Title of PhD project	**Inferring SARS-CoV-2 transmission and its direction from viral genomics and mathematical inference**	
Supervisor	Dr Sam Clifford	LSHTM
Co-Supervisor	Dr Stéphane Hué	LSHTM
Co-Supervisor	Professor Liz Miller	LSHTM
Brief description of project	Reconstructing transmission chains is a cornerstone of infectious disease epidemiology. Attempts to determine who infects who during a viral outbreak or epidemic are made using various types of information, including contact tracing, infection serial intervals and viral genome sequences. But few approaches have explicitly incorporated epidemiological and genomic information into statistical inference frameworks. This project aims to develop and apply a novel statistical framework designed to infer SARS-CoV-2 transmission events and their direction (i.e. who infects whom?) from epidemiological, clinical and viral genomic data collected during a large COVID-19 household transmission study conducted in the UK. The study is expected to provide novel quantitative tools for the study of SARS-CoV-2 transmission and generate fundamental insights into the factors influencing SARS-CoV-2 transmission at the micro-epidemic, e.g. household and clusters thereof, level.	
Skills we expect a student to develop/acquire whilst pursuing this project	Mathematical inference of infectious disease transmission Phylogenetic reconstruction Viral genome sequence analyses Bayesian statistical inference Infectious disease epidemiology Handling of electronic health records Scientific computation project management	
Particular prior educational requirements for a student undertaking this project	This project is in quantitative science, and students should demonstrate an interest and aptitude for statistical inference and mathematical modelling. This project would suit students with a first or subsequent degree with mathematical or statistical content (e.g. bioinformatics, population genetics, population biology as well as mathematics, statistics, data	

	science, physics or computer science). Prior experience with programming, e.g. in R, Python, C++ or MATLAB, is strongly recommended due to the computational nature of the project, although additional training (both formal and informal) will be available. Prior training in genomics and/or virus research is preferable but not essential.
Project key words	SARS-CoV-2 Transmission chain reconstruction Bayesian statistical inference Viral genomes Phylodynamics
Possible under 1+4 route? Master's options identified.	Yes LSHTM – MSc Epidemiology LSHTM – MSc Health Data Science LSHTM – MSc Medical Statistics SGUL – MSc Genomic Medicine
MRC Core Skills developed through this project	Quantitative skills Interdisciplinary skills
MRC LID themes	Health Data Science Infectious Disease
Further reading	Effectiveness of BNT162b2 and ChAdOx1 against SARS-CoV-2 household transmission: a prospective cohort study in England outbreaker2: a modular platform for outbreak reconstruction