

Abstract

Infectious diseases, such as the current COVID-19, have a huge economic and societal impact. The ability to model its transmission characteristics is critical to minimize its impact. 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 well studied 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 behavioural 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 neighbours, 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 given 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 $\langle k \rangle \approx 10\text{--}25$, for all countries tested. Scale Free and Small World networks fail to fit the real data convincingly. Results presented in this work have been produced using the Aristotle University of Thessaloniki (AUTH) High Performance Computing Infrastructure and Resources, which is a structure consisted of heterogeneous connected compute nodes. Regulated by the availability, our results were produced by a structure of 18 nodes of 20 cpus (Intel Xeon E5-2630 v4) or a structure of 5 nodes of 64 cpus (AMD Opteron 6274). It was of utmost importance to use HPC as reliable results required many realizations. Moreover, Monte-Carlo simulations were run to different network topologies and varying $\langle k \rangle$, a small change in which produces different results. A forward-looking statement demonstrating relevance to scientific discoveries, innovation in industry or addressing society's grand challenges. Submissions, as well as the resulting presentations, should be tailored to a wide audience, using layperson's terms and examples where possible. This work has used a network algorithm for studying the spreading of the COVID - 19 disease in several different countries in the world. The aim was to discover which was the closest model of physical contacts of individuals that enhanced the transfer of the disease from person to person. Several different topologies were tried using the real data from the different countries, until the best match was found. It proved to be that people connected in groups of between $\sim 10\text{--}20$ individuals are the most realistic spreaders in most of the world countries.