nature portfolio

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Reporting Summary

Nature Portfolio wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Portfolio policies, see our Editorial Policies and the Editorial Policy Checklist.

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

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n/a	Confirmed
	The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement
x	A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
	The statistical test(s) used AND whether they are one- or two-sided Only common tests should be described solely by name; describe more complex techniques in the Methods section.
	🕱 A description of all covariates tested
	🕱 A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
	A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
	For null hypothesis testing, the test statistic (e.g. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted <i>Give P values as exact values whenever suitable.</i>
x	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
x	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
×	\square Estimates of effect sizes (e.g. Cohen's d , Pearson's r), indicating how they were calculated
,	Our web collection on <u>statistics for biologists</u> contains articles on many of the points above.

Software and code

Policy information about availability of computer code

Data collection Simulation data were generated by code at https://github.com/abliu/early-detection/releases as well as EpiNow2 (v1.3.5).

Data analysis Analyses and figures were generated by code at https://github.com/abliu/early-detection/releases as well as tidyverse (v1.3.1).

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio guidelines for submitting code & software for further information.

Data

Policy information about availability of data

All manuscripts must include a <u>data availability statement</u>. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our policy

Detection time data are available at https://github.com/abliu/early-detection/releases. Estimated COVID-19 case counts in late 2019 and early 2020 are available from Pekar et al. 2022 (https://github.com/sars-cov-2-origins/multi-introduction) and the US wastewater threshold data are from Wu et al. 2021 (https://www.sciencedirect.com/science/article/pii/S0043135421005984?via%3Dihub#sec0019). In the supplementary analyses, the Massachusetts Water Resources Authority wastewater data are from https://www.mwra.com/biobot/biobotdata.htm, national COVID-19 case counts in early 2020 are from the Johns Hopkins Center for Systems Science and Engineering 2023 (https://github.com/CSSEGISandData/COVID-19), and US state COVID-19 case counts in early 2020 are from Lu et

al 2021 (https://jou	rnals plos org/ple	oscompbiol/article?id=10.1371/journal.pcbi.1008994).	
ai. 2021 (https://jou	mais.pios.org/pic	scompholo/article: ld=10.1371/journal.pcbl.1006554).	
Research inv	olving hu	man participants, their data, or biological material	
		with human participants or human data. See also policy information about sex, gender (identity/presentation), ethnicity and racism.	
Reporting on sex a	nd gender	N/A	
Reporting on race, ethnicity, or other socially relevant groupings		N/A	
Population charact	eristics	N/A	
Recruitment		N/A	
Ethics oversight		N/A	
lote that full informa	ation on the appr	oval of the study protocol must also be provided in the manuscript.	
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Life sciences			
		Behavioural & social sciences	
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		points even when the disclosure is negative.	
Sample size	Sample size was 4,800: 100 simulations for each of 48 system-disease-community combinations. These cover 8 diseases simulated in each of these 6 scenarios: (i) hospital system, (ii-v) wastewater in four different catchment sizes, and (vi) air travel monitoring.		
Data exclusions	No data were e	xcluded.	
Replication	We validated the model in two independent datasets: 1. we predicted COVID-19 detection times in each US state with a mean absolute error of 0.97 weeks and 2. we found our wastewater-specific results were consistent with the upper bound implied by Massachusetts COVID-19 wastewater data.		
Randomization		Simulated detection times were generated with random draws from the following distributions: (i) for each case, whether it was detected or not; (ii) the offspring distribution for each case; and (iii) in the case of wastewater, the distribution of sensitivity thresholds from Wu et al. 2021.	
Blinding	Blinding was not applicable because this study is not an experimental trial.		
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		about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.	
Materials & ex	perimental s	ystems Methods	
n/a Involved in the study n/a Involved in the study			
Antibodies			
Fukaryotic cell lines			

Materials & experimental systems		Methods
n/a	Involved in the study	n/a Involved in the study
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×	Eukaryotic cell lines	Flow cytometry
×	Palaeontology and archaeology	MRI-based neuroimaging
×	Animals and other organisms	·
×	Clinical data	
×	Dual use research of concern	
×	Plants	