

專 題 演 講

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演講題目： Biological virus v.s. Computer scientist - an efficient flu simulation system

演講大綱：

Early data from the 2009 H1N1 pandemic (H1N1pdm) suggest that previous studies over-estimated the within-country rate of spatial spread of pandemic influenza. As large spatially resolved data sets are constructed, the need for efficient simulation code with which to investigate the spatial patterns of the pandemic becomes clear.

I will present a significant improvement to the efficiency of an individual-based stochastic disease simulation framework commonly used in multiple previous studies and quantify the efficiency of the revised algorithm and present an alternative parameterization of the model in terms of the basic reproductive number.

The model has been applied to the population of Taiwan during the H1N1 pandemic and demonstrated how the location of the initial seed can influence spatial incidence profiles and the overall spread of the epidemic.

Differences in incidence are driven by the relative connectivity of alternate seed locations. The ability to perform efficient simulation allows us to run a batch of simulations and take account of their average in real time. The averaged data are stable and can be used to differentiate spreading patterns that are not readily seen by only conducting a few runs.