



Random Networks in a Distributed Computing Environment: An Approach to the Transmission Dynamics of Epidemic Diseases

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Abstract

Random networks are emerging in epidemiology as a way of simulation more realistic random contact behaviours. A network is a set of nodes representing individuals. Labels or properties may be assigned to each node, for instance, age, sex, state respect to disease (susceptibility, infection, recovery, etc.). Nodes are connected by ties that represent disease transmission paths. Once the network model and the disease evolution rules are stated, it is possible to simulate the evolution of the network over time and study the effect of disease on the population.

Moreover, random networks provide an easy way of modelling those scenarios where it is required the monitoring of the specific individuals, the design of single or combined vaccination strategies or to control and apply therapies in chosen target groups, something difficult to achieve in continuous models. However, essential aspects in epidemiology like the model fitting with data in order to obtain the transmission rate of a disease in a specific region turns out to be highly complex in computational terms (requiring for an average desktop computer several weeks, months or even years of calculation time) whereas it is an issue with some valid approaches in continuous models which are able to solve the model in an affordable quantity of time.

In this paper, we present the description of a computational system following the paradigm of distributed computing, which will allow the estimation of parameters in random network epidemic models. This paradigm consists of a server that delivers tasks to be carried out by client computers. When the task is finished, the client sends the obtained results to the server to be stored until all tasks are finished and then, ready to be analysed.

Keywords: random network, distributed computing, epidemic diseases, transmission dynamics.

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