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# Geo-social gradients in predicted COVID-19 prevalence in Great Britain: results from 1 960 242 users of the COVID-19 Symptoms Study app

Ruth C E Bowyer,<sup>1</sup> Thomas Varsavsky,<sup>2</sup> Ellen J Thompson,<sup>1</sup> Carole H Sudre,<sup>2,3</sup> Benjamin A K Murray,<sup>2</sup> Maxim B Freidin,<sup>1</sup> Darioush Yarand,<sup>1</sup> Sajaysurya Ganesh,<sup>4</sup> Joan Capdevila,<sup>4</sup> Elco Bakker,<sup>4</sup> M Jorge Cardoso,<sup>2</sup> Richard Davies ,<sup>4</sup> Jonathan Wolf,<sup>4</sup> Tim D Spector,<sup>1</sup> Sébastien Ourselin,<sup>2</sup> Claire J Steves,<sup>1</sup> Cristina Menni

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<sup>1</sup>Twin Research, King's College London, London, UK

<sup>2</sup>School of Biomedical Engineering & Imaging Sciences, King's College London, London, UK

<sup>3</sup>MRC Unit for Lifelong Health and Ageing, University College London, London, UK

<sup>4</sup>Zoe Global Limited, London, UK

## Correspondence to

Dr Cristina Menni, Twin Research, King's College London, London, UK; [cristina.menni@kcl.ac.uk](mailto:cristina.menni@kcl.ac.uk)

RCEB and TV contributed equally.

CJS and CM contributed equally.

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## ABSTRACT

Understanding the geographical distribution of COVID-19 through the general population is key to the provision of adequate healthcare services. Using self-reported data from 1 960 242 unique users in Great Britain (GB) of the *COVID-19 Symptom Study app*, we estimated that, concurrent to the GB government sanctioning lockdown, COVID-19 was distributed across GB, with evidence of 'urban hotspots'. We found a geo-social gradient associated with predicted disease prevalence suggesting urban areas and areas of higher deprivation are most affected. Our results demonstrate use of self-reported symptoms data to provide focus on geographical areas with identified risk factors.

The COVID-19 epidemic has led to large-scale closures and lockdown measures worldwide with the British government sanctioning lockdown from 23 March 2020 (<https://www.gov.uk/government/speeches/pm-address-to-the-nation-on-coronavirus-23-march-2020>).

Early in the pandemic, case distribution was not evenly spread across countries, with dense urban centres being the most affected.<sup>1</sup> Individuals in deprived areas have lower life expectancy,<sup>2</sup> are more likely to have multiple underlying comorbidities, have a higher level of influenza-associated hospitalisation<sup>3</sup> and therefore could be more susceptible to COVID-19.<sup>2</sup>

Based on the known socioeconomic health gradient, we hypothesised that individuals in deprived areas were at greater risk of contracting COVID-19. Understanding the geographical distribution of the virus in a socioeconomic context is key to assist adequate healthcare resourcing, particularly intensive care beds.<sup>4</sup>

Here we investigated the geographical distribution of COVID-19 in Great Britain (GB) and its association with area-level deprivation using self-reported data from almost 2 million users of the *COVID-19 Symptom Study*.<sup>5</sup>

We studied 1 960 242 unique GB app users (20–69 years old) reporting on COVID-19 symptoms, hospitalisation, reverse-transcription PCR (RT-PCR) test outcomes, demographic information and pre-existing medical conditions (online supplemental methods) over 23 days (29 March–19 April) of major social distancing measures ('lockdown').

We computed a proxy of contracting COVID-19, based on reported symptoms<sup>6</sup> (positive predicted value=0.69 (0.66; 0.71) (online supplemental methods)). We then calculated a predicted prevalence as the proportion of app users that we predicted to have COVID-19 within each area (online supplementary figure S1).

Following aggregation of variables to local authority district level (LAD/geographic unit representing ~17 000 individuals), we tested the geographical distribution of predicted prevalence at eight different time points spanning 23 days. We used Local Moran's I tests, which assess for non-random spatial distribution and clustering of a feature and can be used to identify disease hotspots and cold spots relative to the mean GB predicted prevalence<sup>7</sup> (online supplemental methods).

Next, we used data from the eight different time points and used multivariable mixed-effects models to investigate the association of predicted area-level prevalence (at middle super output area level (MSOA)) and deprivation (as captured by the Index of Multiple Deprivation) adjusting for different factors including geo-social mediators and confounders (air pollution, general practitioners per MSOA, household density and urbanicity) area level aggregates of obesity and comorbidities) and area-level adjusted mean age and sex and spatial autocorrelations<sup>8</sup> (online supplemental methods).

table table 1 and online supplemental table S1. The number of predicted COVID-19 positive individuals ranged between 15 991 and 79 378.

Local Moran's I showed that predicted COVID-19 prevalence clustered in urban areas across GB when considered as a proportion of the population per LAD<sup>7</sup> (figure 1 and online supplemental figure S2) adjusting for multiple testing. Predicted prevalence decreased over time, consistent with 'lockdown' (figure 1 and online supplemental figure S2) (pairwise Wilcoxon rank-sum tests, prevalence: all time points except T2:T3 and T1:T4,  $p<0.001$ ), but some hotspots remained.

In the MSOA-level analysis, area-level deprivation was significantly associated with predicted area-level prevalence in all models (M1–M6, see online supplemental table S2), including in the full model (M6) when adjusting for all geo-social covariates and comorbidities (M6: Beta (95% CI)=−0.15



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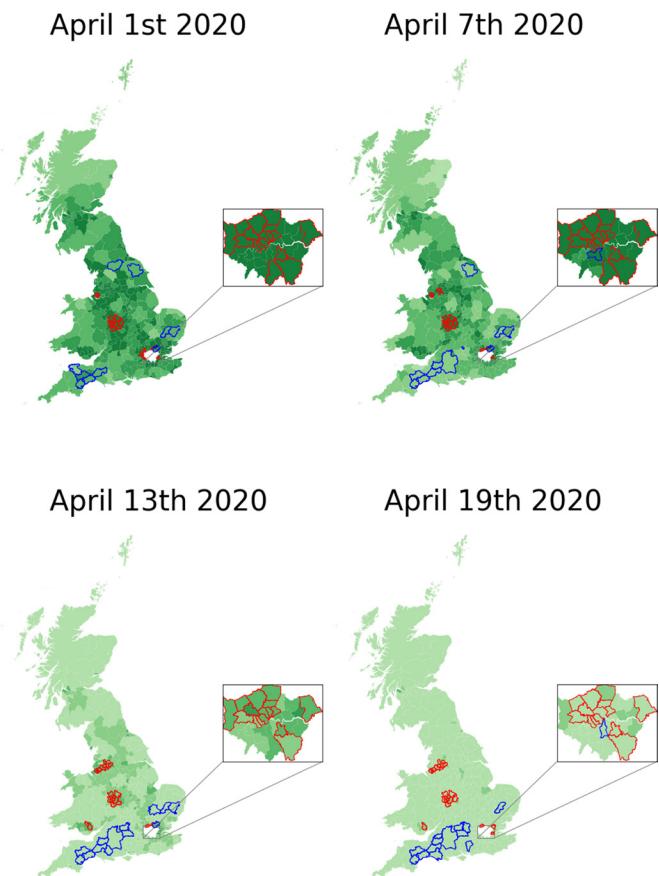
► <http://dx.doi.org/10.1136/thoraxjnl-2020-216673>



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**Figure 1** Geographical distribution of predicted COVID-19 prevalence across four time points. Prevalence is presented as proportional to the responders per local authority district (LAD). Analyses are adjusted for multiple testing using Benjamini-Hochberg false discovery rate correction ( $p<0.05$ ). Inset highlights London where LAD areas are smaller. Hot and cold spots are defined relatively to their neighbours and the mean GB predicted prevalence. Red/blue coloured perimeter lines around each LAD denote hotspot/coldspot.

( $-0.17$  to  $-0.130$ ,  $p<0.001$ ). This suggests that people in deprived areas were at higher risk.

Predicted COVID-19 prevalence was higher in urban areas compared with rural and in more deprived areas compared with less deprived. This could reflect the likelihood of individuals in more deprived areas working/living with people whose vocations mean they are unable to work from home and are thus more likely to be exposed to circulating COVID-19. Accumulation of socioenvironmental exposures across the life course are known to contribute to a greater health deficit and disease burden<sup>2</sup>; our results suggest that COVID-19 is no exception.

Moreover, our study illustrates how app data could be used to successfully monitor COVID-19 over time and identify hotspots as the viral pandemic progresses and social distancing measures are implemented or eased. Using this method, we detected a geo-social gradient associated with prevalence in the context of COVID-19, suggesting the focus of resources should be on deprived urban areas.

Our study has some limitations and assumptions. We used self-reported data on symptoms that can lead to bias. For example, should users in deprived areas report more symptoms due to a facet of the socioeconomic environment (eg, higher air pollution), this could lead to an incorrectly higher predicted prevalence in deprived areas. Second, app users are a self-selected group, not representative of the general population. Our approach to adjust for age and sex differences at MSOA level is unlikely to sufficiently overcome selection and collider bias.<sup>9</sup> Third, our predicted COVID-19 prevalence is not from confirmed tests via RT-PCR, but rather based on self-reported symptoms. Additionally, we assume that people who have symptoms or have been exposed to COVID-19 are equally likely to use the app as those who do not. We performed a sensitivity analysis by rerunning the pooled analysis on individuals who were self-reportedly healthy at sign up and found the observed associations remained (online supplemental table S3), suggesting selection bias associated with being unhealthy at sign up is not influencing the observed associations of COVID-19 and deprivation. We also assume that people report symptoms in the same way and that their drop-out patterns do not differ by space, time and symptom reports. Finally, we aggregated data at MSOA level

**Table 1** Demographic characteristics of the study population at eight time points

	29 March 2020	1 April 2020	4 April 2020	7 April 2020	10 April 2020	13 April 2020	16 April 2020	19 April 2020	All unique users
N	1324843	1431515	1142923	1083601	995157	985860	980608	1164262	1960242
Predicted COVID-19 (n/%)	60827 (4.6)	79378 (5.6)	62508 (5.5)	48418 (4.5)	30132 (3.0)	22352 (2.3)	16586 (1.7)	15991 (1.4)	117614 (6.0)
Average number of reports per user	2.9	3.8	4.2	4.7	5	5	5	4.5	4.4
Age, years (median (IQR))	41 (21)	41 (21)	43 (21)	44 (22)	45 (21)	45 (21)	46 (21)	45 (21)	42.2 (21.8)
Male, (n/%)	426923 (32.2)	459620 (32.1)	365078 (31.9)	353233 (32.6)	327608 (32.9)	327620 (33.3)	327114 (33.3)	388378 (33.4)	654950 (33.4)
Obesity, %	21.3	21.4	20.7	20.3	21.6	22.1	21.4	21.7	21.5
Kidney disease, %	0.5	0.5	0.5	0.5	0.5	0.6	0.6	0.6	0.5
Lung disease, %	12.2	12.3	12.5	12.5	12.4	12.4	12.4	12.4	12.2
Diabetes, %	2.4	2.5	2.7	2.7	2.8	2.9	2.9	2.9	2.4
Smokers, %	10.5	10.5	9.7	9.4	9.0	8.8	8.7	9.0	10.4
Heartdisease, %	1.4	1.4	1.6	1.6	1.7	1.7	1.7	1.7	1.4

Obesity: BMI  $\geq 30 \text{ kg/m}^2$ .

At each time point, we only include users who have made an assessment in the previous 7 days. Exclusion criteria are listed in the supplements. Users are asked daily whether (or not) they have any symptoms. Predicted COVID-19 was calculated on users who reported on symptoms. Users who reported having no symptoms were included in the area-level predicted prevalence estimates (please see the supplements for details).

BMI, body mass index.

that could lead to ecological bias. We also cannot conclude that deprivation increased COVID-19 prevalence, as there could be unmeasured confounders or other factors.

Future work should check our assumptions and seek to integrate these data with data on area-level morbidity, extended pollution data, ethnicity and disease severity. Indeed, higher mortality has been observed among minority ethnic groups,<sup>10</sup> and disentangling the environmental and biological factors contributing to greater disease burden in both deprived areas and among ethnic minorities is an essential focus of future work to ensure resources and intervention are better assigned.

**Twitter** M Jorge Cardoso @mjorgecardoso

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**Contributors** Conceived and designed the experiments: CJS, TDS, SO and CM; analysed the data: RCB and TV. Contributed reagents/materials/analysis tools: MF, CHS, BM, MF, DY, SG, JC, ET, EB, MJC, RD and JW wrote the manuscript: RCB, TV and CM; revised the manuscript: all.

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**Patient consent for publication** Not required.

**Ethics approval** The Ethics for the app has been approved by King's College London ethics Committee (REMAS ID 18210, review reference LRS-19/20-18210), and all users provided consent for non-commercial use. An informal consultation with TwinsUK members over email and social media prior to the app having been launched found that they were overwhelmingly supportive of the project.

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#### ORCID iDs

Richard Davies <http://orcid.org/0000-0003-2050-3994>

Cristina Menni <http://orcid.org/0000-0001-9790-0571>

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**1   Supplementary Methods****2   Study setting and participants**

3   The COVID Symptom Study app developed by Zoe with scientific input from researchers and  
4   clinicians at King's College London and Massachusetts General Hospital, was launched in GB on  
5   Tuesday the 24th March 2020 (<https://covid.joinzoe.com/>) and in the 23 days (March 29<sup>th</sup>–April  
6   19<sup>th</sup>) immediately after the UK lockdown ([https://www.gov.uk/government/speeches/pm-  
7   statement-on-coronavirus-22-march-2020](https://www.gov.uk/government/speeches/pm-statement-on-coronavirus-22-march-2020)) was introduced, it reached 2,266,235 unique GB users,  
8   making 9,108,769 assessments (e.g. an average user is included in 4 out of 8 timepoints).  
9   Referrals/word of mouth, press and eventually partnerships with charities and the Welsh and  
10   Scottish governments drove usage.

11   The app enables capture of self-reported information related to COVID-19 infections. On first use,  
12   the app records self-reported location, age, and core health risk factors. With continued use,  
13   participants provide daily updates on symptoms, health care visits, COVID-19 testing results, and if  
14   they are self-quarantining or seeking health care, including the level of intervention and related  
15   outcomes. Individuals without apparent symptoms are also encouraged to use the app. Through  
16   direct updates, the research team can add or modify questions in real-time to capture new data to  
17   test emerging hypotheses about COVID-19 symptoms and treatments. Importantly, participants  
18   enrolled in ongoing epidemiologic studies, clinical cohorts, or clinical trials, can provide informed  
19   consent to link data collected through the app in a Health Insurance Portability and Accountability  
20   Act (HIPAA) and General Data Protection Regulation (GDPR)-compliant manner with extant study  
21   data they have previously provided or may provide in the future.

22   In this study, we included 1,960,242 unique users as outlined in the flow diagram below (**Figure A**).  
23   Briefly, out of 2,415,843 unique app uses who reported on the COVID-19 symptom Study App  
24   between 29th March 2020 and 19th April 2020, we excluded (i) 149,608 non GB users; (ii) 88,422  
25   users who only reported on the earliest app-version that did not include loss of smell and taste (the  
26   strongest single predictor of COVID-19<sup>1,2</sup>); (iii) 66,975 reporting BMI outside the biological range; (iv)  
27   148,111 users younger than 20 or older than 69; (v) 1007 with missing biological sex at birth or who  
28   were not assigned male or female as their biological sex at birth; (v) 1478 users who did not report  
29   on pre-existing medical conditions (**Figure A**).

30

31 **Figure A. Flow diagram representing the study subjects' inclusion criteria.**

32

33 **Geographic clustering of COVID-19 prevalence**

34 Because we were primarily interested in understanding the geography of COVID-19 distribution, and  
35 how aspects of an area, in particular area-level deprivation, associated with COVID-19 prevalence we  
36 aggregated user data at different GB geographic areas. This was particularly of use as the geosocial  
37 variables considered (please see below) are also defined geographically and are time invariant (as  
38 they are not defined by the app users themselves but by GB geographic area).

39 The maps (**Figure 1, S2**) were created using a shapefile of Local Authority Districts (LADs) from the  
40 Office for National Statistics (ONS) using the geopandas package in Python. Overlaid on the map are  
41 statistically significant 'hot-spots' and 'cold-spots' at LAD level. To assess the significance of these  
42 regions, we used Local Moran's I test, as introduced below. In order to do this, spatial weights were

43 calculated to create a spatially lagged COVID-19 prevalence variable for each LAD. Because our  
44 geographical units share borders we assume a queen criterion, which assumes equal weights of  
45 neighbouring areas, which is appropriate for defining these. Islands were considered to have zero  
46 neighbours. We adjusted for multiple testing using the Benjamini & Hochberg method ('p.adjust')  
47 and used the 'spdep' package in R for the Local Moran's and calculation of the spatial lag. This  
48 approach of calculating the spatial lag was repeated at the middle super output area level (MSOA)  
49 level (below).

50 **Hotspot and Coldspot definition**

51 Predicted prevalence hotspots at LAD levels were defined using Local Moran's I. The Moran's I  
52 statistic gives a value indicating the spatial clustering of a variable relative to its neighbours. Where  
53 there are significant (false discovery rate (FDR)adjusted p < 0.05) high positive local Moran's I in high  
54 value neighbourhood (i.e. where the significant area also had a predicted prevalence greater than  
55 the mean predicted prevalence and greater than the mean of the lagged variable, which effectively  
56 represents how similar COVID-19 prevalence is to the areas that surround it) this implies the area  
57 can be considered a 'hotspot'<sup>3</sup>. This method ensures we do not consider areas as hotspots where  
58 they may have higher predicted prevalence to the surrounding areas but are lower than average for  
59 the UK, although it might miss areas that are surrounded on all borders by other areas which would  
60 be considered hotspots. A coldspot is assessed similarly using Local Moran's I, but where the area is  
61 less than the mean and mean of the lagged variable.

62 **Sources of geographic data**

63 ***Index of Multiple Deprivation (IMD)***

64 The IMD was downloaded from the relevant government websites as below, and the most recent  
65 IMD available at time of analysis was used:

- 66 • English (2019): <https://www.gov.uk/government/statistics/english-indices-of-deprivation-2019>
- 67 • Scottish (2016): <https://www2.gov.scot/Topics/Statistics/SIMD>
- 68 • Welsh (2019): <https://statswales.gov.wales/Catalogue/Community-Safety-and-Social-Inclusion/Welsh-Index-of-Multiple-Deprivation/WIMD-2019>

71 Because the IMD is calculated in each devolved administration using slightly different methodology,  
72 and because of the different number of areas in each country, ranks are not directly comparable.

73 Therefore, we used within-country defined deciles. As the IMD is calculated for smaller area  
74 geographies than MSOA, we calculated the average IMD per MSOA. This was then categorised into  
75 quintiles where 1 is the least deprived and 5 is the most deprived.

76 ***Rural-urban gradient (RUC)***

77 The RUC was downloaded from the relevant government websites as below:

- 78 • England and Wales RUC (2011): <https://data.gov.uk/dataset/9c0e093d-d267-4eb8-90d8-54475ab4d1ff/rural-urban-classification-2011-of-middle-layer-super-output-areas-in-england-and-wales>
- 81 • Scotland RUC (8 fold classification):  
<https://www2.gov.scot/Topics/Statistics/About/Methodology/UrbanRuralClassification>

83 The resulting scale runs from 1 – 8, where 1 is the most urban and 8 is the least.

84 ***Nitrogen Oxide (NOx) data***

85 We used NOx pollution data from the Department of Environment, Food and Rural Affairs  
86 (<https://uk-air.defra.gov.uk/data/>) for England, Scotland and Wales from 2018. Data is provided with  
87 Ordinance Survey 1km<sup>2</sup> grid resolution which was used to calculate per MSOA air pollution by taking  
88 the area-weighted average of the readings.

89 ***General Practitioners (GPs)/MSOA***

90 GPs addresses were used to derive the number of GPs from each MSOA, from the following data  
91 sources:

- 92 • England & Wales: <https://digital.nhs.uk/services/organisation-data-service/data-downloads/gp-and-gp-practice-related-data>
- 94 • Scotland: <https://www.opendata.nhs.scot/ne/dataset/general-practitioner-contact-details/resource/b092b69f-0838-408e-bb89-082562f0e1cd>

96 ***Average household number***

97 This figure was derived from data by dividing the number of houses with at least one usual occupant  
98 with the total population for the same area.

99 Data sources for occupancy data were downloaded from the following sources:

- 100       • England & Wales (table PHP01 2011): <https://www.nrscotland.gov.uk/statistics-and-data/statistics/statistics-by-theme/households/household-estimates/small-area-statistics-on-households-and-dwellings>
- 101       • Scotland: <https://www.nrscotland.gov.uk/statistics-and-data/statistics/statistics-by-theme/households/household-estimates/small-area-statistics-on-households-and-dwellings>
- 102
- 103
- 104

105 **MSOA-level mixed-effects models**

106 We employed multivariable mixed-effects models to understand the relationship of predicted  
107 COVID-19 prevalence at MSOA level with deprivation. As a reminder, these models were ran at  
108 MSOA-level rather than individual-level. This included the following variables:

109 The Index of Multiple Deprivation, our primary explanatory variable (IMD, categorised into quintiles  
110 generated on the average IMD within each MSOA, where 1 is most deprived and 5 is least, and  
111 considered as a continuous variable).

112 Other considered geosocial factors included a rural-urban gradient (RUC, considered as a continuous  
113 variable where 1 is the most urban and 8 is the most rural), General practitioners per population in  
114 MSOA (GPs/MSOA, where a higher number indicates more GPs per individual by MSOA), average  
115 household number (calculated as number of inhabited dwellings/MSOA population, where a higher  
116 number indicates a higher average number of individuals per household). Because it was on a very  
117 different scale to the rest of the predictor variables, GPs/MSOA was scaled to have mean 0 and 1 SD  
118 prior to model inclusion.

119 We additionally adjusted for the following variables derived from app response data, considered as  
120 percentage of responders within the MSOA: those who reported having kidney, heart or lung  
121 disease, and who are diabetic, a smoker or obese (calculated as BMI<30). We derived mean-adjusted  
122 age and sex variables to partially adjust for response bias (i.e. the extent responders in an MSOA  
123 represented the demographic of that MSOA). This was calculated as the difference of the expected  
124 mean/ratio of age.sex in the MSOA (derived from ONS population data) and the observed  
125 mean/ratio of age.sex amongst respondents.

126 We included a spatial lagged variable of the COVID-19 prevalence outcome. Inclusion of the lagged  
127 variable is one method that accounts for spatial autocorrelation (SAC)<sup>4</sup>. It attempts to adjust for  
128 spatial autocorrelation by capturing the variance explained by the influence of neighbouring regions  
129 on the value of interest – in this case COVID-19 severity/prevalence. The lagged variable is calculated  
130 at MSOA level by applying a spatial weights matrix (calculated in this instance under queen's

131 contiguity) to the outcome variable (in this case COVID-19 prevalence) and computing the lag using  
132 the function lag.listw in the ‘spdep’ R package. This variable is then included as a covariate within  
133 the model.

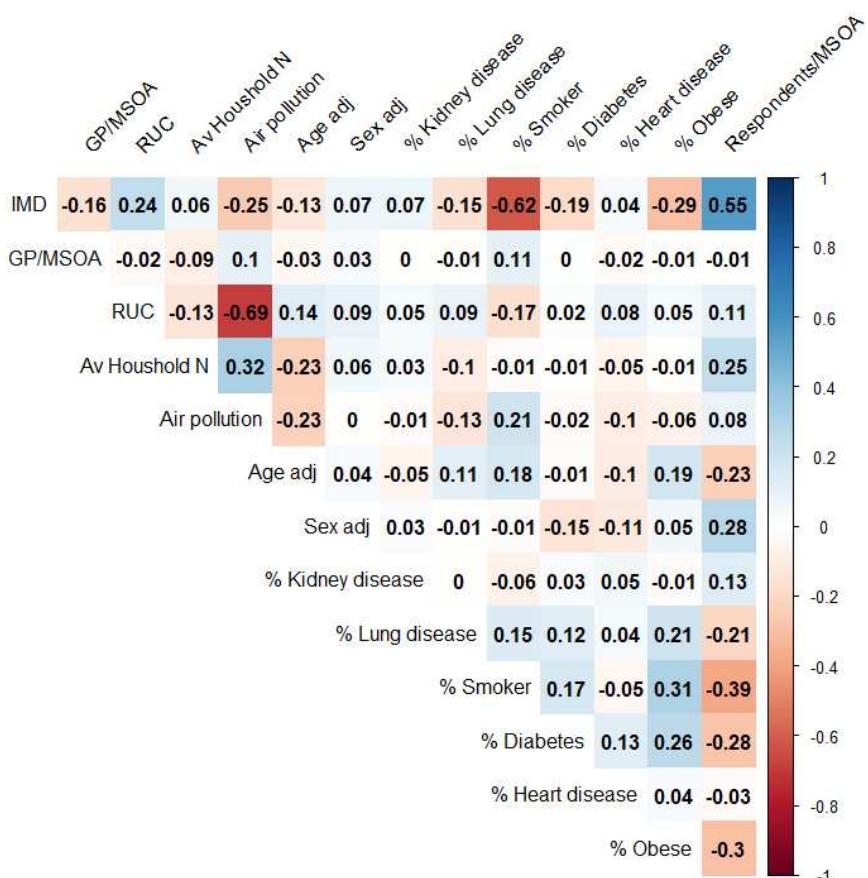
134 Data from eight time points were analysed , calculating the covariates (derived from app  
135 responders) and spatial lag at each time point, a dummy variable adjusting for the different sample  
136 times was included in the model as a random effect (allowing for a random intercept). MSOA was  
137 also included to allow for a random intercept to account for the repeat observations over the eight  
138 time periods, along with country as a fixed effect to account for difference in methodology in  
139 creation of IMD and RUC.

140 The users' distribution across GB is not uniform but all analyses took this into account by considering  
141 only middle super output areas (MSOAs) with at least 20 individuals reporting on the app (n = 8097,  
142 n removed = 387), and we included as a covariate the proportion of responders per MSOA at each  
143 time point, in order to adjust for differences in responders by MSOA. Analysis was conducted in  
144 RStudio v1.1.423 and R v3.6.3.

145 Variables were checked for multicollinearity before model inclusion using Spearman's correlation,  
146 (see **Figure B**) with the *a priori* threshold of > (+/-) 0.7 indicating a variable should be removed.

147

148 **Figure B. Assessment of collinearity between the variables included in the MSOA-level mixed-  
149 effects models. Each cell of the matrix displays Spearman's correlation between two. The table is  
150 colour coded according to the Spearman's correlation, with blue denoting a positive correlation  
151 and red denoting a negative correlation. GP/MSOA= General Practitioners per middle super  
152 output area level; RUC= Rural-urban gradient; Av Household N= average household number.**



153

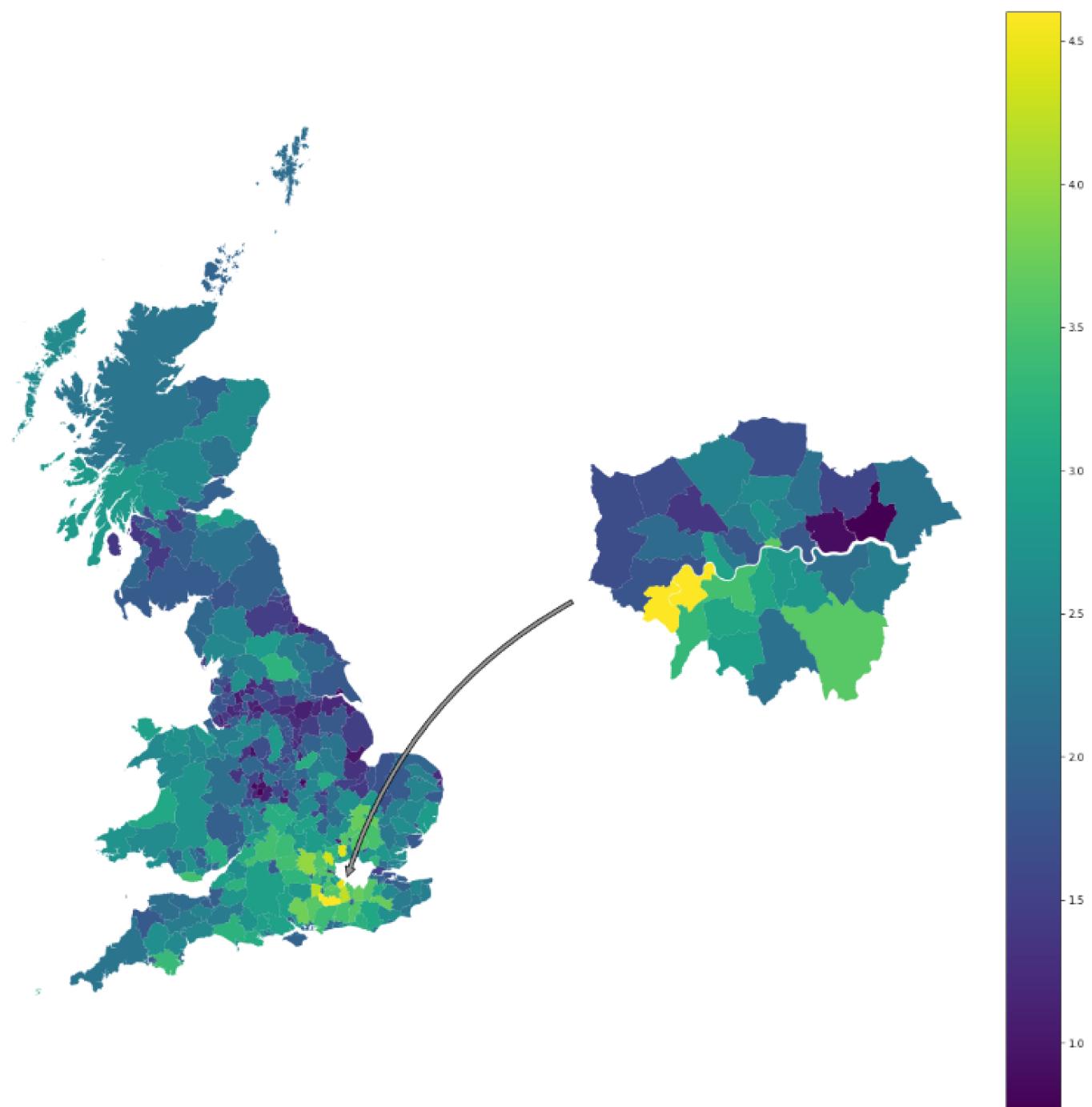
154 The model approach was therefore as follows:

- 155 • Model 1 (M1): Linear regression of the estimated COVID-19 prevalence and the IMD
- 156 • Model 2 (M2): Linear mixed effects model (LMM) of estimated COVID-19 prevalence and the  
157 IMD, adjusted for country, and allowed a random effect of MSOA ID and time (assuming  
158 random intercept for both)
- 159 • Model 3 (M3): Linear mixed effects model of estimated COVID-19 prevalence and the IMD,  
160 adjusted as above in M2, with additional adjustment for spatial autocorrelation (SAC) via  
161 inclusion of a spatial lag.

- 162       • Model 4 (M4): Linear mixed effects model as in M3, with the inclusion of geosocial  
163       mediators and confounders and proportion of MSOA population who were app users.
- 164       • Model 5 (M5): Linear mixed effects model as in M4, with the inclusion of aggregated co-  
165       morbidity as the % of respondents in MSOA with diabetes, kidney, lung or heart disease,  
166       who are obese or are smokers.
- 167       • Model 6 (M6): Covariate + mean-adjusted LMM – Linear mixed effects model as in M6, with  
168       the inclusion of mean-adjusted age and sex variables

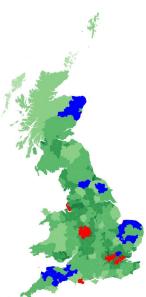
169       **Supplementary References**

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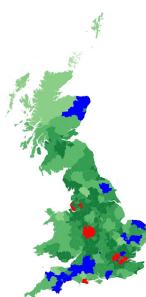


## Predicted Covid-19 +ve cases in GB with highlighted spatially significant hotspots

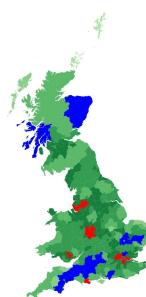
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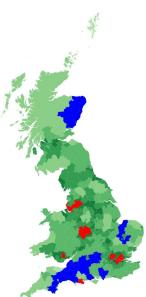
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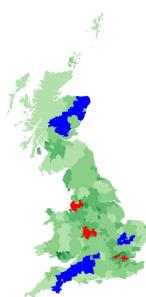
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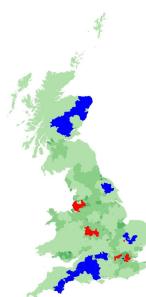
2020/04/07



2020/04/10



2020/04/13



2020/04/16



2020/04/19



- = < 2
- = 2 - 3
- = 3 - 4
- = > 4
- = Not enough contributors
- = Hotspot
- = Coldspot