Dan-Yu Lin

List of Publications by Year
in descending order

14 papers	**1,101** citations	1040056 **9** h-index	1125743 **13** g-index
15 all docs	**15** docs citations	**15** times ranked	**1523** citing authors

#	Article	IF	Citations
1	Design and analysis of bridging studies with prior probabilities on the null and alternative hypotheses. Biometrics, 2020, 76, 224-234.	1.4	1
2	A general framework for integrative analysis of incomplete multiomics data. Genetic Epidemiology, 2020, 44, 646-664.	1.3	9
3	Power and Sample Size for Dose-Finding Studies with Survival Endpoints Under Model Uncertainty. Biometrics, 2019, 75, 308-314.	1.4	3
4	A simple and accurate method to determine genomewide significance for association tests in sequencing studies. Genetic Epidemiology, 2019, 43, 365-372.	1.3	19
5	Semiparametric Regression Analysis of Interval-Censored Data with Informative Dropout. Biometrics, 2018, 74, 1213-1222.	1.4	6
6	Simultaneous Inference on Treatment Effects in Survival Studies with Factorial Designs. Biometrics, 2016, 72, 1078-1085.	1.4	4
7	Maximum likelihood estimation for semiparametric transformation models with interval-censored data. Biometrika, 2016, 103, 253-271.	2.4	109
8	A General Framework for Detecting Disease Associations with Rare Variants in Sequencing Studies. American Journal of Human Genetics, 2011, 89, 354-367.	6.2	251
9	Semiparametric Transformation Models with Random Effects for Joint Analysis of Recurrent and Terminal Events. Biometrics, 2009, 65, 746-752.	1.4	75
10	Simple and Efficient Analysis of Disease Association with Missing Genotype Data. American Journal of Human Genetics, 2008, 82, 444-452.	6.2	87
11	Maximum Likelihood Estimation in Semiparametric Regression Models with Censored Data. Journal of the Royal Statistical Society Series B: Statistical Methodology, 2007, 69, 507-564.	2.2	237
12	Semiparametric variance-component models for linkage and association analyses of censored trait data. Genetic Epidemiology, 2006, 30, 570-581.	1.3	12
13	Likelihood-Based Inference on Haplotype Effects in Genetic Association Studies. Journal of the American Statistical Association, 2006, 101, 89-104.	3.1	127
14	An efficient Monte Carlo approach to assessing statistical significance in genomic studies. Bioinformatics, 2005, 21, 781-787.	4.1	161