The SIR metapopulation model in a temporal commuting network

*Gabriel F. Costa[1], Matheus M. G. Correia[2], Leonardo B. L. Santos[3], Vander L. S. Freitas[4]

1) Department of Physics, Federal University of Ouro Preto, Ouro Preto, Brazil
2) National Institute for Space Research, São José dos Campos, Brazil
3) National Center for Monitoring and Early Warning of Natural Disasters (CEMADEN), São José dos Campos, São Paulo, Brazil
4) Department of Computing, Federal University of Ouro Preto, Ouro Preto, Brazil

Metapopulation models are a powerful tool for theorizing and simulating epidemic dynamics. One possibility of implementation is to have nodes as subpopulations of a given location and the links representing migrations of individuals, obeying a specific mobility rule, from one subpopulation to another in a given time window.

We simulate a SIR metapopulation model on top of a temporal Chinese commuting network, where nodes are cities and weighted connections give the rate of people that reaches or leaves a city. Each node has its metapopulation that interacts with its neighbors. Hence, people may infect and get infected depending on where they meet: i) infection of susceptibles in a certain city by infected people who live there; ii) infected people from other nodes who arrive at the destination and infect the locals; iii) susceptibles who traveled to another node and get infected by the locals; iv) susceptible people that go to a place and meet infected that comes from a third site.

The commuting network has a temporal resolution of 24 hours, which means the network updates its connections once a day. We analyze the dependence of epidemiological variables on the network resolution, by simulating the SIR model under different temporally aggregated versions of the network.

The simulations may help to design strategies for commuting data collection concerning temporal resolution and its impacts on epidemiological surveillance.