

# On the Effect of Space on the Spread of Infections

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## 1 Introduction

A good understanding of how pathogens spread is important to mitigate their effect on individuals in terms of diseases and, as a consequence, on society. The recent case of the COVID-19 pandemic illustrates this fact in many ways. The SARS-CoV-2 virus, which causes the COVID-19 disease, can be found in many locations, some of which are unexpected; and mitigation efforts are successful to varying degrees in different places [8, 9]. The explanations given to such observations often refer to the geographical context, which incorporates besides space also cultures, mundane habits, travel behaviour, and many more aspects. While space is of obvious importance for the transmission of a pathogen, it is also one of the most important aspects of the people’s travel behaviour, an aspect that is relatively easy to control in case of a pandemic. This short paper raises the question in which ways the structure of space influences the spread of such a pathogen.

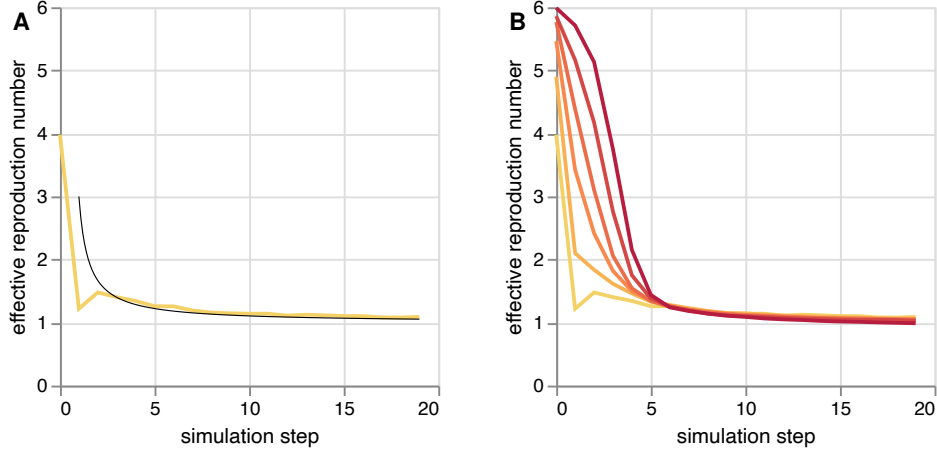
Theoretical considerations often focus on the basic reproduction number  $R_0$ , i.e., the average number of previously uninfected individuals becoming infected by an infectious person. In case of an exponential growth of infections, this number is constant over time [1]. In practice however, it varies in different contexts and over time, resulting in an effective reproduction number  $R$ . When modelling the spread of infections, individuals can be understood as the nodes of a network and their social relations, each of which can lead to the infection of another individual, as edges. In the following, we will examine how the spatial structure of such a network affects the effective reproduction number.

## 2 Results and Discussion

The effective reproduction number can easily be computed in a spatial network setting, which assumes individuals only to infect others in their spatial vicinity. This property translates to neighbouring nodes in the network to be in the same spatial vicinity, in case of which the network inherits spatial characteristics [2, 7]. Previous epidemiological studies often assume spatial grids [10, 11], in contrast to which this study uses instances of the Mocnik model<sup>1</sup>, an example of a non-regular spatial network model [4, 5, 7]. In two-dimensions, each node has  $S = \rho^2$  neighbours in average, where  $\rho$  is a parameter of the model [4, 5]. This number  $S$  will be referred to as the number of social contacts in the following. When choosing  $S$  similar to  $R_0$ , the spread is prototypically influenced by spatial distance – individuals spread infections only in their direct vicinity.

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<sup>1</sup>Other spatial networks yield very similar results. The Mocnik model has been chosen here to blend over between a spatial and a complete network, as is discussed later.



**Figure 1: Simulation of infection spread in an instance of the Mocnik model with 100,000 nodes. A** Spatial case ( $R_0 = S = 6$ ; yellow) compared to the theoretical prediction of Equation 1 (black). **B** Spatial case ( $R_0 = S = 6$ ; yellow) compared with less spatial cases ( $R_0 = 6$ ,  $S = 12, 30, 60, 163, 443$ ; orange to red).

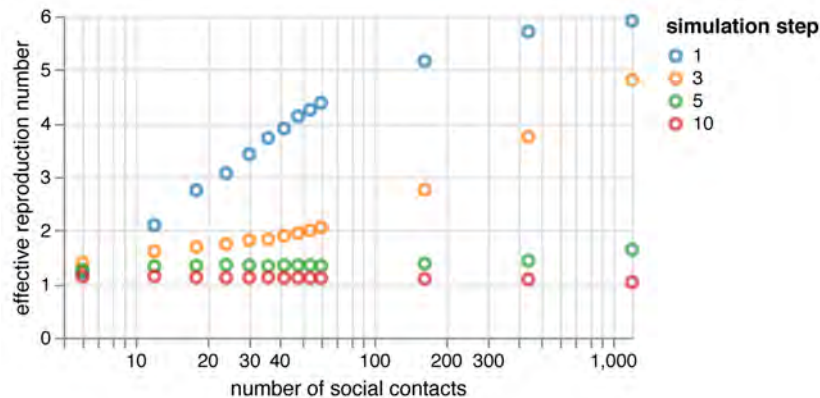
The effective reproduction number  $R$  changes during an outbreak in a spatial network. Starting with one node only, more and more nodes get infected over time. As an already infected neighbour of an infected node cannot be infected anew, infections often follow a sub-exponential growth. More specifically, the *Polynomial Volume Law* claims in case of the two-dimensional Mocnik model that  $1 + n^2$  nodes have statistically been infected until simulation step  $n$  if every neighbouring node of an infected one gets infected itself if not yet being infected [4, 5, 7]. Accordingly,  $n^2 - (n-1)^2$  nodes get infected in step  $n-1$ . These nodes are infectious in step  $n$  and infect  $(n+1)^2 - n^2$  additional nodes. The statistical average of the effective reproduction number is, in case of this model, thus given by

$$\frac{(n+1)^2 - n^2}{n^2 - (n-1)^2} = 1 + \frac{2}{2n-1}. \quad (1)$$

A comparison to a simulation<sup>2</sup> ( $R_0 = S = 6$ ) confirms this consideration (Figure 1A).

The topologies of real social networks are, despite being spatially influenced, more complex in nature – they borrow characteristics from both spatial and complete networks. As the latter can be considered a special case of a Mocnik model with  $S$  approaching the number of nodes, the simulation was run with several values of  $S$  for blending over between both types of networks. The simulations show that the effective reproduction factor  $R$  increases for larger  $S$  but converges to 1 in all cases considered (Figure 1B). Indeed, the circumference of the disk of infected nodes grows only slowly and the ratio of the number of nodes infected in the last step and the ones to infect in the next step converges to 1. At closer inspection, there is little to no influence of  $S$  on  $R$  after some simulation steps (Figure 2). This suggests that the structure of space has a relevant impact on the spread of infections in a network, also beyond the most prototypical cases.

<sup>2</sup>In the simulation, each node infected in step  $n$  is assumed to infect  $R_0$  randomly chosen neighbouring nodes in step  $n+1$ , or less nodes if the node had less neighbours only.



**Figure 2: Influence of the number of social contacts on the effective repr. number**

### 3 Conclusion

The study at hand demonstrates that the spread of diseases in a spatial context tends to yield effective reproduction numbers near to 1. The study is, however, limited by the fact that the network topologies of real networks can be more diverse than the one considered here. Hubs [3] and shortcuts in the network have not yet been considered. Both limitations could be addressed by assuming hierarchical Mocnik models [5]. After having addressed these limitations, more realistic scenarios might be considered [6] to understand the (existing or non-existing) impact of closing country borders or motivating people not to travel, which potentially leads to more spatially structured networks. This study is, however, a first indication that the effect of spatial networks on the spread of infections is robust, even in cases where this structure is less dominant.

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