Here I will outline the issues that caused potential problems early in the COVID-19 pandemic, many of these were slowly resolved as the outbreak progressed but many have resurfaced in the Monkeypox outbreak. I¶d raise five issues as key lessons to be learned

1) As mentioned in Question 6, I feel that better lines of direct communication between the subgroups, that did not have be fed through SAGE, may be of great help in future pandemics. I think more informal meetings between subgroups could be highly beneficial and provide all groups with a more holistic understanding of future outbreaks. We are now seeing a similar situation with Monkeypox, in which the modellers, the clinicians and the behavioural experts are somewhat siloed.
I¶d also state that continuing to have meetings on-line is a definite improvement especially for the majority of academics that live outside London. There is no way I could have generated the output that I did for the COVID-19 pandemic if I also had to attend meetings in person with the associated travel times.

2) Models are only as good as the data that feeds into them, and modern models are often data-hungry. UKHSA (formally PHE) and NHS control access to much of this data. I fully appreciate the ethics of data confidentiality, but often there were substantial bottle-necks that could have impacted what was achieved. While UKHSA/PHE held a large database of reported infection episodes, modellers only had access to partial information that was passed to us on a regular basis. For example, for the majority of 2020 and 2021, the modellers were only told about the first time an individual tested positive ± so any subsequent positive tests were ignored. While there were good reasons for this in the early outbreak (not counting people testing multiple times in succession), later in the outbreak it could have been biasing the modelling results. Even when this was resolved, tests within 90 days were ignored ± again there were reasons for this, but the reinfections within 90 days helps to explain some of the patterns observed just after 90 days. Another continuing issue with the data is the disconnect between case and death data, which was highly detailed and hospital admission data that was aggregated at a relatively course scale. Again, we all appreciate the confidential nature of hospital data, but the differences between data sets seems excessive. In addition, there were often changes to the way that hospital data was counted, meaning that modellers were often fitting to the counting rather than the underlying processes.
Finally, I¶d flag the vast differences in data quality and formatting between the four nations, with different countries providing different data in very different formats. After the initial phase of the epidemic DSTL and later UKHSA did an excellent job of bringing this data into a unified document, but differences in the ways data is reported and recorded caused multiple problems throughout the pandemic.
I had hoped that many of these difficulties would have been resolved for the Monkeypox outbreak, but if anything, the data access issues are worse. Admittedly SAGE and SPI-M are not directly involved in Monkeypox modelling, but the academic community has still been asked for its help. With Monkeypox, the UK data is only available to UKHSA affiliated staff with a UKHSA laptop, and is again siloed so that the entirety of the data sets are not available to all users.
As we move to a new protocol in working with large data sources, it is important that the public-health academic interface matches these innovations. Either academic institutions need to be trusted with large volumes of data, such that the power of university computer systems can be used to analyse the dynamics, or data access needs to be provided in

secure environments with plenty of flexibility and processing power such that the same analyses can be performed.