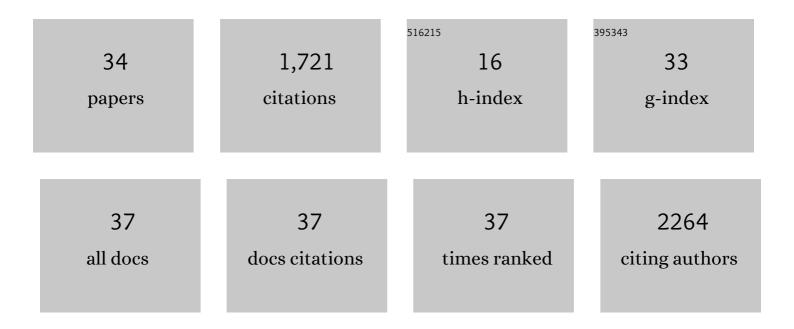
Pieter Trapman

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	A mathematical model reveals the influence of population heterogeneity on herd immunity to SARS-CoV-2. Science, 2020, 369, 846-849.	6.0	540
2	Five challenges for spatial epidemic models. Epidemics, 2015, 10, 68-71.	1.5	148
3	Eight challenges for network epidemic models. Epidemics, 2015, 10, 58-62.	1.5	147
4	Analysis of a stochastic SIR epidemic on a random network incorporating household structure. Mathematical Biosciences, 2010, 224, 53-73.	0.9	123
5	Key questions for modelling COVID-19 exit strategies. Proceedings of the Royal Society B: Biological Sciences, 2020, 287, 20201405.	1.2	106
6	On analytical approaches to epidemics on networks. Theoretical Population Biology, 2007, 71, 160-173.	0.5	92
7	The nosocomial transmission rate of animal-associated ST398 meticillin-resistant <i>Staphylococcus aureus</i> . Journal of the Royal Society Interface, 2011, 8, 578-584.	1.5	72
8	Reproduction numbers for epidemic models with households and other social structures. I. Definition and calculation of RO. Mathematical Biosciences, 2012, 235, 85-97.	0.9	65
9	Threshold behaviour and final outcome of an epidemic on a random network with household structure. Advances in Applied Probability, 2009, 41, 765-796.	0.4	61
10	Five challenges for stochastic epidemic models involving global transmission. Epidemics, 2015, 10, 54-57.	1.5	44
11	Epidemics on random intersection graphs. Annals of Applied Probability, 2014, 24, .	0.6	36
12	Inferring <i>R</i> ₀ in emerging epidemics—the effect of common population structure is small. Journal of the Royal Society Interface, 2016, 13, 20160288.	1.5	33
13	Who is the infector? Epidemic models with symptomatic and asymptomatic cases. Mathematical Biosciences, 2018, 301, 190-198.	0.9	33
14	A useful relationship between epidemiology and queueing theory: The distribution of the number of infectives at the moment of the first detection. Mathematical Biosciences, 2009, 219, 15-22.	0.9	28
15	Reproduction numbers for epidemics on networks using pair approximation. Mathematical Biosciences, 2007, 210, 464-489.	0.9	25
16	Reproduction numbers for epidemic models with households and other social structures II: Comparisons and implications for vaccination. Mathematical Biosciences, 2016, 274, 108-139.	0.9	24
17	Commentary on the use of the reproduction number <i>R</i> during the COVID-19 pandemic. Statistical Methods in Medical Research, 2022, 31, 1675-1685.	0.7	18
18	A branching model for the spread of infectious animal diseases in varying environments. Journal of Mathematical Biology, 2004, 49, 553-576.	0.8	15

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#	Article	IF	CITATIONS
19	Threshold behaviour and final outcome of an epidemic on a random network with household structure. Advances in Applied Probability, 2009, 41, 765-796.	0.4	12
20	Bounding basic characteristics of spatial epidemics with a new percolation model. Advances in Applied Probability, 2011, 43, 335-347.	0.4	10
21	Branching process approach for epidemics in dynamic partnership network. Journal of Mathematical Biology, 2018, 76, 265-294.	0.8	8
22	Modelling: Understanding pandemics and how to control them. Epidemics, 2022, 39, 100588.	1.5	8
23	Bounding basic characteristics of spatial epidemics with a new percolation model. Advances in Applied Probability, 2011, 43, 335-347.	0.4	7
24	Splitting Trees Stopped when the First Clock Rings and Vervaat's Transformation. Journal of Applied Probability, 2013, 50, 208-227.	0.4	6
25	Stochastic Epidemics in Growing Populations. Bulletin of Mathematical Biology, 2014, 76, 985-996.	0.9	6
26	The risk for a new COVID-19 wave and how it depends on <i>R</i> ₀ , the current immunity level and current restrictions. Royal Society Open Science, 2021, 8, 210386.	1.1	5
27	Estimation in branching processes with restricted observations. Advances in Applied Probability, 2006, 38, 1098-1115.	0.4	5
28	Stochastic SIR epidemics in a population with households and schools. Journal of Mathematical Biology, 2016, 72, 1177-1193.	0.8	4
29	SIR epidemics and vaccination on random graphs with clustering. Journal of Mathematical Biology, 2019, 78, 2369-2398.	0.8	4
30	Maximizing the Size of the Giant. Journal of Applied Probability, 2012, 49, 1156-1165.	0.4	3
31	The Tail does not Determine the Size of the Giant. Journal of Statistical Physics, 2018, 173, 736-745.	0.5	2
32	Inferring global network properties from egocentric data with applications to epidemics. Mathematical Medicine and Biology, 2015, 32, 101-114.	0.8	1
33	Who is the infector? General multi-type epidemics and real-time susceptibility processes. Advances in Applied Probability, 2019, 51, 606-631.	0.4	Ο
34	Characterizing the Initial Phase of Epidemic Growth on Some Empirical Networks. Springer Proceedings in Mathematics and Statistics, 2018, , 315-334.	0.1	0