

# Min Yuan

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5828362/publications.pdf>

Version: 2024-02-01

19  
papers

120  
citations

1684188

5  
h-index

1372567

10  
g-index

19  
all docs

19  
docs citations

19  
times ranked

136  
citing authors

#	ARTICLE	IF	CITATIONS
1	Bias correction for multiple covariate analysis using empirical bayesian estimation in mixed-effects models for longitudinal data. <i>Computational Biology and Chemistry</i> , 2022, 99, 107697.	2.3	0
2	SCEBE: an efficient and scalable algorithm for genome-wide association studies on longitudinal outcomes with mixed-effects modeling. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	5
3	Efficient algorithms for covariate analysis with dynamic data using nonlinear mixed-effects model. <i>Statistical Methods in Medical Research</i> , 2021, 30, 233-243.	1.5	1
4	A forward selection algorithm to identify mutually exclusive alterations in cancer studies. <i>Journal of Human Genetics</i> , 2021, 66, 509-518.	2.3	4
5	Stratification of population in NHANES 2009â€“2014 based on exposure pattern of lead, cadmium, mercury, and arsenic and their association with cardiovascular, renal and respiratory outcomes. <i>Environment International</i> , 2021, 149, 106410.	10.0	51
6	Quantitative Trait Loci Identification by Estimating the Genetic Model based on the Extremal Samples. <i>Current Genomics</i> , 2021, 22, 363-372.	1.6	0
7	Basic Reproduction Number of the 2019 Novel Coronavirus Disease in the Major Endemic Areas of China: A Latent Profile Analysis. <i>Frontiers in Public Health</i> , 2021, 9, 575315.	2.7	6
8	Fast and efficient correction for population stratification in multi-locus genome-wide association studies. <i>Genetica</i> , 2021, 149, 313-325.	1.1	1
9	High-throughput and efficient multilocus genome-wide association study on longitudinal outcomes. <i>Bioinformatics</i> , 2020, 36, 3004-3010.	4.1	4
10	A novel quantification of information for longitudinal data analyzed by mixed-effects modeling. <i>Pharmaceutical Statistics</i> , 2020, 19, 388-398.	1.3	2
11	A quick and accurate method for the estimation of covariate effects based on empirical Bayes estimates in mixed-effects modeling: Correction of bias due to shrinkage. <i>Statistical Methods in Medical Research</i> , 2019, 28, 3568-3578.	1.5	5
12	Full covariate modelling approach in population pharmacokinetics: understanding the underlying hypothesis tests and implications of multiplicity. <i>British Journal of Clinical Pharmacology</i> , 2018, 84, 1525-1534.	2.4	17
13	One-sided empirical Bayes test for location parameter in Gamma distribution. <i>Applied Mathematics</i> , 2018, 33, 287-297.	1.0	2
14	Two-sided empirical Bayes test for location parameter in the gamma distribution. <i>Communications in Statistics - Theory and Methods</i> , 2017, 46, 4215-4225.	1.0	2
15	Further Evaluation of Covariate Analysis using Empirical Bayes Estimates in Population Pharmacokinetics: the Perception of Shrinkage and Likelihood Ratio Test. <i>AAPS Journal</i> , 2017, 19, 264-273.	4.4	11
16	Superiority of empirical Bayes estimator of the mean vector in multivariate normal distribution. <i>Science China Mathematics</i> , 2016, 59, 1175-1186.	1.7	5
17	Bayes factors based on robust TDT-type tests for family trio design. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2015, 14, 253-64.	0.6	0
18	Correcting for differential genotyping error in genetic association analysis. <i>Journal of Human Genetics</i> , 2013, 58, 657-666.	2.3	2

#	ARTICLE	IF	CITATIONS
19	Correcting for biases in affected sib-pair linkage analysis caused by uncertainty in sibling relationship. Science China Mathematics, 2012, 55, 1127-1135.	1.7	2