

# Global Analysis for Spread of Infectious Diseases via Transportation Networks

Yukihiko Nakata, Gergely Röst

Bolyai Institute, University of Szeged

nakata@math.u-szeged.hu, rost@math.u-szeged.hu

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We formulate an epidemic model for the spread of an infectious disease along with population dispersal over an arbitrary number of distinct regions. Structuring the population by the time elapsed since the start of travel, we describe the infectious disease dynamics during transportation as well as in the regions. As a result, we obtain a system of delay differential equations. We define the basic reproduction number  $\mathcal{R}_0$  as the spectral radius of a next generation matrix. For multi-regional systems with strongly connected transportation networks, we prove that if  $\mathcal{R}_0 \leq 1$  then the disease will be eradicated from each region, while if  $\mathcal{R}_0 > 1$  there is a globally asymptotically stable equilibrium, which is endemic in every regions. If the transportation network is not strongly connected, then the model analysis shows that numerous endemic patterns can exist by admitting a globally asymptotically stable equilibrium, which may be disease free in some regions while endemic in other regions. We provide a procedure to detect the disease free and the endemic regions according to the network topology and local reproduction numbers. For a system consisting of two regions, we find that due to spatial heterogeneity characterized by different local reproduction numbers,  $\mathcal{R}_0$  may depend non-monotonically on the dispersal rates, thus travel restrictions are not always beneficial.