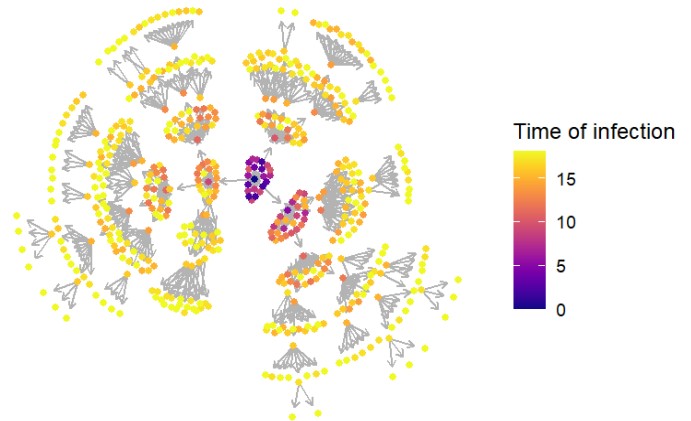




The role of superspreaders

Variation between individuals can have profound effects on populations, through evolution, but also through short-term ecological effects (e.g. Hart et al. 2016). A prime example where variation may have a profound effect is in epidemiology: for a pandemic to spread across the globe it only requires a small number of hosts to travel widely. Indeed, we suspect that the spread of epidemics strongly depends on so-called superspreaders (Wong et al. 2015). In this project, jointly supervised with Sebastian Lequime, we use an individual-based simulator, *nosoi* (Lequime et al. 2020) to simulate disease outbreaks.



In the first step, we will explore under what parameter settings outbreaks rely on a small number of superspreaders and how we can effectively quantify the impact of superspreaders. Once we have this characterization, in a second step, we use approximate Bayesian computation to fit the *nosoi* parameters on data from existing outbreaks of, for example, measles, RSV, NORO, or animal diseases. We then quantify to what extent superspreaders played a role in these outbreaks. The project will require running and analysing simulations, speeding up de *nosoi* code, and using approximate Bayesian computation. Affinity with simulation studies is thus a must. Hopefully, the project will increase our understanding of how individual variation contributes to the spread of diseases.

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Staff member: Koen van Benthem
Daily supervisor:
Expertise group: TRÊS

Contact: k.j.van.benthem@rug.nl
Contact:

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