Project Details	
Project Code	MRC22IIARBr Brooks-Pollock
Title	Multi-scale modelling of COVID-19 transmission, with application to new and on-going vaccination strategies
Research Theme	Infection, Immunity, Antimicrobial Resistance & Repair
Summary	Mathematical models have played a central role in guiding interventions to control COVID-19. Existing models have not captured infection variability within an individual and the dependence on personal characteristics. Using within-host data to capture infection kinetics and surveillance data to capture epidemic dynamics, models will elucidate the role of immunity in long-term COVID control.
Description	BACKGROUND Mathematical models have played a central role in guiding control strategies and interventions to COVID-19 transmission. The most common approach is to use a set of differential equations, known as the S-I-R (Susceptible-Infectious-Recovered) equations, to capture the progression from being uninfected and susceptible to infection to being infectious to others and finally recovered and immune. The supervisors of this PhD have developed multiple models of COVID-19 transmission which have been informed the UK government response via the SAGE modelling subgroup, SPI-M. During the pandemic, co-supervisor Amy Thomas has developed a saliva-based assay to detect COVID-19 antibodies and has validated and tested the antibody assay against known COVID cases and pre-pandemic samples. From the antibody data, there is evidence of a wide variety of immune responses, and that using a single model of disease progression within an individual misses some important features that will become critical as immunity starts playing a larger role in COVID dynamics and transmission. THE PROJECT This project will use antibody and other within-host data generated by the teams within Bristol to develop alternative descriptions of COVID progression within an individual. One of the challenges will be to capture variability of the within host data, while keeping the population-level model as parsimonious and tractable as possible. The models will be calibrated to a variety of population-level data from the UK, including but not limited to national pillar 1 and 2 data. The best performing models, which capture both within and between host dynamics, will be used to investigate vaccination strategies such as prioritising single versus double dose during vaccine rollout based for different levels of on-going COVID transmission, and optimal strategies for using vaccination and immunity in areas of high or low incidence. The models will also be used to identify knowledge gaps in our understanding of COVID transmission. Stage 1: Analyse the antibody and other within host data and identify general patterns to investigate further (lead for within host data Amy Thomas). Stage 2: Develop and calibrate a statistical model of within-host infection kinetics (lead for statistical model calibration TJ McKinley). Potential stage 3: Develop a mechanistic model of COVID-19 infection within a host (lead for mechanistic model development Ellen Brooks-Pollock). Potential stage 4. Evaluate the within-host COVID model performance at community (and possibly spatial) level by calibrating to national-scale surveillance data (lead for data science: Leon Danon). Potential stage 5: Explore the implication of immunity models for vaccine strategies (vaccine policy

	lead Adam Finn). IMPACT This work has the potential to inform long-term vaccination strategies in the UK, as well as improving our understanding of COVID immunity and dynamics. The supervisors' involvement with SPI-M, SAGE and JCVI will ensure impact and link the student to wide academic and non-academic networks.
Supervisory Team	
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