

Peer Review

Review of: "Poisson Network SIR Epidemic Model"

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The manuscript does a general overview of basic SIR models and continuous-time stochastic SIR models, to then analyse SIR on configuration graphs, with a focus on Poisson Network. The authors show that there is a closed form for the likelihood when approaching the problem from a survival analysis perspective and performing inference on Ebola data. I enjoyed reading the paper but have several Minor and Major concerns about the paper. I want to stress that I have given a low rate just because I do not think the paper is ready for publication and I will definitely change it once the authors address my concerns and the ones from the other reviewers.

Major:

- I do not see how to get (2), I suggest to the author to include all calculations. This was also suggested by another reviewer.
- The statement of Theorem 1 is unclear. "describe above" should be replaced by some reference to the text, which is a formal system of equations or something. Also, the second part of the statement is unclear. I think it is crucial to give intuition to the reader why you are doing this. My guess is that in the large population limit (n goes to infinity) you have some form of independence on the interactions between pairs of individuals, is that right?
- Fig. 2 makes me wonder if there are combination of β, γ that could give the same infection curve. If so it seems that all the extensive use of contact networks is kind of lost when aggregating the population. I think this is generally the problem with compartmental models, and a big pro of individual-based models (obviously you pay in terms of computational cost).
- Table 1 increases my concern above, it seems that with the classical SIR the authors already get something. So what are the advantages of the network approach? Which one is better in terms of

likelihood? It is also fine to say something along the lines: “We tried this and it is the same of doing this”, but it needs to be clear in the manuscript. Also it would be good to see the trace plots and have the y-axis scale in Fig. 4.

Minor:

- There is a comma missing above eq. (1), “susceptibles (S) infected (II) ...” should be “susceptibles (S), infected (II) ...”.
- In eq. (1) I think using β instead of b and γ instead of c is more common in the literature. I know they have different interpretations and you use β , γ later, but it would be useful to have the same notation with the right rescaling so the reader can draw connections between the two frameworks.
- If S, I, R are proportions should it not be $S+I+R=1$. Also working with the proportions would require b to scale as $O(N)$, which means that you lose the interpretation of a rate.
- Above fig. 1 the authors use PGF without defining it, I recommend something like: “probability generating function (PGF)...”.
- I think there are connections to be drawn with master equations of individual-based models, see “Deterministic epidemiological models at the individual level” by Sharkey, which is a very cool paper.
- The derivation of (5) should not be done in words, I think having the maths there or in some supplementary material would help a lot.
- There is a typo in Prop. 1 “than” should be “then”. Also the square symbol at the end of Prop. 1 should be used when you complete a proof.

Declarations

Potential competing interests: No potential competing interests to declare.