

Flu, where are you?

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Abstract:

The modelling of the spread of an infectious disease within an individual or a cell culture has typically been done in a non-spatial manner: the population of cells in each state (susceptible, infected, dead, etc.) is tracked and evolved as a function of time alone using ODEs, with no regards for their spatial location. What do we miss when we assume spatial homogeneity? I will review models constructed with various levels of spatial representation for the spread of influenza within a host and/or cell culture. I will explore in which ways spatial distribution can affect the spread and severity of the infection, in particular with respect to cell tropism (preference of the virus for certain cell types) and the production of defective interfering particles.