

Virus genomes reveal factors that spread and sustained

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Citation Report

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Molecular mapping of Zika spread. <i>Nature</i> , 2017, 546, 355-356. | 13.7 | 16 |
| 2 | Multiplex PCR method for MinION and Illumina sequencing of Zika and other virus genomes directly from clinical samples. <i>Nature Protocols</i> , 2017, 12, 1261-1276. | 5.5 | 898 |
| 3 | Opportunities and challenges in modeling emerging infectious diseases. <i>Science</i> , 2017, 357, 149-152. | 6.0 | 113 |
| 4 | Viral outbreaks involve destabilized evolutionary networks: evidence from Ebola, Influenza and Zika. <i>Scientific Reports</i> , 2017, 7, 11881. | 1.6 | 15 |
| 5 | Infectious disease management must be evolutionary. <i>Nature Ecology and Evolution</i> , 2017, 1, 1053-1055. | 3.4 | 4 |
| 6 | Genomic and epidemiological characterisation of a dengue virus outbreak among blood donors in Brazil. <i>Scientific Reports</i> , 2017, 7, 15216. | 1.6 | 40 |
| 7 | Predicting virus emergence amid evolutionary noise. <i>Open Biology</i> , 2017, 7, 170189. | 1.5 | 149 |
| 8 | A model-based clustering method to detect infectious disease transmission outbreaks from sequence variation. <i>PLoS Computational Biology</i> , 2017, 13, e1005868. | 1.5 | 33 |
| 9 | Identifying spatio-temporal dynamics of Ebola in Sierra Leone using virus genomes. <i>Journal of the Royal Society Interface</i> , 2017, 14, 20170583. | 1.5 | 8 |
| 10 | Scalable relaxed clock phylogenetic dating. <i>Virus Evolution</i> , 2017, 3, . | 2.2 | 116 |
| 11 | Pandemic preparedness and forecast. <i>Nature Microbiology</i> , 2018, 3, 265-267. | 5.9 | 5 |
| 12 | Genomic Insights into Zika Virus Emergence and Spread. <i>Cell</i> , 2018, 172, 1160-1162. | 13.5 | 56 |
| 13 | Mapping road network communities for guiding disease surveillance and control strategies. <i>Scientific Reports</i> , 2018, 8, 4744. | 1.6 | 24 |
| 14 | Active Ebola Virus Replication and Heterogeneous Evolutionary Rates in EVD Survivors. <i>Cell Reports</i> , 2018, 22, 1159-1168. | 2.9 | 37 |
| 15 | Landscape attributes governing local transmission of an endemic zoonosis: Rabies virus in domestic dogs. <i>Molecular Ecology</i> , 2018, 27, 773-788. | 2.0 | 50 |
| 16 | Converging and emerging threats to health security. <i>Environment Systems and Decisions</i> , 2018, 38, 198-207. | 1.9 | 33 |
| 17 | TreeTime: Maximum-likelihood phylodynamic analysis. <i>Virus Evolution</i> , 2018, 4, vex042. | 2.2 | 883 |
| 18 | Analytic models for SIR disease spread on random spatial networks. <i>Journal of Complex Networks</i> , 2018, 6, 948-970. | 1.1 | 30 |

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 19 | Clinical sequencing: From raw data to diagnosis with lifetime value. <i>Clinical Genetics</i> , 2018, 93, 508-519. | 1.0 | 75 |
| 20 | Towards a genomics-informed, real-time, global pathogen surveillance system. <i>Nature Reviews Genetics</i> , 2018, 19, 9-20. | 7.7 | 505 |
| 21 | An exploration of the spatiotemporal and demographic patterns of Ebola Virus Disease epidemic in West Africa using open access data sources. <i>Applied Geography</i> , 2018, 90, 272-281. | 1.7 | 1 |
| 22 | Detection of Emerging Zoonotic Pathogens: An Integrated One Health Approach. <i>Annual Review of Animal Biosciences</i> , 2018, 6, 121-139. | 3.6 | 76 |
| 23 | Survey of Ebola Viruses in Frugivorous and Insectivorous Bats in Guinea, Cameroon, and the Democratic Republic of the Congo, 2015â€“2017. <i>Emerging Infectious Diseases</i> , 2018, 24, 2228-2240. | 2.0 | 66 |
| 24 | Spatial infectious disease epidemiology: on the cusp. <i>BMC Medicine</i> , 2018, 16, 192. | 2.3 | 39 |
| 25 | Bayesian phylodynamic inference with complex models. <i>PLoS Computational Biology</i> , 2018, 14, e1006546. | 1.5 | 64 |
| 26 | Design and Analysis of Infectious Disease Studies. <i>Oberwolfach Reports</i> , 2018, 15, 383-432. | 0.0 | 0 |
| 27 | Evolutionary Virology at 40. <i>Genetics</i> , 2018, 210, 1151-1162. | 1.2 | 51 |
| 28 | Recent advances in computational phylodynamics. <i>Current Opinion in Virology</i> , 2018, 31, 24-32. | 2.6 | 45 |
| 29 | How ownership rights over microorganisms affect infectious disease control and innovation: A root-cause analysis of barriers to data sharing as experienced by key stakeholders. <i>PLoS ONE</i> , 2018, 13, e0195885. | 1.1 | 35 |
| 30 | Populations, megapopulations, and the areal unit problem. <i>Health and Place</i> , 2018, 54, 79-84. | 1.5 | 4 |
| 31 | The phylogenomics of evolving virus virulence. <i>Nature Reviews Genetics</i> , 2018, 19, 756-769. | 7.7 | 152 |
| 32 | Genomic Analysis of Lassa Virus during an Increase in Cases in Nigeria in 2018. <i>New England Journal of Medicine</i> , 2018, 379, 1745-1753. | 13.9 | 135 |
| 33 | Predicting reservoir hosts and arthropod vectors from evolutionary signatures in RNA virus genomes. <i>Science</i> , 2018, 362, 577-580. | 6.0 | 140 |
| 34 | Mapping malaria by combining parasite genomic and epidemiologic data. <i>BMC Medicine</i> , 2018, 16, 190. | 2.3 | 68 |
| 35 | Private collection: high correlation of sample collection and patient admission date in clinical microbiological testing complicates sharing of phylodynamic metadata. <i>Virus Evolution</i> , 2018, 4, vey005. | 2.2 | 8 |
| 36 | A Predictive Spatial Distribution Framework for Filovirus-Infected Bats. <i>Scientific Reports</i> , 2018, 8, 7970. | 1.6 | 7 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 37 | MERS-CoV spillover at the camel-human interface. <i>ELife</i> , 2018, 7, . | 2.8 | 172 |
| 38 | The Bayesian optimist's guide to adaptive immune receptor repertoire analysis. <i>Immunological Reviews</i> , 2018, 284, 148-166. | 2.8 | 12 |
| 39 | The epidemiological characteristics and molecular phylogeny of the dengue virus in Guangdong, China, 2015. <i>Scientific Reports</i> , 2018, 8, 9976. | 1.6 | 11 |
| 41 | A comparative computational genomics of Ebola Virus Disease strains: In-silico Insight for Ebola control. <i>Informatics in Medicine Unlocked</i> , 2018, 12, 106-119. | 1.9 | 15 |
| 42 | Ebola Immunity: Gaining a Winning Position in Lightning Chess. <i>Journal of Immunology</i> , 2018, 201, 833-842. | 0.4 | 19 |
| 43 | Mechanisms and Concepts in RNA Virus Population Dynamics and Evolution. <i>Annual Review of Virology</i> , 2018, 5, 69-92. | 3.0 | 101 |
| 44 | Monitoring and redirecting virus evolution. <i>PLoS Pathogens</i> , 2018, 14, e1006979. | 2.1 | 13 |
| 45 | GrapeTree: visualization of core genomic relationships among 100,000 bacterial pathogens. <i>Genome Research</i> , 2018, 28, 1395-1404. | 2.4 | 553 |
| 46 | Rational Engineering and Characterization of an mAb that Neutralizes Zika Virus by Targeting a Mutationally Constrained Quaternary Epitope. <i>Cell Host and Microbe</i> , 2018, 23, 618-627.e6. | 5.1 | 28 |
| 47 | Genomic and epidemiological monitoring of yellow fever virus transmission potential. <i>Science</i> , 2018, 361, 894-899. | 6.0 | 279 |
| 48 | The effects of random taxa sampling schemes in Bayesian virus phylogeography. <i>Infection, Genetics and Evolution</i> , 2018, 64, 225-230. | 1.0 | 12 |
| 49 | Bayesian Phylogeography and Pathogenic Characterization of Smallpox Based on HA, AT1, and CrmB Genes. <i>Molecular Biology and Evolution</i> , 2018, 35, 2607-2617. | 3.5 | 6 |
| 50 | Population mobility reductions associated with travel restrictions during the Ebola epidemic in Sierra Leone: use of mobile phone data. <i>International Journal of Epidemiology</i> , 2018, 47, 1562-1570. | 0.9 | 111 |
| 51 | Long-Range Polymerase Chain Reaction Method for Sequencing the Ebola Virus Genome From Ecological and Clinical Samples. <i>Journal of Infectious Diseases</i> , 2018, 218, S301-S304. | 1.9 | 8 |
| 53 | Outbreaks in a Rapidly Changing Central Africa – Lessons from Ebola. <i>New England Journal of Medicine</i> , 2018, 379, 1198-1201. | 13.9 | 56 |
| 54 | Bayesian phylogenetic and phylodynamic data integration using BEAST 1.10. <i>Virus Evolution</i> , 2018, 4, vey016. | 2.2 | 2,401 |
| 55 | Phylodynamic assessment of intervention strategies for the West African Ebola virus outbreak. <i>Nature Communications</i> , 2018, 9, 2222. | 5.8 | 59 |
| 56 | Networked-oscillator-based modeling and control of unsteady wake flows. <i>Physical Review E</i> , 2018, 97, 063107. | 0.8 | 19 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 57 | Using Genomics to Track Global Antimicrobial Resistance. <i>Frontiers in Public Health</i> , 2019, 7, 242. | 1.3 | 263 |
| 58 | Bayesian phylodynamics of avian influenza A virus H9N2 in Asia with time-dependent predictors of migration. <i>PLoS Computational Biology</i> , 2019, 15, e1007189. | 1.5 | 22 |
| 59 | Bayesian Estimation of Past Population Dynamics in BEAST 1.10 Using the Skygrid Coalescent Model. <i>Molecular Biology and Evolution</i> , 2019, 36, 2620-2628. | 3.5 | 99 |
| 60 | Advances in Visualization Tools for Phylogenomic and Phylodynamic Studies of Viral Diseases. <i>Frontiers in Public Health</i> , 2019, 7, 208. | 1.3 | 15 |
| 61 | Genomic analysis of respiratory syncytial virus infections in households and utility in inferring who infects the infant. <i>Scientific Reports</i> , 2019, 9, 10076. | 1.6 | 19 |
| 62 | High-Performance Computing in Bayesian Phylogenetics and Phylodynamics Using BEAGLE. <i>Methods in Molecular Biology</i> , 2019, 1910, 691-722. | 0.4 | 11 |
| 63 | Communicable Disease Surveillance Ethics in the Age of Big Data and New Technology. <i>Asian Bioethics Review</i> , 2019, 11, 173-187. | 0.9 | 27 |
| 64 | Impacts of environmental and socio-economic factors on emergence and epidemic potential of Ebola in Africa. <i>Nature Communications</i> , 2019, 10, 4531. | 5.8 | 63 |
| 65 | Twenty years of West Nile virus spread and evolution in the Americas visualized by Nextstrain. <i>PLoS Pathogens</i> , 2019, 15, e1008042. | 2.1 | 87 |
| 66 | Phylodynamics of Influenza A/H1N1pdm09 in India Reveals Circulation Patterns and Increased Selection for Clade 6b Residues and Other High Mortality Mutants. <i>Viruses</i> , 2019, 11, 791. | 1.5 | 9 |
| 67 | Inferring time-dependent migration and coalescence patterns from genetic sequence and predictor data in structured populations. <i>Virus Evolution</i> , 2019, 5, vez030. | 2.2 | 20 |
| 68 | Applying next-generation sequencing to track falciparum malaria in sub-Saharan Africa. <i>Malaria Journal</i> , 2019, 18, 268. | 0.8 | 41 |
| 69 | Evaluation of DNA Extraction Methods on Individual Helminth Egg and Larval Stages for Whole-Genome Sequencing. <i>Frontiers in Genetics</i> , 2019, 10, 826. | 1.1 | 30 |
| 70 | Inferring host roles in bayesian phylodynamics of global avian influenza A virus H9N2. <i>Virology</i> , 2019, 538, 86-96. | 1.1 | 13 |
| 71 | The Expectations and Challenges of Wildlife Disease Research in the Era of Genomics: Forecasting with a Horizon Scan-like Exercise. <i>Journal of Heredity</i> , 2019, 110, 261-274. | 1.0 | 9 |
| 72 | Phylodynamic Analysis of Ebola Virus Disease Transmission in Sierra Leone. <i>Viruses</i> , 2019, 11, 71. | 1.5 | 3 |
| 73 | Global phylodynamic analysis of avian paramyxovirus-1 provides evidence of inter-host transmission and intercontinental spatial diffusion. <i>BMC Evolutionary Biology</i> , 2019, 19, 108. | 3.2 | 38 |
| 74 | Fast hierarchical Bayesian analysis of population structure. <i>Nucleic Acids Research</i> , 2019, 47, 5539-5549. | 6.5 | 173 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 75 | A Fast Likelihood Method to Reconstruct and Visualize Ancestral Scenarios. <i>Molecular Biology and Evolution</i> , 2019, 36, 2069-2085. | 3.5 | 153 |
| 76 | Towards Translational Epidemiology: Next-Generation Sequencing and Phylogeography as Epidemiological Mainstays. <i>MSystems</i> , 2019, 4, . | 1.7 | 2 |
| 77 | Outbreak analytics: a developing data science for informing the response to emerging pathogens. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180276. | 1.8 | 118 |
| 78 | Inferring epidemiological links from deep sequencing data: a statistical learning approach for human, animal and plant diseases. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180258. | 1.8 | 14 |
| 79 | Overview of Human Viral Hemorrhagic Fevers. , 2019, , 21-54. | | 1 |
| 80 | Estimating Epidemic Incidence and Prevalence from Genomic Data. <i>Molecular Biology and Evolution</i> , 2019, 36, 1804-1816. | 3.5 | 39 |
| 81 | Retrospective versus real-time Ebola virus sequencing. <i>Lancet Infectious Diseases</i> , The, 2019, 19, 567-568. | 4.6 | 3 |
| 82 | Molecular characterisation of the emerging measles virus from Roraima state, Brazil, 2018. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2019, 114, e180545. | 0.8 | 3 |
| 83 | Emerging Challenges and Opportunities in Infectious Disease Epidemiology. <i>American Journal of Epidemiology</i> , 2019, 188, 873-882. | 1.6 | 14 |
| 84 | Introduction of Ebola virus into a remote border district of Sierra Leone, 2014: use of field epidemiology and RNA sequencing to describe chains of transmission. <i>Epidemiology and Infection</i> , 2019, 147, e88. | 1.0 | 2 |
| 85 | Recent advances in the development and evaluation of molecular diagnostics for Ebola virus disease. <i>Expert Review of Molecular Diagnostics</i> , 2019, 19, 325-340. | 1.5 | 12 |
| 86 | Incorporating sampling uncertainty in the geospatial assignment of taxa for virus phylogeography. <i>Virus Evolution</i> , 2019, 5, vey043. | 2.2 | 12 |
| 87 | Intra-host Ebola viral adaption during human infection. <i>Biosafety and Health</i> , 2019, 1, 14-24. | 1.2 | 9 |
| 88 | The Emergence of Genomic Research in Africa and New Frameworks for Equity in Biomedical Research. <i>Ethnicity and Disease</i> , 2019, 29, 179-186. | 1.0 | 18 |
| 89 | Utilizing general human movement models to predict the spread of emerging infectious diseases in resource poor settings. <i>Scientific Reports</i> , 2019, 9, 5151. | 1.6 | 89 |
| 90 | Bayesian inference of transmission chains using timing of symptoms, pathogen genomes and contact data. <i>PLoS Computational Biology</i> , 2019, 15, e1006930. | 1.5 | 60 |
| 91 | Determinants of Transmission Risk During the Late Stage of the West African Ebola Epidemic. <i>American Journal of Epidemiology</i> , 2019, 188, 1319-1327. | 1.6 | 11 |
| 92 | Precision epidemiology for infectious disease control. <i>Nature Medicine</i> , 2019, 25, 206-211. | 15.2 | 94 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 93 | How Modelling Can Enhance the Analysis of Imperfect Epidemic Data. <i>Trends in Parasitology</i> , 2019, 35, 369-379. | 1.5 | 20 |
| 94 | Ebola virus disease. <i>Lancet, The</i> , 2019, 393, 936-948. | 6.3 | 305 |
| 95 | Pathogen Genomics in Public Health. <i>New England Journal of Medicine</i> , 2019, 381, 2569-2580. | 13.9 | 165 |
| 96 | The ability of single genes vs full genomes to resolve time and space in outbreak analysis. <i>BMC Evolutionary Biology</i> , 2019, 19, 232. | 3.2 | 35 |
| 97 | Reconstruction and prediction of viral disease epidemics. <i>Epidemiology and Infection</i> , 2019, 147, e34. | 1.0 | 29 |
| 98 | Fogarty International Center collaborative networks in infectious disease modeling: Lessons learnt in research and capacity building. <i>Epidemics</i> , 2019, 26, 116-127. | 1.5 | 16 |
| 99 | Phylogeographic Analysis Reveals Multiple International transmission Events Have Driven the Global Emergence of <i>Escherichia coli</i> O157:H7. <i>Clinical Infectious Diseases</i> , 2019, 69, 428-437. | 2.9 | 26 |
| 100 | Tracking virus outbreaks in the twenty-first century. <i>Nature Microbiology</i> , 2019, 4, 10-19. | 5.9 | 305 |
| 101 | Frontiers in Molecular Evolutionary Medicine. <i>Journal of Molecular Evolution</i> , 2020, 88, 3-11. | 0.8 | 18 |
| 102 | A Darwinian Uncertainty Principle. <i>Systematic Biology</i> , 2020, 69, 521-529. | 2.7 | 12 |
| 103 | Emergence of a Plant Pathogen in Europe Associated with Multiple Intercontinental Introductions. <i>Applied and Environmental Microbiology</i> , 2020, 86, . | 1.4 | 57 |
| 104 | Global commercial passenger airlines and travel health information regarding infection control and the prevention of infectious disease: What's in a website?. <i>Travel Medicine and Infectious Disease</i> , 2020, 33, 101528. | 1.5 | 11 |
| 105 | The role of genetic sequencing and analysis in the polio eradication programme. <i>Virus Evolution</i> , 2020, 6, veaa040. | 2.2 | 19 |
| 106 | Genomic epidemiology and evolutionary dynamics of respiratory syncytial virus group B in Kilifi, Kenya, 2015–17. <i>Virus Evolution</i> , 2020, 6, veaa050. | 2.2 | 3 |
| 107 | Species-Specific Evolution of Ebola Virus during Replication in Human and Bat Cells. <i>Cell Reports</i> , 2020, 32, 108028. | 2.9 | 17 |
| 108 | Variation around the dominant viral genome sequence contributes to viral load and outcome in patients with Ebola virus disease. <i>Genome Biology</i> , 2020, 21, 238. | 3.8 | 18 |
| 109 | Molecular epidemiology of the first wave of severe acute respiratory syndrome coronavirus 2 infection in Thailand in 2020. <i>Scientific Reports</i> , 2020, 10, 16602. | 1.6 | 29 |
| 110 | Rapid implementation of SARS-CoV-2 sequencing to investigate cases of health-care associated COVID-19: a prospective genomic surveillance study. <i>Lancet Infectious Diseases, The</i> , 2020, 20, 1263-1271. | 4.6 | 352 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 111 | Origin and evolution of emerging Liao ning Virus (genus Seadornavirus, family Reoviridae). <i>Virology Journal</i> , 2020, 17, 105. | 1.4 | 1 |
| 112 | GeoBoost2: a natural languageprocessing pipeline for GenBank metadata enrichment for virus phylogeography. <i>Bioinformatics</i> , 2020, 36, 5120-5121. | 1.8 | 7 |
| 113 | Going back to the roots: Evaluating Bayesian phylogeographic models with discrete trait uncertainty. <i>Infection, Genetics and Evolution</i> , 2020, 85, 104501. | 1.0 | 3 |
| 114 | Amplicon-Based Detection and Sequencing of SARS-CoV-2 in Nasopharyngeal Swabs from Patients With COVID-19 and Identification of Deletions in the Viral Genome That Encode Proteins Involved in Interferon Antagonism. <i>Viruses</i> , 2020, 12, 1164. | 1.5 | 51 |
| 115 | Accommodating individual travel history and unsampled diversity in Bayesian phylogeographic inference of SARS-CoV-2. <i>Nature Communications</i> , 2020, 11, 5110. | 5.8 | 118 |
| 116 | Urban Vegetation Slows Down the Spread of Coronavirus Disease (COVID-19) in the United States. <i>Geophysical Research Letters</i> , 2020, 47, e2020GL089286. | 1.5 | 37 |
| 117 | Viral genomics in Ebola virus research. <i>Nature Reviews Microbiology</i> , 2020, 18, 365-378. | 13.6 | 30 |
| 118 | The public health response to COVID-19: balancing precaution and unintended consequences. <i>Annals of Epidemiology</i> , 2020, 46, 12-13. | 0.9 | 24 |
| 119 | Tracking echovirus eleven outbreaks in Guangdong, China: a metatranscriptomic, phylogenetic, and epidemiological study. <i>Virus Evolution</i> , 2020, 6, veaa029. | 2.2 | 14 |
| 120 | Multivariate time-series analysis of biomarkers from a dengue cohort offers new approaches for diagnosis and prognosis. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008199. | 1.3 | 7 |
| 121 | Accounting for population structure reveals ambiguity in the Zaire Ebolavirus reservoir dynamics. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008117. | 1.3 | 8 |
| 122 | Estimating the relative probability of direct transmission between infectious disease patients. <i>International Journal of Epidemiology</i> , 2020, 49, 764-775. | 0.9 | 10 |
| 123 | Multiple approaches for massively parallel sequencing of SARS-CoV-2 genomes directly from clinical samples. <i>Genome Medicine</i> , 2020, 12, 57. | 3.6 | 104 |
| 124 | Population structure across scales facilitates coexistence and spatial heterogeneity of antibiotic-resistant infections. <i>PLoS Computational Biology</i> , 2020, 16, e1008010. | 1.5 | 19 |
| 125 | Delayed recognition of Ebola virus disease is associated with longer and larger outbreaks. <i>Emerging Microbes and Infections</i> , 2020, 9, 291-301. | 3.0 | 18 |
| 126 | In Search of Covariates of HIV-1 Subtype B Spread in the United States—A Cautionary Tale of Large-Scale Bayesian Phylogeography. <i>Viruses</i> , 2020, 12, 182. | 1.5 | 15 |
| 127 | Identification of Hidden Population Structure in Time-Scaled Phylogenies. <i>Systematic Biology</i> , 2020, 69, 884-896. | 2.7 | 26 |
| 128 | Standardized phylogenetic and molecular evolutionary analysis applied to species across the microbial tree of life. <i>Scientific Reports</i> , 2020, 10, 1723. | 1.6 | 65 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 129 | Methods for Rapid Mobility Estimation to Support Outbreak Response. <i>Health Security</i> , 2020, 18, 1-15. | 0.9 | 7 |
| 130 | Incubation periods impact the spatial predictability of cholera and Ebola outbreaks in Sierra Leone. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 5067-5073. | 3.3 | 28 |
| 131 | Ebola virus disease. <i>Nature Reviews Disease Primers</i> , 2020, 6, 13. | 18.1 | 340 |
| 132 | Online Bayesian Phylodynamic Inference in BEAST with Application to Epidemic Reconstruction. <i>Molecular Biology and Evolution</i> , 2020, 37, 1832-1842. | 3.5 | 25 |
| 133 | Post-exposure prophylactic vaccine candidates for the treatment of human Risk Group 4 pathogen infections. <i>Expert Review of Vaccines</i> , 2020, 19, 85-103. | 2.0 | 4 |
| 134 | Improving Cross-Border Preparedness and Response: Lessons Learned from 3 Lassa Fever Outbreaks Across Benin, Nigeria, and Togo, 2017-2019. <i>Health Security</i> , 2020, 18, S-105-S-112. | 0.9 | 15 |
| 135 | Community perspectives on the benefits and risks of technologically enhanced communicable disease surveillance systems: a report on four community juries. <i>BMC Medical Ethics</i> , 2020, 21, 31. | 1.0 | 12 |
| 136 | An emergent clade of SARS-CoV-2 linked to returned travellers from Iran. <i>Virus Evolution</i> , 2020, 6, veaa027. | 2.2 | 119 |
| 137 | Genomic and serologic characterization of enterovirus A71 brainstem encephalitis. <i>Neurology: Neuroimmunology and Neuroinflammation</i> , 2020, 7, . | 3.1 | 19 |
| 138 | Permutation Tests for Infection Graphs. <i>Journal of the American Statistical Association</i> , 2021, 116, 770-782. | 1.8 | 0 |
| 139 | Porcine reproductive and respiratory syndrome virus dissemination across pig production systems in the United States. <i>Transboundary and Emerging Diseases</i> , 2021, 68, 667-683. | 1.3 | 31 |
| 140 | Log Transformation Improves Dating of Phylogenies. <i>Molecular Biology and Evolution</i> , 2021, 38, 1151-1167. | 3.5 | 7 |
| 141 | Inference of Nipah virus evolution, 1999â€“2015. <i>Virus Evolution</i> , 2021, 7, veaa062. | 2.2 | 18 |
| 142 | Hostâ€“parasite dynamics set the ecological theatre for the evolution of stateâ€and contextâ€dependent dispersal in hosts. <i>Oikos</i> , 2021, 130, 121-132. | 1.2 | 8 |
| 143 | Spatiotemporal reconstruction and transmission dynamics during the 2016â€“17 H5N8 highly pathogenic avian influenza epidemic in Italy. <i>Transboundary and Emerging Diseases</i> , 2021, 68, 37-50. | 1.3 | 7 |
| 144 | GEViTRec: Data Reconnaissance Through Recommendation Using a Domain-Specific Visualization Prevalence Design Space. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2022, 28, 4855-4872. | 2.9 | 5 |
| 145 | Integrating genomics education into Nigerian undergraduate medical training - A narrative review. <i>Journal of Clinical Sciences</i> , 2021, 18, 3. | 0.0 | 2 |
| 146 | Genome sequencing and its use in public health responses to COVID-19. <i>Microbiology Australia</i> , 2021, 42, 44. | 0.1 | 1 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 147 | Ecological Barrier Deterioration Driven by Human Activities Poses Fatal Threats to Public Health due to Emerging Infectious Diseases. <i>Engineering</i> , 2022, 10, 155-166. | 3.2 | 15 |
| 148 | An approach to integrate population mobility patterns and sociocultural factors in communicable disease preparedness and response. <i>Humanities and Social Sciences Communications</i> , 2021, 8, . | 1.3 | 5 |
| 149 | Analysis of an Ebola virus disease survivor whose host and viral markers were predictive of death indicates the effectiveness of medical countermeasures and supportive care. <i>Genome Medicine</i> , 2021, 13, 5. | 3.6 | 9 |
| 150 | Preparing for Emerging Zoonotic Viruses. , 2021, , 256-266. | | 11 |
| 151 | Ebola virus antibody decayâ€“stimulation in a high proportion of survivors. <i>Nature</i> , 2021, 590, 468-472. | 13.7 | 30 |
| 152 | Establishment and lineage dynamics of the SARS-CoV-2 epidemic in the UK. <i>Science</i> , 2021, 371, 708-712. | 6.0 | 335 |
| 153 | Reconstructing unseen transmission events to infer dengue dynamics from viral sequences. <i>Nature Communications</i> , 2021, 12, 1810. | 5.8 | 12 |
| 155 | Repeated introductions and intensive community transmission fueled a mumps virus outbreak in Washington State. <i>ELife</i> , 2021, 10, . | 2.8 | 13 |
| 156 | Rapid Acquisition of High-Quality SARS-CoV-2 Genome via Amplicon-Oxford Nanopore Sequencing. <i>Virologica Sinica</i> , 2021, 36, 901-912. | 1.2 | 18 |
| 157 | Integration of genomic sequencing into the response to the Ebola virus outbreak in Nord Kivu, Democratic Republic of the Congo. <i>Nature Medicine</i> , 2021, 27, 710-716. | 15.2 | 35 |
| 159 | Comparative analysis of spatial-temporal patterns of human metapneumovirus and respiratory syncytial virus in Africa using genetic data, 2011â€“2014. <i>Virology Journal</i> , 2021, 18, 104. | 1.4 | 1 |
| 160 | Integrating genomics in population models to forecast translocation success. <i>Restoration Ecology</i> , 2021, 29, e13395. | 1.4 | 13 |
| 163 | Untangling introductions and persistence in COVID-19 resurgence in Europe. <i>Nature</i> , 2021, 595, 713-717. | 13.7 | 133 |
| 164 | A dynamic, ensemble learning approach to forecast dengue fever epidemic years in Brazil using weather and population susceptibility cycles. <i>Journal of the Royal Society Interface</i> , 2021, 18, 20201006. | 1.5 | 16 |
| 165 | Evolutionary and Ecological Drivers Shape the Emergence and Extinction of Foot-and-Mouth Disease Virus Lineages. <i>Molecular Biology and Evolution</i> , 2021, 38, 4346-4361. | 3.5 | 14 |
| 167 | Integrating animal movements with phylogeography to model the spread of PRRSV in the USA. <i>Virus Evolution</i> , 2021, 7, veab060. | 2.2 | 14 |
| 168 | Spatiotemporal invasion dynamics of SARS-CoV-2 lineage B.1.1.7 emergence. <i>Science</i> , 2021, 373, 889-895. | 6.0 | 142 |
| 169 | Assignment of epidemiological lineages in an emerging pandemic using the pangolin tool. <i>Virus Evolution</i> , 2021, 7, veab064. | 2.2 | 774 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 170 | Accuracy in Near-Perfect Virus Phylogenies. <i>Systematic Biology</i> , 2022, 71, 426-438. | 2.7 | 8 |
| 171 | Amplicon and Metagenomic Analysis of Middle East Respiratory Syndrome (MERS) Coronavirus and the Microbiome in Patients with Severe MERS. <i>MSphere</i> , 2021, 6, e0021921. | 1.3 | 12 |
| 172 | SARS-CoV-2 Tests: Bridging the Gap between Laboratory Sensors and Clinical Applications. <i>ACS Sensors</i> , 2021, 6, 2815-2837. | 4.0 | 24 |
| 173 | Herramientas biotecnológicas en el diagnóstico, prevención y tratamiento frente a pandemias. <i>Revista Bionatura</i> , 2021, 3, 2091-2113. | 0.1 | 0 |
| 174 | Accounting for the Biological Complexity of Pathogenic Fungi in Phylogenetic Dating. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 661. | 1.5 | 3 |
| 176 | Genomic-informed pathogen surveillance in Africa: opportunities and challenges. <i>Lancet Infectious Diseases, The</i> , 2021, 21, e281-e289. | 4.6 | 97 |
| 177 | Resurgence of Ebola virus in 2021 in Guinea suggests a new paradigm for outbreaks. <i>Nature</i> , 2021, 597, 539-543. | 13.7 | 113 |
| 178 | Conserved ancestral tropical niche but different continental histories explain the latitudinal diversity gradient in brush-footed butterflies. <i>Nature Communications</i> , 2021, 12, 5717. | 5.8 | 33 |
| 179 | Marburg and Ebola Virus mRNA 3' Untranslated Regions Contain Negative Regulators of Translation That Are Modulated by ADAR1 Editing. <i>Journal of Virology</i> , 2021, 95, e0065221. | 1.5 | 8 |
| 180 | Exploiting genomic surveillance to map the spatio-temporal dispersal of SARS-CoV-2 spike mutations in Belgium across 2020. <i>Scientific Reports</i> , 2021, 11, 18580. | 1.6 | 10 |
| 181 | Genetic and evolutionary analysis of SARS-CoV-2 circulating in the region surrounding Islamabad, Pakistan. <i>Infection, Genetics and Evolution</i> , 2021, 94, 105003. | 1.0 | 7 |
| 182 | Omics for Forensic and Post-Mortem Microbiology. , 2021, , 219-240. | | 1 |
| 183 | Sequencing the pandemic: rapid and high-throughput processing and analysis of COVID-19 clinical samples for 21st century public health. <i>F1000Research</i> , 2021, 10, 48. | 0.8 | 6 |
| 184 | Accelerating Vaccine Development During the 2013-2016 West African Ebola Virus Disease Outbreak. <i>Current Topics in Microbiology and Immunology</i> , 2017, 411, 229-261. | 0.7 | 14 |
| 185 | Ebola and Other Haemorrhagic Fevers. , 2019, , 179-205. | | 2 |
| 186 | How countries are using genomics to help avoid a second coronavirus wave. <i>Nature</i> , 2020, 582, 19-19. | 13.7 | 6 |
| 187 | Capturing sequence diversity in metagenomes with comprehensive and scalable probe design. <i>Nature Biotechnology</i> , 2019, 37, 160-168. | 9.4 | 96 |
| 188 | Disease control across urban-rural gradients. <i>Journal of the Royal Society Interface</i> , 2020, 17, 20200775. | 1.5 | 16 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|-----|-----------|
| 189 | Ebola returns to its Congo Basin heartland. <i>Journal of General Virology</i> , 2018, 99, 861-863. | 1.3 | 2 |
| 214 | A Comparison of Geographical Propagation Visualizations. , 2020, , . | | 9 |
| 215 | Cohort study protocol: Bioresource in Adult Infectious Diseases (BioAID). <i>Wellcome Open Research</i> , 2018, 3, 97. | 0.9 | 6 |
| 216 | Rapid in-country sequencing of whole virus genomes to inform rabies elimination programmes. <i>Wellcome Open Research</i> , 2020, 5, 3. | 0.9 | 30 |
| 217 | Hamiltonian Monte Carlo sampling to estimate past population dynamics using the skygrid coalescent model in a Bayesian phylogenetics framework. <i>Wellcome Open Research</i> , 2020, 5, 53. | 0.9 | 15 |
| 218 | Ethical challenges in pathogen sequencing: a systematic scoping review. <i>Wellcome Open Research</i> , 2020, 5, 119. | 0.9 | 6 |
| 219 | Estimating effective population size changes from preferentially sampled genetic sequences. <i>PLoS Computational Biology</i> , 2020, 16, e1007774. | 1.5 | 14 |
| 220 | Genomic sequence of yellow fever virus from a Dutch traveller returning from the Gambia-Senegal region, the Netherlands, November 2018. <i>Eurosurveillance</i> , 2019, 24, . | 3.9 | 9 |
| 221 | Lassa â€“ A latent threat to West Africa: How ready are we?. <i>Journal of Global Infectious Diseases</i> , 2018, 10, 169. | 0.2 | 4 |
| 222 | Genomics of host-pathogen interactions: challenges and opportunities across ecological and spatiotemporal scales. <i>PeerJ</i> , 2019, 7, e8013. | 0.9 | 23 |
| 223 | Why populations are not planets_ gravity and the limits of disease modeling by analogy. <i>Journal of Geography and Regional Planning</i> , 2021, 14, 105-112. | 0.2 | 0 |
| 224 | ADAR Editing in Viruses: An Evolutionary Force to Reckon with. <i>Genome Biology and Evolution</i> , 2021, 13, . | 1.1 | 23 |
| 225 | Progress and challenges in virus genomic epidemiology. <i>Trends in Parasitology</i> , 2021, 37, 1038-1049. | 1.5 | 45 |
| 230 | Simulating the effect of public health interventions using dated virus sequences and geographical data. <i>Peer Community in Evolutionary Biology</i> , 2018, , 100046. | 0.0 | 0 |
| 240 | Innovative Technologies for Advancement of WHO Risk Group 4 Pathogens Research. , 2019, , 437-469. | | 5 |
| 241 | Epidemiology and Management of Lassa Fever in the West African Sub-Region: Overcoming the Socio-cultural Challenges. , 2019, , 41-58. | | 0 |
| 243 | ZooPhy: A bioinformatics pipeline for virus phylogeography and surveillance. <i>Online Journal of Public Health Informatics</i> , 2019, 11, . | 0.4 | 0 |
| 250 | Rapid in-country sequencing of whole virus genomes to inform rabies elimination programmes. <i>Wellcome Open Research</i> , 2020, 5, 3. | 0.9 | 26 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|-----|-----------|
| 256 | Enabling One Health solutions through genomics. Indian Journal of Medical Research, 2021, 153, 273-279. | 0.4 | 0 |
| 258 | Enabling One Health solutions through genomics. Indian Journal of Medical Research, 2021, 153, 273. | 0.4 | 2 |
| 259 | Assessment of Inter-Laboratory Differences in SARS-CoV-2 Consensus Genome Assemblies between Public Health Laboratories in Australia. Viruses, 2022, 14, 185. | 1.5 | 4 |
| 260 | Long-Reads-Based Metagenomics in Clinical Diagnosis With a Special Focus on Fungal Infections. Frontiers in Microbiology, 2021, 12, 708550. | 1.5 | 9 |
| 261 | Multi-Feature Representation Based COVID-19 Risk Stage Evaluation With Transfer Learning. IEEE Transactions on Network Science and Engineering, 2022, 9, 1359-1375. | 4.1 | 6 |
| 262 | From viral evolution to spatial contagion: a biologically modulated Hawkes model. Bioinformatics, 2022, 38, 1846-1856. | 1.8 | 5 |
| 265 | The Carbon Footprint of Bioinformatics. Molecular Biology and Evolution, 2022, 39, . | 3.5 | 29 |
| 267 | Phylogeography Reveals Association between Swine Trade and the Spread of Porcine Epidemic Diarrhea Virus in China and across the World. Molecular Biology and Evolution, 2022, 39, . | 3.5 | 35 |
| 268 | Phycova " a tool for exploring covariates of pathogen spread. Virus Evolution, 2022, 8, veac015. | 2.2 | 3 |
| 269 | Methods for sequencing the pandemic: benefits of rapid or high-throughput processing. F1000Research, 0, 10, 48. | 0.8 | 5 |
| 270 | Spatial model of Ebola outbreaks contained by behavior change. PLoS ONE, 2022, 17, e0264425. | 1.1 | 1 |
| 271 | Therapeutic Strategies against Ebola Virus Infection. Viruses, 2022, 14, 579. | 1.5 | 16 |
| 273 | Phylodynamic analysis of the highly pathogenic avian influenza H5N8 epidemic in France, 2016"2017. Transboundary and Emerging Diseases, 2022, 69, . | 1.3 | 6 |
| 274 | Epidemiological characteristics of imported respiratory infectious diseases in China, 2014"2018. Infectious Diseases of Poverty, 2022, 11, 22. | 1.5 | 0 |
| 275 | Modeling international mobility using roaming cell phone traces during COVID-19 pandemic. EPJ Data Science, 2022, 11, 22. | 1.5 | 9 |
| 276 | The need for linked genomic surveillance of SARS-CoV-2. Canada Communicable Disease Report, 2022, 48, 131-139. | 0.6 | 13 |
| 281 | Phylogenetic and phylodynamic approaches to understanding and combating the early SARS-CoV-2 pandemic. Nature Reviews Genetics, 2022, 23, 547-562. | 7.7 | 70 |
| 282 | Phylogenetic analysis of migration, differentiation, and class switching in B cells. PLoS Computational Biology, 2022, 18, e1009885. | 1.5 | 40 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|-----|-----------|
| 283 | Nanopore Sequencing as a Rapid Tool for Discrimination between Epidemic and Vaccine Strains of Classical Swine Fever Viruses in Japan. Nippon Juishikai Zasshi Journal of the Japan Veterinary Medical Association, 2022, 75, e83-e90. | 0.0 | 0 |
| 284 | A microfluidic cell chip for virus isolation via rapid screening for permissive cells. Virologica Sinica, 2022, , . | 1.2 | 6 |
| 285 | Accommodating sampling location uncertainty in continuous phylogeography. Virus Evolution, 2022, 8, . | 2.2 | 8 |
| 288 | Prospective surveillance study to detect antimalarial drug resistance, gene deletions of diagnostic relevance and genetic diversity of <i>Plasmodium falciparum</i> in Mozambique: protocol. BMJ Open, 2022, 12, e063456. | 0.8 | 7 |
| 291 | The Evolution of Medical Countermeasures for Ebola Virus Disease: Lessons Learned and Next Steps. Vaccines, 2022, 10, 1213. | 2.1 | 11 |
| 292 | Robust Phylodynamic Analysis of Genetic Sequencing Data from Structured Populations. Viruses, 2022, 14, 1648. | 1.5 | 6 |
| 293 | Molecular adaptations during viral epidemics. EMBO Reports, 2022, 23, . | 2.0 | 18 |
| 294 | Viral informatics: bioinformatics-based solution for managing viral infections. Briefings in Bioinformatics, 2022, 23, . | 3.2 | 10 |
| 296 | Scalable Bayesian phylogenetics. Philosophical Transactions of the Royal Society B: Biological Sciences, 2022, 377, . | 1.8 | 9 |
| 298 | Using multiple sampling strategies to estimate SARS-CoV-2 epidemiological parameters from genomic sequencing data. Nature Communications, 2022, 13, . | 5.8 | 10 |
| 299 | Phylogeographic analysis reveals an ancient East African origin of human herpes simplex virus 2 dispersal out-of-Africa. Nature Communications, 2022, 13, . | 5.8 | 1 |
| 301 | A high scale SARS-CoV-2 profiling by its whole-genome sequencing using Oxford Nanopore Technology in Kazakhstan. Frontiers in Genetics, 0, 13, . | 1.1 | 2 |
| 302 | Data Integration in Bayesian Phylogenetics. Annual Review of Statistics and Its Application, 2023, 10, 353-377. | 4.1 | 2 |
| 303 | Spatially explicit phylogeographical reconstruction sheds light on the history of the forest cover in the Congo Basin. Journal of Biogeography, 0, , . | 1.4 | 1 |
| 304 | Applications of Long-Read Sequencing Technology in Clinical Genomics. Advances in Molecular Pathology, 2022, 5, 85-108. | 0.2 | 0 |
| 306 | Distinguishing imported cases from locally acquired cases within a geographically limited genomic sample of an infectious disease. Bioinformatics, 2023, 39, . | 1.8 | 1 |
| 307 | Advancing disease genomics beyond COVID-19 and reducing health disparities: what does the future hold for Africa?. Briefings in Functional Genomics, 0, , . | 1.3 | 1 |
| 310 | Gaps in mobility data and implications for modelling epidemic spread: A scoping review and simulation study. Epidemics, 2023, 42, 100666. | 1.5 | 2 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 311 | Minimal Antigenic Evolution after a Decade of Norovirus GII.4 Sydney_2012 Circulation in Humans. <i>Journal of Virology</i> , 2023, 97, . | 1.5 | 8 |
| 312 | Impact and mitigation of sampling bias to determine viral spread: Evaluating discrete phylogeography through CTMC modeling and structured coalescent model approximations. <i>Virus Evolution</i> , 2023, 9, . | 2.2 | 13 |
| 313 | Diverse pathways toward a cure. <i>IScience</i> , 2023, 26, 106052. | 1.9 | 0 |
| 314 | Comparing the transmission potential from sequence and surveillance data of 2009 North American influenza pandemic waves. <i>Infectious Disease Modelling</i> , 2023, 8, 240-252. | 1.2 | 0 |
| 315 | Outbreak.info genomic reports: scalable and dynamic surveillance of SARS-CoV-2 variants and mutations. <i>Nature Methods</i> , 2023, 20, 512-522. | 9.0 | 111 |
| 316 | Toward a global virus genomic surveillance network. <i>Cell Host and Microbe</i> , 2023, 31, 861-873. | 5.1 | 13 |
| 317 | Linked Mutations in the Ebola Virus Polymerase Are Associated with Organ Specific Phenotypes. <i>Microbiology Spectrum</i> , 2023, 11, . | 1.2 | 1 |
| 318 | Deciphering the Hantavirus Host Range Combining Virology and Species Distribution Models with an Emphasis on the Yellow Pygmy Rice Rat (<i>Oligoryzomys flavescens</i>). <i>Transboundary and Emerging Diseases</i> , 2023, 2023, 1-15. | 1.3 | 0 |
| 320 | Into a Brighter Future. , 2023, , 143-149. | | 0 |
| 321 | Future Pandemics. , 2023, , 135-142. | | 0 |
| 325 | Emerging and Zoonotic Diseases. , 2023, , 111-122. | | 0 |
| 341 | Ebola and Marburg viruses. , 2024, , 2281-2308. | | 0 |
| 342 | Principles of diagnostic virology and virus discovery. , 2024, , 2595-2604. | | 0 |