Penetration of SARS-CoV-2 variants in England

B. Arregui, J. Ramasco and S. Meloni

IFISC (CSIC-UIB) Palma de Mallorca - Spain

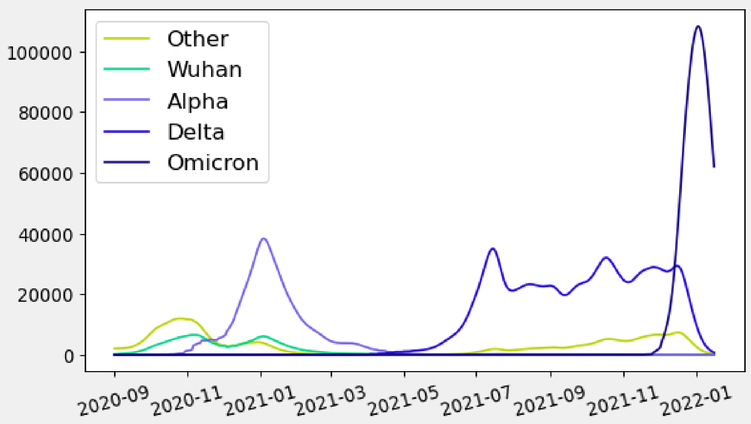
beatriz@ifisc.uib-csic.es

Abstract

Many efforts have been globally made against the COVID-19 pandemic since the appearance of the wild-strain of SARS-CoV-2 in early 2020. The propagation of this variant was strongly enhanced by human mobility[1,2] and measures have primarily consisted of lockdowns, social distancing, usage of masks and ultimately, vaccination strategies to allow a recovery of mobility. Nevertheless, some mutations of the virus developed a higher transmissibility causing a major impact on the epidemic spreading. Those mutations are known as Variants of Concern (VOCs). We hereby study the key-factors fuelling the emergence and transmission of the new VOCs.

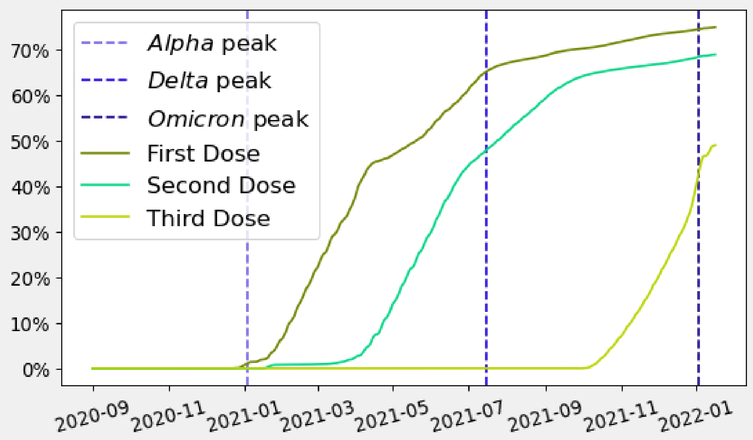
Data

Incidence



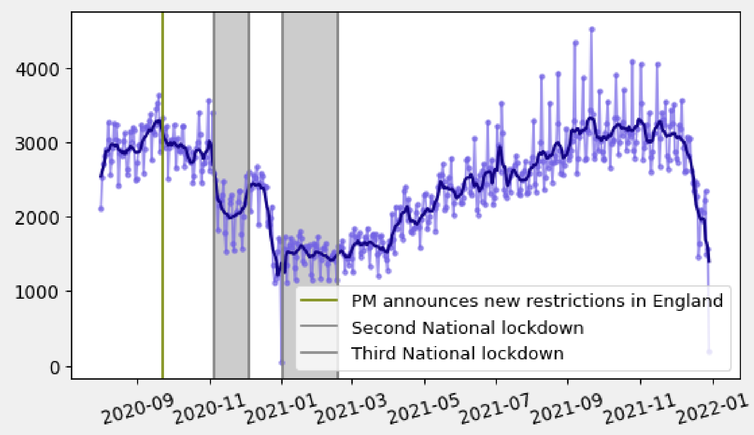
Incidence of the SARS-CoV 2 cases by lineage: *Original* (lineage B.1.177), *Alpha* (B.1.1.7), *Delta* (B.1.617.2 and sub-lineage AY.4.2), *Omicron* (BA.1) and the rest of lineages grouped as *Other*.

Vaccination



Full green lines are the cumulative percentage of people vaccinated in England. Blue dashed lines are the dates where the different VOCs reached their peak incidence.

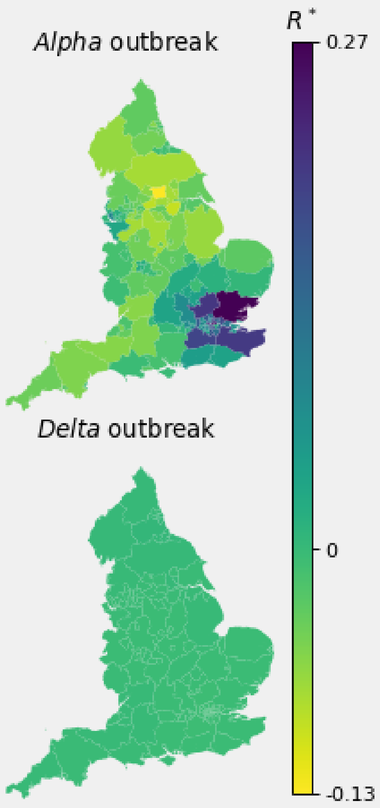
Mobility



Number of trips computed from Twitter geolocalization data. In dark blue we show the moving average over a week. The grey areas span over the National Lockdown periods.

Epicenter analysis

Incidence



The coefficient R^* is a correlation measure computed as $R^* = R_p \frac{n_o}{N_{max}}$. Where R_p is the Pearson coefficient between the peak incidence of any district and the incoming mobility from the possible source, n_o is the number of different destinations from o, and N_{max} is the maximum number of destinations from any district in England.

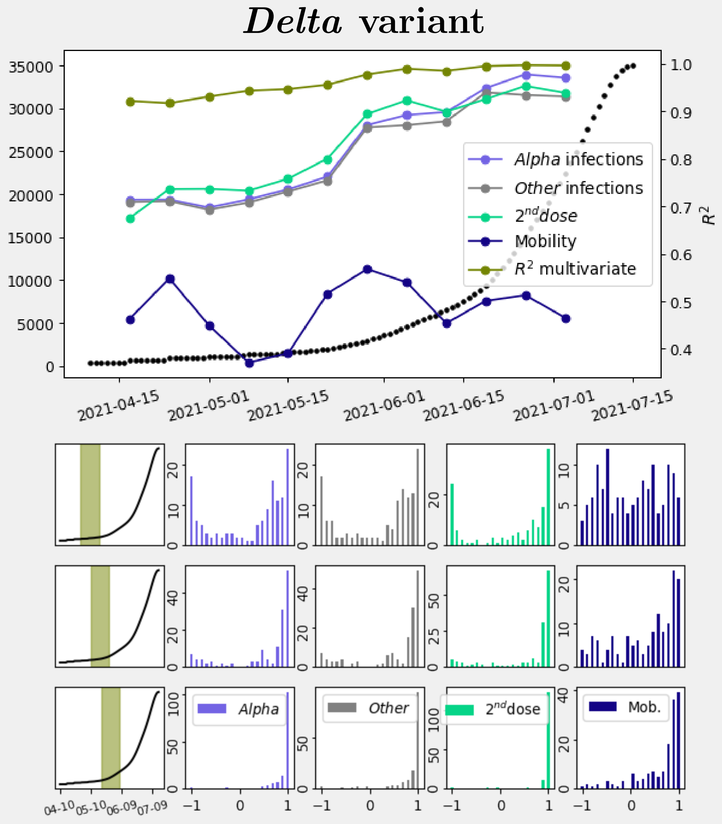
1. Tian et al. *Science* **368** (6490), 2020.
2. Kraemer et al. *Science* **368** (6490), 2020.
3. Mazzoli et al. *PLoS Computational Biology* **17** (10), 2021.
4. Tian et al. *Journal of Medical Biology* **1-8** 2022.
5. Kraemer et al. *Science* **367** (6557), 2021.

Methodology

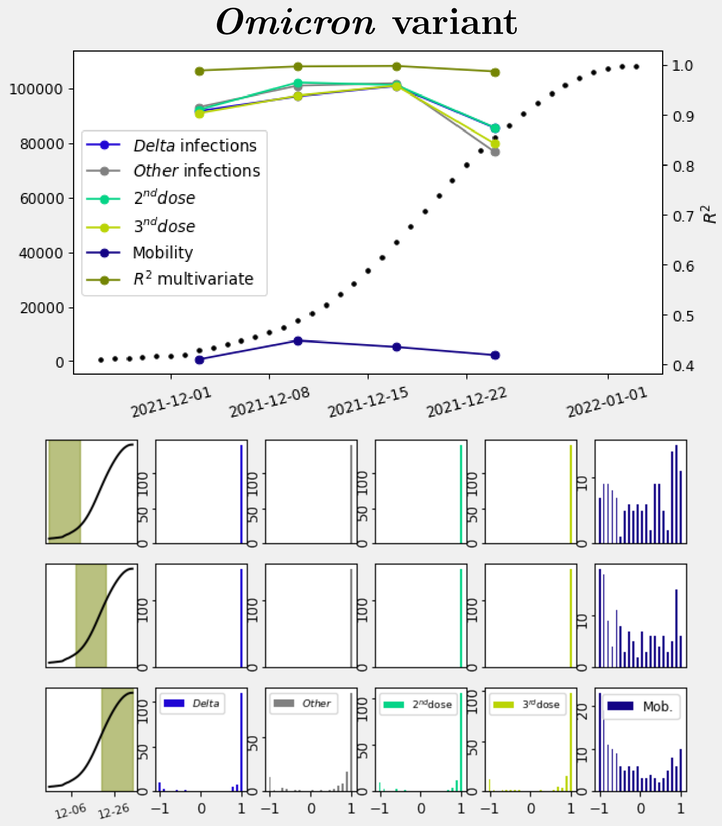
Large-scale sequencing of SARS-CoV-2 allowed us to analyse the spreading of the most dominant VOCs since September 2020 in every district in England. Along with public data on vaccination, we obtained a spatio-temporal understanding on the epidemiological situation spanning the past years. Mobility data is recovered from Twitter geolocalizations. Applying appropriate filters we compute the daily number of trips among districts.
Via a multivariate analysis including epidemiological and social data, we identify the key variables contributing to a higher incidence. At last, we use mobility data to identify the epicenter of the epidemic[3].

Multivariate analysis

Delta variant



Omicron variant



Top panels: The dotted curves are the total incidence of *Delta* and *Omicron* cases in England. We perform a correlation analysis during the early stage of each outbreak since there are at least 30 infected districts. We computed the regression coefficient R^2 between the different variables and the incidence per district evaluated over a period of 10 days every week. The different variables under study are the cumulative cases in every district of *Alpha* (for the *Delta* case) and *Delta* (in the *Omicron* case) lineage until the previous two weeks, the same for all the other cumulative cases of SARS-CoV-2 (*Other*), the fraction of vaccinated people per district, and the incoming mobility per capita in the district from three to one weeks before. Each point is the average of the R^2 of every district. Bottom panels: The first column shows, over the incidence curve, the time period analysed in each row. The following columns are the distribution of the $R_{pearson}$ coefficients between the incidence and the variables explained before for each district.

Conclusions

- We found a high correlation between the *Alpha* and *Delta* variants incidence and the previous immunization, which becomes more acute near the peak incidence. Correlation with human mobility varies all over the curve and plays a minor role with respect to the previous infections.
- *Omicron* exhibits the fastest spreading and no trend is captured in the correlation with the other variables. This different behaviour may be explained by the high number of mutations of this strain[4].
- The epicenter analysis doesn't bring any conclusive results on the onset of *Delta* and *Omicron* variants. The fact that they are variants not originated within the country may explain a multi-seeding outbreak which we are not able to capture. However the source of the *Alpha* wave is well located in the Outer London districts and Kent region, which is consistent with previous works [5].