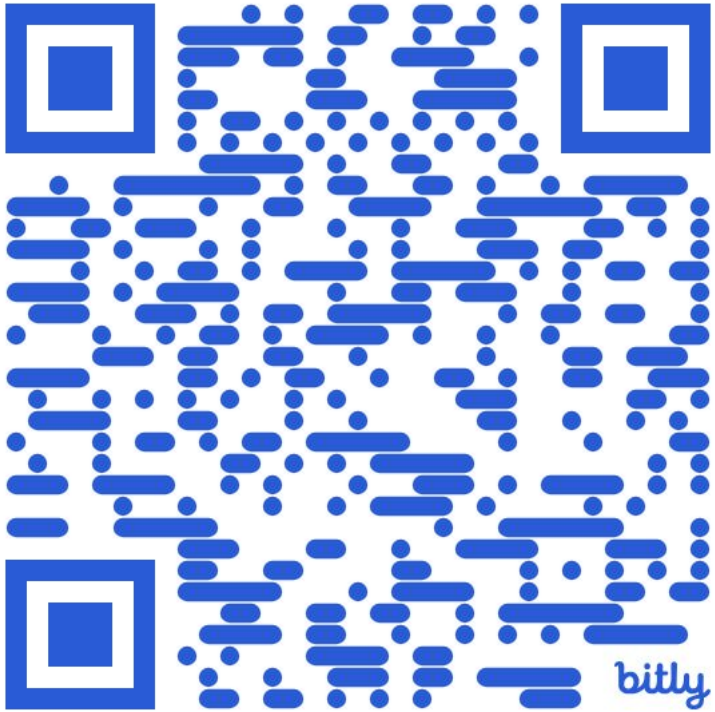
Why am I so late?

Delays and nowcasting for situational awareness



bit.ly/idm-sam

A review of work over 5 years of outbreaks.

Are we being useful?

Are we getting better?

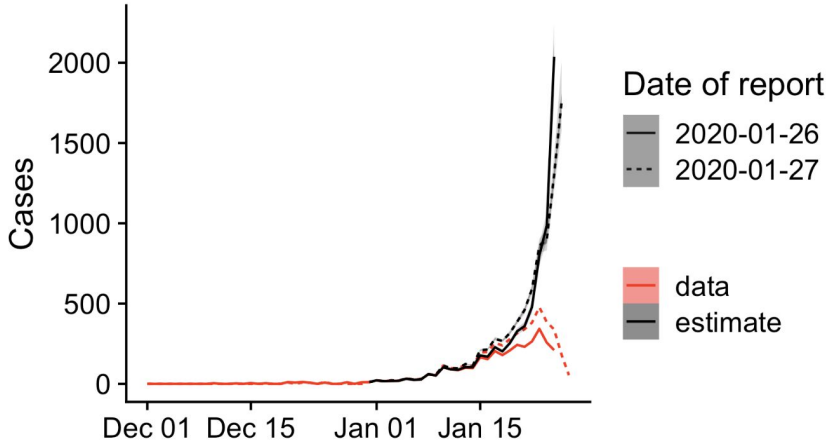
Where it started

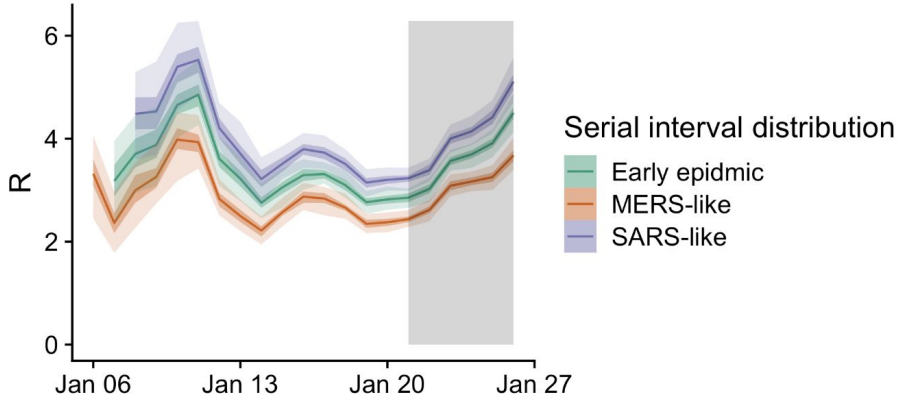
Reporting delays and temporal variation in transmission in China during the 2019-nCoV outbreak

Status: In Progress | First online: 30-01-2020 | Last update: 30-01-2019

Authors: *Sebastian Funk*, Sam Abbott, Stefan Flasche & CMMID COVID-19 working group.*

* corresponding author





Where it started

Temporal variation in transmission during the COVID-19 outbreak

Status: In Progress | First online: 02-03-2020 | Last update: 04-04-2020

Authors: *Sam Abbott*, Joel Hellewell, James D Munday, June Young Chun, Robin N. Thompson, Nikos I Bosse, Yung-Wai Desmond Chan, Timothy W Russell, Christopher I Jarvis, CMMID COVID-19 working group, Stefan Flasche, Adam J Kucharski, Rosalind M Eggo & Sebastian Funk.*

* corresponding author

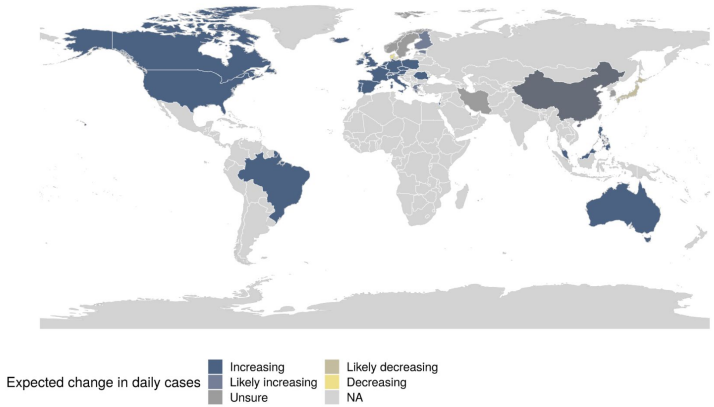


Figure 1: Global map of the expected change in daily cases based on data from the 2020-03-19. Note: only country level estimates are shown.

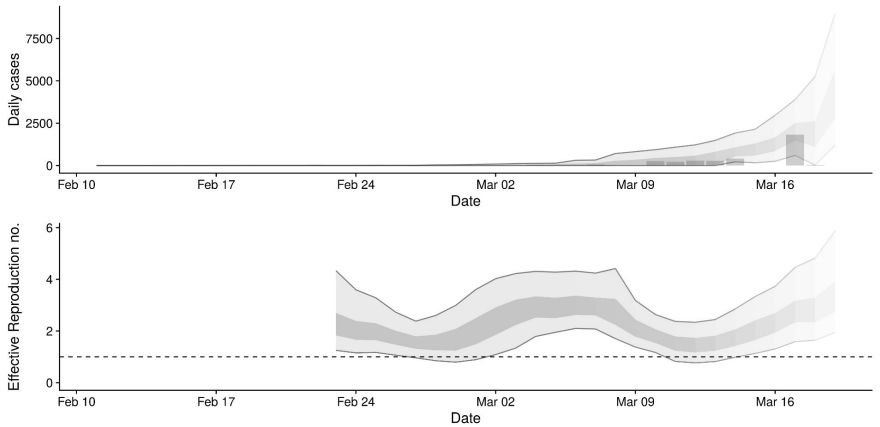
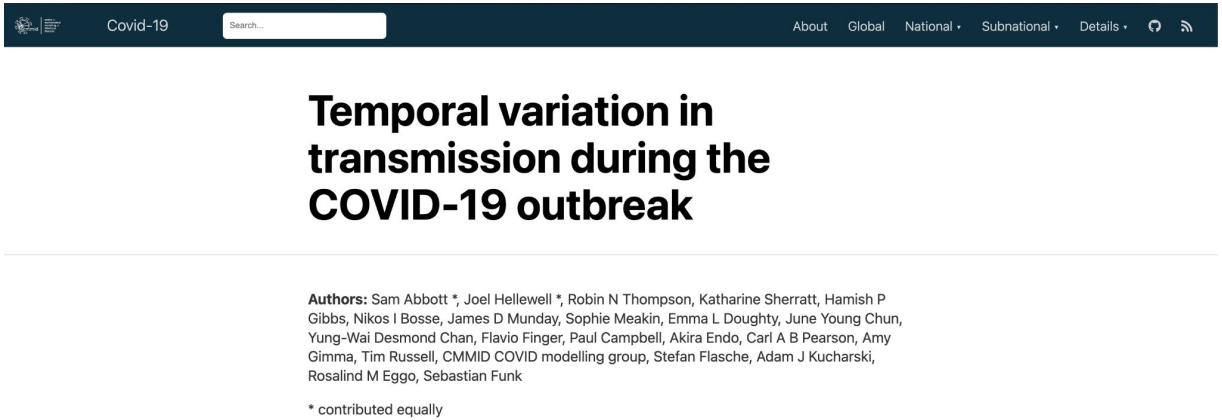


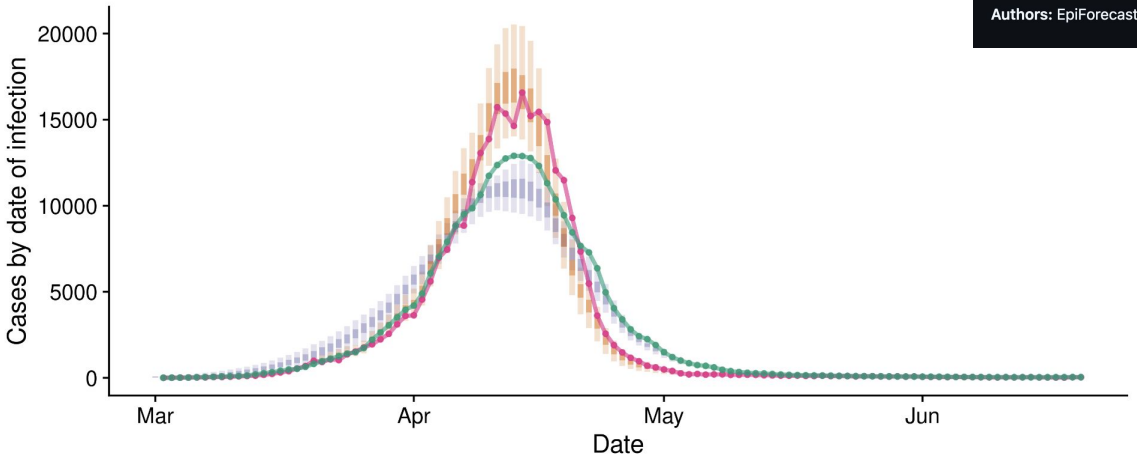
Figure 4: A.) Cases by date of report (bars) and estimated cases by date of onset. B.) Time-varying estimate of the effective reproduction number. Light grey ribbon = 95% credible interval. Dark grey ribbon = the interquartile range. Based on data from the 2020-03-19. Confidence in the estimated values is indicated by shading with reduced shading corresponding to reduced confidence.

Where it started



EpiNow: Estimate realtime case counts and time-varying epidemiological parameters

What went wrong - back sampling delays



Evaluating approaches to backcalculating cases counts by date of infection from cases counts by date of report

Authors: EpiForecasts, CMMID Covid working group, Sebastian Funk

Practical considerations for measuring the effective reproductive number, R_t

Katelyn M. Gostic, Lauren McGough, Edward B. Baskerville, Sam Abbott, Keya Joshi, Christine Tedijanto, Rebecca Kahn, Rene Niehus, James A. Hay, Pablo M. De Salazar, Joel Hellewell, Sophie Meakin, James D. Munday, [···], Sarah Cobey

[view all]

Published: December 10, 2020 • https://doi.org/10.1371/journal.pcbi.1008409

Where it ended

Temporal variation in transmission during the COVID-19 outbreak

Authors: Sam Abbott *, Joel Hellewell *, Robin N Thompson, Katharine Sherratt, Hamish P Gibbs, Nikos I Bosse, James D Munday, Sophie Meakin, Emma L Doughty, June Young Chun, Yung-Wai Desmond Chan, Flavio Finger, Paul Campbell, Akira Endo, Carl A B Pearson, Amy Gimma, Tim Russell, CMMID COVID modelling group, Stefan Flasche, Adam J Kucharski, Rosalind M Eggo, Sebastian Funk

* contributed equally

EpiNow2: Estimate real-time case counts and time-varying epidemiological parameters

Reflections on two years estimating effective reproduction numbers

Over the last two years we have estimated reproduction numbers daily for several thousand locations, presented thes estimates as a curated data set and visualised them at epiforecasts.io/covid. In this post we reflect on this project, summarising its utility, its integration with other projects, unanticipated challenges, and finally whether we would do it again.

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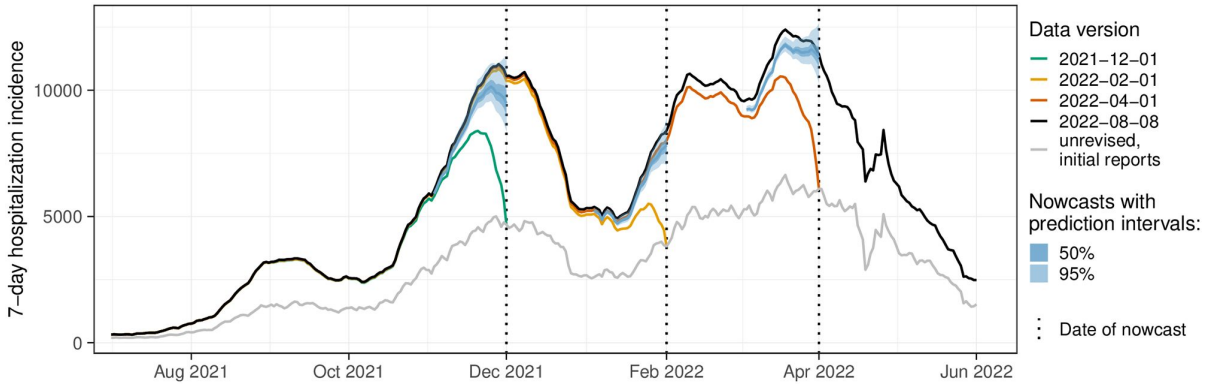
March 25, 2022

DOI
10.59350/8apn9-8h048

What went wrong - right truncation

Collaborative nowcasting of COVID-19 hospitalization incidences in Germany

Daniel Wolffram, Sam Abbott, Matthias an der Heiden, Sebastian Funk, Felix Günther, Davide Hailer, Stefan Heyder, Thomas Hotz, Jan van de Kassteele, Helmut Küchenhoff, Sören Müller-Hansen, Diellë Syliqi, Alexander Ullrich, [...], Johannes Bracher [view all]

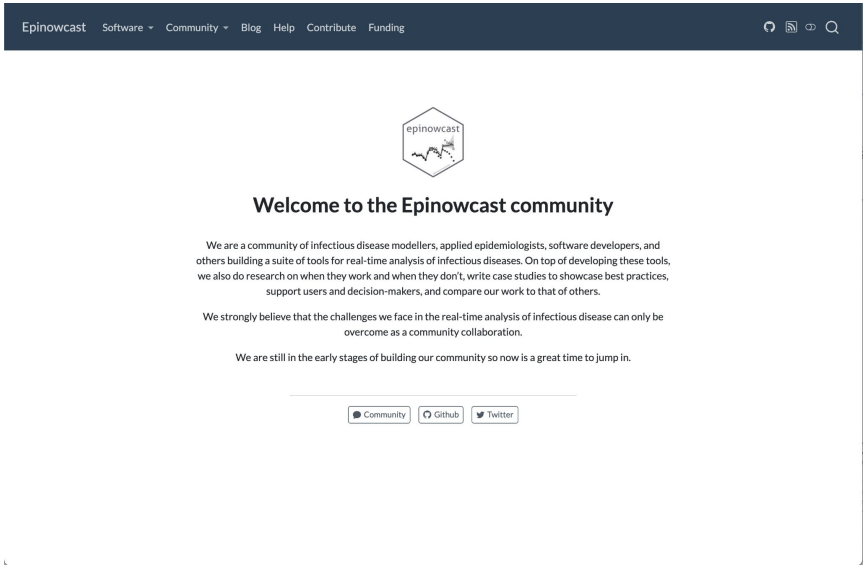


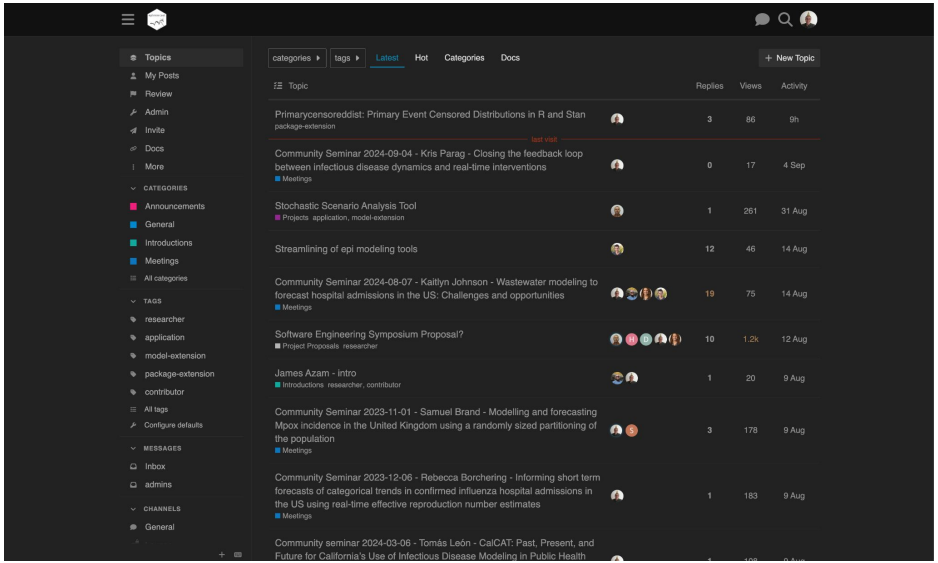
Flexible Hierarchical Nowcasting

Summary

Tools to enable flexible and efficient hierarchical nowcasting of right-truncated epidemiological time-series using a semi-mechanistic Bayesian model with support for a range of reporting and generative processes. Nowcasting, in this context, is gaining situational awareness using currently available observations and the reporting patterns of historical observations. This can be useful when tracking the spread of infectious disease in real-time: without nowcasting, changes in trends can be obfuscated by partial reporting or their detection may be delayed due to the use of simpler methods like truncation. While the package has been designed with epidemiological applications in mind, it could be applied to any set of right-truncated time-series count data.

What went wrong - teamwork





mpox - 2022

Nowcasting examples

This repository contains two example approaches to nowcasting, one using the EpiNow2 package, and one using the epinowcast package which is currently being developed to eventually replace `EpiNow2` for real-time applications.

Nowcasting and forecasting the 2022 U.S. mpox outbreak: Support for public health decision making and lessons learned

Kelly Charniga [a 1], Zachary J. Madewell [b 1], Nina B. Masters [c], Jason Asher [d], Yoshinori Nakazawa [a], Ian H. Spicknall [e]

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RESEARCH ARTICLE

Nowcasting the 2022 mpox outbreak in England

Christopher E. Overton, Sam Abbott, Rachel Christie, Fergus Cumming, Julie Day, Owen Jones, Rob Paton, Charlie Turner, Thomas Ward

Research » Special Paper

Transmission dynamics of monkeypox in the United Kingdom: contact tracing study

BMJ 2022 ; 379 doi: https://doi.org/10.1136/bmj-2022-073153 (Published 02 November 2022)
Cite this as: *BMJ* 2022;379:e073153

Linked Editorial
The dynamics of monkeypox transmission

Article | Related content | Metrics | Responses | Peer review

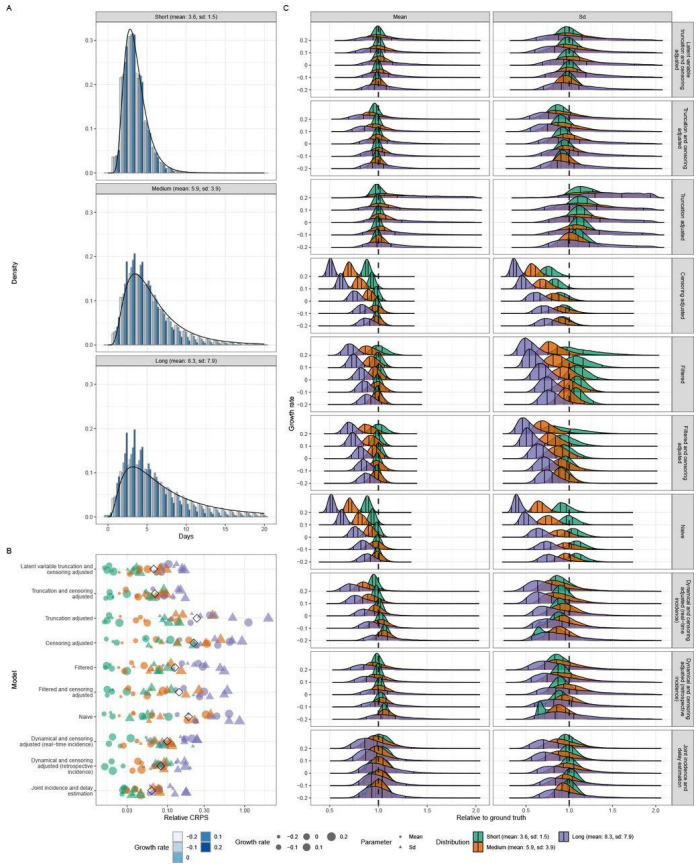
Thomas Ward, head of infectious disease modelling [1], Rachel Christie, senior data scientist [1], Robert S Paton, senior infectious disease modeller [1], Fergus Cumming, deputy director for advanced analytics [1], Christopher E Overton, principal infectious disease modeller [1 2 3]

The dynamics of monkeypox transmission

BMJ 2022 ; 379 doi: https://doi.org/10.1136/bmj.o2504 (Published 02 November 2022)
Cite this as: *BMJ* 2022;379:o2504

Linked Research
Transmission dynamics of monkeypox in the United Kingdom

What went wrong - delay distributions in outbreaks



Estimating epidemiological delay distributions for infectious diseases

Sang Woo Park, Andrei R. Akhmetzhanov, Kelly Charniga, Anne Cori, Nicholas G. Davies, Jonathan Dushoff, Sebastian Funk, Katie Gostic, Bryan Grenfell, Natalie M. Linton, Marc Lipsitch, Adrian Lison, Christopher E. Overton, Thomas Ward, Sam Abbott

doi: https://doi.org/10.1101/2024.01.12.24301247

What went wrong - delay distributions in outbreaks

Bias	Interval censoring	Right truncation	Dynamical bias
Details	The exact timing of the primary event or secondary event (single interval censoring) or both events (double interval censoring) is unknown (e.g., except for experimental studies, exposure is usually reported as a date or range of dates, rather than a time of day).	Right truncation is a type of sampling bias. It arises because only cases whose secondary event has occurred can be observed. In an ongoing epidemic, right truncation biases the incubation period and serial interval toward shorter intervals because individuals with longer incubation periods may not have developed symptoms or have been reported yet.	Dynamical bias is another type of sampling bias that can be present when case ascertainment is based on the secondary event. It is related to epidemic dynamics: during a growth phase, cases that developed symptoms recently are overrepresented in the observed data, while during a declining phase, these cases are underrepresented. This means that the backward distribution is not representative of the forward distribution during these periods.
Impact	Not accounting for interval censoring can lead to biased estimates of a delay's standard deviation. Incorrectly accounting for it can also bias the mean.	Not accounting for right truncation can lead to underestimation of the mean delay [23].	Not adjusting for dynamical bias when estimating the forward distribution from the backward distribution can lead to under- or overestimation of delay intervals depending on whether the epidemic is in a growth or declining phase, respectively.
Diseases for which this bias has been considered in analyses	Incubation period: mpox [36]; Zika [96]; COVID-19 [97]; 6 vector-borne diseases [88] Serial interval: mpox [36]	Incubation period: COVID-19 [25,97] Serial interval: mpox [24]	Incubation period: COVID-19 [89] Serial interval: mpox [24]
Possible solutions	Use methods, such as Reich and colleagues [44], that adjust for double interval censoring; however, this method does not adjust for right truncation. Alternatively, use Ward and colleagues' double interval censoring and right truncation adjusted model, which adjusts for interval censoring and right truncation simultaneously [23,24].	Use an approximate latent variable method, such as Ward and colleagues' double interval censoring and right truncation adjusted model [24] or similar alternatives [23].	If both primary and secondary event dates are known and the incidence of primary events is changing exponentially at a constant rate, it is possible to use the approach of Verity and colleagues, Britton and colleagues, and Park and colleagues [26,46,47] to adjust for dynamical bias; however, uncertainty in both growth rate estimates and observed delays need to be taken into account carefully with this approach and the assumption of constant growth rates may not be met in practice. Park and colleagues present a version of this method that allows for a time-varying growth rate, but it requires untruncated incidence data or assumptions to be made about the recent growth rate [23]. For most settings, considering the forward distribution and accounting for right truncation is recommended.
Practices to avoid	Do not adjust for single censoring if the data are doubly interval-censored as this will result in a biased mean [23]. Note that even if both primary and secondary events are reported to have occurred on a single date, the data should be considered doubly interval-censored. Do not use a midpoint imputation rule on interval-censored data as this may introduce bias [50].	Do not adjust for right truncation and dynamical bias at the same time early in an outbreak as doing this can lead to overadjustment of the downward bias and therefore to overestimation of the delay [23].	Avoid adjusting for right truncation and dynamical bias at the same time [23]. When analyzing the forward distribution, adjust for right truncation; when analyzing the forward distribution via the backward distribution, adjust for dynamical bias. We recommend the former when possible.

https://doi.org/10.1371/journal.pcbi.1012520.t001

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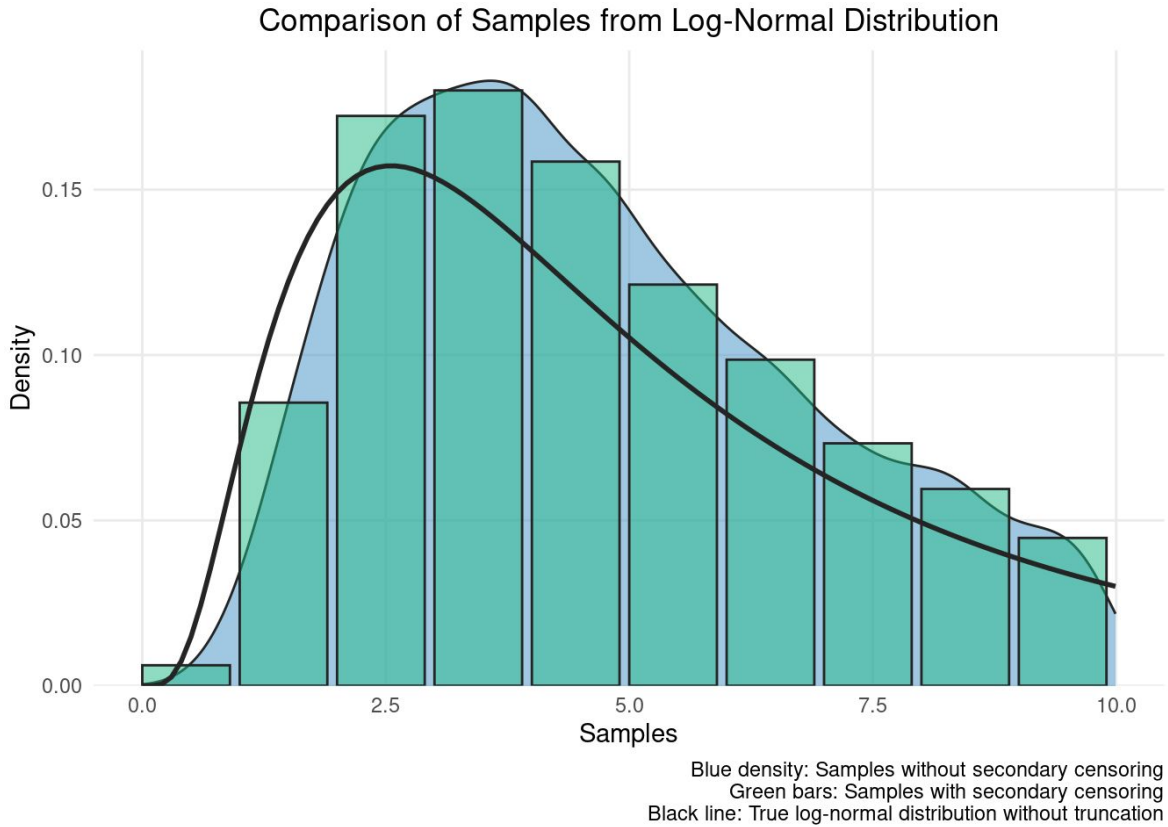
PERSPECTIVE

Best practices for estimating and reporting epidemiological delay distributions of infectious diseases

Kelly Charniga, Sang Woo Park, Andrei R. Akhmetzhanov, Anne Cori, Jonathan Dushoff, Sebastian Funk, Katelyn M. Gostic, Natalie M. Linton, Adrian Lison, Christopher E. Overton, Juliet R. C. Pulliam, Thomas Ward, Simon Cauchemez, Sam Abbott

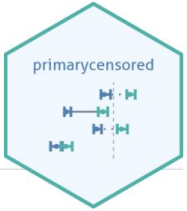
Published: October 28, 2024 • https://doi.org/10.1371/journal.pcbi.1012520

Where it ended? Double censoring and right truncation



Where it ended? Double censoring and right truncation

Primary event censored distributions



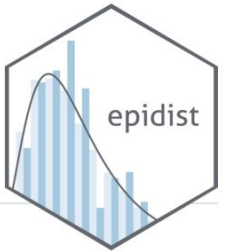
r-universe 1.0.0 | License MIT | contributors 6 | DOI 10.5281/zenodo.14001749

Summary

Provides functions for working with primary event censored distributions and 'Stan' implementations for use in Bayesian modeling. Primary event censored distributions are useful for modeling delayed reporting scenarios in epidemiology and other fields (Charniga et al. (2024) doi:10.48550/arXiv.2405.08841). It also provides support for arbitrary delay distributions, a range of common primary distributions, and allows for truncation and secondary event censoring to be accounted for (Park et al. (2024) doi:10.1101/2024.01.12.24301247). A subset of common distributions also have analytical solutions implemented, allowing for faster computation. In addition, it provides multiple methods for fitting primary event censored distributions to data via optional dependencies.

Where it ended? Double censoring and right truncation

Estimate epidemiological delay distributions with `brms`



Warning! This package is a prototype and is under active development. Breaking changes are likely.

Summary

Understanding and accurately estimating epidemiological delay distributions is important for public health policy. These estimates directly influence epidemic situational awareness, control strategies, and resource allocation. In this package, we provide methods to address the key challenges in estimating these distributions, including truncation, interval censoring, and dynamical biases. Despite their importance, these issues are frequently overlooked, often resulting in biased conclusions.

Mpox clade 1

- Are recent delay distribution estimates accounting for double censoring and right truncation?

- Are real time considerations like delayed reporting and changing ascertainment being incorporated into more complex models that are being developed?

- If not why not?

What went wrong - composable modelling

EpiAware.jl

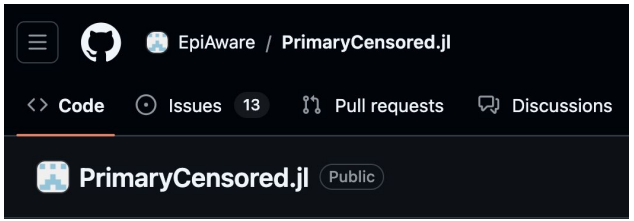
Infectious disease situational awareness modelling toolkit for Julia.

Package Features

- Flexible: The package is designed to be flexible and extensible, and to provide a consistent interface for fitting and simulating models.
- Modular: The package is designed to be modular, with a clear separation between the model and the data.
- Extensible: The package is designed to be extensible, with a clear separation between the model and the data.
- Consistent: The package is designed to provide a consistent interface for fitting and simulating models.
- Efficient: The package is designed to be efficient, with a clear separation between the model and the data.

Interoperability of statistical models in pandemic preparedness: principles and reality

George Nicholson [1,+], Marta Blangiardo [2,+], Mark Briers [3,4], Peter J Diggle [7,+], Tor Erlend Fjelde [9,+], Hong Ge [9,+], Robert J B Goudie [8], Radka Jersakova [5,+], Ruairidh E King [6,+], Brieuc C L Lehmann [1,+], Ann-Marie Mallon [6,+], Tullia Padellini [2,+], Yee Whye Teh [1,+], Chris Holmes [1,5,6,+,#], Sylvia Richardson [5,8,+,#]



Thanks for listening!

Questions?

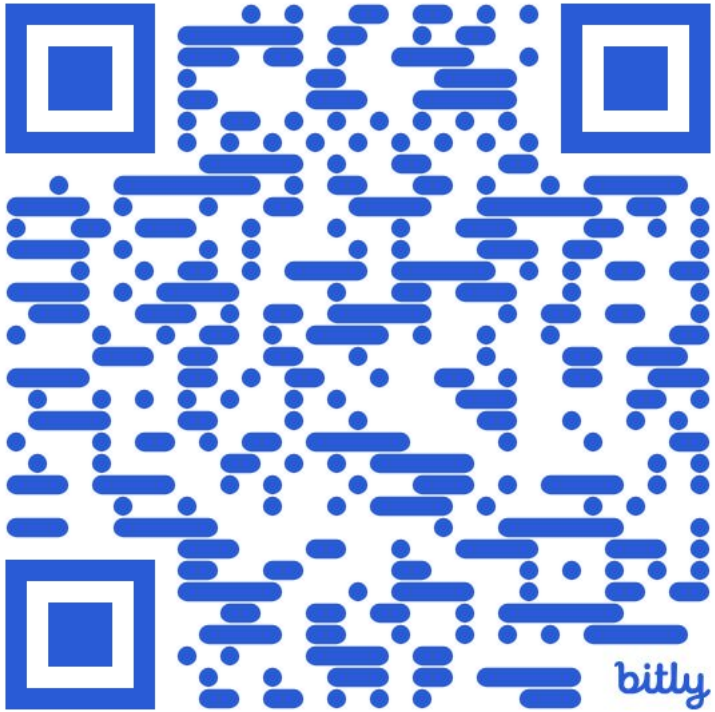
Where its going

- Expanding epidist to include methods for generation time and case fatality ratio estimation.

- Continuing to support and grow the epinowcast community project and related R based tools and methods

- Expanding the EpiAware ecosystem with more modules including:
  - wastewater modelling
  - viral load modelling
  - reporting triangle modelling
  - support for differential equation infection processes
  - deep learning compatibility.

- Methods development and evaluation for all of the above



bit.ly/idm-sam