Contact heterogeneity and epidemic spread

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The way social contacts are structured is known to have a strong impact on epidemic spread. While the first epidemic models considered uniformly mixing populations, meaning that all individuals encounter one another at the same frequency, several ways of including contact heterogeneity have been developed since. For instance, it is possible to consider that contacts occur at different frequencies between several groups of individuals (*e.g.* age structure), or that the epidemic spreads on a graph representing the contact network.

The aim of this Bachelor Thesis is to explore some of the means of taking into account contact heterogeneity, and the way they influence epidemic key characteristics such as the herd immunity threshold and final size. Further, they offer different options for simulating lockdown-like control measures. After briefly considering the case of the uniformly mixing *SIR* model for reference (Diekmann and Heesterbeek 2000), the student will study a recent article (Di Lauro et al. 2021) and aim at reproducing some of the results obtained therein. This leads to the following key points:

- Understanding the ways different forms of contact heterogeneity can be included in epidemic models.

- Conducting a simulation study to explore the behaviour of each of these models, and compare different ways of modelling lockdown-like control measures.

- Interpretation of the obtained results.

The focus will be put on network-based *SIR* models, as well as an age-structured *SEIRD* model in a COVID-like setting. For the latter, real-world data has been used to parametrise mortality and contact rates per age group (Mossong et al. 2008; Verity et al. 2020), and these realistic parameters will be used throughout the Bachelor Thesis.

Depending on the student's interest and motivation, the emphasis can be lain on different aspects of this topic to complement the above objectives, including for instance other epidemic models in the study.

References

Di Lauro, F. et al. (2021). "The Impact of Contact Structure and Mixing on Control Measures and Disease-Induced Herd Immunity in Epidemic Models: A Mean-Field Model Perspective". In: *Bulletin of Mathematical Biology* 83.11, p. 117. DOI: 10.1007/s11538-021-00947-8.

Diekmann, O. and J. A. P. Heesterbeek (2000). *Mathematical Epidemiology of Infectious Diseases: Model Building, Analysis and Interpretation*. Wiley Series in Mathematical and Computational Biology. Chichester: John Wiley & Sons. DOI: 10.1093/ije/30.1.186.

Mossong, J. et al. (2008). "Social Contacts and Mixing Patterns Relevant to the Spread of Infectious Diseases". In: *PLoS Medicine* 5.3. Ed. by Steven Riley. DOI: 10.1371/journal.pmed.0050074.

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