

Reply to “Comment on ‘Nodal infection in Markovian susceptible-infected-susceptible and susceptible-infected-removed epidemics on networks are non-negatively correlated’ ”

Eric Cator,^{1,*} Peter Donnelly,^{2,†} and Piet Van Mieghem^{3,‡}

¹Faculty of Science, P. O. Box 9010, 6500 GL Nijmegen, The Netherlands

²Wellcome Centre for Human Genetics, University of Oxford, Roosevelt Drive, Oxford OX3 7BN, United Kingdom

³Faculty of Electrical Engineering, Mathematics and Computer Science, P.O. Box 5031, 2600 GA Delft, The Netherlands



(Received 29 May 2018; published 3 August 2018)

We emphasize that correlations between infection states in both the SIS and SIR model are always positive and that the title of the article “Nodal infection in Markovian susceptible-infected-susceptible and susceptible-infected-removed epidemics on networks are non-negatively correlated” [Phys. Rev. E **89**, 052802 (2014)] is correct. The history and motivation that led to the proof is placed in perspective.

DOI: [10.1103/PhysRevE.98.026302](https://doi.org/10.1103/PhysRevE.98.026302)

Cator and Van Mieghem are grateful to the authors of the Comment [1] on the paper [2], which focused mainly on the susceptible-infected-susceptible (SIS) model, for two reasons. First, Cator and Van Mieghem carelessly assumed that the proof in Ref. [2] also holds for the susceptible-infected-removed (SIR) model. Rodriguez *et al.* [1] rightly point out that the monotonicity, which is crucial in the proof in Ref. [2], does not hold for the SIR model, although monotonicity applies to the SIS model. Second, Rodriguez *et al.* [1, Ref. [2]] refer to a paper [3] by Donnelly, which was unfortunately overlooked in Ref. [2]. Let the Bernoulli random variable $Y_i(t) = 1$, when node i is infected at time t , and otherwise $Y_i(t) = 0$. Donnelly [3] has used a different graphical construction for the SIR and SIS model than in Ref. [2] to prove that $Y_i(t)$ and $Y_j(s)$ are positively correlated. Moreover, his method extends to more general epidemic models. In summary, we wish to emphasize that *correlations between infection states in both the SIS and SIR model are always positive*. Hence, the main message as well as the title of [2] is correct.

The counterexample in the Comment [1] seems to contradict positive correlations in SIS and SIR, but we argue that the counterexample is misleading. Rodriguez *et al.* [1] consider the correlation between $X_t(i)$ and $X_t(j)$ in the SIR model, where $X_t(i) \in \{S, I, R\}$ is the state of node i at time t and they choose $S = 0$ for the susceptible, $I = 1$ for the infected, and $R = 2$ for the removed state. However, it seems more natural as in Refs. [2] and [3] to consider the correlations between the random variables $Y_i(t)$ at each node i in the

graph. Indeed, a positive correlation between $Y_i(t)$ and $Y_j(s)$ means that the probability that node j is infected at time $s \geq t$ grows, given that node i is infected at time t (i.e., the infection states of any pair of nodes i and j are positively correlated). Physically and intuitively, positive correlations in SIS and SIR epidemics mean that an infection in some node in the network can only increase the probability of infection in other nodes. The covariance between $X_t(i)$ and $X_t(j)$ in Ref. [1] is difficult to physically interpret, in contrast to $Y_i(t)$ and $Y_j(s)$, and, moreover, depends on the somewhat arbitrary coding of the states. Indeed, by choosing the states $X_t(i) \in \{0, 1, -1\}$, a different sign in the covariance $\text{cov}(X_t(i), X_t(j))$ can be found.

On several occasions before 2014, when presenting the N -intertwined mean-field approximation (NIMFA) for SIS epidemics on any network [4,5] that implicitly assumed positive correlations, a debate started on whether the covariance between two infectious nodes is always non-negative in any graph. Any mean-field approximation [6] assumes that the covariance is equal to zero. The advantage of a non-negative correlation is that NIMFA always overestimates—though slightly—the actual probability of nodal infection. Hence, from a practical point of view, to prevent epidemics in a network, NIMFA puts us always on the safe side. The exact Markovian SIS model [4] has a state space of 2^N linear equations, which can only be solved for small networks of size $N < 20$. Therefore, mean-field theory is popular [7], because large networks can be computed. At that time in 2014, Cator and Van Mieghem assumed that the non-negative SIS correlation result was unknown and embarked on a proof.

We hope that this rebuttal will spread the non-negative SIS and SIR correlation property more widely and that the original paper of Donnelly [3] will be recognized as its first demonstration.

*E.Cator@science.ru.nl

†Donnelly@well.ox.ac.uk

‡P.F.A.VanMieghem@tudelft.nl

[1] P. M. Rodriguez, A. Roldan-Correra, and L. A. Valencia, Comment on ‘Nodal infection in Markovian susceptible-infected-susceptible and susceptible-infected-removed epidemics on networks are non-negatively correlated,’ Phys. Rev. E **98**, 026301 (2018).

[2] E. Cator and P. Van Mieghem, Nodal infection in Markovian SIS and SIR epidemics on networks are non-negatively correlated, Phys. Rev. E **89**, 052802 (2014).

[3] P. Donnelly, The correlation structure of epidemic models, Math. Biosci. **117**, 49 (1993).

- [4] P. Van Mieghem, J. S. Omic, and R. E. Kooij, Virus spread in networks, *IEEE/ACM Trans. Network.* **17**, 1 (2009).
- [5] P. Van Mieghem, The N -intertwined SIS epidemic network model, *Computing* **93**, 147 (2011).
- [6] K. Devriendt and P. Van Mieghem, Unified mean-field framework for SIS epidemics on networks, based on graph partitioning and the isoperimetric inequality, *Phys. Rev. E* **96**, 052314 (2017).
- [7] R. Pastor-Satorras, C. Castellano, P. Van Mieghem, and A. Vespignani, Epidemic processes in complex networks, *Rev. Mod. Phys.* **87**, 925 (2015).