

Resource Summary Report

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EpiEstim

RRID:SCR_018538

Type: Tool

Proper Citation

EpiEstim (RRID:SCR_018538)

Resource Information

URL: <https://cran.r-project.org/web/packages/EpiEstim/index.html>

Proper Citation: EpiEstim (RRID:SCR_018538)

Description: Framework and software to estimate time varying reproduction numbers during epidemics. Tools to quantify transmissibility throughout epidemic from analysis of time series of incidence. Used to estimate time varying instantaneous reproduction numbers from incidence time series.

Synonyms: Estimate Time Varying Reproduction Numbers from Epidemic Curves

Resource Type: software resource, data analysis software, software toolkit, data processing software, software application

Defining Citation: [PMID:24043437](#)

Keywords: Estimate time varying, reproduction number, epidemics, quantify transmissibility, time series analysis, reproductionc number analysis, incidence time series, bio.tools

Funding: United Kingdom Medical Research Council

Availability: Free, Available for download, Freely available

Resource Name: EpiEstim

Resource ID: SCR_018538

Alternate IDs: biotools:EpiEstim

Alternate URLs: <https://bio.tools/EpiEstim>

Record Creation Time: 20220129T080340+0000

Record Last Update: 20260807T042920+0000

Ratings and Alerts

No rating or validation information has been found for EpiEstim.

No alerts have been found for EpiEstim.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 35 mentions in open access literature.

Listed below are recent publications. The full list is available at [NIF](#) .

De Arcos-Jimenez JC, et al. (2026) Social Determinants and Outbreak Dynamics of the 2025 Measles Epidemic in Mexico: A Nationwide Analysis of Linked Surveillance Data. *Viruses*, 18(2).

Smolko P, et al. (2025) Spatio-Temporal Dynamics of African Swine Fever in Free-Ranging Wild Boar (*Sus scrofa*): Insights from Six Years of Surveillance and Control in Slovakia. *Veterinary sciences*, 12(11).

Chauvel C, et al. (2025) Community and Hospital-Based Laboratory Surveillance for Influenza, Respiratory Syncytial Virus, and SARS-CoV-2 During the 2023-2024 Season, Lyon, France. *Journal of medical virology*, 97(9), e70549.

Cleary E, et al. (2025) Comparing lagged impacts of mobility changes and environmental factors on COVID-19 waves in rural and urban India: A Bayesian spatiotemporal modelling study. *PLOS global public health*, 5(4), e0003431.

Clancey E, et al. (2025) Time-varying reproductive number estimation for practical application in structured populations. *Epidemiologic methods*, 14(1).

Kabami Z, et al. (2024) Ebola disease outbreak caused by the Sudan virus in Uganda, 2022: a descriptive epidemiological study. *The Lancet. Global health*, 12(10), e1684.

Kehoe AD, et al. (2024) SARS-CoV-2 Transmission in Alberta, British Columbia, and Ontario, Canada, January 2020-January 2022. *Emerging infectious diseases*, 30(5), 956.

Wei F, et al. (2023) COVID-19 transmission driven by age-group mathematical model in Shijiazhuang City of China. *Infectious Disease Modelling*, 8(4), 1050.

Dai C, et al. (2023) A new method for the joint estimation of instantaneous reproductive number and serial interval during epidemics. *PLoS computational biology*, 19(3), e1011021.

Wei Y, et al. (2022) Global COVID-19 Pandemic Waves: Limited Lessons Learned Worldwide over the Past Year. *Engineering (Beijing, China)*, 13, 91.

Rui J, et al. (2022) Optimal control strategies of SARS-CoV-2 Omicron supported by invasive and dynamic models. *Infectious diseases of poverty*, 11(1), 115.

Ji H, et al. (2022) The effectiveness of travel restriction measures in alleviating the COVID-19 epidemic: evidence from Shenzhen, China. *Environmental geochemistry and health*, 44(9), 3115.

Zhou Z, et al. (2022) Estimation of heterogeneous instantaneous reproduction numbers with application to characterize SARS-CoV-2 transmission in Massachusetts counties. *PLoS computational biology*, 18(9), e1010434.

Chen Z, et al. (2022) Epidemiological characteristics and transmission dynamics of the outbreak caused by the SARS-CoV-2 Omicron variant in Shanghai, China: a descriptive study. *medRxiv : the preprint server for health sciences*.

Chen Z, et al. (2022) Epidemiological characteristics and transmission dynamics of the outbreak caused by the SARS-CoV-2 Omicron variant in Shanghai, China: A descriptive study. *The Lancet regional health. Western Pacific*, 29, 100592.

Siddle KJ, et al. (2022) Transmission from vaccinated individuals in a large SARS-CoV-2 Delta variant outbreak. *Cell*, 185(3), 485.

Lal R, et al. (2022) An assessment of transmission dynamics via time-varying reproduction number of the second wave of the COVID-19 epidemic in Fiji. *Royal Society open science*, 9(8), 220004.

Huisman JS, et al. (2022) Estimation and worldwide monitoring of the effective reproductive number of SARS-CoV-2. *eLife*, 11.

Bolze A, et al. (2022) SARS-CoV-2 variant Delta rapidly displaced variant Alpha in the United States and led to higher viral loads. *Cell reports. Medicine*, 3(3), 100564.

Petrie JG, et al. (2022) The variant-specific burden of SARS-CoV-2 in Michigan: March 2020 through November 2021. *Journal of medical virology*, 94(11), 5251.