The effect of SARS-CoV-2 variant B.1.1.7 on symptomatology, re-infection and transmissibility

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Abstract

The new SARS-CoV-2 variant B.1.1.7 was identified in December 2020 in the South-East of England, and rapidly increased in frequency and geographic spread. While there is some evidence for increased transmissibility of this variant, it is not known if the new variant presents with variation in symptoms or disease course, or if previously infected individuals may become reinfected with the new variant. Using longitudinal symptom and test reports of 36,920 users of the Covid Symptom Study app testing positive for COVID-19 between 28 September and 27 December 2020, we examined the association between the regional proportion of B.1.1.7 and reported symptoms, disease course, rates of reinfection, and transmissibility. We found no evidence for changes in reported symptoms, disease severity and disease duration associated with B.1.1.7. We found a likely reinfection rate of around 0.7% (95% CI 0.6-0.8), but no evidence that this was higher compared to older strains. We found an increase in R(t) by a factor of 1.35 (95% CI 1.02-1.69). Despite this, we found that regional and national lockdowns have reduced R(t) below 1 in regions with very high proportions of B.1.1.7.

Introduction

In early December 2020, a phylogenetically distinct cluster of SARS-CoV-2 was genetically characterised in the South-East of England. The majority of cases had been detected in November with a small number detected as early as September[1]. Genomic surveillance reveals that this new variant, termed B.1.1.7, has a number of mutations of immunologic significance and is growing rapidly in frequency and spread.[2]

Preliminary evidence from epidemiological studies suggests the new strain is more transmissible. Davies et. al. found the new strain is 56% (95% CI 50-74) more transmissible[3] and Volz et. al. found the new strain increases the effective reproduction number R(t) by a factor of 1.4-1.8[4]. There is early data to suggest B.1.1.7 increases risk of death by ~1.3.[5] However, there is much that is still unknown. Little is known about the disease course of infections due to the new variant. Early evidence suggested that the new variant does not affect rates of hospitalisation[3], but it is crucial to assess whether the new variant alters the symptomatology, duration, and severity of disease. It is also important to understand whether B.1.1.7 alters the rate of asymptomatic infection and reinfection. Furthermore, early estimates of the new transmissibility of B.1.1.7 are uncertain and there is a need for additional estimates using independent data sources.

We make use of data from the COVID Symptom Study (CSS)[6] to investigate the symptomatology, disease course, and transmissibility of the new variant. The longitudinal dataset provides symptom reports and test results from a population of over 4 million adults living in the UK using the mobile application. By combining these data with surveillance data from the Covid-19 UK Genetics Consortium (COG-UK)[7] and a spike-gene target failure correlate in community testing data, we performed associative studies to study the symptoms, disease course, rates of reinfection, and transmissibility of the new variant.

Methods

Symptom study data

Longitudinal data were prospectively collected using the CSS app, developed by Zoe Global with input from King's College London (London, UK), the Massachusetts General Hospital (Boston, MA, USA), and Lund and Uppsala Universities (Sweden). The app guides users through a set of enrolment questions, establishing baseline demographic and health information. Users are asked to record each day whether they feel physically normal, and if not, to log any symptoms. Users are also asked to maintain a record of any COVID-19 tests, their type, and their results in the app. Users are able to record the same data on behalf of others, such as family members, to increase data coverage amongst those unlikely to use mobile applications, such as the elderly. More details about the app can be found in a study by Drew and colleagues[6].

Genomic data

We used data released on 13 January 2020 from COG-UK to extract time-series of the percentage of daily cases that came from the B.1.1.7 lineage in Scotland, Wales, and each of the seven National Health Service (NHS) regions in England. Northern Ireland was excluded due to the low number of samples in the COG-UK dataset. These data are produced by sequencing a sample of polymerase chain reaction (PCR) tests carried out in the community. Due to the delay of approximately two weeks[2] between PCR and genomic sequencing, we only used data from samples taken up to 31 December to avoid censoring effects.

Additionally, we used data from Public Health England (PHE) on the probable new variant captured in community cases in England using spike gene target failure (SGTF). It has been observed that one of the spike gene mutations in B.1.1.7 causes an SGTF in the test used in three of England's large laboratories used for analysis of community cases.[1] This failure results in a marker that is sensitive to B.1.1.7, but not necessarily specific, as other circulating variants also contain the mutation leading to an SGTF. Comparison to genomic data finds that from 30 November 2020 onwards more than 96% of cases with the SGTF were from lineage B.1.1.7[8]. The proportion of SGTF cases is made available in England for each of the 316 "Lower Tier" Local Authorities. We grouped these data to each NHS region using a population-weighted average to enable integration with other data sources.

Disease symptoms and course

In order to assess whether the symptomatology of infection from B.1.1.7 differed from previous variants, we investigated the change in symptom reporting from 28 September to 27 December 2020, covering 15 complete weeks over the period when the proportion of B.1.1.7 grew most notably in London, South East and East of England. We took the symptom reports from users reporting a positive swab test (PCR or lateral flow) in this period and examined the association between the proportion of B.1.1.7 in each region and the proportion of reports per week for each

symptom, accounting for age, sex, and two seasonal environmental confounders: regional temperature and humidity, in a linear regression. Seasonal confounders were calculated each day as the average of the temperature and relative humidity at two meters above the surface, averaged across each region considered.[9]

We also examined the relation between proportion of B.1.1.7 and disease burden, measured here as the total number of different symptoms reported over a period of two weeks before and two weeks after the test, and the relation with asymptomatic infection, defined as users reporting a positive test result but no symptoms in the two weeks before or after the test. Using similar corrections for demographic and seasonal environmental confounders, we investigated the rate of self-reported hospital visits. We also investigated the proportion of individuals reporting long symptom duration using a previously published definition of continuous symptoms reported for at least 28 days.[10] To avoid censoring effects, both hospitalisation and long duration analyses included symptom reports extended up to 18 January, and the long duration analysis only considered reports of positive tests up to 21 December.

Reinfection

We defined possible reinfection as the presence of two reported positive tests separated by more than 90 days with a period of reporting no symptoms for more than seven days before the second positive test. We calculated the proportion of possible reinfection among individuals reporting their first positive test before 1 October 2020 and the correlation between number of possible reinfections and number of reported positive tests. To assess whether the risk of reinfection was stronger in the presence of the new variant, we calculated the correlations between the number of possible reinfections and the proportion of B.1.1.7 cases regionally over time.

Transmissibility

Daily incidence for Scotland, Wales, and each of the seven NHS regions in England were produced from the period 1 October 2020 to 27 December 2020 using data from the CSS app and previously described methodology[11]. These data were used to determine the number of new daily cases from both old variants and from B.1.1.7 in each region. R(t) was estimated separately for the old and new variants using methods described in[11]. We compared both multiplicative and additive differences of the new and old R values for days when the proportion of B.1.1.7 in a region was greater than 3%. While data is not available for the proportion of B.1.1.7 in January, we also computed total incidence and R from 1 October to 16 January to see the effect of national lockdown in England on these measures.

Results

Symptom study data

Table 1 shows the demographic data for the cohort studied. From 24 March to 27 December 2020, 4,327,245 participants from the UK signed up to use the app. We excluded users living in Northern Ireland due to the low number of sign-ups (38,976), 383,352 users lacking information on sex, and 2,175,979 who had not logged in the app during the period 28 September to 27 December 2020, leaving a total of 1,767,914 users. Between them, these users recorded 65,606,869 logs in the app between 28 September and 27 December. In this period, 497,989 users reported a swab test. 55,192 of these reported a positive test, and we investigated the symptom reports of 36,920 of those whose region was known and who reported as healthy on app sign-up.

		Overall		Tested		Tested positive		Signed up healthy with reporting around positive test	
		N	%	N	%	N	%	N	%
Users		1,767,914	---	497,989	---	55,192	---	40,463	
Daily reports*		65,613,697		19,154,601		1,514,244			
Age in years mean (std)		48.4 (19.3)	---	46.06 (17.8)	---	42.1 (16.8)	---	42.9 (17.0)	
	≤18	163,112	9.2	40,717	8.2	5,468	9.9	3,874	9.6
	19 - 64	1,234,259	69.8	381,900	76.7	45,149	81.8	32,878	81.2
	≥ 65	370,543	20.9	72,741	14.6	4,367	7.9	3,600	8.9
	Invalid	5,576	0.3	2,631	0.5	208	0.3	111	0.3
Sex	Female	1,046,074	59.2	315,875	63.4	34,516	62.5	24,844	61.4
	Male	720,562	40.8	181,110	36.4	20,546	37.2	15,545	38.4
	Intersex	79	<0.1	21	<0.1	3	<0.1	3	<0.1
	Prefer not to say	1,199	0.1	983	0.2	127	0.2	71	0.2
Region	South East	342,881	19.4	97,143	19.5	8,762	16.0	6,555	16.2

	East of England	196,063	11.1	57,680	11.6	5,373	9.8	4,037	10.0
	London	227,004	12.8	81,940	16.5	9,733	17.8	7,384	18.2
	Midlands	198,350	11.2	57,582	11.6	6,695	12.2	4,756	11.8
	North East and Yorkshire	156,999	8.9	42,986	9.1	5,292	9.7	3,744	9.3
	North West	123,201	7.0	45,156	9.1	6,180	11.3	4,399	10.9
	South West	186,372	10.5	46,780	9.4	3,685	6.7	2,637	6.5
	Scotland	87,263	4.9	13,793	2.8	1,589	2.9	1,049	2.6
	Wales	82,886	4.7	16,471	3.3	3,092	5.6	2,359	5.8
	Not known	165,164	9.3	38,458	7.5	4,638	8.0	3,543	8.8

Table 1. Characteristics of GB app users active in the period 28 September - 27 December 2020

* Reports logged between 28 September - 27 December. For some analyses we took further reports from an extended time period 14 September 2020 - 18 January 2021

**May be more than one test per individual as the overall number contains failed tests and unknown results

Genomic data

In the period between 27 September 2020 and 31 December 2020, 98,170 sequences were made available by COG-UK, corresponding to 4.4% of the 2,207,476 cases recorded in this period.[12] 16,224 sequences (16.5%) were variant B.1.1.7. Considering the mean of the rolling average across December, the three regions with the largest proportion of B.1.1.7 are the South East, London, and East of England. The three regions with the lowest proportion are Wales, the North East and Yorkshire, and the North West. SGTF data was made available in England on a weekly basis from 10 November 2020 to 29 December 2020. Of the 700,590 cases reported in this period, 295,404 (42.2%) caused an SGTF. Examining the COG-UK data from England in the same time period, we find 34.6% cases are B.1.1.7. The difference is in part attributable to the SGTF being a nonspecific marker of B.1.1.7: in the week from 9-15 November 81% of cases with an SGTF were B.1.1.7, while from 30 November at least 96% of cases with the SGTF were from B.1.1.7. Figure 1 shows how the proportion of the new variant changed over time in regions of the UK using COG-UK and the SGTF data.

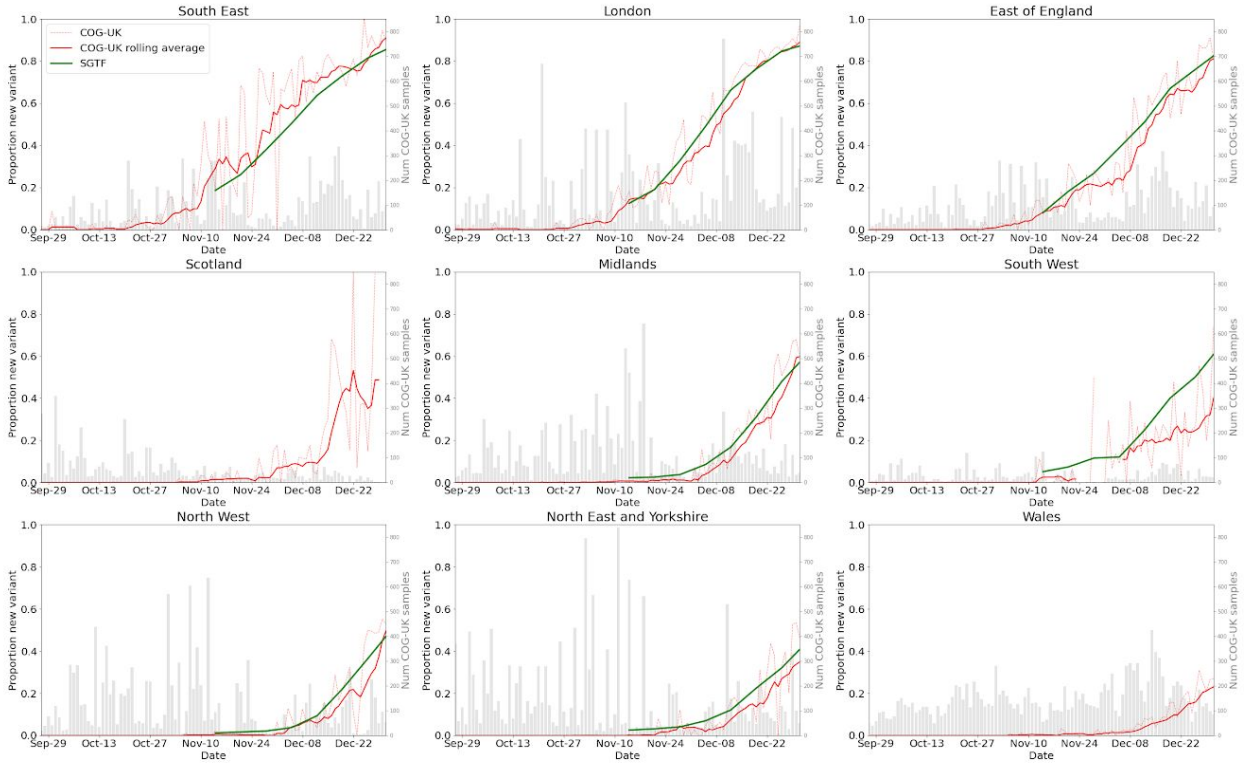

Figure 1. Presence of B.1.1.7 in each of the 7 NHS regions in England, and Scotland and Wales, as measured using genomic surveillance data (COG-UK) and SGTF data. SGTF data are not available for Scotland or Wales.

Disease symptoms and course

Figure 2 illustrates the variation of symptom occurrence over time considering a one-week window smoothed over 3 time points as a function of time, and Supplementary Figure 1 shows how these symptoms vary as a function of the proportion of B.1.1.7. These results show no change in the proportion of users reporting each symptom with the new variant.

Figure 3 shows the variation of total number of symptoms reported, the total number of asymptomatic infections, self-reported hospital visits, and symptoms of long duration over time; Supplementary Figure 2 shows how these plots vary with proportion of B.1.1.7. When correcting for mean age, sex, ambient temperature and humidity there was no evidence of an association between B.1.1.7 and either the number of symptoms reported over a 4-week window, the number of hospitalisations, long symptom duration, or proportion of asymptomatic case (Supplementary Table 1).

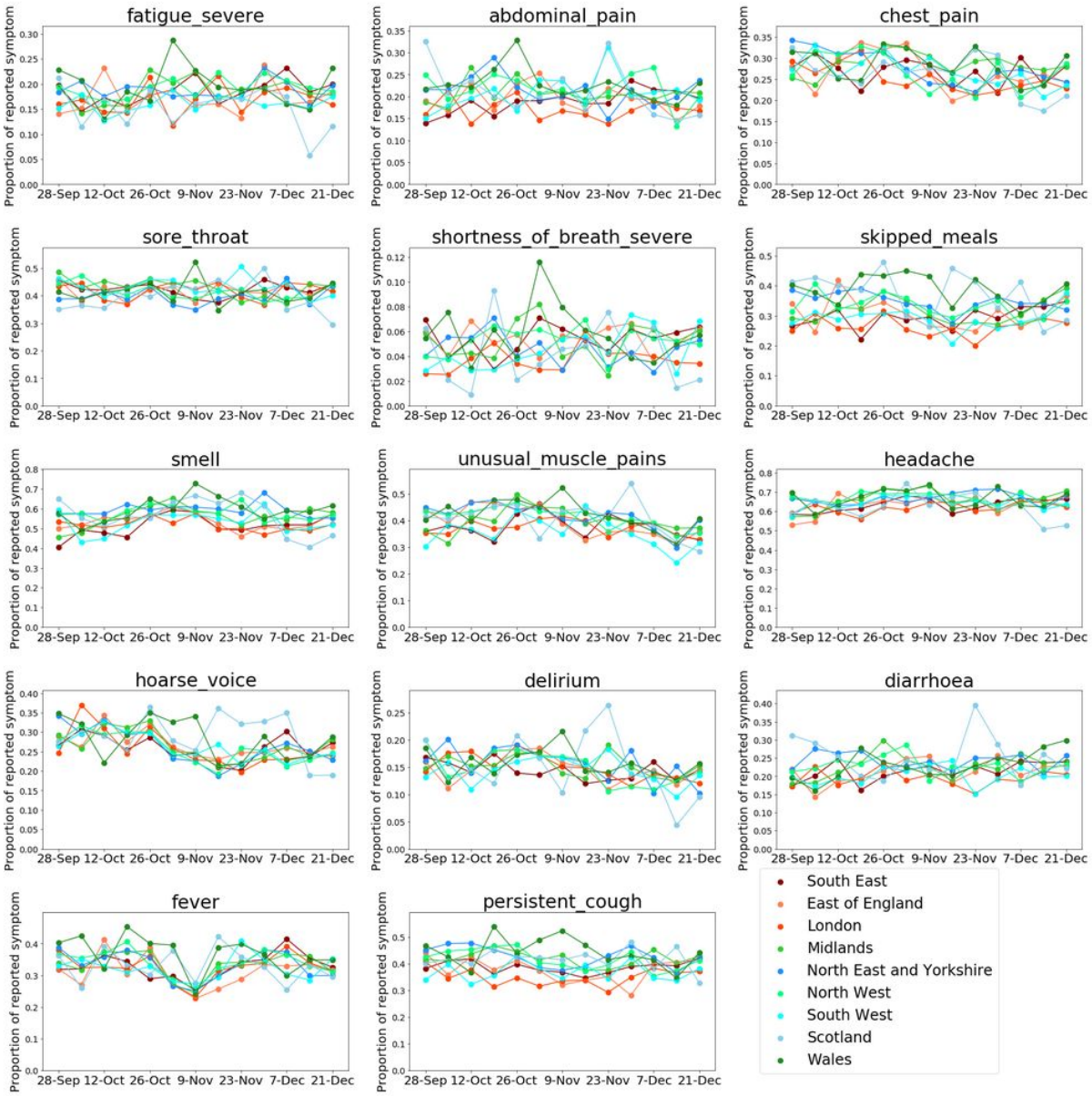

Figure 2. Regional plots of the frequency of reporting of symptoms over time for each reported symptom. Drop in fever reporting in early November was caused by a change in the question wording; this wording was subsequently reverted a week later.

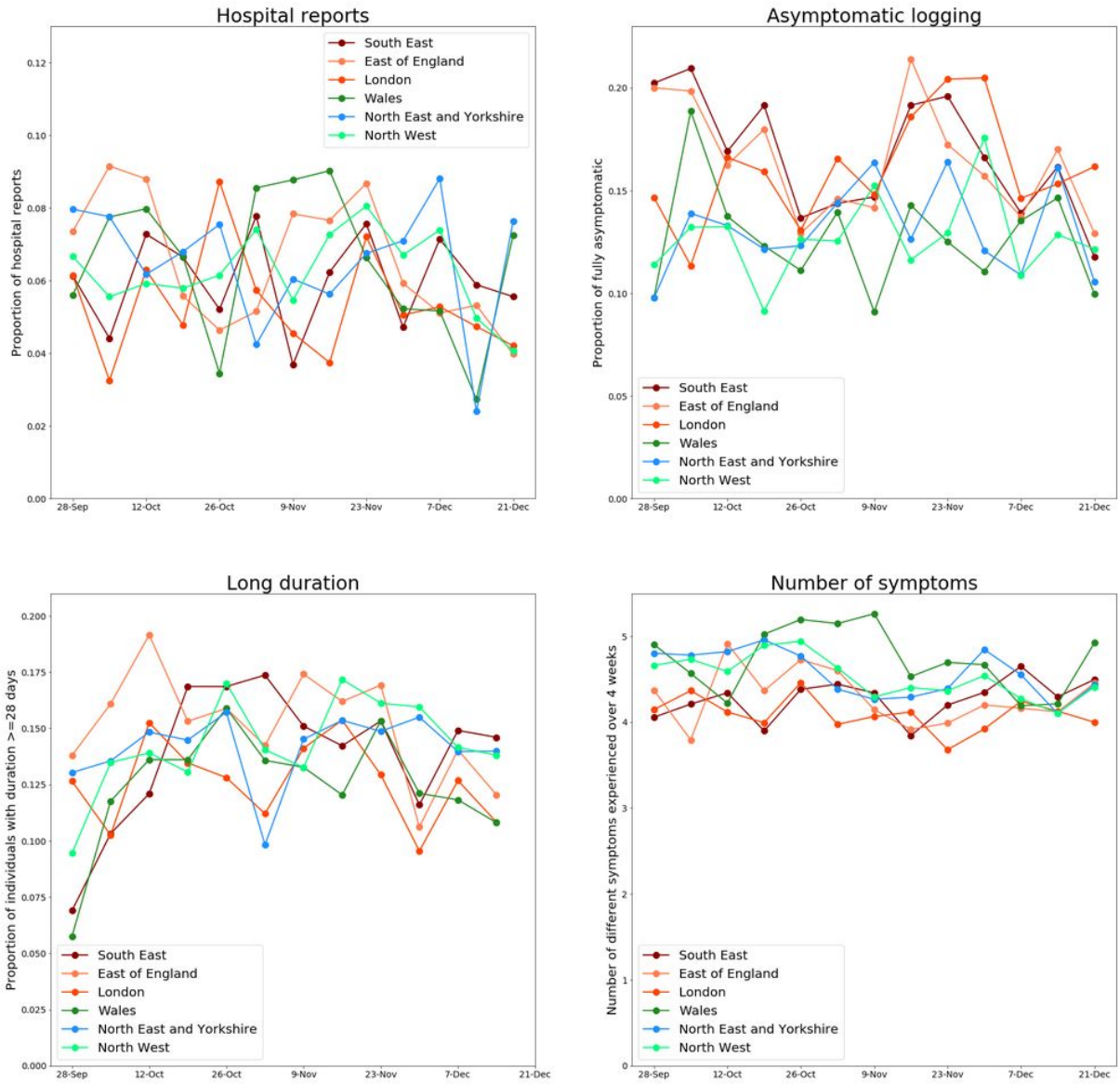

Figure 3. Regional plot of hospitalisation report, proportion of asymptomatic, report of long duration and number of experienced symptoms around test. For the study of long duration, tests are only considered up to 21 December counting reports up to 18 January 2021 to limit right censoring. Only symptomatic individuals for which duration can be ascertained are included.

Reinfection

Overall, we identified 304 individuals reporting two positive tests with more than 90 days between the two. Among these individuals, symptom reporting allowed us to identify 249 for which there is a period of at least 7 symptom-free days in between positive tests among the 36,509 individuals having reported a positive swab test before 1 October 2020 (0.7%, 95% CI 0.6-0.8). Among those 249, daily reports were available in the periods around both of the positive tests for 173. There was no difference in reinfection reporting rates across the different NHS regions (p=0.1). Figure 4 shows the evolution in the number of possible reinfections along

with reported positive cases (red line) and proportion of B.1.1.7 (green line). For all regions (except Scotland), reinfection occurrences were more positively correlated with the overall regional rise in cases rather than the regional rise in the new variant percentage (Number of cases:reinfection, Spearman rho 0.55 to 0.69 [$p<0.05$] for South East, London and East of England; % new variant:reinfection, Spearman rho 0.37 to 0.55 in the same regions). Supplementary Table 2 shows the bootstrapped median values of correlation compared across the different regions and the outcome of a Mann-Whitney U test across the bootstrapped distributions.

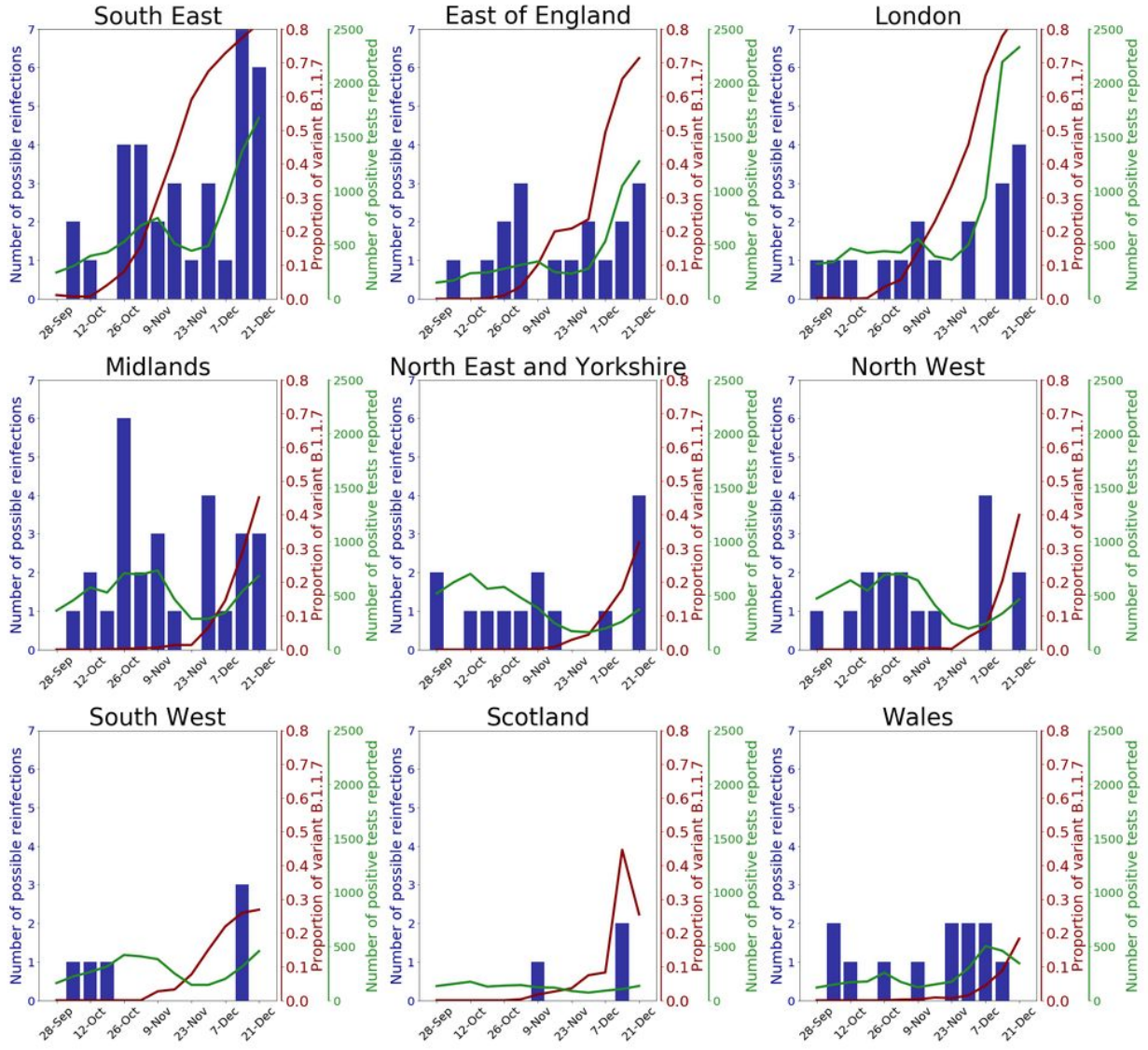

Figure 4. Number of reinfection reports by region according to week of second infection, along with the total number of positive tests reported through the app and the proportion of B.1.1.7 in circulation.

Transmissibility

Figure 5 shows incidence and R(t) for the old and new variants in the three regions in England with the highest proportions of the new variant. Results consistently show the R(t) of B.1.1.7 to be greater than that of other variants. The mean (95% CI) of the additive increase in R for B.1.1.7 was 0.34 (0.02-0.66), and the multiplicative increase was 1.35 (1.02-1.69). England exited its second national lockdown on 2 December, leading to a change in behaviour and R(t). When considering only the period after the second lockdown ended, we find 0.28 (0.01-0.61) for the additive and 1.28 (1.02-1.61) for the multiplicative increases. Supplementary Figure 3 shows the same using the SGTF data, with analysis limited to the period after 1 December when at least 95% of all SGTF cases were B.1.1.7. These data are provided weekly, and linear interpolation was used to obtain daily estimates, leading to smoother estimates for variant-specific incidence and R(t). Using these values, we find R(t) of B.1.1.7 has an additive increase of 0.26 (0.15-0.37) and a multiplicative increase of 1.25 (1.17-1.34).

On 19 December 2020 London and much of the South East and East of England were placed in 'Tier 4' restrictions, enforcing stricter rules for social distancing and decreased human-to-human contact that stopped short of nationwide measures. On 5 January 2021 the whole of England was placed in national lockdown. Figure 6 shows overall incidence and R(t) for the longer period from 1 October 2020 to 16 January 2021 in the three regions with the largest proportion of B.1.1.7. The proportion of B.1.1.7 in these regions in January is at least 80%, assuming the proportion has not decreased from the end of December. The combination of Tier 4 and national lockdown measures were able to bring R(t) to ~ 0.8 in all three of these regions.

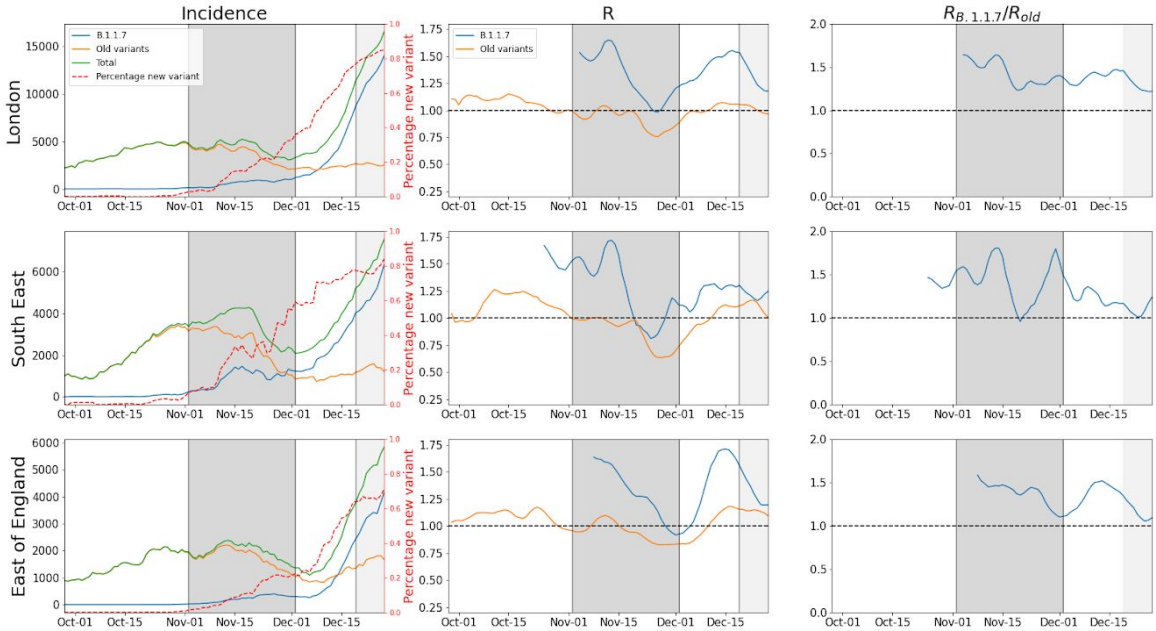

Figure 5. Incidence and R(t) for the old and new variants, along with the ratio between these R values, for the three regions in England with the largest proportion of B.1.1.7. Dark grey regions indicate national lockdowns, light grey the period where London and much of the South East and East of England were placed in Tier 4 restrictions.

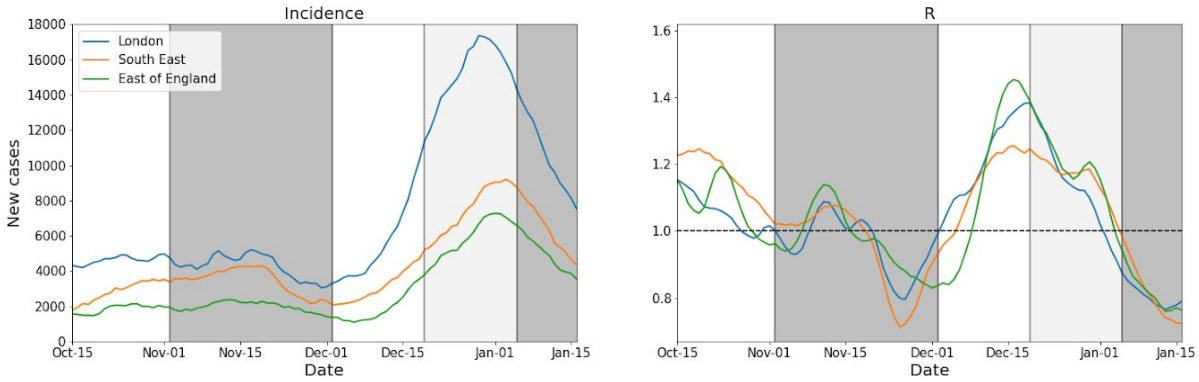

Figure 6. Total incidence and R(t) for the three regions with the highest proportion of B.1.1.7 in December, extended to capture the third national lockdown beginning 5 January 2021. Dark grey regions indicate national lockdowns, light grey indicate the period where London and much of the South East and East of England were placed in Tier 4 restrictions.

Discussion

Using data collected through community reporting of symptoms and tests via the COVID Symptom Study app, we investigated whether the appearance of the variant B.1.1.7, first detected in a sample from England in September 2020, was related to differences in symptom reporting, disease duration, hospitalisation, asymptomatic infection, risks of reinfection, and transmissibility for users reporting a positive test result between 28 September and 27 December 2020.

We did not find associations between the proportion of B.1.1.7 in circulation and disease severity, either measured by the number of different reported symptoms over the 4-week window around each positive test, hospitalisations, any of the different symptoms, or the proportion of individuals with long symptom duration when correcting for variations in demographic characteristics (age, sex) and seasonal variables (temperature, humidity). The proportion of individuals with duration of symptoms ≥28 days without a break of more than seven days did not change in association with the presence of variant B.1.1.7. Likewise the proportion of users with asymptomatic disease did not significantly change as B.1.1.7 increased in prevalence.

A recent study reported that individuals infected with B.1.1.7 were more likely to report a cough, sore throat, fatigue, myalgia and fever in the seven days preceding the test, and less likely to report a loss of taste or smell.[13] It is not clear if this report adjusted for age, sex, and environmental factors. If we do not correct for these factors we find some significant changes in symptom reporting but in our view these are not likely to be due to B.1.1.7 (Supplementary Figure 4). The periods considered also differed; we considered symptoms reported both two weeks before and after the positive test result. Further opportunity to study symptoms with B.1.1.7 in different contexts are required to be definitive.

We observed, based on 249 potential cases, a very low rate of possible reinfection of 0.7% (95% CI 0.6- 0.8). This rate is consistent with another study of 6614 healthcare workers that had previously tested positive for Covid-19, finding 44 possible reinfections (0.66%).[14] Our reinfection rate did not vary consistently across regions or time, which would be consistent with the hypothesis that reinfection is no more likely in the context of B.1.1.7. This may mean that if adequate immunity is built over the first infection it may be sufficient to protect against reinfection in the presence of B.1.1.7. Ultimately this is a positive sign that the immunity built through vaccination against the old variants could also be useful against B.1.1.7. This is in line with initial reports regarding the efficacy of vaccines designed for early strains against this newer variant.[15,16]

We found an increase in the reproduction number R(t) in association with the B.1.1.7 variant: we found a multiplicative increase in R(t) of ~ 1.35 (95% 1.02-1.69), compatible with estimates from Volz et al.[3,4], of 1.4-1.8, and Davies et al. who estimated a transmissibility increase of 1.56 (95% CI 1.50-1.74).[3,4] These increases in transmissivity have worrying implications for the ability of lockdown measures to control B.1.1.7, given R(t) was estimated to be 0.7-0.9 during the first national lockdown in England.[17] Despite this, we found R(t) to be ~ 0.8 in the three regions in England with at least 80% of B.1.1.7, with very clear response to lockdown measures. This could indicate that the true increase in transmissivity is at the lower end of the available estimates, or that the increase in transmissivity estimated outside of lockdown cannot be extrapolated to lockdown, perhaps due to B.1.1.7 responding differently to lockdown measures than the old variants.

Strengths

The large, longitudinal nature of the CSS data, with good coverage of the UK population, provides a unique opportunity to study potential changes in symptomatology, symptom severity, and disease duration. The ability to match tests and symptom reports over long periods further allows us to measure possible reinfection rates. Our data also offers the ability to provide a valuable complementary measure to existing measurements of the increased transmissibility of B.1.1.7: we were able to use real-time, representative incidence estimates to measure R(t), whilst other studies have relied on deaths and hospitalisations, which are lagged, or community case numbers which do not reflect true infection numbers.

Limitations

Our study is limited by reliance on self-report of symptoms and test results, although previous publications from our group show that our figures triangulate well with other study designs[11]. Despite the ability of the app users to correct any wrong input of their test results, errors still may be made. We make the assumption that testing positive for SARS CoV2 after an interval of 90 days with at least seven days of freedom from symptoms in the interval is consistent with reinfection. Repeated positive testing has been reported shortly after hospital discharge[18] and showed that PCR positivity could be detected up to 28 days post symptom resolution. While the chosen cut-off of 90 days between two positive tests is unlikely to be due to prolonged PCR positivity, this cannot be ruled out, but would only affect a small number of cases. Viral sequencing of the two infections would ideally be required to confirm reinfection. Despite correcting for changes in temperature and humidity, a possible limitation in the study is that comparisons in symptoms are made across time, and seasonal effects (e.g. on symptoms) may not have been fully taken into account[19]. As we lack information on the disease strain of individual positive infections reported through the app, the study is associative in nature; and we cannot account for the effects of other potentially circulating variants.

Conclusions

We examined the effect of SARS-CoV-2 variant B.1.1.7 on the symptoms, disease course, rates of reinfection, and transmissibility in the UK. We found no change in symptoms and no increase in overall disease severity. We found a low rate of reinfection (0.7%) and no evidence of increased rates associated with B.1.1.7. We found an increase in R(t) of ~ 1.38 (95% CI 1.06-1.71), but evidence that lockdown measures are effective even in regions with very high (>80%) proportions of B.1.1.7.

Ethics

Ethics has been approved by KCL Ethics Committee REMAS ID 18210, review reference LRS-19/20-18210 and all participants provided consent.

Data sharing

Data collected in the COVID Symptom Study smartphone application are being shared with other health researchers through the UK National Health Service-funded Health Data Research UK (HDRUK) and Secure Anonymised Information Linkage consortium, housed in the UK Secure Research Platform (Swansea, UK). Anonymised data are available to be shared with researchers according to their protocols in the public interest (https://web.www.healthdatagateway.org/dataset/fddcb382-3051-4394-8436-b92295f14259). US investigators are encouraged to coordinate data requests through the Coronavirus Pandemic Epidemiology Consortium (https://www.monganinstitute.org/cope-consortium).

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Declaration of interests

AM, LP, SS, JCP, CH, JW are employees of Zoe Global Ltd. TDS is a consultant to Zoe Global Ltd. DAD and ATC previously served as investigators on a clinical trial of diet and lifestyle using a separate smartphone application that was supported by Zoe Global.

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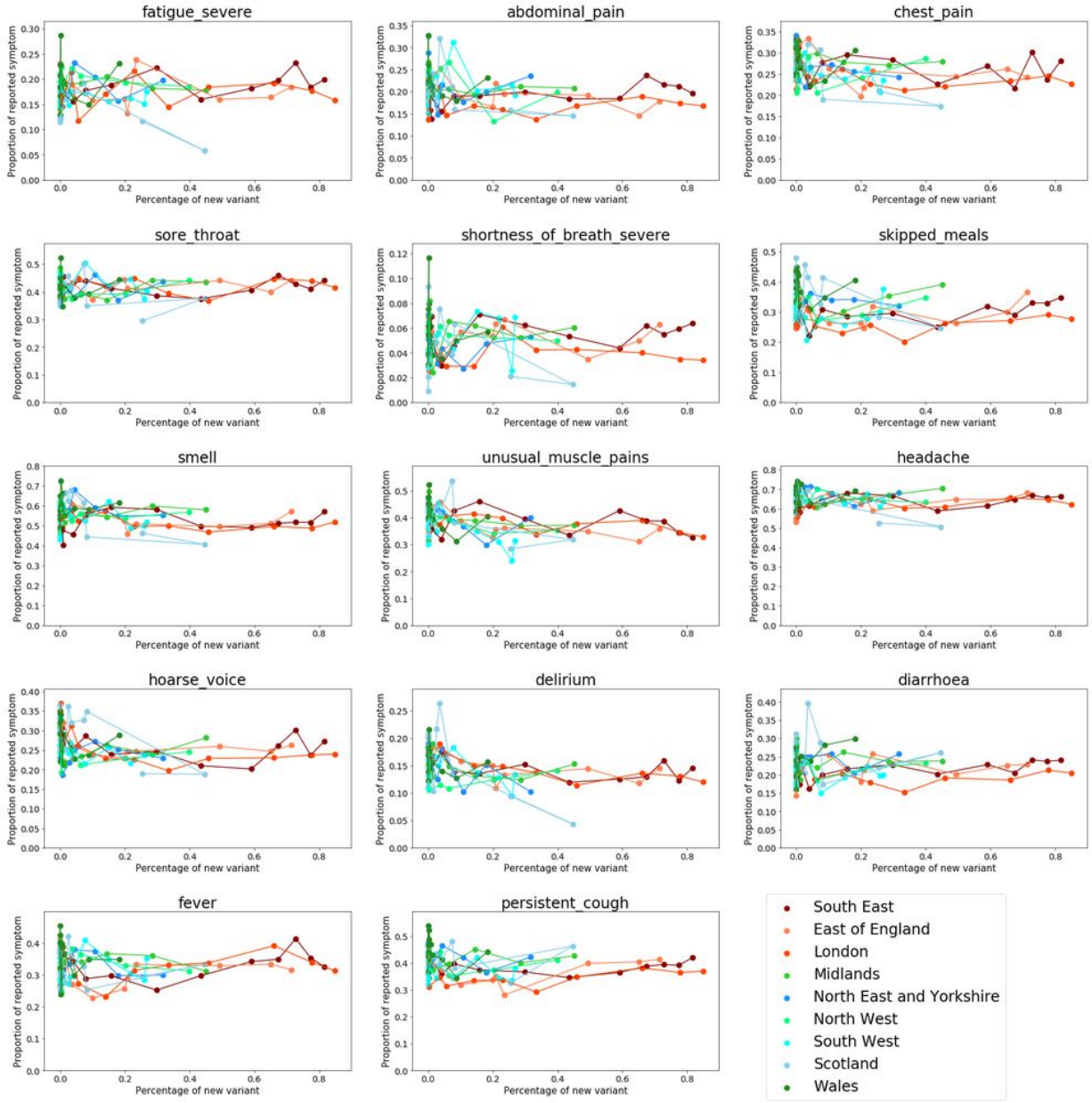
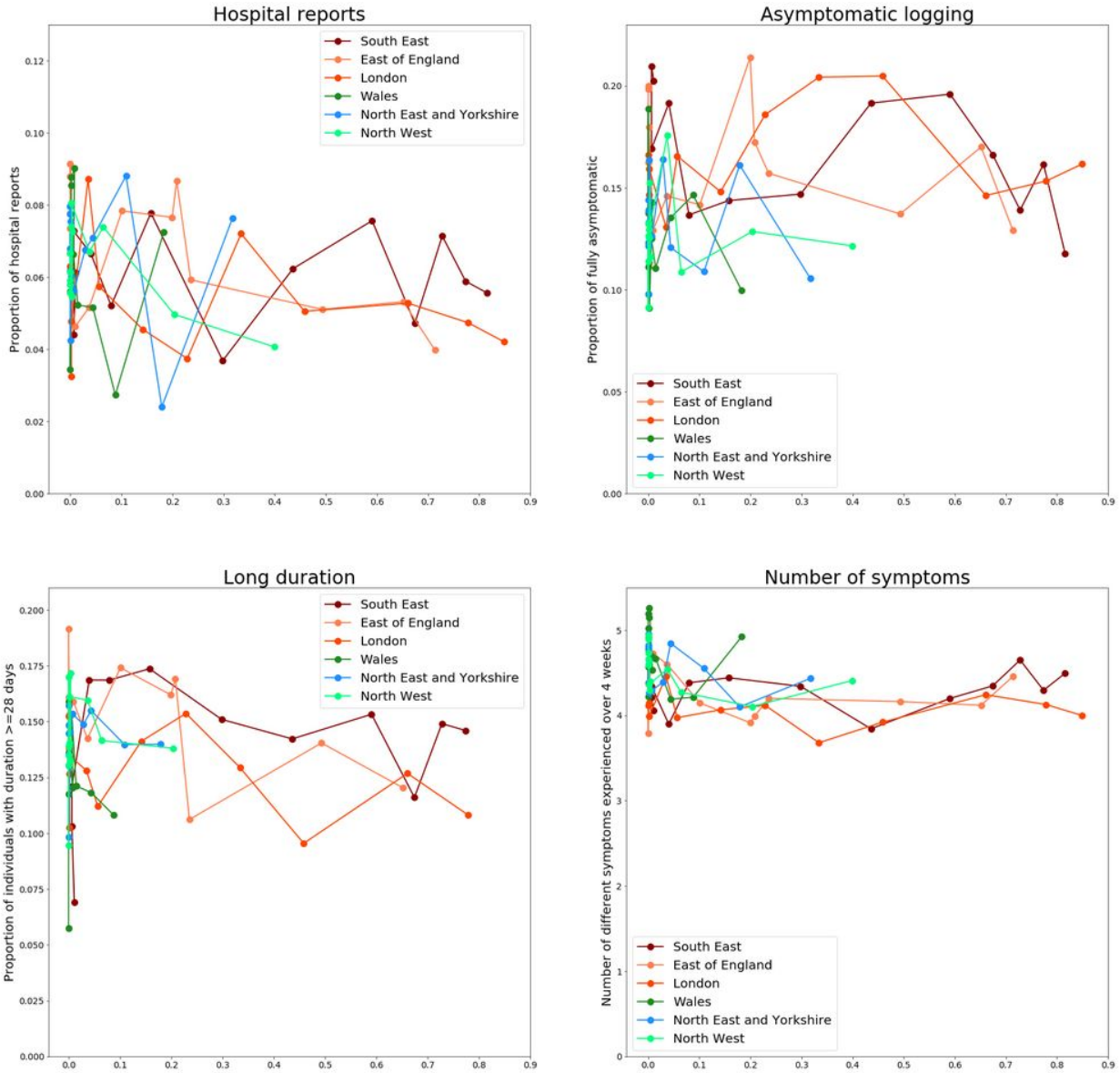
Supplementary material

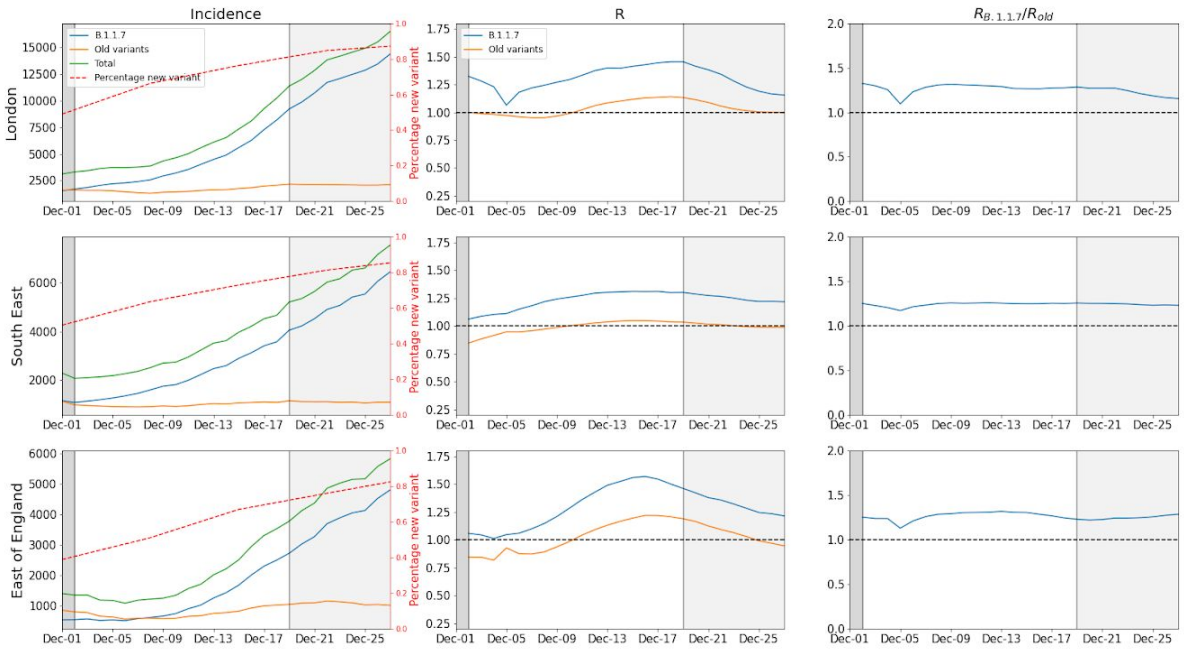
Supplementary tables and figures



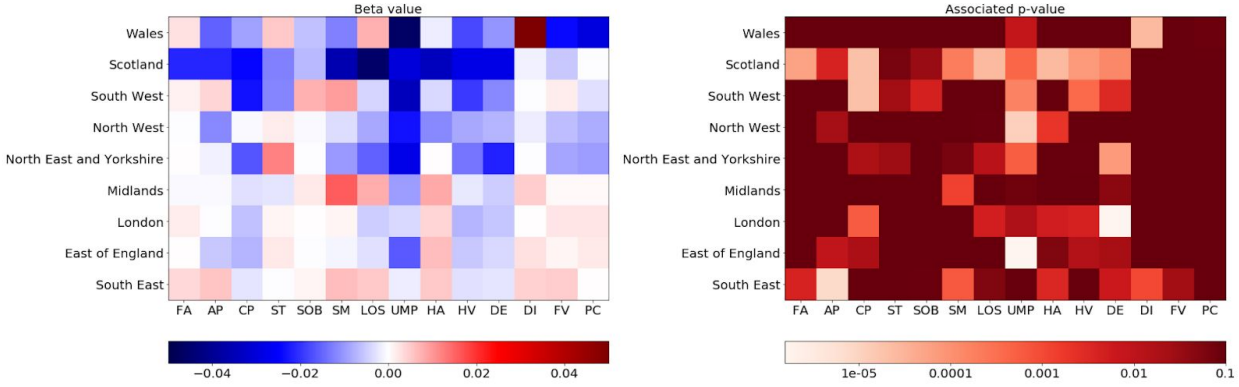
Supplementary Figure 1. Regional plots of the frequency of reporting of symptoms over time for each reported symptom, against the proportion of B.1.1.7.. Drop in fever reporting in early November was caused by a change in the question wording; this wording was subsequently reverted a week later.



Supplementary Figure 2. Regional plot of hospitalisation report, proportion of asymptomatic, report of long duration and number of experienced symptoms around test against proportion of B.1.1.7. For the study of long duration, tests are only considered up to 21 December counting reports up to 18 January 2021 to limit right censoring. Only symptomatic individuals for which duration can be ascertained are included.



Supplementary Figure 3. Incidence and R(t) for the old and new variants, along with the ratio between these R values, for the three regions in England with the largest proportion of B.1.1.7, using SGTF data. Dark grey regions indicate national lockdowns, light grey shaded the period where London and much of the South East and East of England were placed in Tier 4 restrictions.



Supplementary Figure 4: Colour plot of beta values and associated p-values for each region and symptoms when investigating association between symptom report (in a 4 week window around the test) and proportion of variant B.1.1.7 and without any correction for personal characteristic or seasonal feature. Note that the p-values are capped at 0.1. Beta-values are presented for an increase of 0.1 in the proportion of variant B.1.1.7.

Key: FA - fatigue, AP - abdominal pain, CP - chest pain, ST - sore throat, SOB - shortness of breath, SM - skipped meals, LOS - loss of smell, UMP - unusual muscle pains, HA - headache, HV - hoarse voice, DE - delirium, DI - diarrhoea, FV - fever, PC - persistent cough

	Proportion of fully asymptomatic	Number of symptoms reported over 4 weeks around test	Proportion of hospital reports	Proportion of individuals with symptom duration >= 28days
South East	0.001 [-0.015;0.017] ; 0.901	-0.021 [-0.163;0.121] ; 0.733	-0.002 [-0.011;0.007] ; 0.624	-0.003 [-0.009;0.004] ; 0.37
East of England	0.002 [-0.008;0.012] ; 0.588	-0.012 [-0.153;0.13] ; 0.851	-0.002 [-0.01;0.006] ; 0.52	-0.002 [-0.015;0.01] ; 0.689
London	-0.005 [-0.014;0.005] ; 0.298	0.031 [-0.055;0.116] ; 0.423	-0.002 [-0.007;0.003] ; 0.298	-0.002 [-0.013;0.009] ; 0.682
Midlands	-0.016 [-0.028;-0.004] ; 0.014	0.02 [-0.133;0.173] ; 0.766	-0.002 [-0.007;0.003] ; 0.328	0.002 [-0.01;0.015] ; 0.671
North East and Yorkshire	-0.011 [-0.046;0.023] ; 0.462	-0.086 [-0.444;0.272] ; 0.586	-0.011 [-0.04;0.019] ; 0.426	0.015 [-0.022;0.052] ; 0.349
North West	-0.005 [-0.023;0.013] ; 0.512	-0.053 [-0.218;0.111] ; 0.468	-0.009 [-0.015;-0.004] ; 0.005	0 [-0.031;0.031] ; 0.98
South West	0.015 [-0.011;0.04] ; 0.217	-0.261 [-0.437;-0.085] ; 0.01	-0.001 [-0.02;0.018] ; 0.902	-0.048 [-0.091;-0.004] ; 0.036
Scotland	0.022 [-0.013;0.058] ; 0.177	-0.4 [-0.711;-0.088] ; 0.019	-0.018 [-0.037;0.002] ; 0.073	-0.012 [-0.027;0.003] ; 0.107
Wales	-0.002 [-0.05;0.047] ; 0.943	-0.041 [-0.683;0.601] ; 0.884	-0.008 [-0.045;0.028] ; 0.602	-0.053 [-0.141;0.035] ; 0.192

Supplementary Table 1: Beta coefficient of the variant proportion when evaluating association with number of reported symptoms, asymptomatic rate, proportion of hospital report and proportion of individuals with duration >28 days (among symptomatic) across the different regions when correcting for age, sex, temperature and humidity. All values are presented for an increase in 0.1 in the proportion of variant B.1.1.7. All results are presented in the form mean [CI]; p-value

Region	Correlation Variant/Reinfection	Correlation New cases/Reinfection	p-value
South East	0.55	0.69	<0.001
East of England	0.51	0.56	<0.001
London	0.46	0.62	<0.001
Midlands	0.28	0.75	<0.001
North East and Yorkshire	-0.02	0.30	<0.001
North West	0.06	0.43	<0.001
South West	-0.35	0.05	<0.001
Scotland	0.59	-0.15	<0.001
Wales	0.07	0.26	<0.001

Supplementary Table 2: Comparison of regional correlation over time between proportion of B.1.1.7 and number of possible reinfections and between new reported cases and number of possible reinfections. Medians over 100 bootstrapped samples are calculated for each and compared using a Mann-Whitney U test.

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