

HIPS/21/71 – Spatial And Network Analysis Of SARS-Cov-2 Sequences To Inform COVID-19 Control In Scotland.

Viral phylogenetic data (i.e. the family trees of viruses obtained from infected individuals) provide unprecedented detail on virus spread and inform our understanding of “who infected whom?” However, data issues, including variations in evolutionary rates and incomplete, biased sampling can hamper their utility, and influence our interpretation of events. For example, the number of transmission events that are deemed to occur before or after a policy change influences our understanding of its efficacy and our estimates of this is skewed by biases. As COVID-19 genetic data relies heavily on self-reported community tests, these biases can be substantial. By combining viral genetic data with Scotland-specific demographic and COVID-19 cases data (including dates and locations of tests, types of test, age and gender), we shall generate analytical tools to account for these issues and ask important questions about the COVID-19 epidemic’s control, including:

- i) How close did Scottish measures come to eradicating COVID-19 in the summer of 2020, and how important was travel with other countries in perpetuating the epidemic?
- ii) What impact could long distance movement restrictions have had in slowing down the spread of the Alpha and Delta variants across Scotland?
- iii) Can we estimate region-specific differences in control measure efficacy?

By addressing these questions, we shall be developing methods that will allow us, in future, to robustly inform policy questions in real time. These tools will also be invaluable for analysing other infectious diseases in Scotland such as influenza or future pandemics), further increasing the utility of this project.