. Human Heredity, 2018, 83, 175-195.	0.8	4
12	A Bayesian latent variable approach to aggregation of partial and top–ranked lists in genomic studies. Statistics in Medicine, 2018, 37, 4266-4278.	1.6	4
13	Logistic Bayesian LASSO for genetic association analysis of data from complex sampling designs. Journal of Human Genetics, 2017, 62, 819-829.	2.3	10
14	A model for individualized risk prediction of contralateral breast cancer. Breast Cancer Research and Treatment, 2017, 161, 153-160.	2.5	38
15	Detecting Rare and Common Haplotype–Environment Interaction under Uncertainty of Gene–Environment Independence Assumption. Biometrics, 2017, 73, 344-355.	1.4	8
16	Residual Isocyanates in Medical Devices and Products: A Qualitative and Quantitative Assessment. Environmental Health Insights, 2016, 10, EHI.S39149.	1.7	5
17	Association of rare haplotypes on ULK4 and MAP4 genes with hypertension. BMC Proceedings, 2016, 10, 363-369.	1.6	13
18	A two-stage approach to genetic risk assessment in primary care. Breast Cancer Research and Treatment, 2016, 155, 375-383.	2.5	13

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19	Comparison of haplotype-based statistical tests for disease association with rare and common variants. Briefings in Bioinformatics, 2016, 17, 657-671.	6.5	19
20	A model for predicting individualized absolute risk of contralateral breast cancer.. Journal of Clinical Oncology, 2016, 34, 1567-1567.	1.6	4
21	Recent Enhancements to the Genetic Risk Prediction Model BRCAPRO. Cancer Informatics, 2015, 14s2, CIN.S17292.	1.9	34
22	An Improved Version of Logistic Bayesian LASSO for Detecting Rare Haplotype-Environment Interactions with Application to Lung Cancer. Cancer Informatics, 2015, 14s2, CIN.S17290.	1.9	20
23	Computer Simulation, Bioinformatics, and Statistical Analysis of Cancer Data and Processes. Cancer Informatics, 2015, 14s2, CIN.S32525.	1.9	0
24	Detecting Rare Haplotypeâ€Environment Interaction With Logistic Bayesian LASSO. Genetic Epidemiology, 2014, 38, 31-41.	1.3	18
25	Populationâ€Based Association and Gene by Environment Interactions in Genetic Analysis Workshop 18. Genetic Epidemiology, 2014, 38, S49-56.	1.3	3
26	Reclassification of predictions for uncovering subgroup specific improvement. Statistics in Medicine, 2014, 33, 1914-1927.	1.6	4
27	Evaluation of logistic Bayesian LASSO for identifying association with rare haplotypes. BMC Proceedings, 2014, 8, S54.	1.6	12
28	Impact of a Community Based Implementation of REACH II Program for Caregivers of Alzheimer's Patients. PLoS ONE, 2014, 9, e89290.	2.5	38
29	Simplifying clinical use of the genetic risk prediction model BRCAPRO. Breast Cancer Research and Treatment, 2013, 139, 571-579.	2.5	24
30	Factors associated with attention deficit/hyperactivity disorder among US children: Results from a national survey. BMC Pediatrics, 2012, 12, 50.	1.7	73
31	Assessing the added value of breast tumor markers in genetic risk prediction model BRCAPRO. Breast Cancer Research and Treatment, 2012, 133, 347-355.	2.5	21
32	Logistic Bayesian LASSO for Identifying Association with Rare Haplotypes and Application to Ageâ€Related Macular Degeneration. Biometrics, 2012, 68, 587-597.	1.4	39
33	Reciprocal Regulation of Annexin A2 and EGFR with Her-2 in Her-2 Negative and Herceptin-Resistant Breast Cancer. PLoS ONE, 2012, 7, e44299.	2.5	56
34	Accounting for Disease Model Uncertainty in Mapping Heterogeneous Traits â€" A Bayesian Model Averaging Approach. Human Heredity, 2010, 69, 242-253.	0.8	0
35	Bayesian clinical trials at the University of Texas M. D. Anderson Cancer Center. Clinical Trials, 2009, 6, 205-216.	1.6	106
36	Association between Obesity and Asthma in US Children and Adolescents. Journal of Asthma, 2009, 46, 642-646.	1.7	40

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37	Incorporating covariates in mapping heterogeneous traits: a hierarchical model using empirical Bayes estimation. Genetic Epidemiology, 2007, 31, 684-696.	1.3	3
38	A Parallel Phase I/II Clinical Trial Design for Combination Therapies. Biometrics, 2007, 63, 429-436.	1.4	96
39	Building and validating a prognostic index for biomarker studies. Cancer Biomarkers, 2006, 2, 97-101.	1.7	2
40	A Bayesian Approach for Incorporating Variable Rates of Heterogeneity in Linkage Analysis. Journal of the American Statistical Association, 2006, 101, 1341-1351.	3.1	4