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Structures of networks and application to models of disease spreading

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In the last twenty years Statistical Physics has contributed immensely to other scientific fields, mainly by the introduction of networks. The main reason has been the creation of the internet, which has been ubiquitous in daily life. The different structures of networks will be shown, together with their characteristics, with several different applications from real situations, which help us to understand dynamic phenomena in many different fields, such as social networks, economic networks, linguistics, etc.

One important application is the spreading of diseases, such as the recent Covid-19 in a population in the form of a pandemic. In fact, predicting how fast an infection is spreading could be a major factor in deciding on the severity, extent and strictness of the applied mitigation measures, such as the recent lockdowns. Even though modelling epidemics is a wellstudied subject, usually models do not include quarantine or other social measures, such as those imposed in the recent pandemic. The current work builds upon a recent paper by Maier and Brockmann (2020), where a compartmental SIRX model was implemented. That model included social or individual behavioral changes during quarantine, by introducing state X, in which symptomatic quarantined individuals are not transmitting the infection anymore, and described well the transmission in the initial stages of the infection. The results of the model were applied to real data from several provinces in China, quite successfully. In our approach we use a Monte-Carlo simulation model on networks. Individuals are network nodes and the links are their contacts. We use a spreading mechanism from the initially infected nodes to their nearest neighbors, as has been done previously. Initially, we find the values of the rate constants (parameters) the same way as in Maier and Brockmann (2020) for the confirmed cases of a country, on a daily basis, as published by the Johns Hopkins University. We then use different types of networks (random Erdős-Rényi, Small World, and Barabási-Albert Scale-Free) with various characteristics in an effort to find the best fit with the real data for the same geographical regions as reported in Maier and Brockmann (2020). Our simulations show that the best fit comes with the Erdős-Rényi random networks. We then apply this method to several other countries, both for large size countries, and small size ones. In all cases investigated we find the same result, i.e. best agreement for the evolution of the pandemic with time is for the Erdős-Rényi networks. Furthermore, our results indicate that the best fit occurs for a random network with an average degree of the order of $\langle k \rangle \sim 10-25$, for all countries tested. Scale Free and Small World networks fail to fit the real data convincingly.

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