

Abbott et al.

MMED 2023

Sam Abbott

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“Could the faculty/faculty observers introduce themselves” - Anonymous

“Include background, challenges you faced, and relationship to public health” - Anonymous

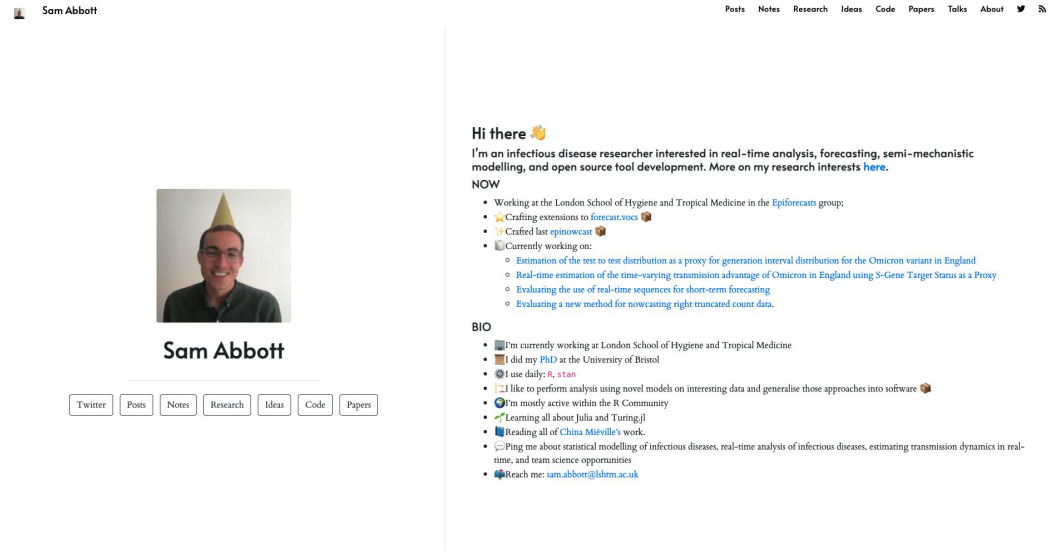
Overview

- Who am I - a primer
- Real-time analysis case studies from the COVID-19 pandemic
- Real-time estimation of the effective reproduction number
- My pandemic (a very abridged tail)
- Epinowcast: Flexible hierarchical nowcasting

Who am I - primer

I'm an infectious disease researcher interested in real-time analysis, forecasting, semi-mechanistic modelling, and open source tool development.

- Consultant with the Centre for forecasting and outbreak analysis at the US CDC
- Research Fellow (i.e., a postdoc) at the London School of Hygiene and Tropical Medicine
- PhD in modelling Tuberculosis and the optimal use of the BCG vaccine
- Background in mathematical biology, mathematics, and theoretical physics



The image shows a GitHub profile for Sam Abbott. At the top, the name "Sam Abbott" is displayed next to a small profile picture icon. Below this is a navigation bar with links for "Posts", "Notes", "Research", "Ideas", "Code", "Papers", "Talks", and "About". The main content area features a profile picture of Sam Abbott wearing a yellow party hat. Below the photo is the name "Sam Abbott" and a row of social media links: "Twitter", "Posts", "Notes", "Research", "Ideas", "Code", and "Papers". The bio section begins with "Hi there 🍷" and describes him as an infectious disease researcher. It lists his current work at the London School of Hygiene and Tropical Medicine, his PhD at the University of Bristol, and his interests in performing analysis using novel models and generalising approaches into software. It also mentions his involvement in the R Community and his learning about Julia and Turing.jl. The bio concludes with a link to his research interests and a reach link to his GitHub profile.

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Real-time analysis case studies from the COVID-19 pandemic

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An 80% right paper before a policy decision is made is worth ten 95% right papers afterwards, provided the methodological limitations imposed by doing it fast are made clear.

Case studies

Routine

- Effective reproduction number estimation
- Short-term forecasting
- Nowcasting

Reactive

- Estimating the transmission advantage of variants of concern
- Estimating changes in the generation time

Real-time analysis case studies from the COVID-19 pandemic

Routine

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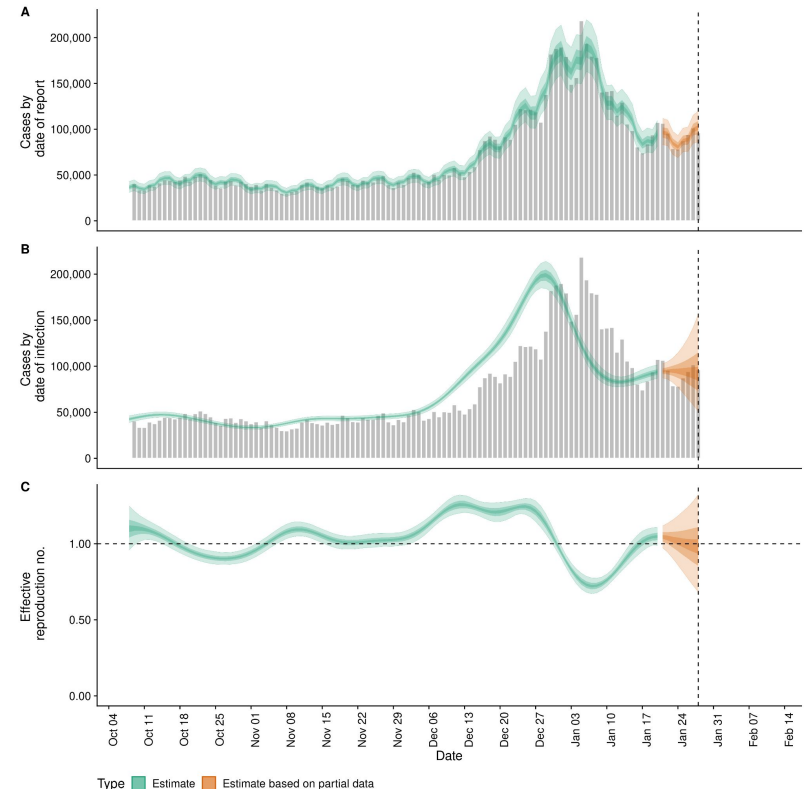
Reactive

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Effective reproduction number estimation

The average number of secondary infections produced by a single infected person.

- A helpful metric to track transmission (?)
- Tricky to estimate as depends on infections and on the interval between primary and secondary infections.
- Estimating using various methodologies from February 2020.
- Estimates submitted as part of the SPI-M consensus estimate each week for two years.
- Estimates also published each day for over 1000 locations from April 2020 to March 2022 on epiforecasts.io/covid w/ 1 million+ views.
- Used by various governments/WHO/CDC etc.



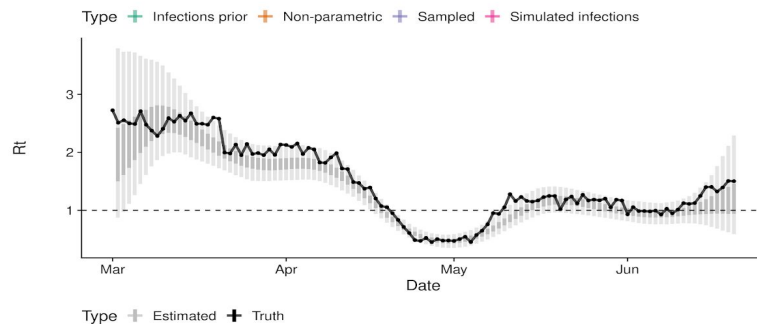
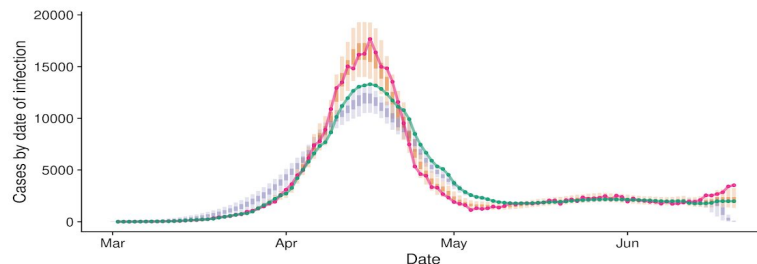
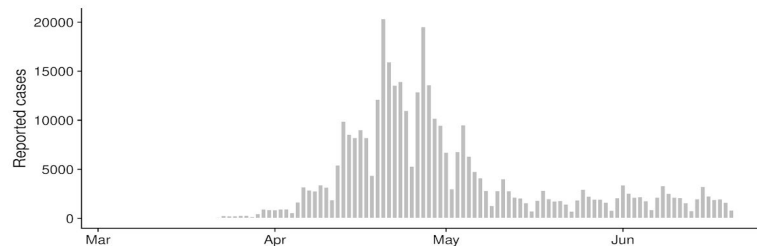
Effective reproduction number estimation

Key Challenges

- We care about linking policy changes with changes in transmission but only observe delayed proxies like reported cases and deaths.
- Surveillance data subject to a range of difficult to account for biases.
- Estimation at scale in real-time is currently computationally challenging.

Mitigations

- Generative model of expected infections.
- Worked with the **Met Office** to develop production ready code using resources donated by **Microsoft Azure**.
- Estimate independently on a range of data sources.



Effective reproduction number estimation

Reflections on two years estimating effective reproduction numbers

Over the last two years we have estimated reproduction numbers daily for several thousand locations, presented these 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.

AUTHORS

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Sebastian Funk [↗](#)

AFFILIATION

London School of Hygiene and Tropical Medicine

London School of Hygiene and Tropical Medicine

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March 25, 2022

On this page

[An attempt to design a useful resource for situational awareness](#)

[Assessing utility](#)

[Feeding into analysis pipelines](#)

[Unanticipated challenges](#)

[Back to 2020...would we do it again?](#)

[Addendum 13/6/2022](#)

[Edit this page](#)

[View source](#)

Blog post: epiforecasts.io/posts/2022-03-25-rt-reflections/

Lessons learnt

- Routine work can be a useful way to gain situational awareness.
- Real-time analysis often builds on analyses, tools, and data pipelines previously developed.
- Outputs are easiest to use when they are **robust, modular, evaluated, and available**.
- Combining estimates from a range of sources and methodologies are likely to improve decision making versus using a single analysis.
- Work that is good enough tends to be work that is available.

Case studies

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- **Short-term forecasting**
- Nowcasting

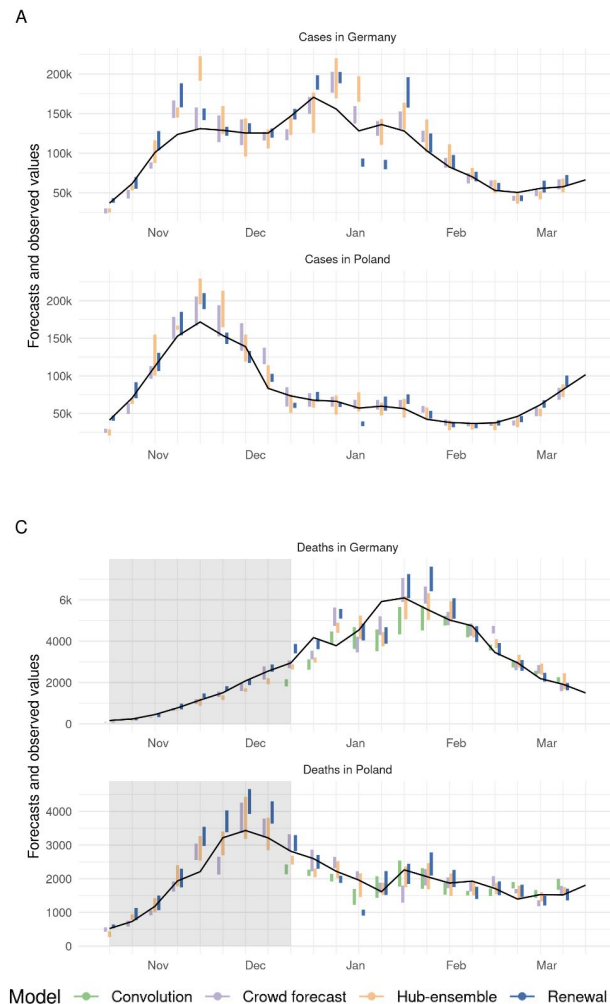
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Short-term forecasts

What do we think will happen to reported metrics over the next 1-4 weeks

- Using the reproduction number renewal model and similar discrete convolution models.
- Submitting to the ECDC and CDC forecasting hubs weekly as well as to SPI-M 3 times a week until mid 2020.
- Performed wellish compared to other models but outperformed by an all-model ensemble.
- Also outperformed by a human judgement model.
- All forecasts struggle to account for policy changes and behavioural changes.



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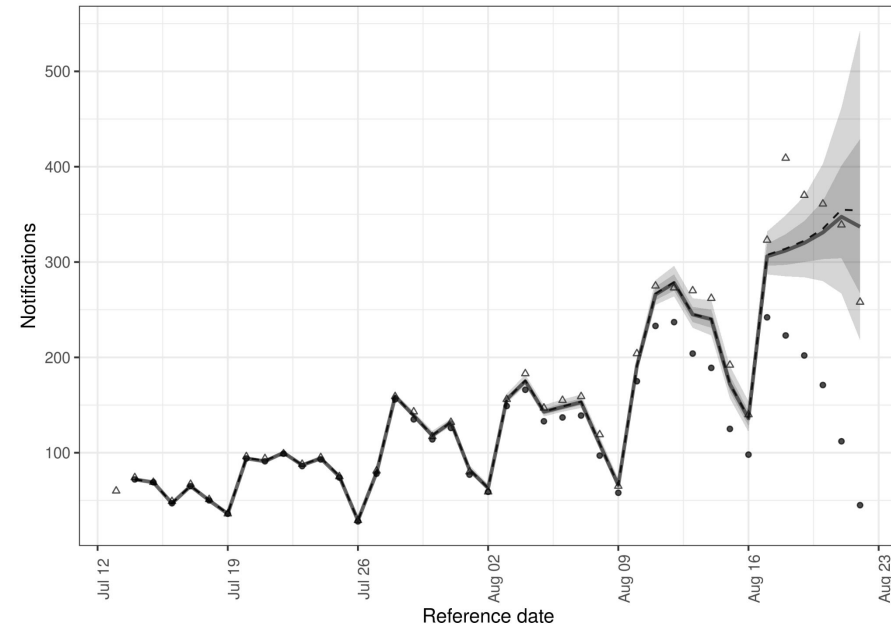
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Nowcasts

What is happening now to metrics we partially observe

- **International collaboration** estimating 7-day hospital admissions by date of positive test in Germany (the key metric used by decision makers).
- Statistical approach is to decompose the model into forecast and reporting delay components.
- Multi-method ensemble outperforms any single model.
- Nowcasting is conceptually difficult to understand and so potentially under used.
- Open access tools, such as **epinowcast**, make access easier.



Bracher et al. covid19nowcasthub.de

Wolffram et al: epinowcast.org/posts/2023-05-08-collab-nowcasting-covid19-germany

Abbott et al. github.com/epiforecasts/epinowcast

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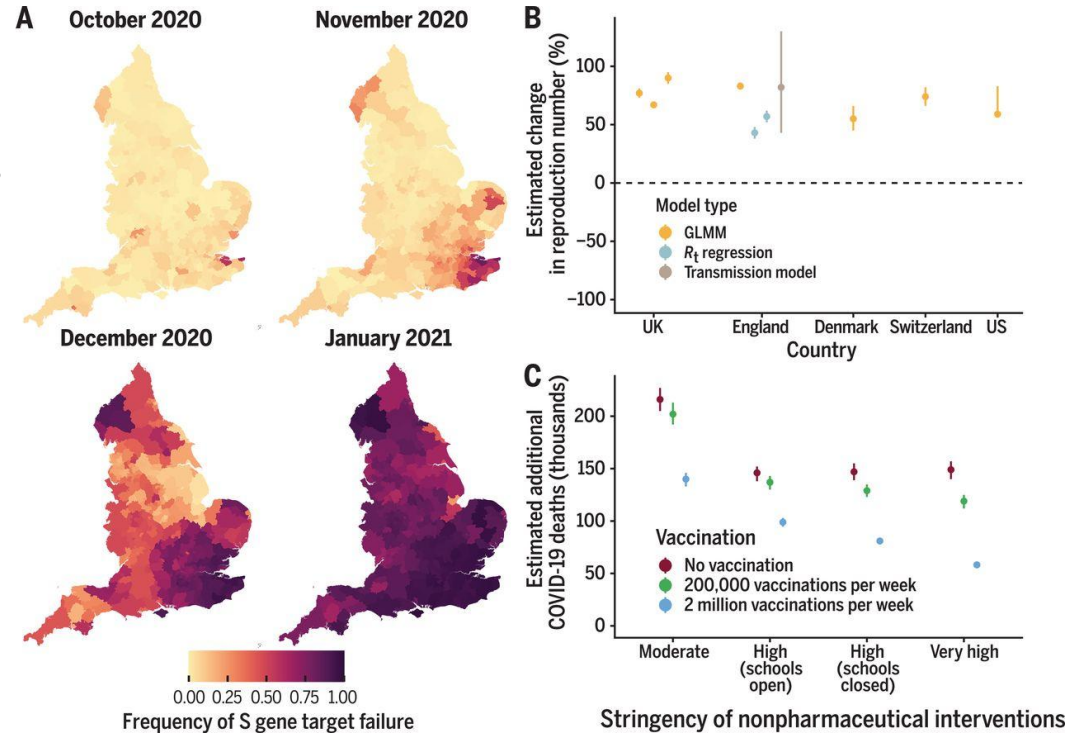
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Estimating the transmission advantage of Alpha

How much more transmissible is Alpha than wild-type?

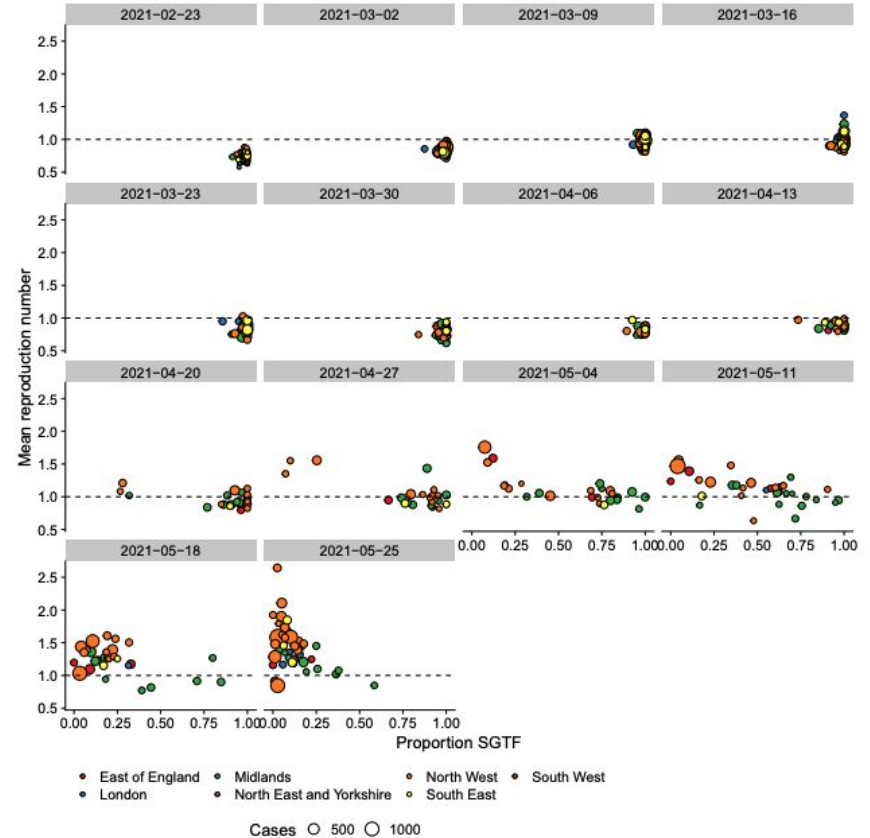
- Part of a multi-method approach by Davies et al.
- Used **reproduction number estimates** by Lower-Tier local authority as "data" + S-gene target failure status (SGTF) as a proxy for variant status.
- Estimated the transmission advantage using an extended regression model adjusted for confounders
- Work done between December 20th 2020 and January 1st 2021.



Estimating the transmission advantage of Delta

How much more transmissible is Delta than Alpha?

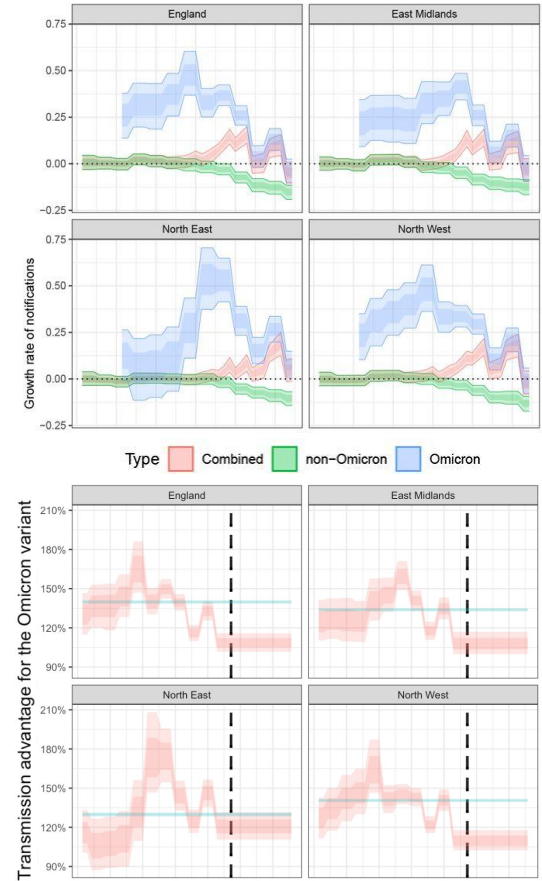
- Repurposed the approach used for Alpha using **reproduction number estimates** as data.
- Extended the methodology to include uncertainty for the reproduction number estimates and SGTF status.
- Estimates combined with others as part of the SPI-M consensus statement.



Estimating the transmission advantage of Omicron

How much more transmissible is Omicron than Delta and does it vary over time?

- **Early evidence** from South Africa suggested that Omicron may be more successful than Delta at escaping prior immunity.
- This would be identifiable as variation over time in the transmission advantage (in the model we were using). Our previous analysis didn't support this.
- Repurposed methodology developed to evaluate the role of sequences for forecasting ([forecast.vocs](https://forecast.vocs.org) 📦).
- Identified a reduction in transmission advantage prior to Christmas (rather than the increase expected due to immune escape).
- A real-time report developed, submitted to SPI-M, and updated daily from the 18th of December 2021 to the 1st of January 2022.



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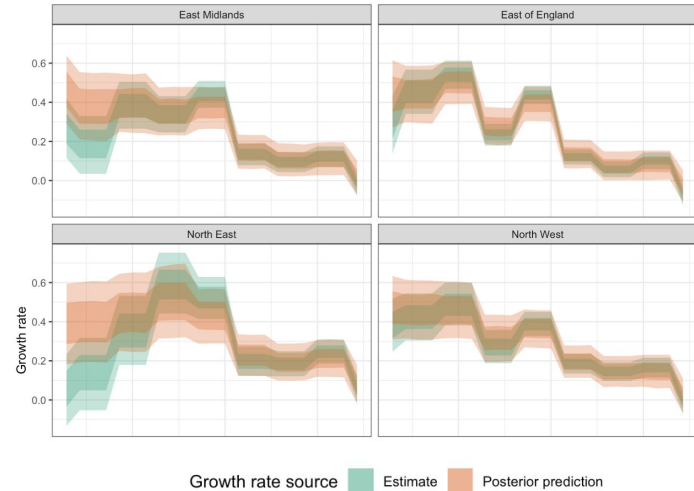
- Estimating the transmission advantage of variants of concern
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Estimating the generation time of Omicron

Is Omicron's generation time shorter than Delta's?

- Observed reduction in transmission advantage could indicate a shorter generation time.
- This is due to the relationship between the daily growth rate and the reproduction number.
- Used growth rates for Omicron and Delta to explore this and found that a shorter generation time was plausible.
- Findings supported by a study from UKHSA using household contact data.
- Results available in early January and formed part of the SPI-M consensus statement.

$$R = \left(1 + \bar{G}kr\right)^{\frac{1}{k}}$$



Park et al. medRxiv, 2021, DOI: [10.1101/2021.05.03.21256545](https://doi.org/10.1101/2021.05.03.21256545)

Abbott et al. medRxiv, 2021, DOI: [10.1101/2022.01.08.22268920](https://doi.org/10.1101/2022.01.08.22268920)

Park et al. medRxiv, 2022, DOI: [10.1073/pnas.222188712](https://doi.org/10.1073/pnas.222188712)

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Real-time analysis case studies from the COVID-19 pandemic

Summary

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Lessons learnt

- Higher standards can be achieved via **teamwork**, more **pre-emptive work**, and **evaluation**. These are currently all **poorly incentivised**.
- **Real-time analysis is hard** and those doing it **need to be well trained** in statistical methodology, software engineering, and public communication of limitations.
- This skillset is **poorly rewarded by traditional academic incentives** and **difficult to acquire** through currently available training.

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Real-time estimation of the effective reproduction number

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Overview



Overview

Challenges

Tools

Case studies

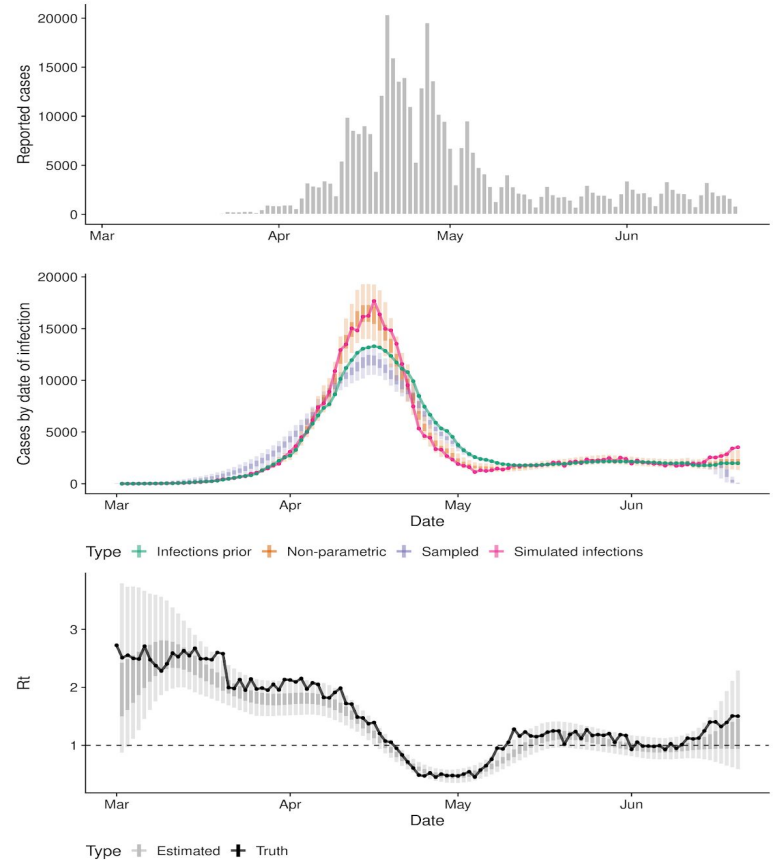
What is left to do?

Summary

Effective reproduction number estimation

Objectives

- Develop a model that can be used for real-time surveillance, nowcasting, and short-term forecasting.
- Include known epidemiological structure of the infection and reporting process (i.e., delayed reporting, partial ascertainment, day of week effects).
- The model should include a parameter that is referenced to the infection process and that can be used to compare disparate surveillance data source.
- The model should ideally capture changes in trend as quickly as possible to make it useful for situational awareness.



Effective reproduction number estimation

EpiNow2 1.3.3.10 Home News Functions

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

License MIT contributors 12 PRs welcome commits since v1.3.2 85 DOI 10.5281/zenodo.5036949

This package estimates the time-varying reproduction number, growth rate, and doubling time using a range of open-source tools ([Abbott et al.](#)), and current best practices ([Gostic et al.](#)). It aims to help users avoid some of the limitations of naive implementations in a framework that is informed by community feedback and is under active development.

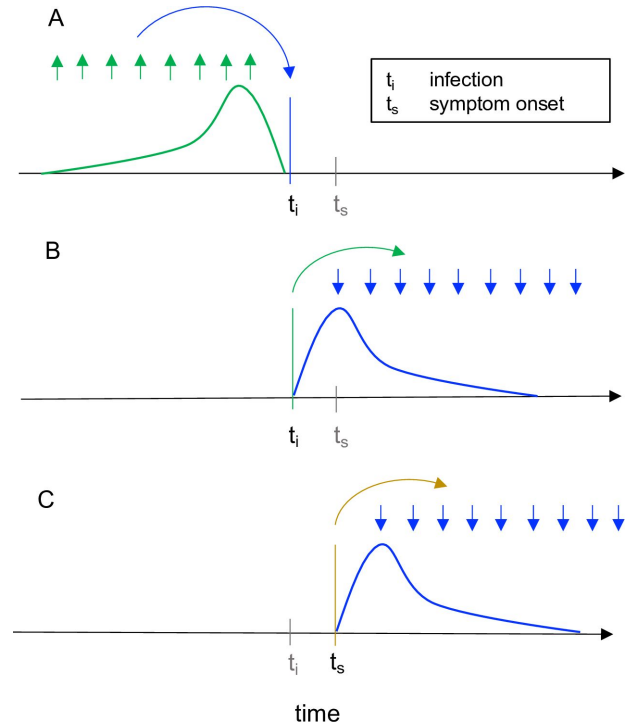
How do we define the reproduction number?

Instantaneous reproduction number

- Transmission at a specific point in time
- Backwards looking
- Can be derived from compartmental models (i.e SEIR)
- Real-time method
- Potentially useful for understanding how transmission changes at a given time-point.

$$R_t^{\text{inst}} = \beta(t)S(t)D$$

$$R_t = \frac{I_t}{\sum_{s=1}^t I_{t-s}W_s},$$

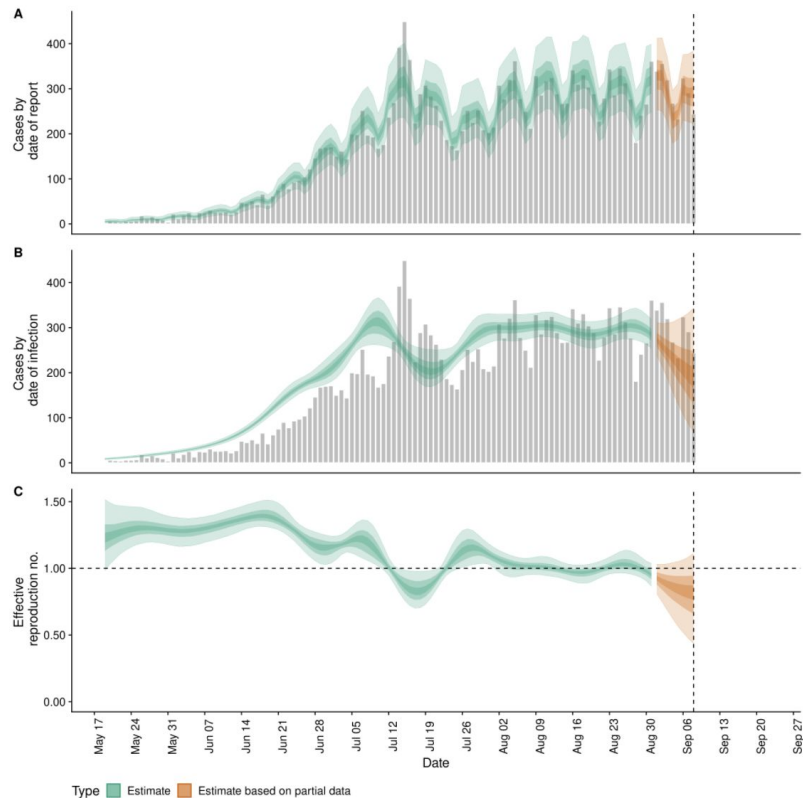


Practical considerations for measuring the effective reproductive number, R_t

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]

Our general approach

- Bayesian approach combining nowcasting and R estimation
- Uncertain generation interval estimates allowing for negative serial interval
- Latent process for estimating I_t
- Negative binomial reporting with multiplicative day-of-the-week effect
- R_t estimates with correlation between R_{t+1} and R_t based on a Gaussian Process prior (with other options).



The model

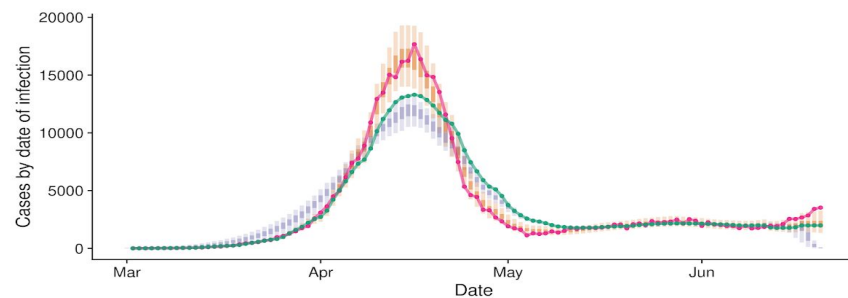
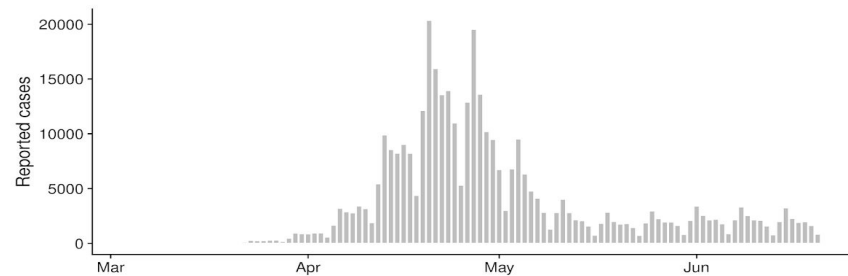
$$\log R_t = \log R_{t-1} + GP_t$$

$$I_t = R_t \sum_{\tau=1}^{15} w(\tau | \mu_w, \sigma_w) I_{t-\tau}$$

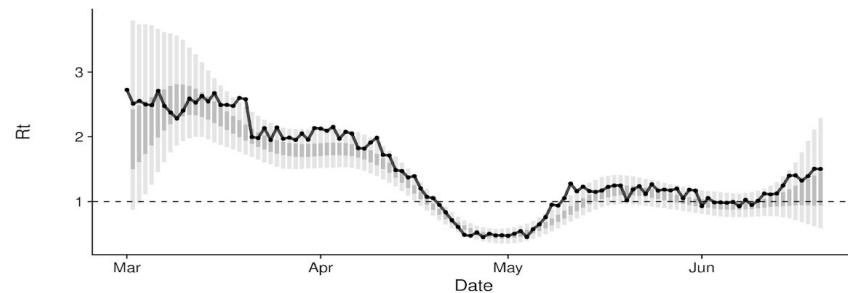
$$O_t = \sum_{\tau=0}^{15} \xi_O(\tau | \mu_{\xi_O}, \sigma_{\xi_O}) I_{t-\tau}$$

$$D_t = \alpha \sum_{\tau=0}^{15} \xi_D(\tau | \mu_{\xi_D}, \sigma_{\xi_D}) O_{t-\tau}$$

$$C_t \sim \text{NB}(\omega_{(t \bmod 7)} D_t, \phi)$$



Type + Infections prior + Non-parametric + Sampled + Simulated infections



Type + Estimated + Truth

Method: doi.org/10.12688/wellcomeopenres.16006.2

Stan code: git.io/JUxRt

Real-time estimation of the effective reproduction number?

Challenges

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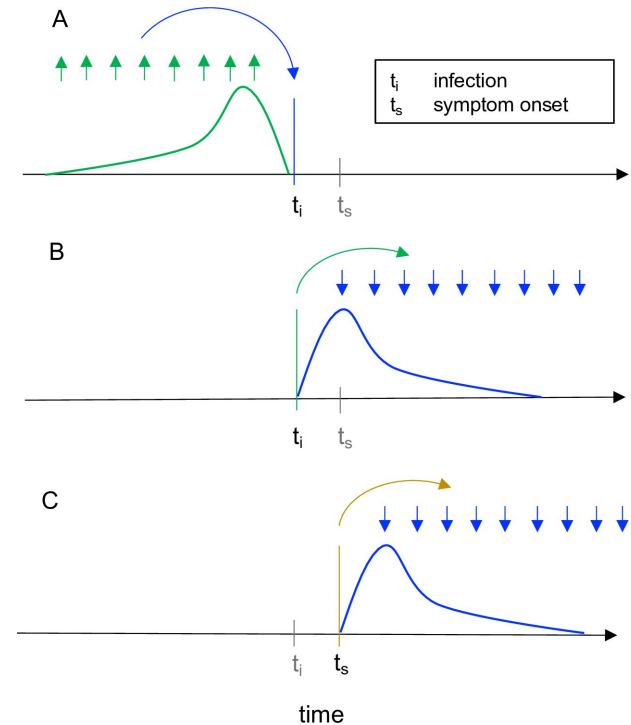
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What are we actually trying to do?

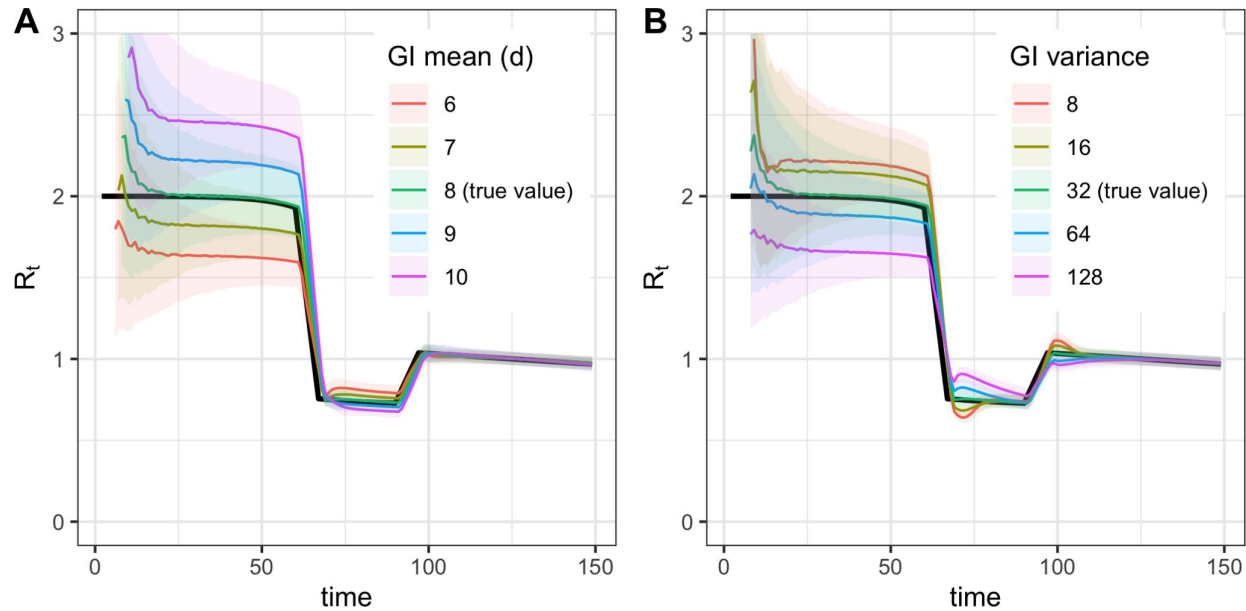
- What kind of reproduction number are we estimating (case, instantaneous etc).
- Are we trying to estimate the reproduction number for the true latent infection process or using observed data as a proxy?
- Do we want a non-parametric estimate, a forecast of future transmission, or an understanding of the impact of NPIs etc.
- What do we a priori believe about how the reproduction number and generation time evolve over time.



Practical considerations for measuring the effective reproduction number, R_t

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Generation interval misspecification

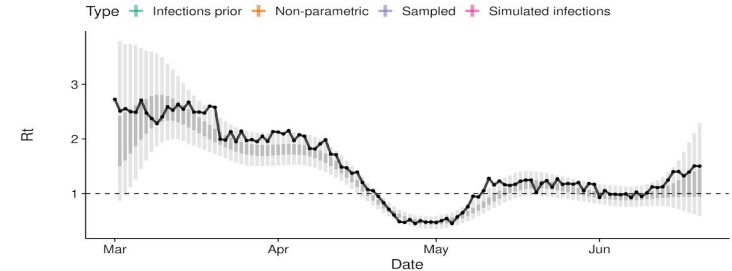
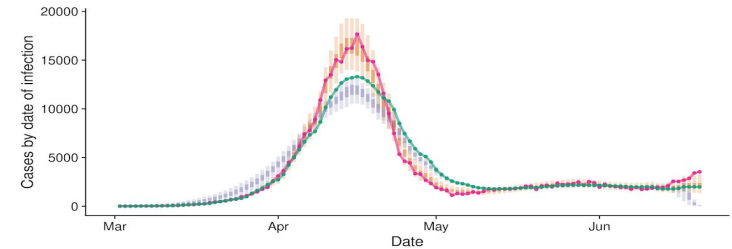
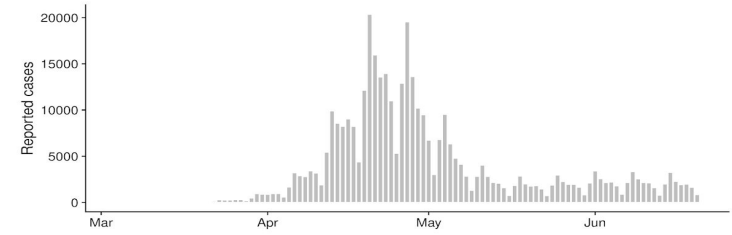
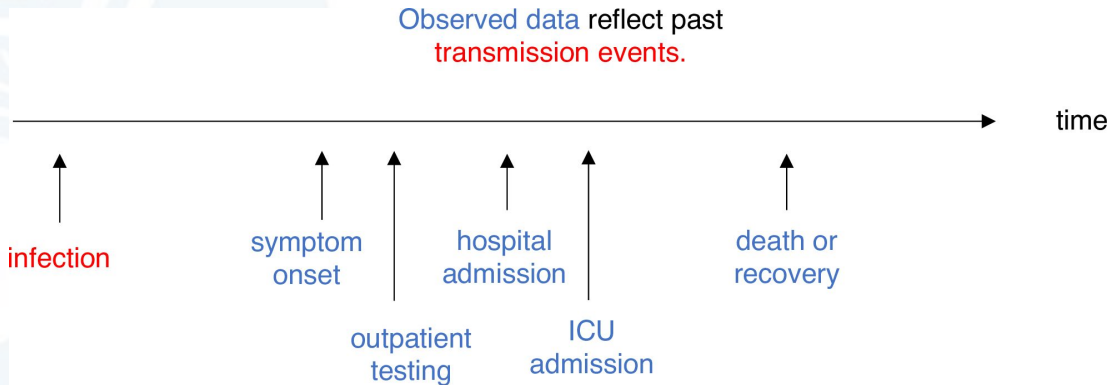


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Adjusting for delays

We observe some later proxy for infections delayed by a mixture delay distributions and observation processes



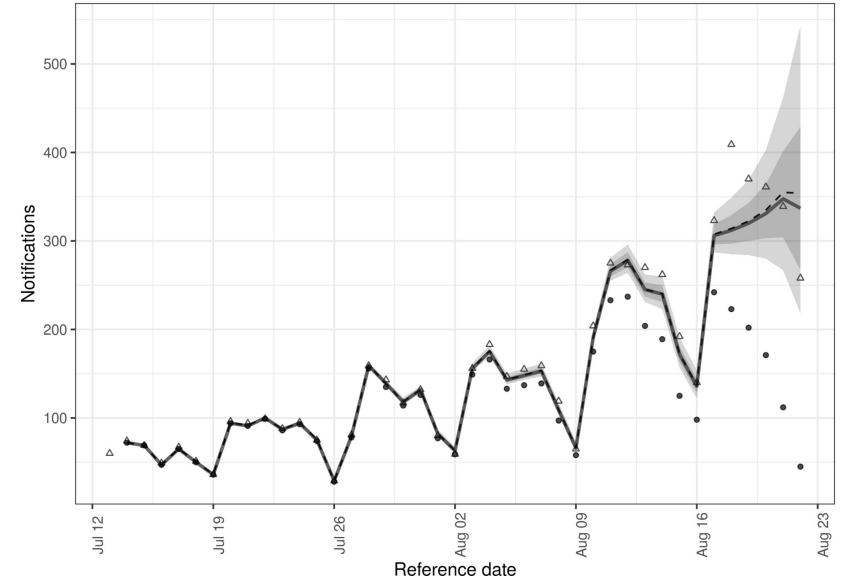
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Adjusting for right truncation

Incoming data can be delayed meaning what we currently observed isn't what we will ultimately observe.

Equally as infections are observed via a delay after reconstructing them they are also not fully observed.



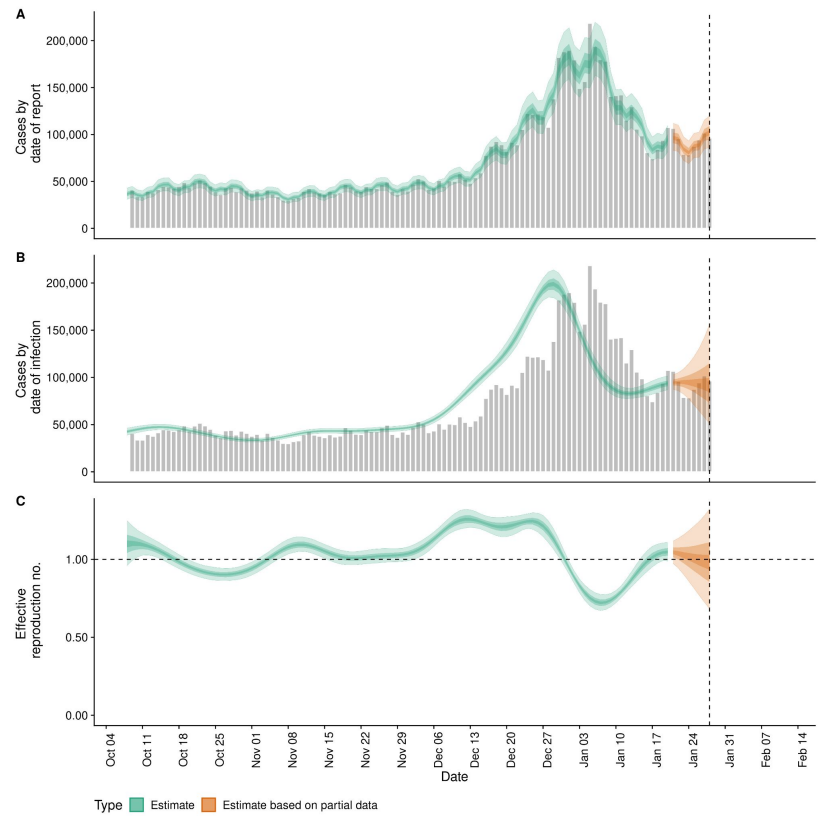
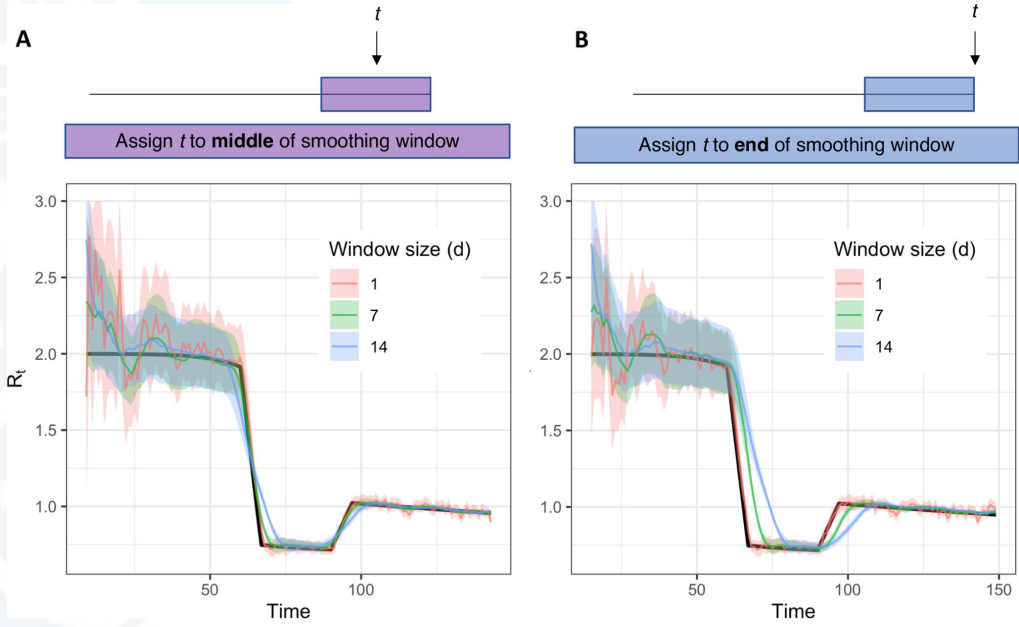
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Published: December 10, 2020 • <https://doi.org/10.1371/journal.pcbi.1008409>

How to smooth

How does the reproduction number evolve over time and how much of that do we want to include in our estimates?



Practical considerations for measuring the effective reproductive number, R_t

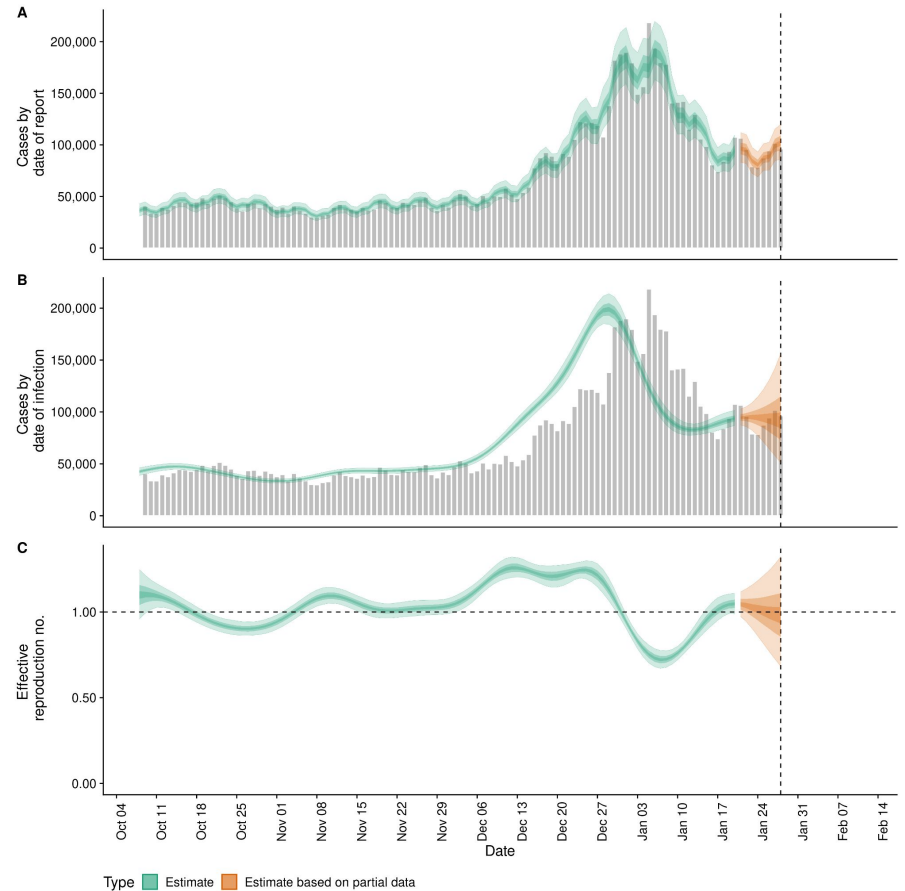
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Retrospective or real-time?

Real-time = Orange.

This is computationally expensive to care about.

$$\log R_t = \log R_{t-1} + GP_t$$



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Epidemia - Hierarchical regression + flexible model options



epidemia

Flexibly specify and fit Bayesian, regression-oriented models for infectious diseases. The implemented models define a likelihood for all observed data while also explicitly modeling transmission dynamics: an approach often termed as *semi-mechanistic*. Multiple regions can be modeled simultaneously with multilevel models. Key epidemiological quantities, including reproduction numbers and latent infections, may be estimated within the framework. The models may be used to evaluate the determinants of changes in transmission rates, including the effects of control measures. Epidemic dynamics may be simulated either from a fitted model or a "prior" model; allowing for prior/posterior predictive checks, experimentation, and forecasting.

[Source Code](#) [License : GPL-3](#) [Citation](#) [Authors](#)










Getting Started

After [installing](#) the software, the best way to get started is to become familiar with the [model](#) and its [implementation](#). Once familiar with the model, there are a few articles showcasing the main features of the package using real example data. The simplest such article is [here](#).

EpiEstim - A fast implementation of the renewal equation

EpiEstim: Estimate Time Varying Reproduction Numbers from Epidemic Curves

Tools to quantify transmissibility throughout an epidemic from the analysis of time series of incidence as described in Cori et al. (2013) <[doi:10.1093/aje/kwt133](https://doi.org/10.1093/aje/kwt133)> and Wallinga and Teunis (2004) <[doi:10.1093/aje/kwh255](https://doi.org/10.1093/aje/kwh255)>.

Version: 2.2-4
Depends: R (≥ 2.10)
Imports: [coarseDataTools](#) (≥ 0.6-4), stats, graphics, [reshape2](#), [ggplot2](#), [gridExtra](#), [fitdistrplus](#), [coda](#), [incidence](#) (≥ 1.7.0), [scales](#), grDevices
Suggests: [testthat](#), utils, [vdiff](#), [covr](#), [knitr](#), [rmarkdown](#)
Published: 2021-01-07
Author: Anne Cori  [aut, cre], Simon Cauchemez [ctb], Neil M. Ferguson  [ctb], Christophe Fraser  [ctb], Elisabeth Dahlquist  [ctb], P. Alex Demarsh [ctb], Thibaut Jombart  [ctb], Zhian N. Kamvar  [ctb], Justin Lessler  [ctb], Shikun Li [ctb], Jonathan A. Polonsky  [ctb], Jake Stockwin [ctb], Robin Thompson  [ctb], Rolina van Gaalen [ctb]
Maintainer: Anne Cori <a.cor@imperial.ac.uk>
BugReports: <https://github.com/mrc-ide/EpiEstim/issues>
License: [GPL-2](#) | [GPL-3](#) [expanded from: GPL (≥ 2)]
URL: <https://github.com/mrc-ide/EpiEstim>
NeedsCompilation: no
Materials: [README NEWS](#)
In views: [Epidemiology](#)
CRAN checks: [EpiEstim results](#)

Documentation:

Reference manual: [EpiEstim.pdf](#)
Vignettes: [EpiEstim demonstration](#)

Downloads:

Package source: [EpiEstim_2.2-4.tar.gz](#)
Windows binaries: r-devel: [EpiEstim_2.2-4.zip](#), r-release: [EpiEstim_2.2-4.zip](#), r-oldrel: [EpiEstim_2.2-4.zip](#)
macOS binaries: r-release (arm64): [EpiEstim_2.2-4.tgz](#), r-oldrel (arm64): [EpiEstim_2.2-4.tgz](#), r-release (x86_64): [EpiEstim_2.2-4.tgz](#), r-oldrel (x86_64): [EpiEstim_2.2-4.tgz](#)
Old sources: [EpiEstim archive](#)



Reverse dependencies:

Reverse imports: [covid19india](#), [earlyR](#), [EpiLPS](#)
Reverse suggests: [epidemia](#), [projections](#)

Linking:

Please use the canonical form <https://CRAN.R-project.org/package=EpiEstim> to link to this page.

Flexible hierarchical nowcasting

lifecycle experimental  R-CMD-check passing  codecov 97%r-universe 0.2.2 License MIT contributors 9DOI [10.5281/zenodo.7924463](https://doi.org/10.5281/zenodo.7924463)

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.

Getting started and learning more

This README is a good place to get started with `epinowcast`, in particular the following installation and quick start sections. As you make use of the package, or if your problem requires a richer feature set than presented here, we also provide a range of other documentation, case studies, and spaces for the community to interact with each other. Below is a short list of current resources.

- [Package website](#): This includes a function reference, model outline, and case studies making use of the package. This site refers to the release version of our package which can be installed from our Universe or from the latest GitHub release (see installation instructions). The development version of our documentation (corresponding to our `main` branch on GitHub) is available [here](#).
- [Organisation website](#): This includes links to our other resources as well as guest posts from community members and schedules for any related seminars being run by community members.
- [Directory of example scripts](#): Not as fleshed out as our complete case studies these scripts are used during package development and each showcase a subset of package functionality. Often newly

Links

[Browse source code](#)[Report a bug](#)

License

[Full license](#)MIT + file [LICENSE](#)


Community

[Contributing guide](#)[Code of conduct](#)

Citation

[Citing epinowcast](#)

Developers

[Sam Abbott](#)Author, maintainer 

Adrian Lison

Author 

Sebastian Funk

Author

Carl Pearson

Author 

Hugo Gruson

Author 

Felix Guenther

Author [More about authors...](#)

Real-time estimation of the effective reproduction number?

Learning more

Sam Abbott

@seabbs

samabbott.co.uk

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& TROPICAL
MEDICINE





Tools for real-time nowcasting and R_t estimation

Katie Gostic, PhD

Modeling and data science lead

CDC Center for Forecasting and Outbreak Analytics

CSTE Infectious Disease Forecasting Workshop

2023-06-25

Summary



Overview

Challenges

Tools

Learning more

Overview

- Who am I - a primer
- Real-time analysis case studies from the COVID-19 pandemic
- Real-time estimation of the effective reproduction number
- My pandemic (a very abridged tail)
- Epinowcast: Flexible hierarchical nowcasting

My pandemic (a very abridged tail)

MMED 2023

Sam Abbott

@seabbs

samabbott.co.uk

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MEDICINE

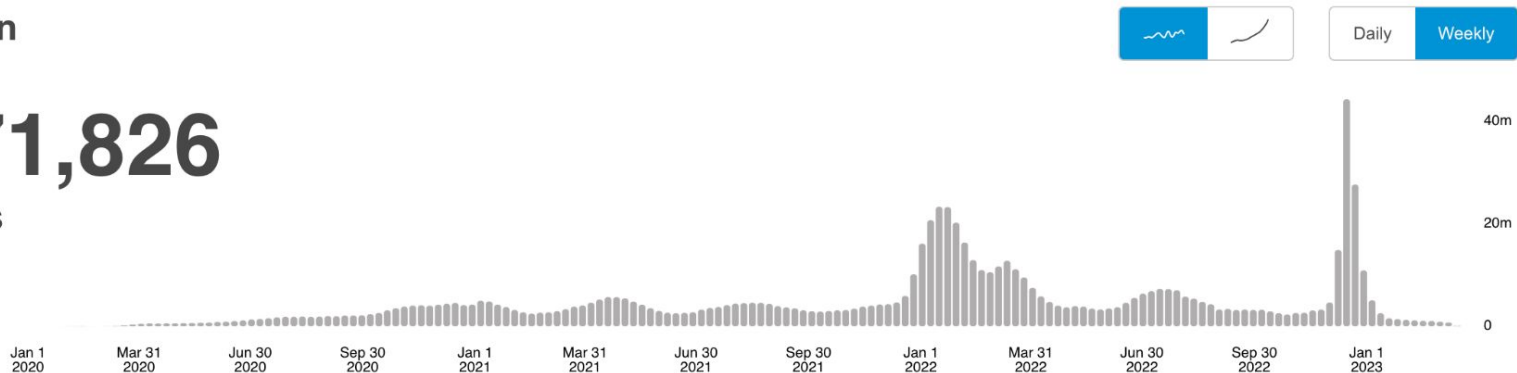


Globally, as of **6:06pm CET, 21 March 2023**, there have been **761,071,826 confirmed cases** of COVID-19, including **6,879,677 deaths**, reported to WHO. As of **21 March 2023**, a total of **13,260,401,200 vaccine doses** have been administered.

Global Situation

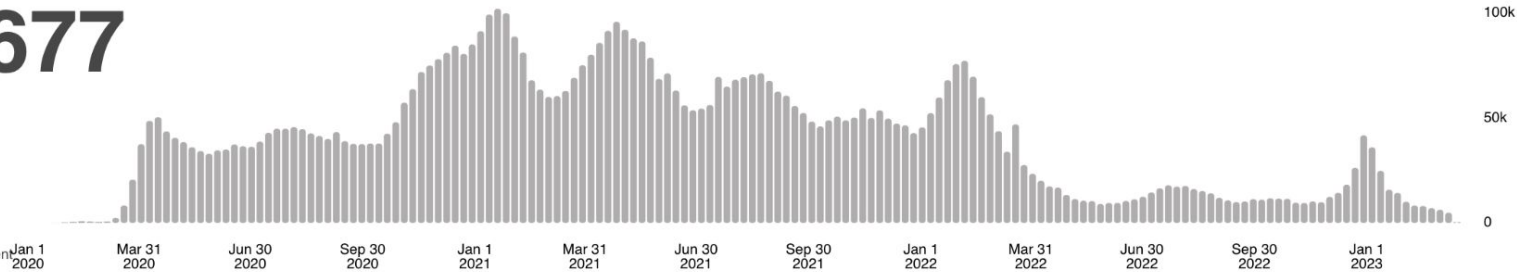
761,071,826

confirmed cases



6,879,677

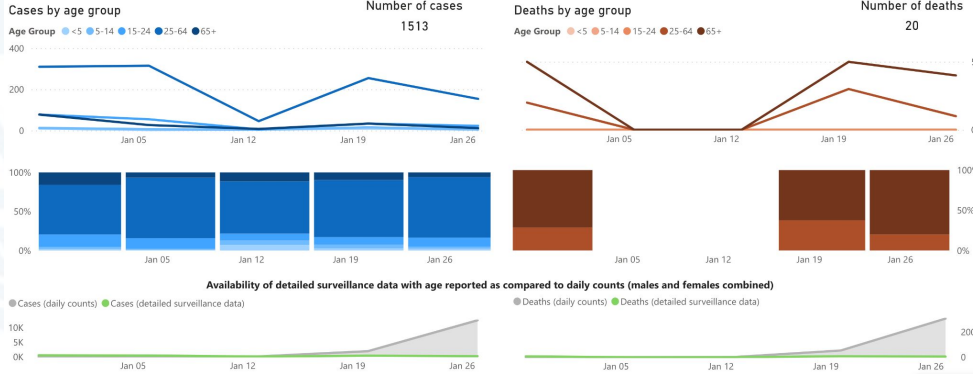
deaths



Source: World Health Organization

Data may be incomplete for the current day or week.

2020: January



- Jan 6th: Joined the school to work on real-time forecasting of infectious disease
- Jan 18th: First COVID-19 working group meeting -> Full-time on COVID-19.
- Jan 30th: Report: **Reporting delays and R_t in China** (led by Sebastian Funk)
- Jan 30th: Paper: **Size of spillover and reproduction number estimates**

RESEARCH ARTICLE

The transmissibility of novel Coronavirus in the early stages of the 2019-20 outbreak in Wuhan: Exploring initial point-source exposure sizes and durations using scenario analysis [version 1; peer review: 2 approved]

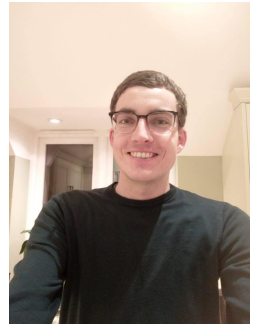
Sam Abbott , Joel Hellewell , James Munday , CMMID nCoV working group, Sebastian Funk

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

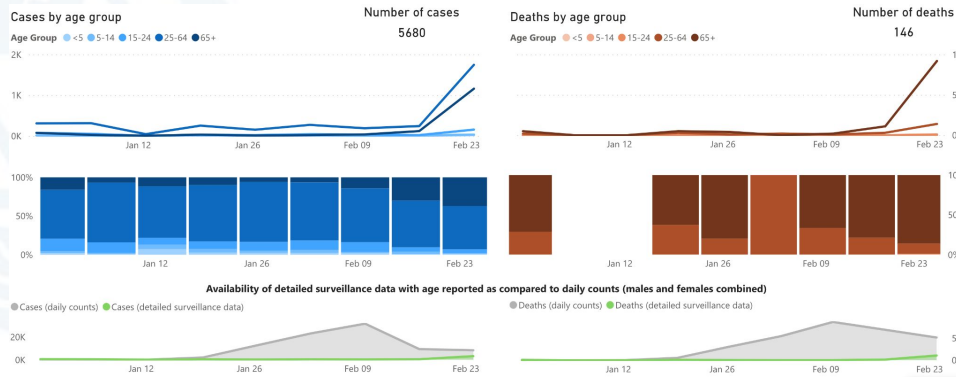
Status: In Progress | First online: 30-01-2020 | Last update: 30-01-2019

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

* corresponding author



2020: February



- Feb 5th: Presented PhD work to the JVCI BCG meeting (first Dr Abbott plaque)
- Feb 7th: Feasibility of contact tracing (led by Joel Hellewell)
- Feb 19th: In person PhD graduation @Bristol
- Feb: 1st/20+ reports to SPI-M-O (??)



Feasibility of controlling COVID-19 outbreaks by isolation of cases and contacts

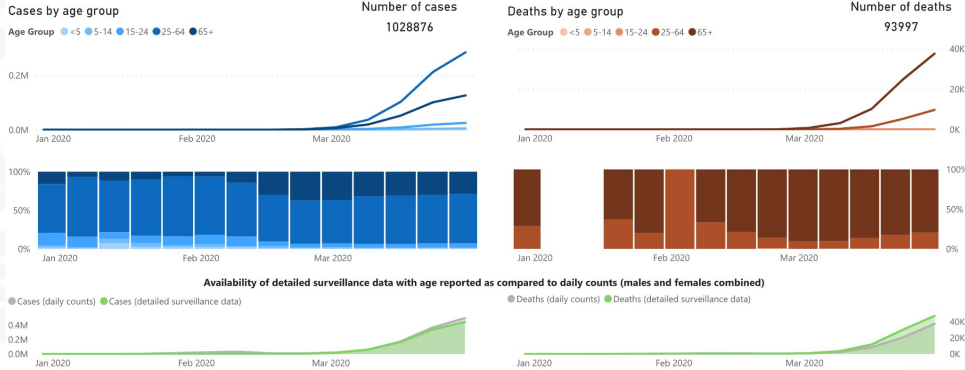
Joel Hellewell, PhD • Sam Abbott, PhD * • Amy Gimma, MSc * • Nikos I Bosse, BSc • Christopher I Jarvis, PhD •

Timothy W Russell, PhD • et al. [Show all authors](#) • [Show footnotes](#)

[Open Access](#) • Published: February 28, 2020 •

DOI: [https://doi.org/10.1016/S2214-109X\(20\)30074-7](https://doi.org/10.1016/S2214-109X(20)30074-7)

2020: March



- March 2nd: Temporal variation in transmission (R_t) + release of EpiNow
- March 10th: In person teaching (first and last @LSHTM)
- March 10th: Pointing at graphs as an intro to John's newnight interview



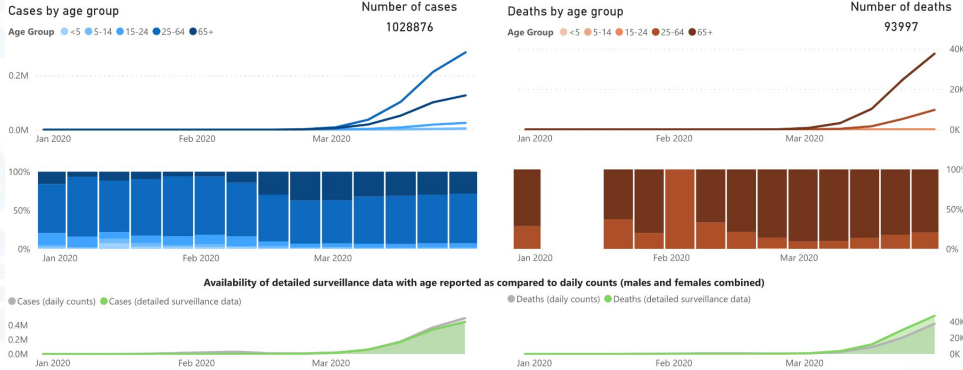
Temporal variation in transmission during the COVID-19 outbreak

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

2020: March



- March 20th: Partner flew back from Postdoc in the US
- March 23rd: London -> Bristol
- March 31st: epiforecasts.io/covid
 - Rt + short-term forecasts
 - Daily for 2+ years
 - Initially manually
 - 2000+ locations



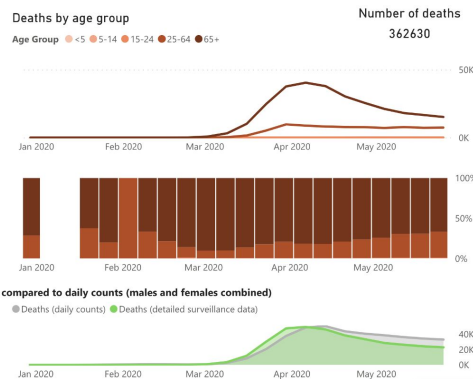
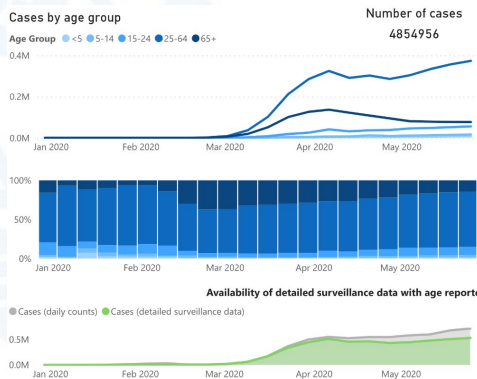
RESEARCH ARTICLE

UPDATE Estimating the time-varying reproduction number of SARS-CoV-2 using national and subnational case counts [version 2; peer review: 1 approved, 1 approved with reservations]

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



2020: April - May



- April 1st: Start of 3 times a week short-term forecasts and Rt estimates for SPI-M-O
- April: More reports (5+(?)) for SPI-M-O
- April: Became effectively non-verbal outside of work.
- May: Forecasts -> Weekly

Estimates of nosocomial and community transmission of COVID-19 in the England

Authors: Sam Abbott, Joel Hellewell, Jonathan Read, Nikos I Bosse, Kath Sherratt, James D Munday, and Sebastian Funk on behalf of the LSHTM COVID-19 Modelling Team

Date: 2020-04-12

Aim

To identify changes in the reproduction number, rate of spread, and doubling time during the course of the COVID-19 outbreak in nosocomial and community populations whilst accounting for potential biases due to delays in case reporting.

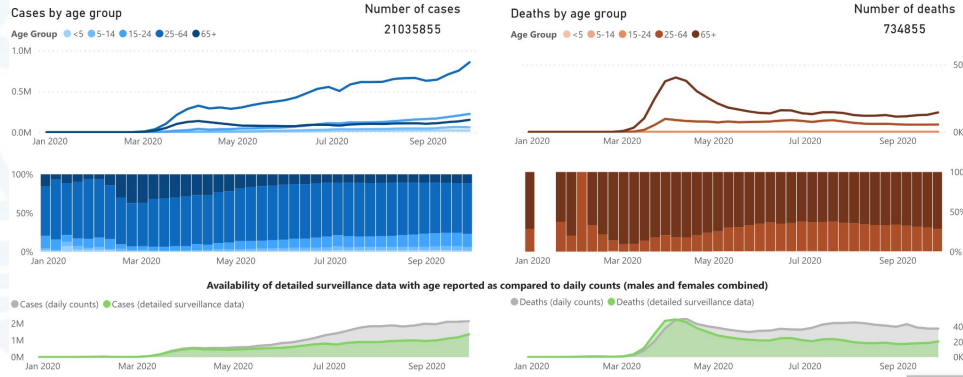
Short-term forecasts to inform the response to the Covid-19 epidemic in the UK

© S Funk, © S Abbott, BD Atkins, M Baguelin, © JK Baillie, P Birrell, J Blake, © NI Bosse, © J Burton, J Carruthers, © NG Davies, D De Angelis, L Dyson, WJ Edmunds, © RM Eggo, NM Ferguson, K Gaythorpe, © E Gorsich, © G Guyver-Fletcher, J Hellewell, © EM Hill, © A Holmes, TA House, C Jewell, © M Jit, T Jombart, I Joshi, © MJ Keeling, E Kendall, ES Knock, AJ Kucharski, KA Lythgoe, © SR Meakin, © JD Munday, © PJM Openshaw, CE Overton, © F Pagani, J Pearson, PN Perez-Guzman, L Pellis, F Scarabel, © MG Semple, K Sherratt, M Tang, MJ Tildesley, © E Van Leeuwen, © LK Whittles, CMMID COVID-19 Working Group, Imperial College COVID-19 Response Team, ISARIC4C Investigators

doi: <https://doi.org/10.1101/2020.11.11.20220962>

This article is a preprint and has not been peer-reviewed [what does this mean?]. It reports new medical research that has yet to be evaluated and so should not be used to guide clinical practice.

2020: June - September



- June: Stopped forecasts and started projections for SPI-M-O
- June: Started speaking outside of work again.
- June: Email from Katie Gostic + James Hay -> Rt method is flawed
- June: Start forecasting weekly for the CDC forecast hub
- July 23rd: First stable EpiNow2 release
- Sept 31st: Moved in with parents in Cornwall to try and deal with panic attacks

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]

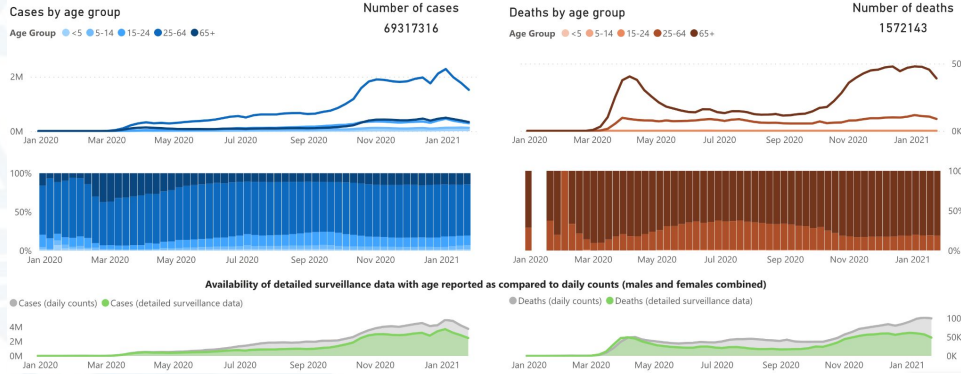
Published: December 10, 2020 • <https://doi.org/10.1371/journal.pcbi.1008409>

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

lifecycle maturing R-CMD-check passing codecov 75% downloads 2.1K

License MIT contributors 13 r-universe 1.3.4 commits since v1.3.4 16 DOI 10.5281/zenodo.7611804

2020-2021: October - January



- Oct 22nd: Grandma's funeral (10 people)
- Oct 22nd: Worked overnight implementing susceptibility for SPI-M-O projections.
- Oct: Sisters wedding (14 people)
- Nov-Jan: Worked with Met office to productionise our Rt estimates
- Jan 1st: Moved to partner's parent's house to start our own house hunt
- Jan 8th: Local area Rt and S-gene target failure



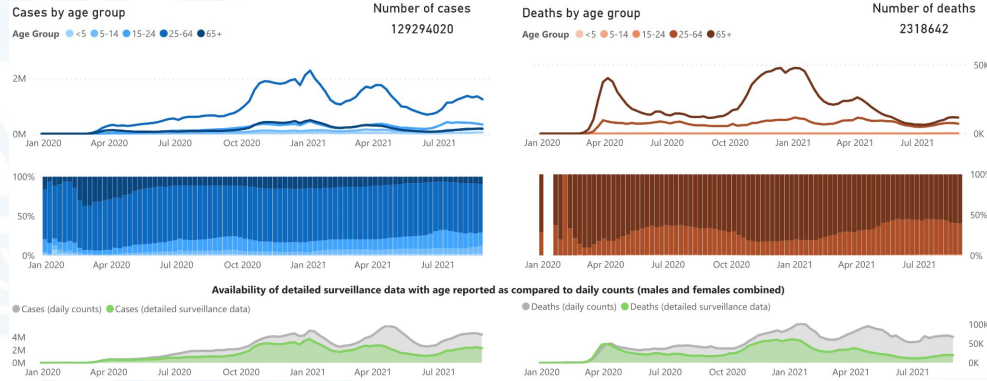
Local area reproduction numbers and S-gene target failure

Status: Real time report | First online: 08-01-2021 | Last update: 08-01-2021

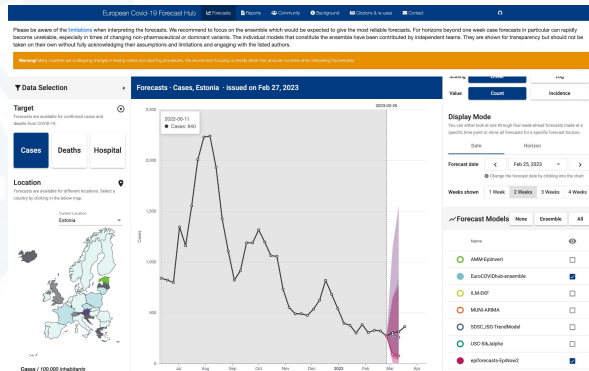
Authors: Sam Abbott, Sebastian Funk* & CMMID COVID-19 working group.

* corresponding author

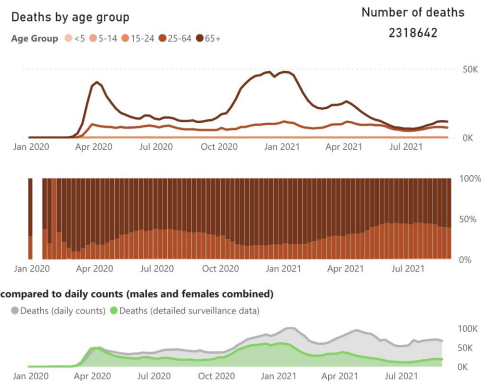
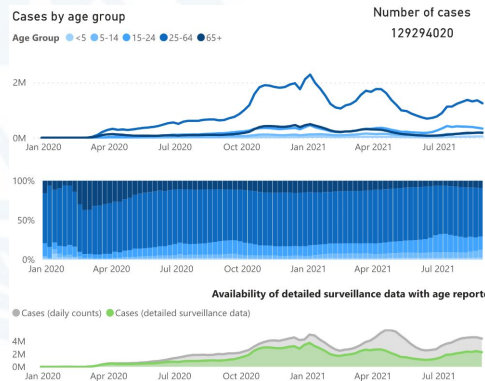
2021: February - August



- Feb: Started forecasting weekly for the European forecasting Hub
- March 1st: Start on EpiNow2 v2 dev
- March 18th: Moved out of and sold Bristol flat
- 20th April: Gave up on house buying -> Cornwall



2021: February - August



- April: Started being able to talk to people in shops etc. again
- April 21st: Grandad's funeral (30 people)
- May: Burned out on EpiNow2 dev
- May - August: Short-term forecasts of variant dynamics + cases

forecast.vocs 0.1.0-2000 Reference Articles · Changelog Search for

Forecast case and sequence notifications using variant of concern strain dynamics

Overview · GitHub · Issues · Discussions

Contains models and tools to produce short-term forecasts for both case and sequence notifications assuming circulation of either one or two variants. Tools are also provided to allow the evaluation of the use of sequence data for short-term forecasts in both real-world settings and in user-generated scenarios.

Installation

Installing the package

Install the stable development version of the package with:

```
!install_stable() {"forecast.vocs", repo = "https://gitlab.com/forecast.vocs-dev"}

Install the unstable development from GitHub using the following.
```

```
!remotes::install_github("epiforecasts/forecast.vocs", dependencies = TRUE)
```

Installing CmdStan

If you don't already have CmdStan installed then, in addition to installing `forecast.vocs`, it is also necessary to install CmdStan using CmdStan's `install_cmdstan()` function to enable model fitting in `forecast.vocs`. A suitable C++ compiler is also required. Instructions are provided in the [Getting started with CmdStan vignette](#). See the [CmdStanB documentation](#) for further details and support.

```
!cmdstanr::install_cmdstan()
```

Quick start

Links

- [Browse source code](#)
- [Report a bug](#)

License

- [Full license](#)
- [MIT - No license](#)

Community

- [Code of conduct](#)
- [Citation](#)
- [Citing forecast.vocs](#)

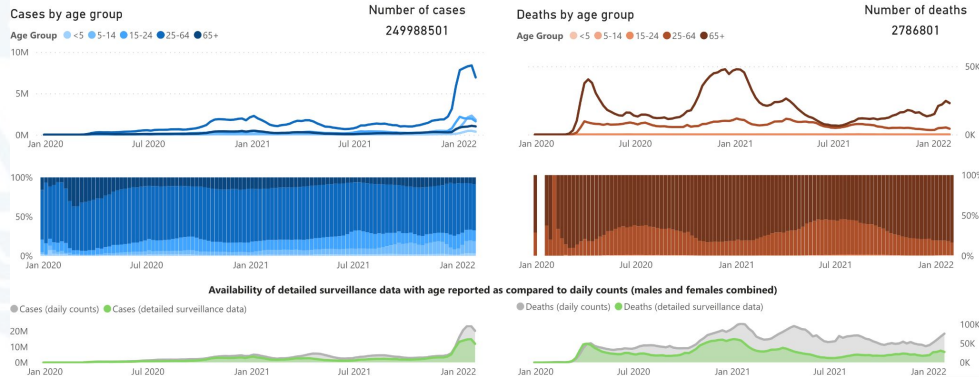
Developers

- [Sam Abbott](#)
- Author, maintainer
- [More about authors...](#)

Dev status

- [EpiNow2](#)
- [EpiNow2](#)

2021-2022: September - January



- Sept 1st: Cornwall -> Bristol (staff flat).
House buying round 2

- Oct 1st: Dev on epinowcast.org begins

- Nov: Niece born + 1st day
@office since 2020



- Nov 21st: Daily nowcasting of
hospitalisations in Germany

- Dec 22nd: Daily Omicron short-term
forecasts

- Jan 1st: Had 1st round of COVID-19

- Jan 7th: Estimate of Omicron's generation
time (last SPI-M-O report)

Estimation of the test to test distribution as a proxy for generation interval distribution for the Omicron variant in England

Sam Abbott, Katharine Sherratt, Moritz Gerstung, Sebastian Funk

doi: <https://doi.org/10.1101/2022.01.08.22268920>

2022-2023: Feb - Now

Globally, as of 6:06pm CET, 21 March 2023, there have been **761,071,826 confirmed cases** of COVID-19, including **6,879,677 deaths**, reported to WHO. As of 21 March 2023, a total of **13,260,401,200 vaccine doses** have been administered.

Global Situation

761,071,826

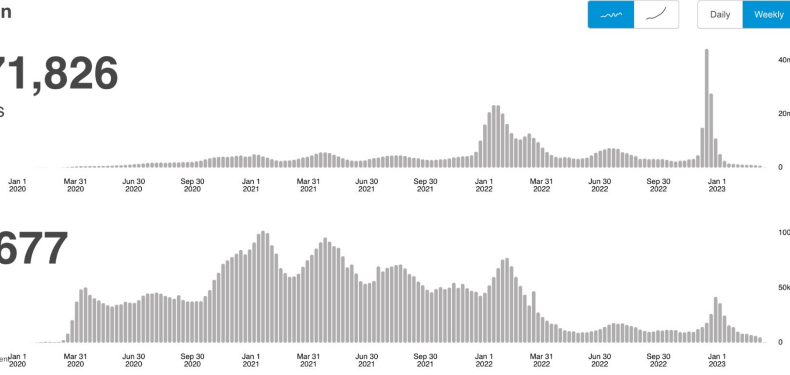
confirmed cases

6,879,677

deaths

Source: World Health Organization

Data may be incomplete for the current day or week.



Sem Abbott

Posts Notes Research Ideas Code Papers Talks About 1k

Reflections on two years estimating effective reproduction numbers

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

Author: Sem Abbott
London School of Hygiene and Tropical Medicine
MRC Centre for Global Infectious Disease Analysis

This post was originally posted to [github.com](#) and has been reposted here with consent of the author.

31 March, in just under a week time, we'll mark the last day we are producing global national and subnational Rt estimates and forecasts at [https://github.com/semab/globalest-rt-forecasts](#). It's a good opportunity to reflect on what we have learned from this, what went well and what went wrong, and what we would aim to do better next time.

An attempt to design a useful resource for **cultural awareness**

- March 10th: First successful house offer (note 1st...)
- March 17th: Had COVID round 2
- March 25th: Turned off Rt pipeline after 2 years
 - 500k unique users
 - 1.2 million page views
 - Was it worth it?



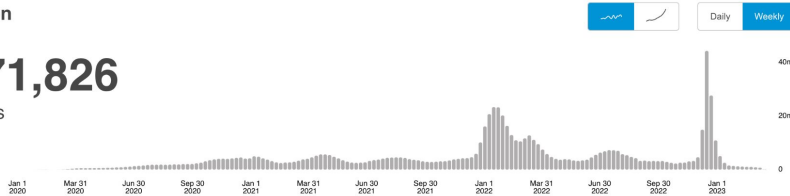
Now

Globally, as of 6:06pm CET, 21 March 2023, there have been **761,071,826 confirmed cases** of COVID-19, including **6,879,677 deaths**, reported to WHO. As of 21 March 2023, a total of **13,260,401,200 vaccine doses** have been administered.

Global Situation

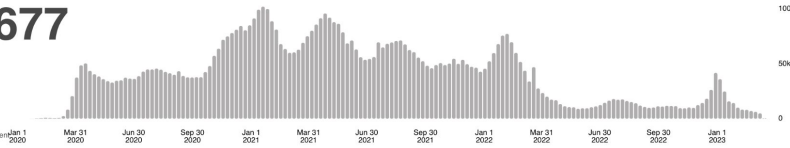
761,071,826

confirmed cases



6,879,677

deaths



Source: World Health Organization

Data may be incomplete for the current day or week.

(in the sense of nearly now and in the sense of right truncated count correction)

EpinoCast: Flexible hierarchical nowcasting

Forecasting infectious disease incidence for public health

w/ Adrian Lison, Sang Woo Park, Felix Gunther, Kelly Charniga, Johannes Bracher, Carl Pearson, Hannah Choi, Michael DeWitt, Sebastian Funk and many more

Sam Abbott

fosstodon.org/@seabbs

samabbott.co.uk

Slides: samabbott.co.uk/presentations/2023/royal-society-epinowcast.pdf












- First Christmas not working in 3 years
- Sept 2022: House (yay!)
- Working on
 - Estimating delay distributions during outbreaks
 - Flexible methods for situational awareness during outbreaks (epinowcast.org)
- Start at CDC-CFA as a consultant on 1st April 12th -> July 31st
- August 1st: ???



What was your pandemic like?

Improving modelling for epidemic responses: reflections from members of the UK infectious disease modelling community on their experiences during the COVID-19 pandemic

 Katharine Sherratt, Anna C. Carnegie, Adam Kucharski, Anne Cori, Carl A. B. Pearson, Christopher I. Jarvis, Christopher Overton, Dale Weston,  Edward M. Hill, Edward Knock, Elizabeth Fearon,  Emily Nightingale, Joel Hellewell, W. John Edmunds, Julián Villabona Arenas, Kiesha Prem,  Li Pi, Marc Baguelin, Michelle Kendall,  Neil Ferguson,  Nicholas Davies, Rosalind M. Eggo,  Sabine van Elsland,  Timothy Russell,  Sebastian Funk, Yang Liu, Sam Abbott

doi: <https://doi.org/10.1101/2023.06.12.544667>

Summary: epinowcast.org/posts/2023-06-18-improving-modelling-for-epidemic-responses/

Preprint: biorxiv.org/content/10.1101/2023.06.12.544667v1

Overview

- Who am I - a primer
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(in the sense of nearly now and in the sense of right truncated count correction)

Epinowcast: Flexible hierarchical nowcasting

MMED 2023

w/ Adrian Lison, Sang Woo Park, Felix Gunther, Kelly Charniga, Johannes Bracher, Carl Pearson, Hannah Choi, Michael DeWitt, Sebastian Funk and many more

Sam Abbott

@seabbs

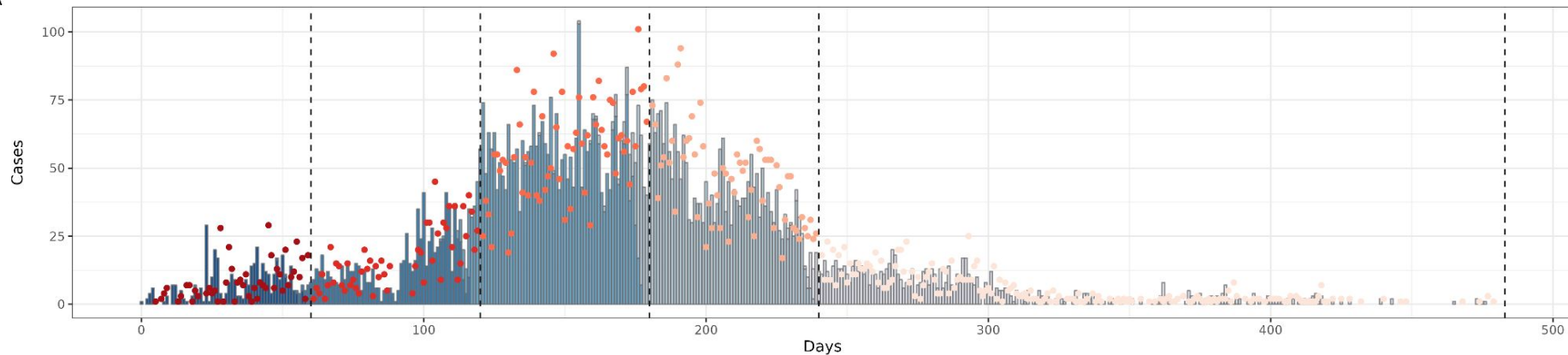
samabbott.co.uk

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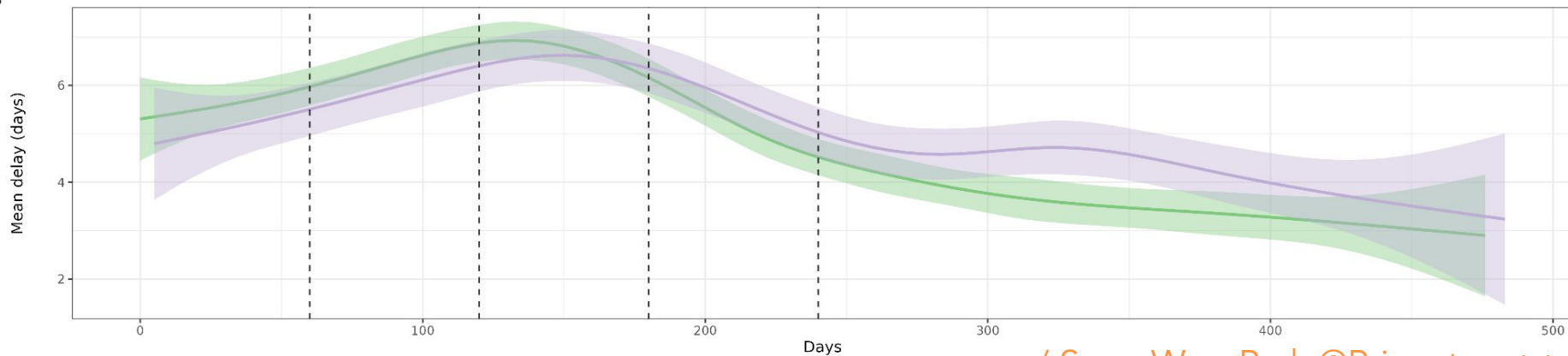


Sierra Leone Ebola virus disease outbreak (Fang et al.) - doi.org/10.1073/pnas.1518587113

A

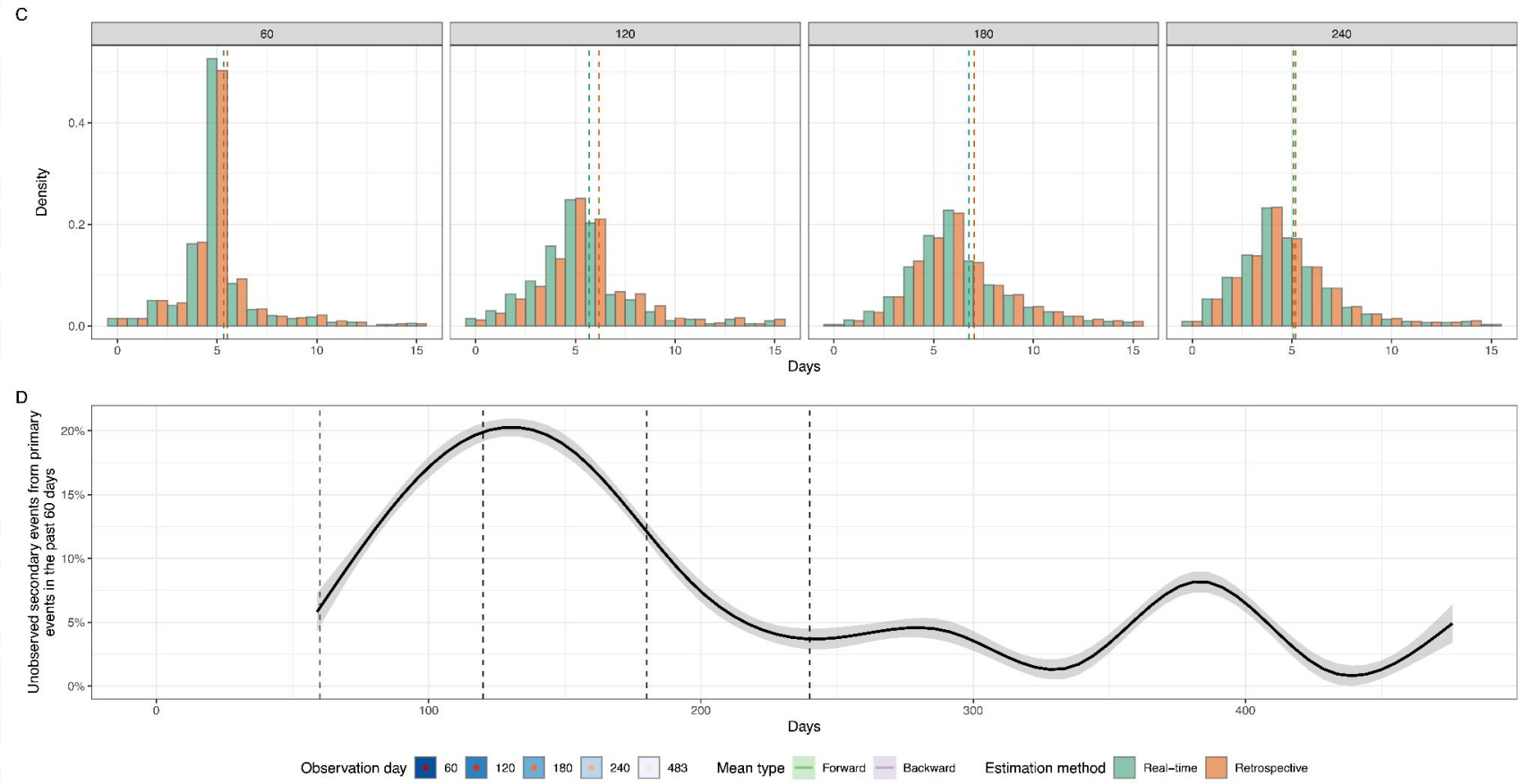


B



w/ Sang Woo Park @Princeton ++

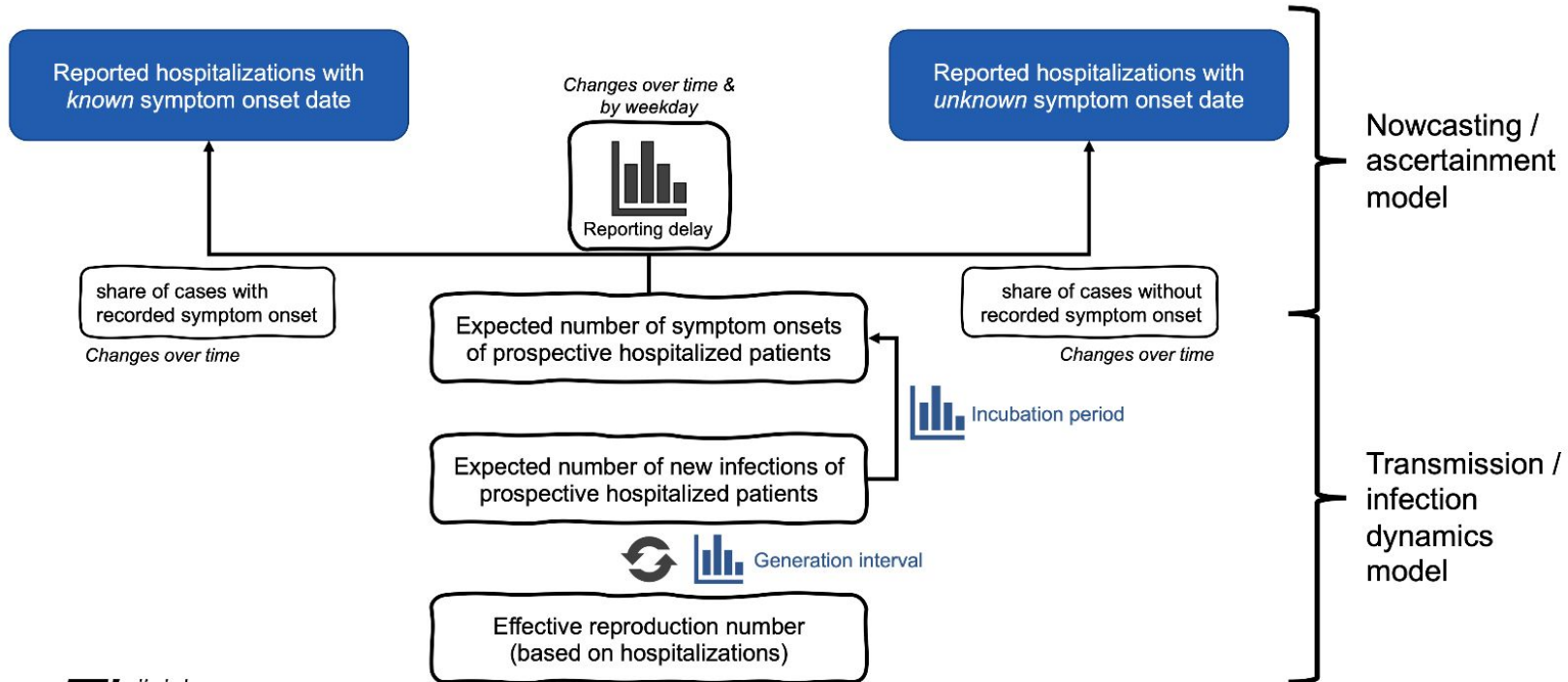
Sierra Leone Ebola virus disease outbreak (Fang et al.) - doi.org/10.1073/pnas.1518587113

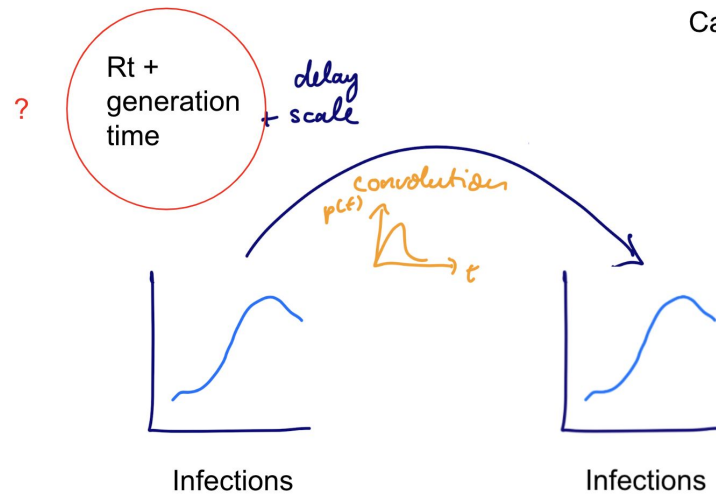
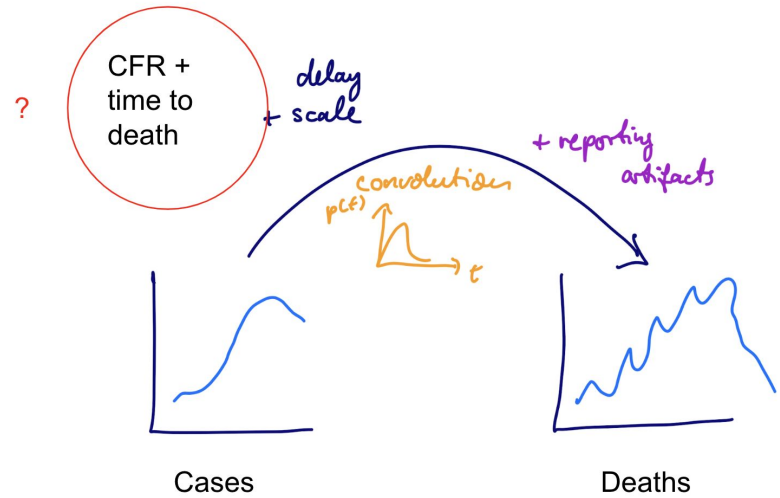
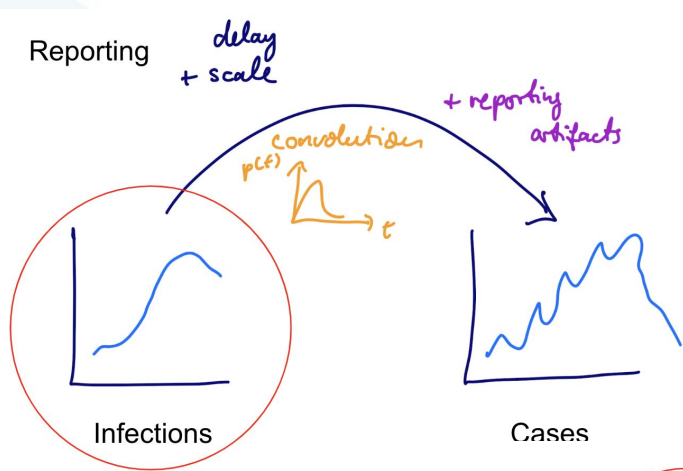


w/ Sang Woo Park @Princeton ++

Nowcasting R_t from hospitalization linelist data

Bayesian hierarchical model

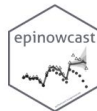




All by:

- Space/location
- Time
- Risk factors
- Society structure

Stolen without permission
from Sebastian Funk



Welcome to the Epinowcast community

We are a community of infectious disease modellers, applied epidemiologists, software developers, and others building a suite of tools for real-time analysis of infectious diseases. On top of developing these tools, we also do research on when they work and when they don't, write case studies to showcase best practices, support users and decision-makers, and compare our work to that of others.

We strongly believe that the challenges we face in the real-time analysis of infectious disease can only be overcome as a community collaboration.

We are still in the early stages of building our community so now is a great time to jump in.

[Community](#)

[Github](#)

[Twitter](#)

Flexible hierarchical nowcasting

lifecycle experimental R-CMD-check passing codecov 97%r-universe 0.2.2 License MIT contributors 9DOI [10.5281/zenodo.7924463](https://doi.org/10.5281/zenodo.7924463)

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.

Getting started and learning more

This README is a good place to get started with `epinowcast`, in particular the following installation and quick start sections. As you make use of the package, or if your problem requires a richer feature set than presented here, we also provide a range of other documentation, case studies, and spaces for the community to interact with each other. Below is a short list of current resources.

- [Package website](#): This includes a function reference, model outline, and case studies making use of the package. This site refers to the release version of our package which can be installed from our Universe or from the latest GitHub release (see installation instructions). The development version of our documentation (corresponding to our `main` branch on GitHub) is available [here](#).
- [Organisation website](#): This includes links to our other resources as well as guest posts from community members and schedules for any related seminars being run by community members.
- [Directory of example scripts](#): Not as fleshed out as our complete case studies these scripts are used during package development and each showcase a subset of package functionality. Often newly

Links

[Browse source code](#)[Report a bug](#)

License

[Full license](#)MIT + file [LICENSE](#)


Community

[Contributing guide](#)[Code of conduct](#)

Citation

[Citing epinowcast](#)

Developers

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Adrian Lison

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Author

Carl Pearson



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Author 

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Author [More about authors...](#)

Community

Categories

- Announcements
- General
- Introductions
- Meetings
- All categories

Messages

- Inbox
- admins


Channels

- # General
- # Lounge
- # Staff


Personal chat

- sangwoopark
- alison, johannes
- alison
- teocryan
- FelixGuenther
- kcharrniga
- medewitt
- OvertonC
- dwollfram

To make launching your new site easier, you are in bootstrap mode. All new users will be granted trust level 1 and have daily email summary emails enabled. This will be automatically turned off when 50 users have joined.

 Send invitations

all categories
all tags
Latest
Top
Categories
Docs

 New Topic

Topic	Replies	Views	Activity
Community Seminar 2023-03-15 ■ Meetings	0	1	3m
last visit			
How should we talk about nowcasting horizons?	2	28	7d
Community Seminar 2023-03-01 - Adrian Lison - Generative modeling approaches to nowcasting with incomplete line list data ■ Meetings	0	177	14d
European forecasting hub moves to nowcasting hospital admissions	1	21	15d
Adding a new package to epinowcast github ■ Project Proposals	2	92	15d
Propagating uncertainty between models in EpiNow2 ■ Other Resources application	1	50	20d
Community meeting 2023-02-15 ■ Meetings	1	165	28d
Handling delayed entry of symptom onset dates in line lists ■ Developers model-extension	9	124	8 Feb
Community Seminar 2023-02-01 - Johannes Bracher - Collaborative nowcasting of COVID-19 hospitalization incidences in Germany ■ Meetings researcher, application, real-time-seminar	2	260	1 Feb
Community seminars for real-time infectious disease modelling ■ Meetings	1	161	1 Feb
Epinowcast meeting (2023-01-18) ■ Meetings	2	48	18 Jan
General-audience nowcasting FAQ	2	101	18 Jan

Learning more and getting involved

Talk to me?

epinowcast.org - A community of infectious disease modellers, applied epidemiologists, software developers, and others building a suite of tools for real-time analysis of infectious diseases. See our package docs, the community site and our GitHub organisation.

Straight to the maths - package.epinowcast.org/articles/model

See the stan code (here be demons) - github.com/epinowcast/epinowcast/tree/main/inst/stan

Summary slides from an application in Germany - samabbott.co.uk/presentations/2022/nowcasting-sacema.pdf

Summary

- Who am I - a primer
- Real-time analysis case studies from the COVID-19 pandemic
- Real-time estimation of the effective reproduction number
- My pandemic (a very abridged tail)
- Epinowcast: Flexible hierarchical nowcasting

Abbott et al.

MMED 2023

Questions!?! (or feel free to come and chat anytime)

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HYGIENE
& TROPICAL
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