ESTIMATING THE DATE OF EMERGENCE OF AN EPIDEMIC FROM DETECTION DATA: APPLICATIONS TO COVID-19 Jijón S¹, Czuppon P², Blanquart F³ and Débarre F¹

¹Institute of ecology and environmental sciences of Paris (iEES-Paris, UMR 7618), Sorbonne Université, CNRS, UPEC, IRD, INRAE ²Institute for Evolution and Biodiversity, University of Münster ³Center for Interdisciplinary Research in Biology, CNRS, Collège de France, PSL Research University

Background

Estimates of dates of emergence for COVID-19

Dating attempts for the first human SARS-CoV-2 infection [1–2], as well as the emergence of SARS-CoV-2 variants of concern [3].

Main estimates of the date of emergence. Abbreviations: CrI = Credibility interval; Ref. = Reference.

Epi context	Estimated date of	Method	Ref.
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Findings

A-priori

Input par

Estimating the date of the first infection with the "Alpha" variant in the UK

Data: N=406 detected cases sequenced by Nov 11, 2020 [4].





	emergence		
COVID-19 in Wuhan	Mid-Oct to mid-Nov, 2019	Transmission model coupled with genomic data.	[1]
	Nov 18, 2019 (95%CrI: Oct 23 to Dec 8)	Estimates were recently updated.	[2]
B.1.1.7 ("Alpha") variant in the United Kingdom (UK)	Early August 2020	Stochastic model of early epidemics dynamics estimating the time of the first detection event.	[3]

Objective

To estimate the delay from emergence (i.e., first infection) to the N-th observed (i.e., detected) case, using available data.

Methods

Modelling infectious disease spread

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ori parameters. Darameters as in [3].			Estimates of the emergence date and other epidemiological indicators. Median values (IQR), unless stated otherwise.			
Param.	Value		Indicator	Median (IQR)		
R	1.50					
ĸ	0.57		Number of days from 1st infection to N-th case	114.9 (106.7–125.9)		
p_{detect}	0.01		Date of first Alpha infection	Jul 20 (09–28), 2020		
κ_t	0.83		Mean number of secondary infections (sd)	1.5 (2.3)		
$ heta_t$	6.60		Epidemic size	1104 (433–2193)		
$\kappa_{ au}$	0.58		Proportion of detected infections	62.3% (4.2%-81.0%)		
$ heta_{ au}$	12.0					

Estimating the date of emergence of COVID-19 in Wuhan

Data: N=174 reported cases of COVID-19 with symptom onset up to Dec 31, 2019 [5].





Process

We extended the model presented in [3], to model infectious disease spread from a single infectious individual (\bigcirc) to N observed cases. The times and probabilities for pathogen transmission () and detection events (\bigcup , n = 1, ..., N) are drawn from the following distributions:

- Number of secondary cases $\sim NegBinom(\kappa, p = \frac{\kappa}{\kappa+R})$, where $\kappa :=$ dispersion parameter and R := effective reproduction number.
- Number of detected infections $\sim Binom(n = I(t), p = p_{detect})$, where I(t) := Infected individuals at time t and $p_{detect} :=$ probability of detection.
- Times of infection (t_i) and detection $(\tau_n) \sim Gamma(\kappa_x, \theta_x)$, with $x \in \{t, \tau\}$, respectively.

Model calibration

oriori	param	eters.				
		Dof	Estimates of the emergence date and other epie	Estimates of the emergence date and other epidemiological indicators.		
4111.			Indicator	Median (IQR)		
	0.10	[6] [7]	Number of days from 1st infection to N -th case	43.1 (38.6–48.7)		
0.15 0.83		[6] [3]	Mean number of secondary infections (sd)	2.6 (3.7)		
6.60 [[[3] 81	Epidemic size	957 (567–1440)		
6.25		[8]	Proportion of detected infections	18.6% (12.4%–31.4%		

Sensitivity analyses. Distributions of time from 1st infection to N-th reported case, varying the transmission (R) and detection (p_{detect}) parameters, without the calibration constraints. Median values are depicted by a dashed line.



The numerical simulations (sim) are calibrated to reproduce i) the observed (obs) time period between the first and the N-th case:

$$\left| \left(\tau_N^{\text{obs}} - \tau_1^{\text{obs}} \right) - \left(\tau_N^{\text{sim}} - \tau_1^{\text{sim}} \right) \right| \le \delta_{tol} \left(\tau_N^{\text{obs}} - \tau_1^{\text{obs}} \right),$$

and

ii) the observed daily number of cases:

$$|y_i^{\mathsf{obs}} - y_i^{\mathsf{sim}}| \le \delta_{tol}' N, \qquad \forall i = 1, 2, \dots, N$$

where $\delta_{tol} = 0.2$ and $\delta'_{tol} = 0.9$.

Abbreviations: IQR = interquartile range, Param. = parameter, sd = standard deviation, Ref. = reference.

Conclusions

• We propose a generic and flexible modelling framework that can be applied to date epidemic outbreak emergence.

• Our results fall within the ranges previously estimated, by using different methods.

References

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[6] Hao et al. (2020) *Nature* [7] Endo et al. (2020) Wellcome Open Res. [8] Backer et al (2020) *Eurosurveillance*





Contact information: Sofía JIJON ALBAN Mathematical epidemiology sofia.jijon alban@sorbonne-universite.fr

