Mathematical modelling of SARS-CoV-2: Alpha variant (B.1.1.7)

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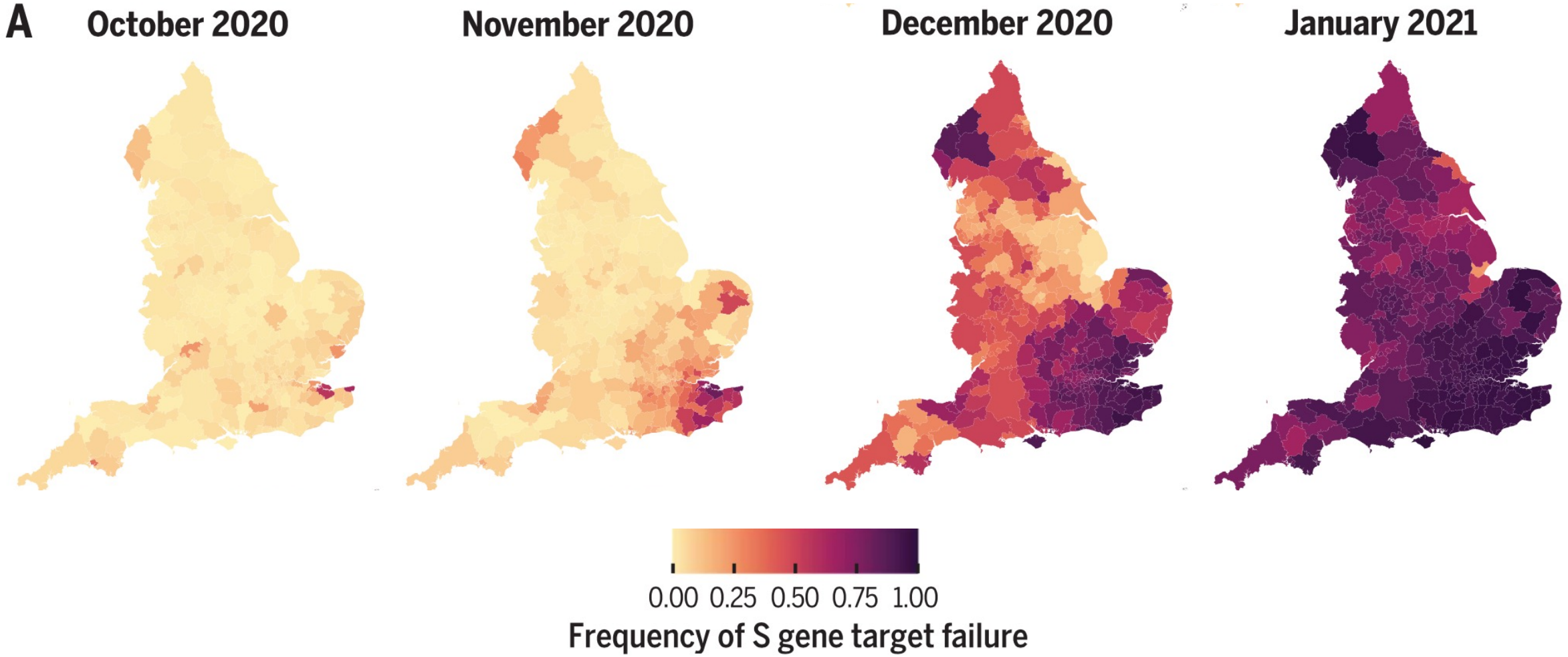
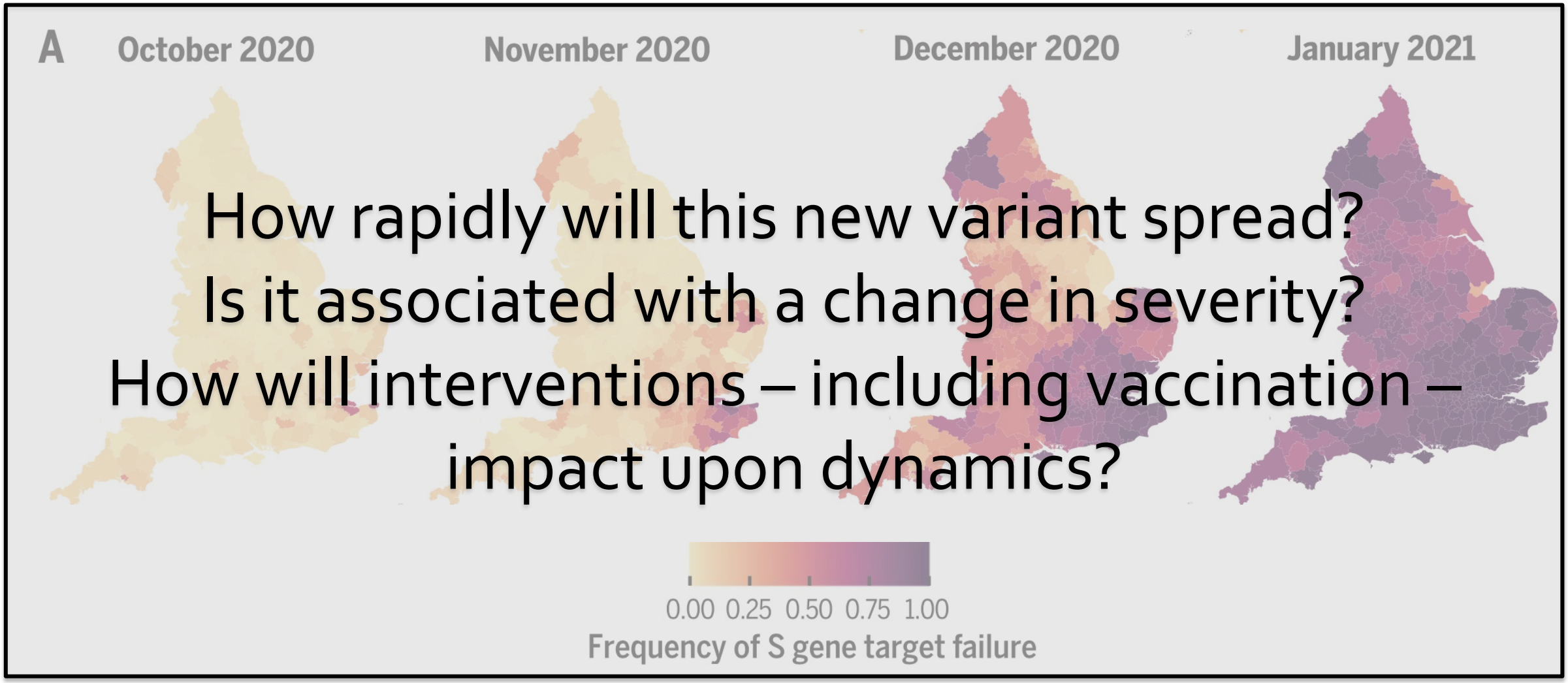
6 July, 2023

Emergence of the Alpha variant…



Key questions as of mid-December 2020



Mathematical model: **covidm**

SEIR-type model, age-stratified

Two strains

Age group *i*:

λ_i = force of infection

u_i = susceptibility

y_i = clinical fraction

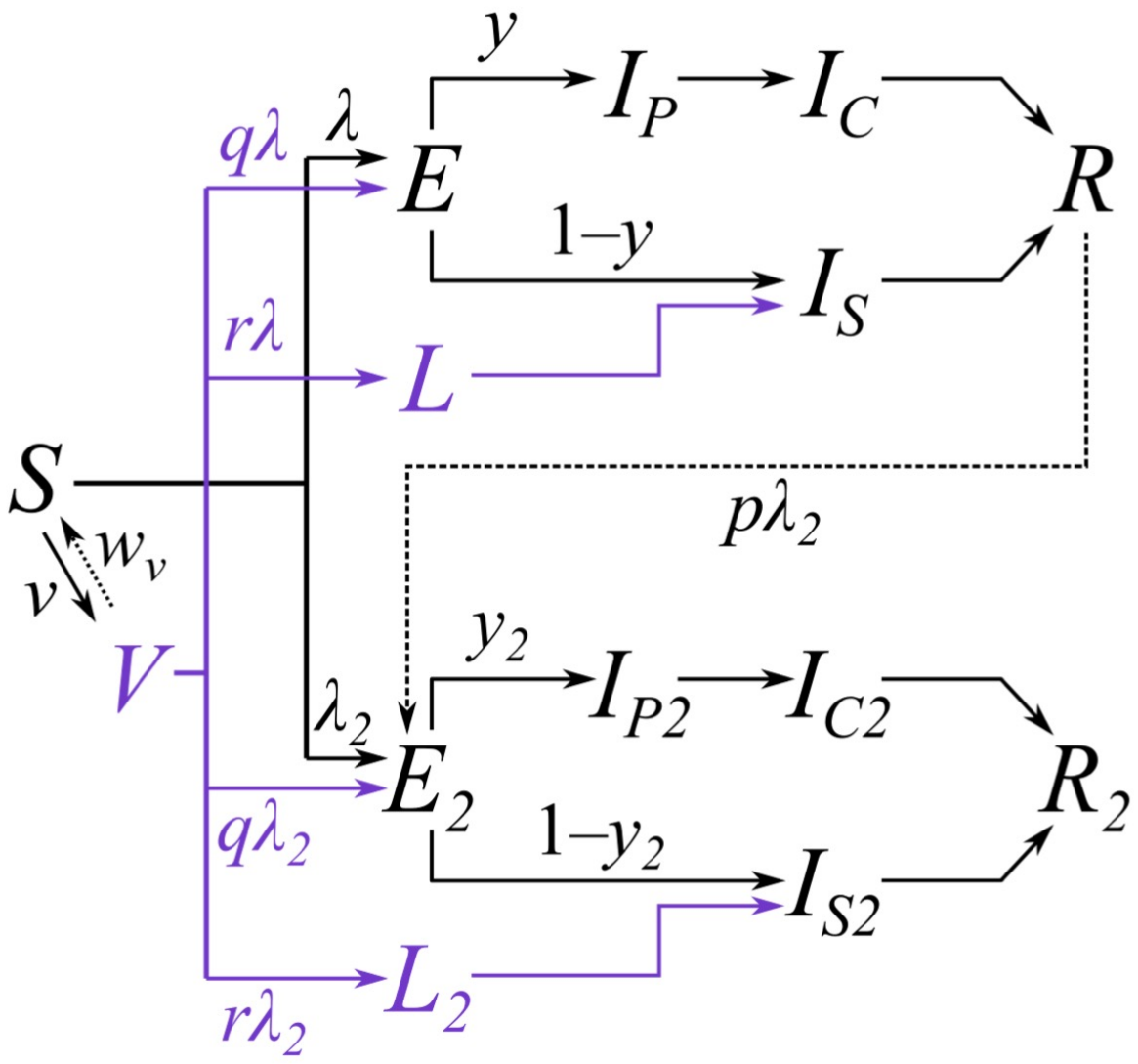
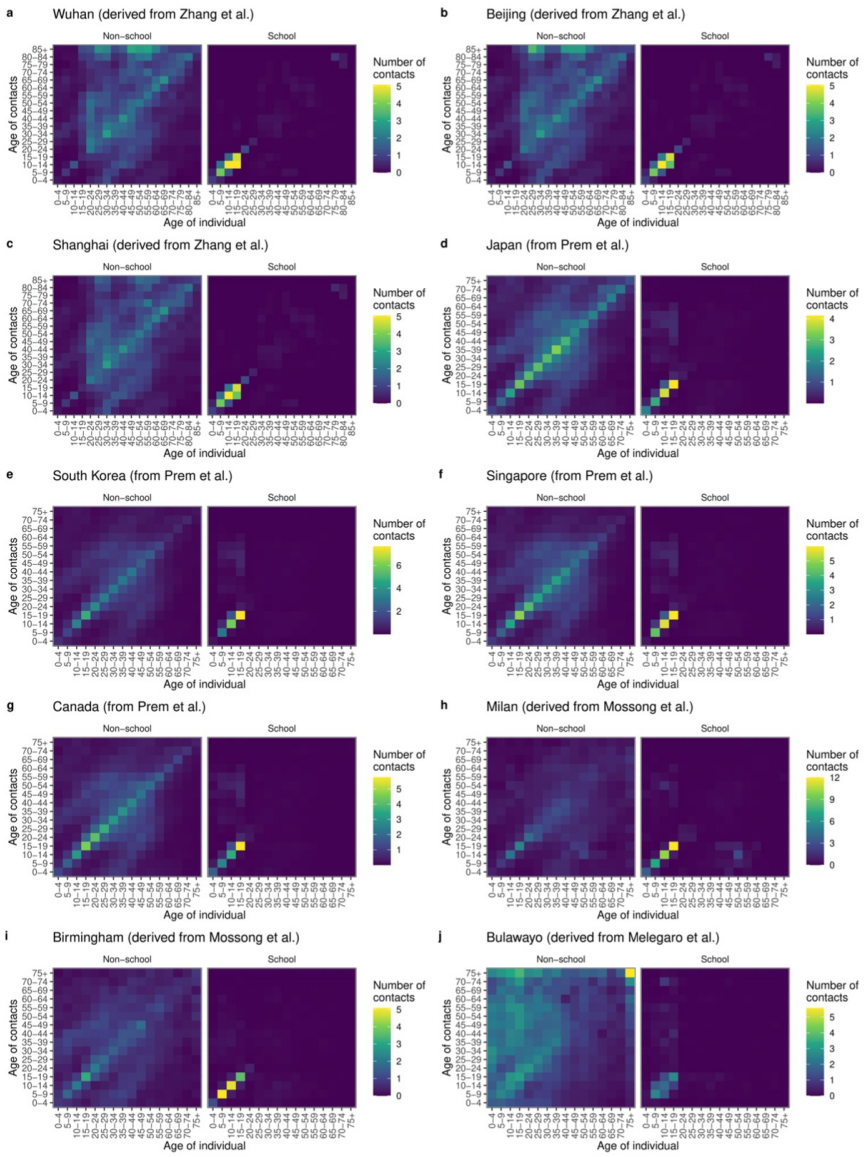


Table S3.

Model parameters not subject to fitting.

Parameter	Description	Value	Notes
d_E	Latent period (E to I_P, E to I_S, L to I_S; days)	~gamma(μ = 2.5, k = 2.5)	Set to 2.5 so that incubation period (latent period plus period of preclinical infectiousness) is 5 days(*70*)
d_P	Duration of preclinical infectiousness (I_P to I_C; days)	~gamma(μ = 2.5, k = 4)	Assumed to be half the duration of total infectiousness in clinically-infected individuals (*14*)
d_C	Duration of clinical infectiousness (I_C to R; days)	~gamma(μ = 2.5, k = 4)	Infectious period set to 5 days, to result in a serial interval of approximately 6 days(*71–73*)
d_S	Duration of subclinical infectiousness (I_S to R; days)	~gamma(μ = 5.0, k = 4)	Assumed to be the same duration as total infectious period for clinical cases, including preclinical transmission
y_i	Probability of clinical symptoms given infection for age group i	Estimated from case distributions across 6 countries	(*19*)
f	Relative infectiousness of subclinical cases	50%	Assumed (*15*, *19*)
$c_{i,j}$	Number of age-j individuals contacted by an age-i individual per day, prior to changes in mobility	UK-specific contact matrix	(*74*)

Age-specific clinical fraction & susceptibility



Using contact matrices specific to each of the 32 regions, calculated the expected distribution of infections given a candidate age-specific profile of susceptibility and symptom severity.

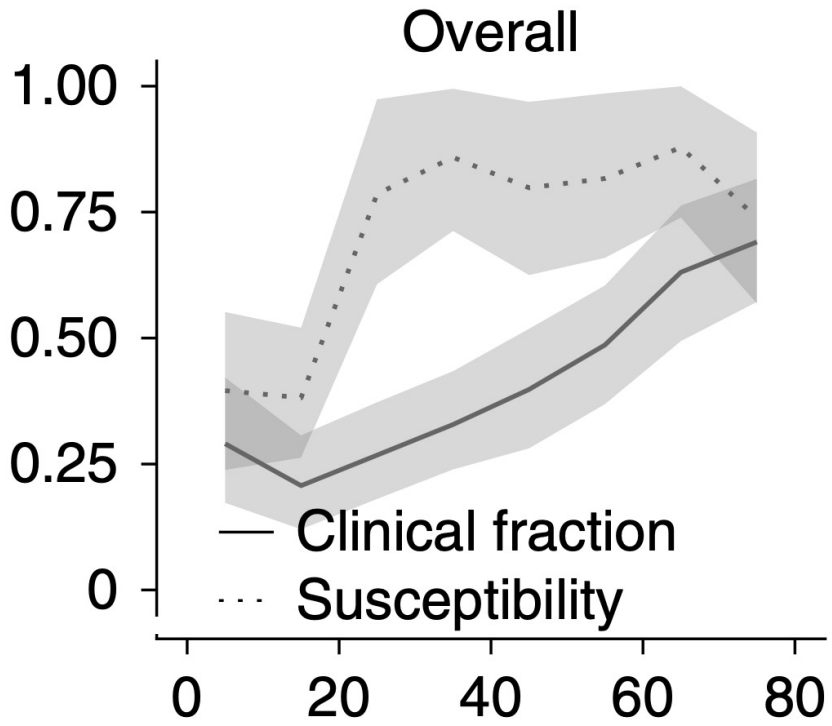


Table S3.

Model parameters not subject to fitting.

Parameter	Description	Value	Notes
N_i	Number of age-*i* individuals	From demographic data	(*75*)
Δt	Time step for discrete-time simulation	0.25 days	
$P(\text{ICU})_i$	Proportion of hospitalised cases that require critical care for age group *i*	Estimated from CO-CIN data	(*66*)
w_s	Waning rate of seropositivity	224 days^{-1}	Estimated from serology data
los_{hosp}	Length of stay in hospital	~lognormal(μ_{log} = 11.08, sd_{log} = 1.20)	Estimated from CO-CIN data (*66*)
los_{icu}	Length of stay in ICU	~lognormal(μ_{log} = 13.33, sd_{log} = 1.25)	Estimated from CO-CIN data (*66*)
$detect_0$, $detect_1$, $detect_{s0}$, $detect_{s1}$	Delay from hospital admission to SARS-CoV-2 test	$detect_0$ = 14 $detect_1$ = 1 $detect_{s0}$ = 5.86 $detect_{s1}$ = 33.4	To capture substantial delays in testing at the beginning of the epidemic in the UK, we assume that the delay from hospital admission to confirmed SARS-CoV-2 infection is $asc(t/366, detect_0, detect_1, detect_{s0}, detect_{s1})$, where *t* is time in days since 1 January 2020. Estimated from a previous round of model fitting.

Mathematical model: **covidm**

Table S2.

Details of fitted parameters.

Parameter	Description	Prior distribution	Notes
`tS`	Start date of epidemic in days after 1 January 2020	~uniform(0, 60)	Determines date at which seeding begins in region; starting on this date, one random individual per day contracts SARS-CoV-2 for 28 days
`u`	Basic susceptibility to infection	~normal(0.09, 0.02)	Determines basic reproduction number R_0
`death_mean`	Mean delay in days from start of infectious period to death	~normal(15, 2)	Delay is assumed to follow a gamma distribution with shape parameter 2.2. Prior and shape of distribution informed by analysis of CO-CIN data (*66*).

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Mathematical model: **covidm**

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Parameters for VOC 202012/01 strain

Parameter	Description	Prior distribution	Notes
`v2_when`	Introduction date of VOC 202012/01 in days after 1 January 2020	~uniform(144, 365)	On this date, ten random individuals contract VOC 202012/01
`v2_hosp_rlo`	Relative log-odds of hospitalisation for VOC 202012/01, compared to preexisting variants	~normal(0, 0.1)	Vague prior
`v2_icu_rlo`	Relative log-odds of ICU admission for VOC 202012/01, compared to preexisting variants	~normal(0, 0.1)	Vague prior
`v2_cfr_rlo`	Relative log-odds of death for VOC 202012/01, compared to preexisting variants	~normal(0, 0.1)	Vague prior

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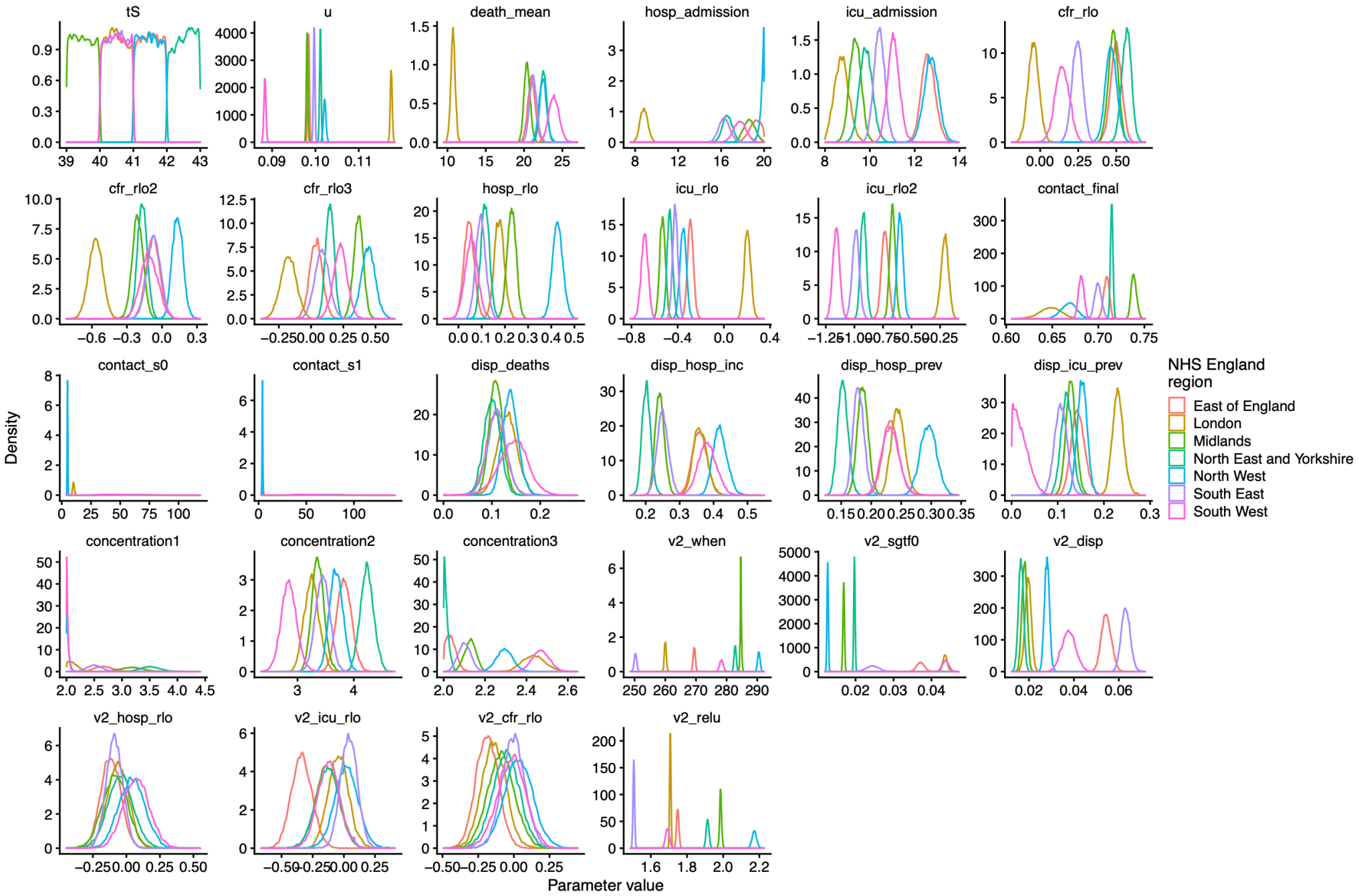
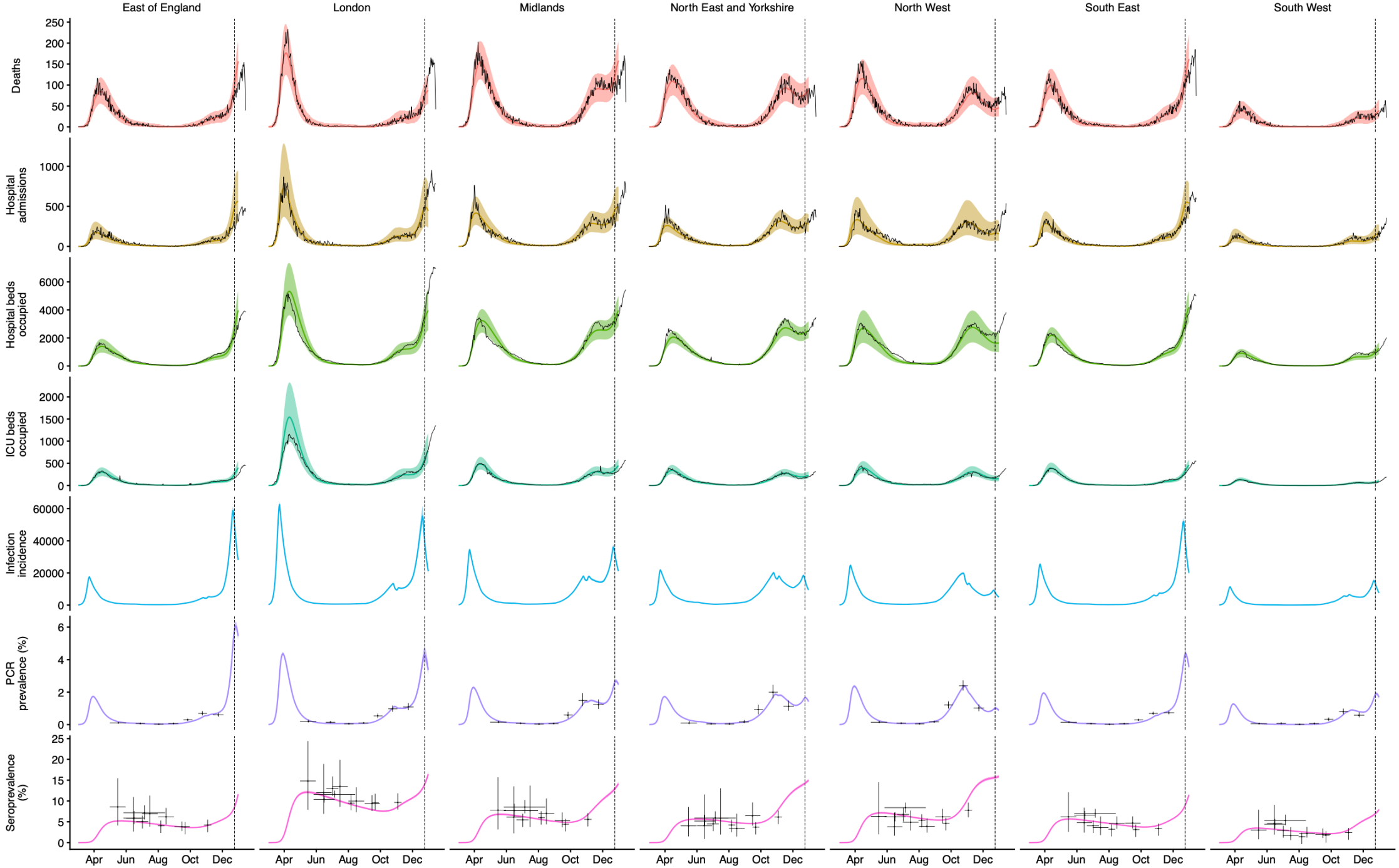
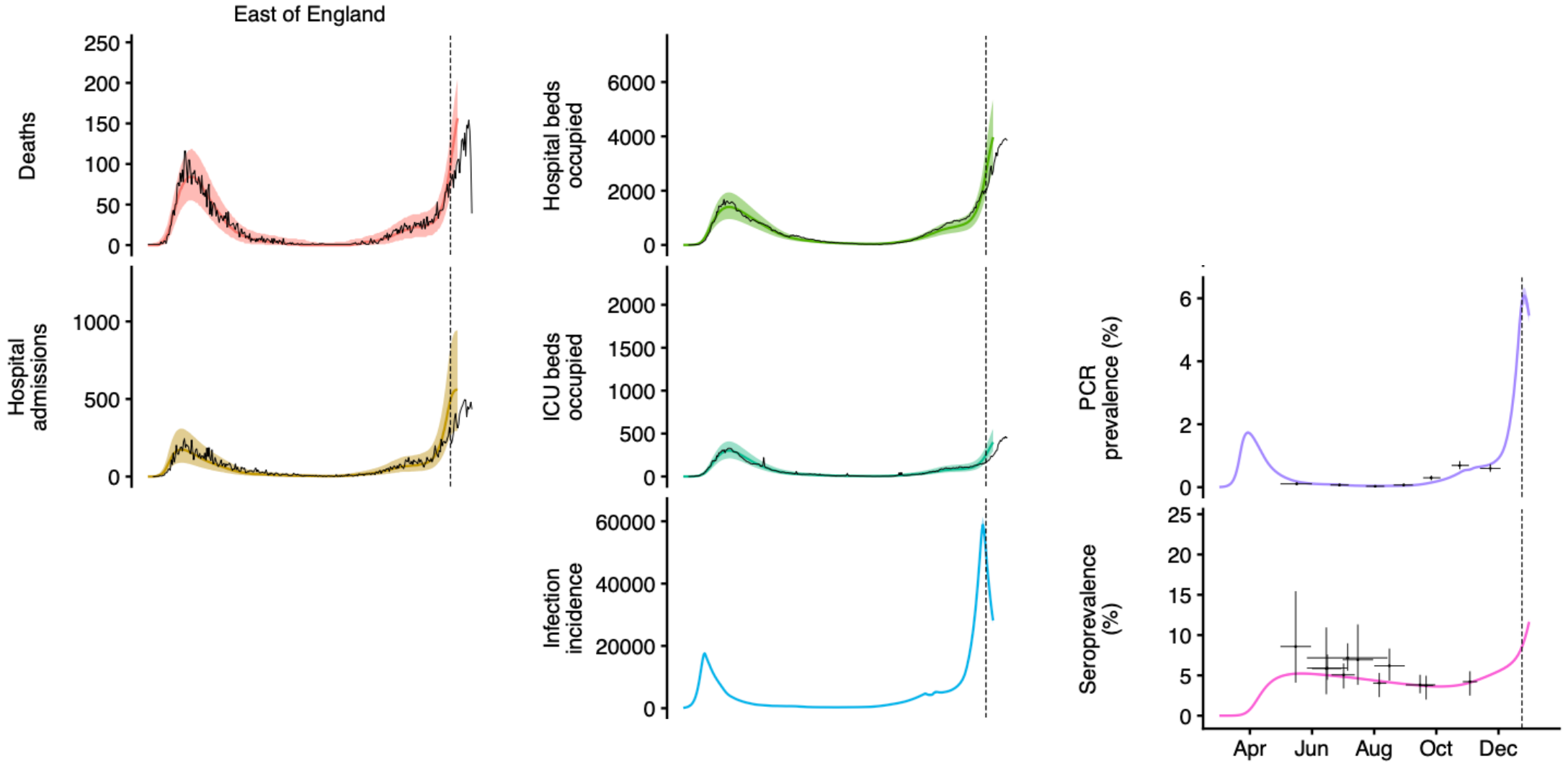

tS
u
death_mean
hosp_admission
icu_admission
cfr_rlo
cfr_rlo2
cfr_rlo3
hosp_rlo
icu_rlo
icu_rlo2
contact_final
contact_s0
contact_s1
disp_deaths
disp_hosp_inc
disp_hosp_prev
disp_icu_prev
concentration1
concentration2
concentration3
v2_when
v2_sgtf0
v2_disp
v2_hosp_rlo
v2_icu_rlo
v2_cfr_rlo
v2_relu
Density
Parameter value
NHS England region
East of England
London
Midlands
North East and Yorkshire
North West
South East
South West

Mathematical model: **covidm**

When fitting deaths, hospital admissions, hospital bed occupancy and ICU bed occupancy, we used a negative binomial likelihood with a fitted size parameter for each series and region. For seroprevalence and PCR prevalence, we used a skew-normal likelihood for each data point fitted to produce the same mean and 95% confidence interval as was reported for the data, and took the expected value of the model prediction over the date range during which the prevalence was measured. For fitting to VOC 202012/01 relative frequency over time in the three heavily affected NHS England regions, we used a beta-binomial likelihood with the daily proportion of detected samples that were VOC 202012/01 and a fitted dispersion parameter.

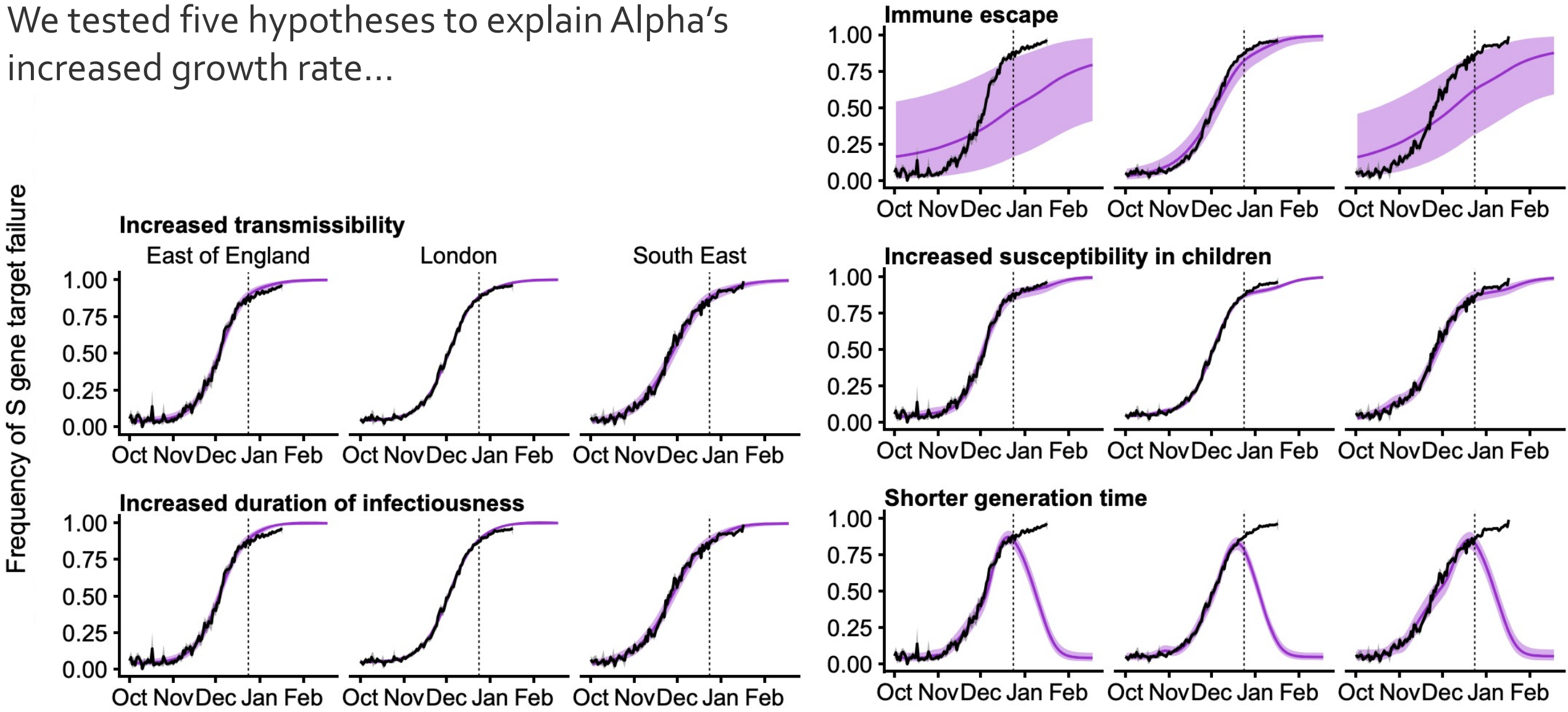

East of England
London
Midlands
North East and Yorkshire
North West
South East
South West
Deaths
Hospital admissions
Hospital beds occupied
ICU beds occupied
Infection incidence
PCR prevalence (%)
Seroprevalence (%)
Apr
Jun
Aug
Oct
Dec

Mathematical model: **covidm**



Mechanistic hypotheses for the rapid spread

We tested five hypotheses to explain Alpha's increased growth rate…



Mechanistic hypotheses for the rapid spread

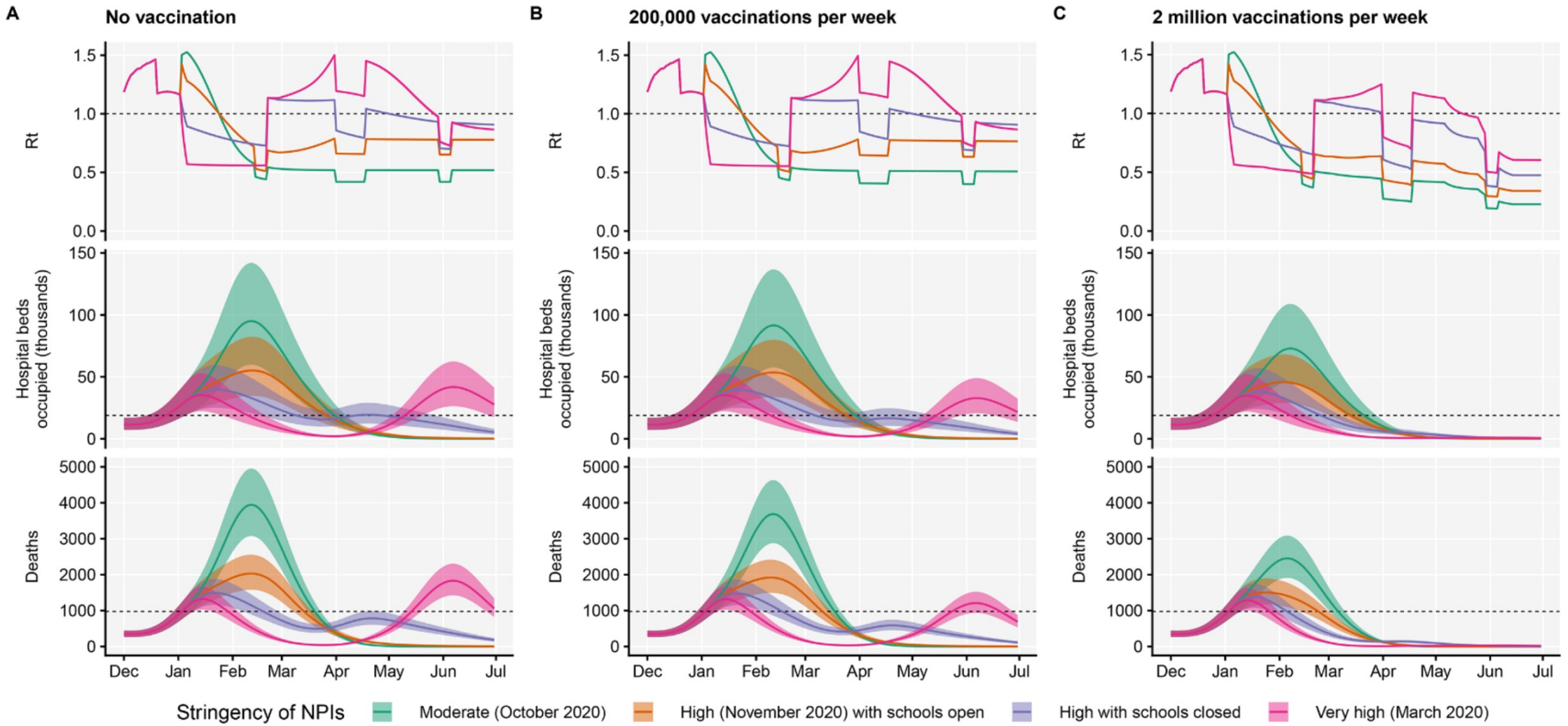
We tested five hypotheses to explain Alpha's increased growth rate…

Table S4.

Model comparison for dynamic transmission models.

Hypothesis	DIC	Predictive deviance	ΔDIC	ΔPD	Rank
Increased transmissibility	16246	6872	4	0	1
Increased duration of infectiousness	16242	8188	0	1316	2
Immune escape	19988	9314	3747	2442	4
Increased susceptibility in children	16385	8056	144	1184	3
Shorter generation time	17205	58373	963	51501	5
Combined	16295	18141	53	11269	—

Projections for vaccination and NPIs



N G Davies, S Abbott, R C Barnard, C I Jarvis, A J Kucharski, J Munday, C AB Pearson, T W Russell, D C Tully, A D Washburne, T Wenseleers, A Gimma, W Waites, K LM Wong, K van Zandvoort, J D Silverman, K Diaz-Ordaz, R Keogh, R M Eggo, S Funk, M Jit, K E Atkins, W J Edmunds, CMMID COVID-19 Working Group. 2021. Estimated transmissibility and impact of SARS-CoV-2 lineage B.1.1.7 in England. *Science* 372: eabg3055.

Thank you

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Thank you for your attention!