
Applied Mathematics Seminar



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Modelling viral dynamics on networks using a pair-based approach

With the ever-growing rate of antibiotic-resistant diseases, new ways of tackling epidemics must be considered, as we are losing the ability to fight them effectively with drugs. As such, prevention is as important as a cure. The goal of this contribution is to model the likelihood of paths that a disease may take and to identify areas that will be most affected.

To achieve this we consider a class of SIS, SIR and SIRS models, which are realized as a temporal network. We present a pair-based description to study the spreading of epidemics. The shift in perspective from individual-based to pair-based quantities enables exact modelling of Markovian epidemic processes on temporal tree graphs. On arbitrary graphs, the proposed pair-based model provides a substantial increase in accuracy at a low computational and conceptual cost compared to the individual-based model. Using the pair-based model, we derive useful analytical expressions, such as the epidemic threshold for testing the global susceptibility to epidemic outbreaks.

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