

When details do matter: detecting superspreader farms in livestock diseases

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Livestock infectious diseases spread between farms (network nodes) via both *direct contacts*, i.e. animal trade, and *indirect contacts*, due to visitors and vehicles that can act as pathogen vectors. The diffusion process can well be captured by temporal two-layer network models. While animal movements are registered in national databases in many EU-countries, little or no information about on-farm visits is available and rarely collected in a systematic manner.

Here we evaluate how and to what extent different levels of detail in describing indirect contact networks can result into qualitative and quantitative different outcomes of epidemic spread, in terms of both superspreaders identification and final epidemic size.

We focus on a dairy farm system in Emilia Romagna (Northern Italy) as resulting from a 3-month comprehensive data collection campaign on itineraries of trucks for calves transportation. The indirect contact layer of the network is described at two different levels of detail. In the *common contractors network (CCN)*, farms are connected with indirect links if visited by trucks of the same company. In the *truck itineraries network (TIN)*, directed links connect each farm to those later visited by the same truck. Disease spread is simulated through a stochastic Susceptible-Infectious model initialized with one-at-a-time farm acting as epidemic seed. CCN, coarsely-described layering systematically brings to overestimations of final epidemic sizes compared to TIN, finely-described layering. Moreover, the identified sets of superspreaders (farms leading to the top 5% of final epidemic sizes), are very different using CCN or TIN. Most important, while epidemics starting from CCN-superspreaders typically infect the same farms, outbreaks seeded at TIN-superspreaders involve quite diversified sets of farms. We conclude that not only the detail of indirect contacts description deeply influences the identification of superspreaders, but also the set of infected farms, with non-trivial consequences in designing surveillance and control measures.

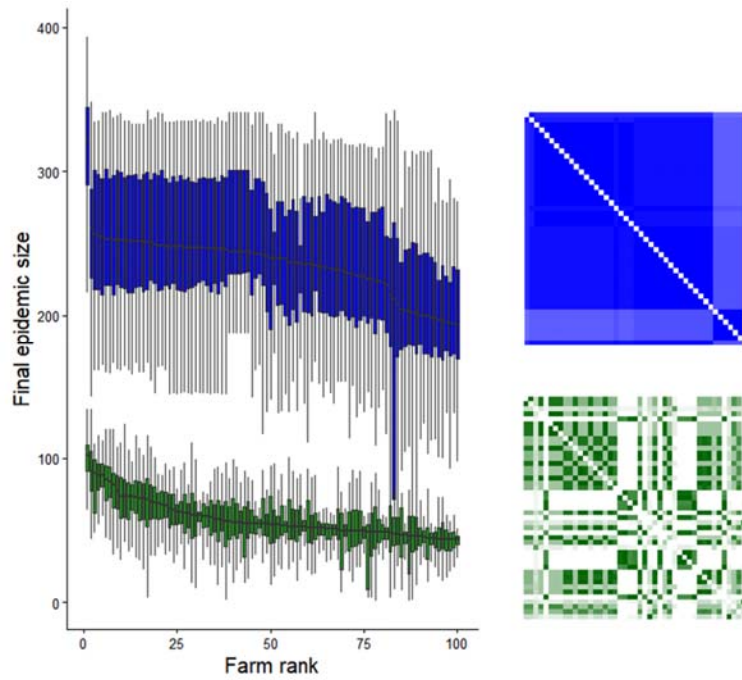


Figure 1 Left panel shows the comparison between the distributions of the final epidemic size obtained with the two temporal multilayer networks. Each x-axis point represents an epidemic seed and, for each of them, are reported the 100 final epidemic sizes obtained. Right panel shows the Jaccard index heatmaps obtained pairwise comparing the sets of farms that could be potentially infected from a seed; only superspreaders are considered. Blue identifies results obtained with the CCN, while green represents results obtained with the TIN.