Pandemic Diseases and the Aviation Network: SARS, a case study

LARS HUFNAGEL, KITP, Santa Barbara, CA, DIRK BROCKMANN, MPI for Dynamics and Selforganization, THEO GEISEL, MPI for Dynamics and Selforganization — We investigate the mechanisms of the worldwide spread of infectious diseases in a modern world in which humans travel on all scales. We introduce a probabilistic model which accounts for the worldwide spread of infectious diseases on the global aviation network. The analysis indicates that a forecast of the geographical spread of an epidemic is indeed possible, provided that local dynamical parameters of the disease such as the basic reproduction number are known. The model consists of local stochastic infection dynamics and stochastic transport of individuals on the worldwide aviation network which takes into account over 95 civil aviation traffic. Our simulations of the SARS outbreak are in surprisingly good agreement with published case reports. Despite the fact that the system is stochastic with a high number of degrees of freedom the outcome of a single simulation exhibits only a small magnitude of variability. We show that this is due to the strong heterogeneity of the network ranging from a few two over 25,000 passengers between nodes of the network. Thus, we propose that our model can be employed to predict the worldwide spread of future pandemic diseases and to identify endangered regions in advance. Based on the connectivity of the aviation network we evaluate the performance of different control strategies and show that a quick and focused reaction is essential to inhibit the global spread of infectious diseases.