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Contagion in a Clustered Context

Mathematical models are now routinely used in infectious disease epidemiology to inform public health policy. One of the key features of the contacts that transmit most infectious diseases is transitivity: a lot of your contacts are each others' contacts, too. But modelling this feature is tricky because of the correlations that build up on the network of contacts.

This talk will report advances on three relatively recent approaches to this problem: First, specialisation of the network topology to a local-global system (or *hypergraph*); secondly, proposal of improved moment closure schemes; and thirdly methods based on non-independent Bernoulli trials that can also be adapted to behavioural / 'complex' contagion processes.

Biological insights gained include:

1. The role of different types of transitivity in slowing disease spread – i.e. does it matter if most of the triangles are in complete graphs of size four or above?

2. A counter-intuitive result about contact tracing / hyperparasitism.

3. Intuitions for why clustering enhances the spread of some complex contagions.

These will be discussed alongside the mathematical methodology.