As of the 28th of June, over 300,000 individuals have been confirmed to have acquired infection with the SARS-CoV-2 virus. Amongst these over 40,000 have died. Over the last months we have learnt that the UK COVID-19 pandemic has three contexts: community, hospitals and care homes. A lock-down was introduced on the 23rd of March and we are gradually easing it, desperately trying to go back to normal life. Behind this knowledge and its input to policy, lies the work of many individuals: epidemiologists, mathematicians, statisticians and behavioural scientists who became members of relevant advisory groups. Figure 1 explains the structure of this interaction involving the Civil Contingencies Committee (COBR), the Scientific Advisory Group for Emergencies (SAGE), the New and Emerging Respiratory Virus Threats Advisory Group (NERVTAG), and the Scientific Pandemic Influenza Groups on Modelling (SPI-M-O) and Behaviours (SPI-B).

SPI-M-O is the committee providing quantitative evidence to SAGE, particularly on the dynamics of SARS-CoV-2 transmission. Constituted during the H1N1 Pandemic in 2009, it has been maintained over the years to ensure preparedness in the event of an influenza pandemic and recently extended to deal with other emerging diseases. Members come from a number of research institutions who freely accepted the invitation to contribute to the work. Regular commissions are received from Cabinet Office.

Figure 1
The models adopted by the groups contributing to SPI-M-O have a much more complex structure than the simple SIR model in Figure 2. They typically include a higher number of compartments and further stratify the population by age groups, geography and contexts (e.g. workplace, schools etc.). The interaction between susceptible and infected individuals in the different population strata, expressed as the average numbers of daily contacts, drives disease transmission and generates new infections until there are no longer susceptible individuals, or an intervention that reduces this interaction is introduced. In this more realistic context, the aim is to monitor the pandemic evolution over time by estimating the level of transmission, the number of new infections and predict future burden, in different age groups and regions.

In the last four months, the Medical Research Council Biostatistics Unit (MRC-BSU) at Cambridge University, has contributed, in collaboration with Public Health England (PHE), to SPI-M-O by providing regular updates on the state of the pandemic in England from a transmission model. The population is subdivided into four categories: susceptible, infected but not infectious, infected and infectious, recovered. We further stratify by age groups (< 1, 1–4, 5–14, 15–24, 25–44, 45–64, 65–74, 75+ years old) and by the seven National Health Service regions. The transmission between groups is informed by the POLYMOD study (Mossong et al, 2008), giving the mean number of contacts between the different age groups and contexts, updated throughout the pandemic to account for changes in behaviour (E. van Leeuwen, F. Sandmann, 2020); literature from the Chinese pandemic provides information on the natural history of SARS-CoV-2 (Li et al, 2020; Verity et al, 2020); and sequential serological surveys from testing blood donors over time and in different regions provide information on the proportion of the population that has already been infected (https://www.gov.uk/government/publications/national-covid-19-surveillance-reports/sero-surveillance-ance-of-covid-19 ). All these data sources are then combined with data on daily numbers of age and region-specific deaths in individuals with laboratory confirmed SARS-CoV-2 to reconstruct the underlying number of infections and characterise transmission nationally and in the different regions. Death data, although a lagged signal of infection, provide information on the shape of the epidemic curve; and data from serological studies, giving information on the proportion of the population in different age group with antibodies, inform the magnitude of the pandemic. The typical output, produced regularly (https://www.mrc-bsu.cam.ac.uk/now-casting/), included: the reconstructed number of infections over time; trends in $R_0$, the effective reproduction number (now referring to a population not totally susceptible), an indicator of ongoing transmission; and
short-term predictions for the number of deaths. Figure 3 gives an example of these outputs, portraying the probability of \( R_t \) being above the value of 1 in the different regions at the beginning of June.

It this type of quantification, provided by the different groups, that gave evidence to policy makers to monitor levels of transmission and inform decisions.

Currently, transmission appears to be slowing down in all regions of England and the number of daily infections is decreasing over time. The estimated proportions of already infected individuals in the various age groups and regions are, however, low, alerting to the possibility of a second wave of infection. So, continued monitoring remains essential. The approach taken until now will need to be complemented by more granular surveillance tools aimed at identifying and managing local outbreaks.

These interesting times offer plenty of exciting professional experience to a statistician studying disease transmission like me!

