M2 Internship Opportunity: Multiscale mathematical modelling of respiratory virus transmission

Context

The transmission of a respiratory virus occurs through interactions between an infected individual and a susceptible individual. It depends on multiple factors, including the amount of infectious virus emitted, symptoms, behaviours, the frequency and proximity of contacts, and the susceptibility of exposed individuals. These factors vary over the course of infection and between individuals, contributing to heterogeneity in transmission. Among them, viral load is an accessible measurement that provides an indication of transmission potential [1].

Recent work by the research team has integrated viral load trajectories into a mathematical model of household transmission. In this framework, the relationship between viral load and infectiousness is assumed, and the approach has been evaluated using simulated households [2].

However, viral load is sometimes only weakly associated with infectiousness [1]. In a study involving healthy volunteers experimentally exposed to influenza A virus [3], the amount of infectious virus detected in saliva and nasopharyngeal samples was compared with the amount expelled in respiratory particles during talking, coughing, and sneezing. The study highlighted substantial inter-individual variability in the relationships between infectious viral load, symptoms, and the amount of virus expelled into the air.

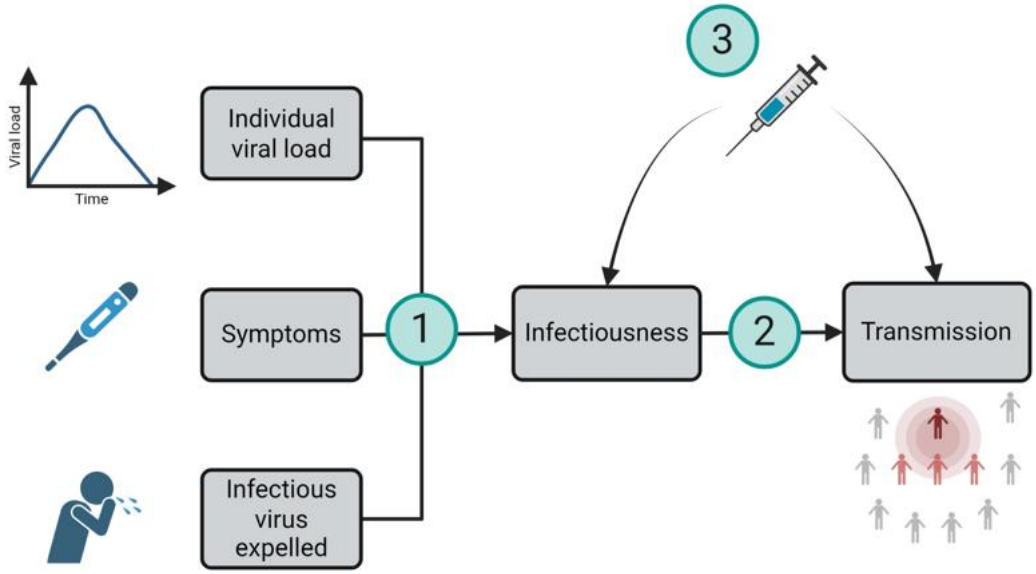
Vaccination, by reducing symptoms and viral load, also plays a role in preventing both infection and transmission.

Objective

The main objective of this internship will be to develop a mathematical model linking measured viral load, symptoms, and inter-individual heterogeneity to the emission of infectious virus, and to investigate how these factors translate into transmission risk in structured populations.

Proposed work

1. **Linking viral load to infectious virus emitted into the air**. Statistical models will be developed to analyse experimental measurements [3]. The relationships between viral load, symptoms, and infectious virus emitted into the air will be estimated using mixed-effects models to account for inter-individual variability.
2. **Investigating transmission within households**. An individual-based model will integrate viral load, viral emission, contacts, behaviours, and the susceptibility of exposed individuals. Parameters that have not yet been identified will be explored under different scenarios. Previous studies on influenza A and B, RSV, and SARS-CoV-2 will provide virus-specific points of comparison [4-6]. Outbreaks will be simulated to assess heterogeneity in outbreak dynamics and sizes. An extension to nursing homes may be considered to explore the impact of a different contact structure.
3. **Exploring the role of vaccination in preventing transmission**. While vaccine-induced protection against infection is well characterised, protection against onward transmission remains less well understood. Among infected individuals, we will investigate the potential effects of vaccination on viral load, symptoms, the amount of infectious virus expelled into the air, and subsequent transmission. Scenarios will be informed by available data, particularly studies of COVID-19 vaccination [7].



Candidate profile

We are looking for a second-year Master's student (M2) or a final-year engineering student with a background in biostatistics or biomathematics. Good proficiency in R, skills in statistical modelling, and interest in interdisciplinary approaches are desirable.

Research environment and supervision

The internship will take place within the MOCLID research team, IMR 1137 IAME Inserm, based at Bichat Hospital in Paris. The internship will be remunerated in accordance with Inserm regulations.

Supervision : Laura Mulas, Nathanaël Hozé, Jérémie Guedj et François Blanquart.

Contact : laura.mulas@inserm.fr ; nathanael.hoze@inserm.fr; jeremie.guedj@inserm.fr; françois.blanquart@college-de-france.fr

References

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