

# Jack Kuipers

## List of Publications by Year in descending order

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Version: 2024-02-01

37  
papers

1,591  
citations

430874

18  
h-index

361022

35  
g-index

48  
all docs

48  
docs citations

48  
times ranked

2116  
citing authors

#	ARTICLE	IF	CITATIONS
1	Discovering gene regulatory networks of multiple phenotypic groups using dynamic Bayesian networks. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	3
2	The variance of causal effect estimators for binary v-structures. <i>Journal of Causal Inference</i> , 2022, 10, 90-105.	1.2	1
3	scAmpliâ€™ A versatile pipeline for single-cell RNA-seq analysis from basics to clinics. <i>PLoS Computational Biology</i> , 2022, 18, e1010097.	3.2	8
4	Tracing Clonal Dynamics Reveals that Two- and Three-dimensional Patient-derived Cell Models Capture Tumor Heterogeneity of Clear Cell Renal Cell Carcinoma. <i>European Urology Focus</i> , 2021, 7, 152-162.	3.1	34
5	The Tumor Profiler Study: integrated, multi-omic, functional tumor profiling for clinical decision support. <i>Cancer Cell</i> , 2021, 39, 288-293.	16.8	71
6	Spatial Distribution of Private Gene Mutations in Clear Cell Renal Cell Carcinoma. <i>Cancers</i> , 2021, 13, 2163.	3.7	10
7	Universal S -matrix correlations for complex scattering of wave packets in noninteracting many-body systems: Theory, simulation, and experiment. <i>Physical Review E</i> , 2021, 103, 052209.	2.1	4
8	Establishing standardized immune phenotyping of metastatic melanoma by digital pathology. <i>Laboratory Investigation</i> , 2021, 101, 1561-1570.	3.7	15
9	Comparing mutational pathways to lopinavir resistance in HIV-1 subtypes B versus C. <i>PLoS Computational Biology</i> , 2021, 17, e1008363.	3.2	2
10	Statistical tests for intra-tumour clonal co-occurrence and exclusivity. <i>PLoS Computational Biology</i> , 2021, 17, e1009036.	3.2	6
11	Clonal evolution of acute myeloid leukemia revealed by high-throughput single-cell genomics. <i>Nature Communications</i> , 2020, 11, 5327.	12.8	208
12	Computational Model Reveals a Stochastic Mechanism behind Germinal Center Clonal Bursts. <i>Cells</i> , 2020, 9, 1448.	4.1	16
13	Predicting colorectal cancer risk from adenoma detection via a two-type branching process model. <i>PLoS Computational Biology</i> , 2020, 16, e1007552.	3.2	16
14	Computational Analysis of DNA and RNA Sequencing Data Obtained from Liquid Biopsies. <i>Recent Results in Cancer Research</i> , 2020, 215, 347-368.	1.8	1
15	Integrative inference of subclonal tumour evolution from single-cell and bulk sequencing data. <i>Nature Communications</i> , 2019, 10, 2750.	12.8	101
16	netprioR: a probabilistic model for integrative hit prioritisation of genetic screens. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2019, 18, .	0.6	1
17	Single-cell mutation identification via phylogenetic inference. <i>Nature Communications</i> , 2018, 9, 5144.	12.8	75
18	Mutational interactions define novel cancer subgroups. <i>Nature Communications</i> , 2018, 9, 4353.	12.8	26

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19	Improved pathway reconstruction from RNA interference screens by exploiting off-target effects. <i>Bioinformatics</i> , 2018, 34, i519-i527.	4.1	8
20	Partition MCMC for Inference on Acyclic Digraphs. <i>Journal of the American Statistical Association</i> , 2017, 112, 282-299.	3.1	33
21	Detailed simulation of cancer exome sequencing data reveals differences and common limitations of variant callers. <i>BMC Bioinformatics</i> , 2017, 18, 8.	2.6	40
22	Advances in understanding tumour evolution through single-cell sequencing. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2017, 1867, 127-138.	7.4	95
23	Using Directed Acyclic Graphs in Epidemiological Research in Psychosis: An Analysis of the Role of Bullying in Psychosis. <i>Schizophrenia Bulletin</i> , 2017, 43, 1273-1279.	4.3	78
24	pathTiME: Joint Inference of Mutually Exclusive Cancer Pathways and Their Progression Dynamics. <i>Journal of Computational Biology</i> , 2017, 24, 603-615.	1.6	35
25	Single-cell sequencing data reveal widespread recurrence and loss of mutational hits in the life histories of tumors. <i>Genome Research</i> , 2017, 27, 1885-1894.	5.5	156
26	Tree inference for single-cell data. <i>Genome Biology</i> , 2016, 17, 86.	8.8	257
27	Large-scale inference of conjunctive Bayesian networks. <i>Bioinformatics</i> , 2016, 32, i727-i735.	4.1	21
28	Multiparticle Correlations in Mesoscopic Scattering: Boson Sampling, Birthday Paradox, and Hong-Ou-Mandel Profiles. <i>Physical Review Letters</i> , 2016, 116, 100401.	7.8	25
29	Efficient semiclassical approach for time delays. <i>New Journal of Physics</i> , 2014, 16, 123018.	2.9	29
30	Sequential Monte Carlo EM for multivariate probit models. <i>Computational Statistics and Data Analysis</i> , 2014, 72, 252-272.	1.2	6
31	Addendum on the scoring of Gaussian directed acyclic graphical models. <i>Annals of Statistics</i> , 2014, 42, .	2.6	27
32	Universality in chaotic quantum transport: The concordance between random-matrix and semiclassical theories. <i>Physical Review E</i> , 2012, 85, 045201.	2.1	34
33	Weak Localization in Mesoscopic Hole Transport: Berry Phases and Classical Correlations. <i>Physical Review Letters</i> , 2011, 106, 146801.	7.8	7
34	Semiclassics for chaotic systems with tunnel barriers. <i>Journal of Physics A: Mathematical and Theoretical</i> , 2009, 42, 425101.	2.1	16
35	The semiclassical continuity equation for open chaotic systems. <i>Nonlinearity</i> , 2009, 22, 1945-1964.	1.4	7
36	Semiclassical universality of parametric spectral correlations. <i>Journal of Physics A: Mathematical and Theoretical</i> , 2007, 40, 935-948.	2.1	12

#	ARTICLE	IF	CITATIONS
37	Semiclassical expansion of parametric correlation functions of the quantum time delay. Nonlinearity, 2007, 20, 909-926.	1.4	18