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	Bayesian clinical trials at the University of Texas M. D. Anderson Cancer Center. Clinical Trials, 2009, 6, 205-216.	1.6	106
2	A Parallel Phase I/II Clinical Trial Design for Combination Therapies. Biometrics, 2007, 63, 429-436.	1.4	96
3	Factors associated with attention deficit/hyperactivity disorder among US children: Results from a national survey. BMC Pediatrics, 2012, 12, 50.	1.7	73
4	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
5	Association between Obesity and Asthma in US Children and Adolescents. Journal of Asthma, 2009, 46, 642-646.	1.7	40
6	Logistic Bayesian LASSO for Identifying Association with Rare Haplotypes and Application to Ageâ€Related Macular Degeneration. Biometrics, 2012, 68, 587-597.	1.4	39
7	A model for individualized risk prediction of contralateral breast cancer. Breast Cancer Research and Treatment, 2017, 161, 153-160.	2.5	38
8	Impact of a Community Based Implementation of REACH II Program for Caregivers of Alzheimer's Patients. PLoS ONE, 2014, 9, e89290.	2.5	38
9	Recent Enhancements to the Genetic Risk Prediction Model BRCAPRO. Cancer Informatics, 2015, 14s2, CIN.S17292.	1.9	34
10	Simplifying clinical use of the genetic risk prediction model BRCAPRO. Breast Cancer Research and Treatment, 2013, 139, 571-579.	2.5	24
11	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
12	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
13	Comparison of haplotype-based statistical tests for disease association with rare and common variants. Briefings in Bioinformatics, 2016, 17, 657-671.	6.5	19
14	Validation of a personalized risk prediction model for contralateral breast cancer. Breast Cancer Research and Treatment, 2018, 170, 415-423.	2.5	19
15	Detecting Rare Haplotypeâ€Environment Interaction With Logistic Bayesian LASSO. Genetic Epidemiology, 2014, 38, 31-41.	1.3	18
16	Association of rare haplotypes on ULK4 and MAP4 genes with hypertension. BMC Proceedings, 2016, 10, 363-369.	1.6	13
17	A two-stage approach to genetic risk assessment in primary care. Breast Cancer Research and Treatment, 2016, 155, 375-383.	2.5	13
18	Evaluation of logistic Bayesian LASSO for identifying association with rare haplotypes. BMC Proceedings, 2014, 8, S54.	1.6	12

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19	Logistic Bayesian LASSO for genetic association analysis of data from complex sampling designs. Journal of Human Genetics, 2017, 62, 819-829.	2.3	10
20	A preliminary risk prediction model for cannabis use disorder. Preventive Medicine Reports, 2020, 20, 101228.	1.8	9
21	Detecting Rare and Common Haplotypeâ€“Environment Interaction under Uncertainty of Geneâ€“Environment Independence Assumption. Biometrics, 2017, 73, 344-355.	1.4	8
22	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
23	Residual Isocyanates in Medical Devices and Products: A Qualitative and Quantitative Assessment. Environmental Health Insights, 2016, 10, EHI.S39149.	1.7	5
24	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
25	Bivariate logistic Bayesian LASSO for detecting rare haplotype association with two correlated phenotypes. Genetic Epidemiology, 2019, 43, 996-1017.	1.3	5
26	A Bayesian learning model to predict the risk for cannabis use disorder. Drug and Alcohol Dependence, 2022, 236, 109476.	3.2	5
27	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
28	Reclassification of predictions for uncovering subgroup specific improvement. Statistics in Medicine, 2014, 33, 1914-1927.	1.6	4
29	A Family-Based Rare Haplotype Association Method for Quantitative Traits. Human Heredity, 2018, 83, 175-195.	0.8	4
30	A Bayesian latent variable approach to aggregation of partial and topâ€ranked lists in genomic studies. Statistics in Medicine, 2018, 37, 4266-4278.	1.6	4
31	A model for predicting individualized absolute risk of contralateral breast cancer.. Journal of Clinical Oncology, 2016, 34, 1567-1567.	1.6	4
32	Incorporating covariates in mapping heterogeneous traits: a hierarchical model using empirical Bayes estimation. Genetic Epidemiology, 2007, 31, 684-696.	1.3	3
33	Populationâ€Based Association and Gene by Environment Interactions in Genetic Analysis Workshop 18. Genetic Epidemiology, 2014, 38, S49-56.	1.3	3
34	Comparison of haplotype-based tests for detecting geneâ€“environment interactions with rare variants. Briefings in Bioinformatics, 2020, 21, 851-862.	6.5	3
35	Building and validating a prognostic index for biomarker studies. Cancer Biomarkers, 2006, 2, 97-101.	1.7	2
36	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

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37	A Bayesian Hierarchical Framework for Pathway Analysis in Genome-Wide Association Studies. Human Heredity, 2019, 84, 240-255.	0.8	1
38	Detecting rare haplotype association with two correlated phenotypes of binary and continuous types. Statistics in Medicine, 2021, 40, 1877-1900.	1.6	1
39	Accounting for Disease Model Uncertainty in Mapping Heterogeneous Traits â€“ A Bayesian Model Averaging Approach. Human Heredity, 2010, 69, 242-253.	0.8	0
40	Computer Simulation, Bioinformatics, and Statistical Analysis of Cancer Data and Processes. Cancer Informatics, 2015, 14s2, CIN.S32525.	1.9	0