Organised by

National Centre for Infectious Diseases

NCID MONTHLY RESEARCH MEETING:

BRINGING PEOPLE TOGETHER,

BRIDGING SCIENCE AND MEDICINE

15 Jul 2022 | Friday | 11.00am – 12.00pm

About the Meeting

Our research meetings are held every 3rd Friday of the month, with the aim to:

1) Inspire research ideas and participation
2) Provide guidance on research studies
3) Foster research collaborations

Who should attend

All who are interested in research are welcome to attend.

To register

This will be a Zoom meeting. Register here or scan the QR code below.

*CME/CPE points will be awarded

Programme

11:00 AM **Integrating Multimodal Data to Improve Clinical Outbreak Investigations**
Mr Ashleigh Myall
PhD Student
Imperial College London

11:30 AM **Comparing Results from Alternative Approaches for Estimating the Severity of the Different SARS-CoV-2 Lineages in Singapore**
Dr Mark Chen I-Cheng
Consultant, National Public Health & Epidemiology Unit,
Head of Research Office,
National Centre for Infectious Diseases

5 to 10 mins Q&A will follow after each talk

Integrating Multimodal Data to Improve Clinical Outbreak Investigations

by **Mr Ashleigh Myall**
PhD Student
Imperial College London

Contact tracing is a key tool in epidemiology to identify and control outbreaks of infectious diseases. It yields contact maps of cases to identify outbreak clusters that can be targeted with infection control measures.

What constitutes a contact is typically based on binary definitions, that is, a contact has occurred or not. However, missing data, indirect contacts, and different contact requirements for transmission between diseases can substantially limit analyses. Here, we present StEP, a Spatial-temporal Epidemiological Proximity model that accounts for imperfect data and pathogen-specific contact, by learning probabilistic definitions of contact based on background spatial-temporal proximity. We showcase its potential using clinical data from outbreaks of Carbapenemase-producing Enterobacteriaceae within a large hospital group in London, UK. In addition to recovering core contact structures, StEP identifies missing contacts that link seemingly unconnected outbreak clusters and thus reveal a larger extent of transmission than estimated by conventional contact tracing methods

Three Learning Points

1. Routinely collected data holds novel reconstructive power for Carbapenemase-producing Enterobacteriaceae outbreaks.
2. In lieu of full/rapid genomic sequencing learnt definitions off contact can provide quick low-cost insights to clinicians.
3. Indirect and missed transmission is a strong driver of Carbapenemase-producing Enterobacteriaceae transmission.

Comparing Results from Alternative Approaches for Estimating the Severity of the Different SARS-CoV-2 Lineages in Singapore

by **Dr Mark Chen I-Cheng**
Consultant, National Public Health & Epidemiology Unit,
Head of Research Office, National Centre for Infectious Diseases

Since the delta variant, Singapore has been confronted with successive variants and sub-lineages of SARS-CoV-2. The impact of each new variant is a function of its likely attack rate, and the severity of the disease it may cause on the backdrop of the existing immune landscape. When a new lineage emerges, there is a necessity to rapidly project if it will cause more severe strain on the health system or lead to more mortality than previous waves. However, an emerging variant or lineage may initially co-circulate with earlier variants, thereby complicating how well we can estimate its severity by disentangling the contribution of circulating variants.

We compare results from several different approaches to estimating severity of key SARS-CoV-2 lineages in Singapore, in terms of the results obtained, but also how quickly we can obtain an estimate with some level of confidence. We then propose an approach which we think may be applicable to deriving early estimates of severity in an “endemic state” with co-circulating variants and lineages. We also suggest how different approaches may be needed to corroborate and “calibrate” the findings of other approaches.