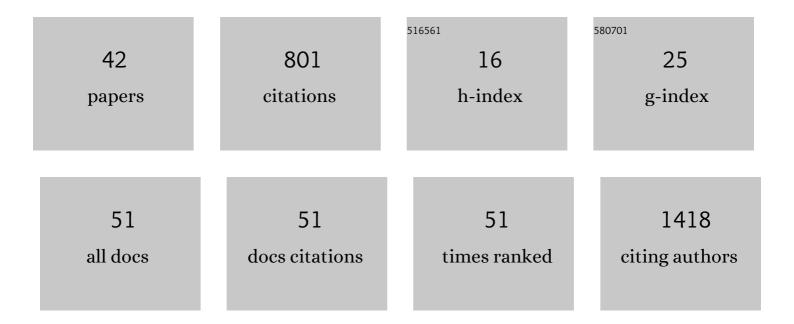
## Nicholas M Fountain-Jones

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2035396/publications.pdf

Version: 2024-02-01



#	Article	lF	CITATIONS
1	Moving beyond the guild concept: developing a practical functional trait framework for terrestrial beetles. Ecological Entomology, 2015, 40, 1-13.	1.1	85
2	Microclimate through space and time: Microclimatic variation at the edge of regeneration forests over daily, yearly and decadal time scales. Forest Ecology and Management, 2014, 334, 174-184.	1.4	65
3	Towards an ecoâ€phylogenetic framework for infectious disease ecology. Biological Reviews, 2018, 93, 950-970.	4.7	63
4	Urban landscapes can change virus gene flow and evolution in a fragmentationâ€sensitive carnivore. Molecular Ecology, 2017, 26, 6487-6498.	2.0	40
5	Pathogens in space: Advancing understanding of pathogen dynamics and disease ecology through landscape genetics. Evolutionary Applications, 2018, 11, 1763-1778.	1.5	37
6	How to make more from exposure data? An integrated machine learning pipeline to predict pathogen exposure. Journal of Animal Ecology, 2019, 88, 1447-1461.	1.3	33
7	Living near the edge: Being close to mature forest increases the rate of succession in beetle communities. Ecological Applications, 2015, 25, 800-811.	1.8	31
8	Using host traits to predict reservoir host species of rabies virus. PLoS Neglected Tropical Diseases, 2020, 14, e0008940.	1.3	29
9	Global emergence and evolutionary dynamics of bluetongue virus. Scientific Reports, 2020, 10, 21677.	1.6	26
10	Speciesâ€ <b>s</b> pecific spatiotemporal patterns of leopard, lion and tiger attacks on humans. Journal of Applied Ecology, 2019, 56, 585-593.	1.9	24
11	Parasites as conservation tools. Conservation Biology, 2022, 36, .	2.4	24
12	Urbanization impacts apex predator gene flow but not genetic diversity across an urbanâ€rural divide. Molecular Ecology, 2019, 28, 4926-4940.	2.0	23
13	Linking social and spatial networks to viral community phylogenetics reveals subtypeâ€specific transmission dynamics in African lions. Journal of Animal Ecology, 2017, 86, 1469-1482.	1.3	22
14	Mitochondrial genome sequencing reveals potential origins of the scabies mite Sarcoptes scabiei infesting two iconic Australian marsupials. BMC Evolutionary Biology, 2017, 17, 233.	3.2	22
15	Emerging phylogenetic structure of the SARS-CoV-2 pandemic. Virus Evolution, 2020, 6, veaa082.	2.2	21
16	Trophic position determines functional and phylogenetic recovery after disturbance within a community. Functional Ecology, 2017, 31, 1441-1451.	1.7	20
17	Host relatedness and landscape connectivity shape pathogen spread in the puma, a large secretive carnivore. Communications Biology, 2021, 4, 12.	2.0	20
18	Crossâ€species transmission and evolutionary dynamics of canine distemper virus during a spillover in African lions of Serengeti National Park. Molecular Ecology, 2020, 29, 4308-4321.	2.0	18

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#	Article	IF	CITATIONS
19	Frequent cross-species transmissions of foamy virus between domestic and wild felids. Virus Evolution, 2020, 6, vez058.	2.2	17
20	Incorporating genomic methods into contact networks to reveal new insights into animal behaviour and infectious disease dynamics. Behaviour, 2018, 155, 759-791.	0.4	16
21	Microbial associations and spatial proximity predict North American moose ( <i>Alces alces</i> ) gastrointestinal community composition. Journal of Animal Ecology, 2020, 89, 817-828.	1.3	16
22	Endemic infection can shape exposure to novel pathogens: Pathogen coâ€occurrence networks in the Serengeti lions. Ecology Letters, 2019, 22, 904-913.	3.0	14
23	Gut microbiota and their putative metabolic functions in fragmented Bengal tiger population of Nepal. PLoS ONE, 2019, 14, e0221868.	1.1	13
24	Group density, disease, and season shape territory size and overlap of social carnivores. Journal of Animal Ecology, 2021, 90, 87-101.	1.3	12
25	MrIML: Multiâ€response interpretable machine learning to model genomic landscapes. Molecular Ecology Resources, 2021, 21, 2766-2781.	2.2	12
26	Mainstreaming Microbes across Biomes. BioScience, 2020, 70, 589-596.	2.2	11
27	Temporal persistence of edge effects on bryophytes within harvested forests. Forest Ecology and Management, 2016, 375, 223-229.	1.4	10
28	The Expectations and Challenges of Wildlife Disease Research in the Era of Genomics: Forecasting with a Horizon Scan-like Exercise. Journal of Heredity, 2019, 110, 261-274.	1.0	9
29	Distance, environmental and substrate factors impacting recovery of bryophyte communities after harvesting. Applied Vegetation Science, 2018, 21, 64-75.	0.9	8
30	Machine learning in molecular ecology. Molecular Ecology Resources, 2021, 21, 2589-2597.	2.2	8
31	Does the virus cross the road? Viral phylogeographic patterns among bobcat populations reflect a history of urban development. Evolutionary Applications, 2020, 13, 1806-1817.	1.5	7
32	Novel smacoviruses identified in the faeces of two wild felids: North American bobcat and African lion. Archives of Virology, 2019, 164, 2395-2399.	0.9	5
33	Anemia or other comorbidities? using machine learning to reveal deeper insights into the drivers of acute coronary syndromes in hospital admitted patients. PLoS ONE, 2022, 17, e0262997.	1.1	5
34	Hunting alters viral transmission and evolution in a large carnivore. Nature Ecology and Evolution, 2022, 6, 174-182.	3.4	5
35	Beetle communities associated with the tree fern <i>Dicksonia antarctica</i> Labill. in Tasmania. Australian Journal of Entomology, 2012, 51, 154-165.	1.1	4
36	Machine-learning model led design to experimentally test species thermal limits: The case of kissing bugs (Triatominae). PLoS Neglected Tropical Diseases, 2021, 15, e0008822.	1.3	4

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37	Environment, vector, or host? Using machine learning to untangle the mechanisms driving arbovirus outbreaks. Ecological Applications, 2021, 31, e02407.	1.8	4
38	Strong trait correlation and phylogenetic signal in North American ground beetle (Carabidae) morphology. Ecosphere, 2021, 12, .	1.0	3
39	Comparative phylodynamics reveals the evolutionary history of SARS-CoV-2 emerging variants in the Arabian Peninsula. Virus Evolution, 2022, 8, .	2.2	3
40	Cross-sectional association of Toxoplasma gondii exposure with BMI and diet in US adults. PLoS Neglected Tropical Diseases, 2021, 15, e0009825.	1.3	1
41	Domestic horses within the Maya biosphere reserve: A possible threat to the Central American tapir (Tapirus bairdii). Caldasia, 2018, 40, 188-191.	0.1	0
42	Interspecies bacterial communication produces a delicate balance between Vibrio cholerae and the chironomid egg mass microbiome. Molecular Ecology, 2021, 30, 1571-1573.	2.0	0