The importance of the temporal sequence of indirect contacts: the case study of a dairy farm system in the Emilia Romagna region (Northern Italy)

Alba Bernini[1,2], Luca Bolzoni[2], and Renato Casagrandi[1]

[1] Dipartimento di Elettronica, Informazione e Bioingegneria (DEIB), Politecnico di Milano, 20133 Milan, Italy
[2] Risk Analysis Unit, Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia Romagna, 43126 Parma, Italy
alba.bernini@polimi.it
luca.bolzoni@izsler.it
renato.casagrandi@polimi.it

1 Introduction

Among the many real-world processes that can be represented as dynamical systems on networks, epidemics spread is one of the most notable examples. In the case of live-stock diseases, the diffusion of epidemics in farm systems can cause serious negative impacts both from economic and social perspectives [?]. Thus, quantitative epidemiological studies are key in supporting the design of more effective control measures. In this context, nodes can represent farms, considered as epidemiological units, while links can describe the possible between-farm pathogen transmission routes, which can in turn be distinguished between direct contacts, i.e. animal movements, and indirect ones, such as the sharing of equipment or movement of workers and vehicles. The role of indirect contacts in disease transmission is still poorly understood due to limitations deriving from their highly diverse and complex nature. Indeed, while animal movements (such as bovine and swine) are registered in national databases in many EU-countries (Commission Decision 2006/132/EC), little information is available to date on workers visits. As a consequence, when accounted for in modelling, indirect contacts have been described through the use of commercial networks, where links between farms are traced on the basis of common contractors [?]. However, this approach can lead to descriptions of the contact networks that are misleading, since *(i)* a common contractor does not imply common personnel and vehicles visiting a pair of farms and *(ii)* the temporal sequence of contacts is lost. Here, we analyzed how different levels of detail in the representation of indirect contacts may affect the description of the epidemic spread process, to the point that different conclusions can sometimes be obtained. In such cases, the detection of superspreaders, i.e. the farms that play a crucial role in the diffusion process, is falsified and potential control actions might become ineffective.

2 Materials and methods

We considered a system of dairy farms in the Emilia Romagna region (Northern Italy) involved in a comprehensive data collection campaign on calves transportation occurred

COMPLEX NETWORKS

The 6th International Conference on Complex Networks & Their Applications. Nov. 29 - Dec. 01, 2017, Lyon (France)

between September and November 2014. Based on these data, we reconstructed the daily routes of the trucks belonging to different transportation companies active in the area. As a matter of fact, the contamination of trucks (such as for milk, feed, and live animals transportation) represents one of the main indirect route of between-farm transmission. For the same period and the same farms, information about direct contacts were collected from the Italian National Database for Animal Identification and Registration. The between-farm contacts were represented as a daily temporal multilayer network [**?**,**?**] with two layers: one for direct (i.e. animal movements) and the other for indirect contacts (derived from the sharing of transportation trucks). We derived the indirect contacts network using two different levels of detail. Indeed, our aim was to evaluate to what extent the knowledge of the sequence of on-farm visits is relevant to establish the final size of an epidemic in the unfortunate case of a disease diffusion. On the one hand, we built a bipartite network based on the commercial relations between the farms and the transportation companies and we projected it on the space of the farms to obtain the *common contractors network (CCN)*. On the other hand, taking advantage of the available data on the truck identifiers and the sequence of visits, the *truck itineraries network (TIN)* was assembled assigning a directed link from a given farm to those later visited by the same truck in the same day. It is worth remarking that the TIN is different with respect to the CCN not only because of the introduction of the links directionality, but also because of the different number of links, since some transportation companies own more than one truck. To remark the crucial role played by the topology of the network, we kept the description of the disease diffusion process as simple as possible. Therefore, the system was modeled on both multilayer networks through a boolean Susceptible-Infectious (SI) compartmental model, where the probability of disease transmission was designed according to Bates *et al.* [**?**]. At the beginning of each simulation, all farms were assumed susceptible but one (namely, the epidemic seed). One at a time, each farm was selected as epidemic seed and 100 simulations were performed. At the end of each simulation, the final epidemic size was recorded and the 5% of farms that led to the larger final epidemic sizes were classified as superspreaders and characterized in terms of their topological characteristics.

3   Results and discussion

The distributions of the final epidemic sizes obtained with the two multilayer networks CCN and TIN were significantly different, as shown in Fig.1. Each point on the x-axis represents an epidemic seed and the vertical segments surrounding the median final epidemic sizes on the y-axis represent the ranges out of the 100 simulations performed describing the indirect contacts through the CCN (grey) and TIN (black). Farms are ranked in decreasing order of median final epidemic size predicted either using the CCN or the TIN. As emerging from Fig.1, the use of the CCN systematically resulted in an overestimation of the final epidemic size. Interestingly, we found that the superspreading farms identified through the simulations on the CCN (red dots) rarely match the superspreaders in the TIN (Kendalls coefficient between the two rankings equals 0.41). This result has significant consequences on the surveillance and control of livestock diseases, especially in the case of implementation of risk-based biosecurity measures.

The 6th International Conference on Complex Networks & Their Applications. Nov. 29 - Dec. 01, 2017, Lyon (France)

COMPLEX NETWORKS

Specifically, if the network structure used to identify the superspreaders is inadequate, the intervention will focus on the wrong farms. Among all the indicators considered to potentially characterize the superspreaders, the best resulted to be the out degree and the outgoing infection chain [**?**], which seem to be good candidates for selecting the farms where starting to implement biosafety measures.
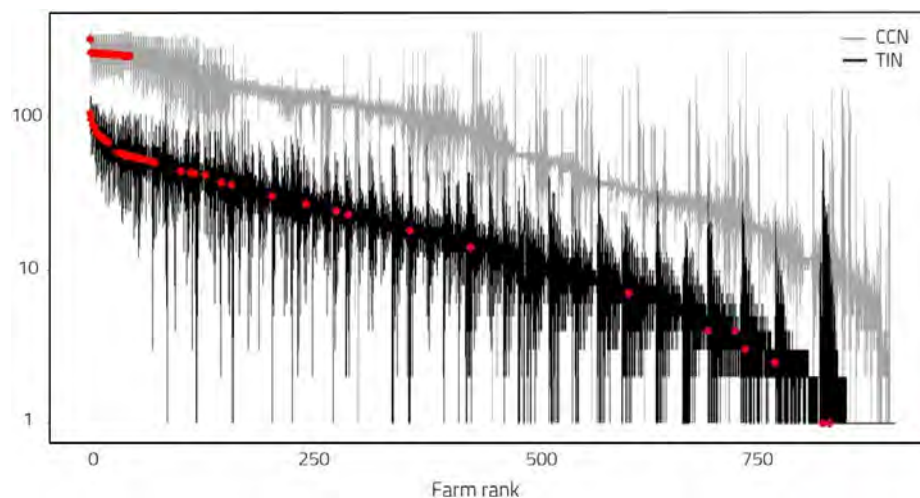

Fig. 1. Comparison between the distributions of the final epidemic size obtained with the two temporal multilayer networks. Each x-axis point represents an epidemic seed and, for each of them, are reported on semi logarithmic scale the 100 final epidemic sizes obtained. The red dots represent the positions in the two rankings of the farms associated to the largest 5% median final epidemic sizes in the commercial network, i.e. the superspreaders.

References

1. Anderson, I.: Foot and mouth disease 2001: lessons to be learned inquiry. The Stationery Office, London, (2002)
2. Fournié, G., Guitian, J., Desvaux, S., Cuong, V. C., Pfeiffer, D. U., Mangtani, P., Ghani, A. C.: Interventions for avian influenza A (H5N1) risk management in live bird market networks. Proc. Natl. Acad. Sci. USA 110, 91779182 (2013)
3. Holme, P., Saramäki, J.: Temporal networks. Physics reports 519(3), 97-125 (2012)
4. Boccaletti, S., Latora, V., Moreno, Y., Chavez, M., Hwang, D. U.: Complex networks: Structure and dynamics. Physics reports, 424(4), 175-308 (2006)
5. Bates, T. W., Thurmond, M. C., Carpenter, T. E.:Description of an epidemic simulation model for use inevaluating strategies to control an outbreak of foot-and-mouth disease. Am. J. Vet. Res. 64, 195204 (2003)
6. Dubé, C., Ribble, C., Kelton, D., McNab, B.: Comparing network analysis measures to determine potential epidemic size of highly contagious exotic diseases in fragmented monthly networks of dairy cattle movements in Ontario, Canada. Transbound. Emerg. Dis. 55, 382-92 (2008)