Reviewer’s report

Title: Differential sexual network connectivity offers a parsimonious explanation for population-level variations in the prevalence of bacterial vaginosis: a data-driven, model-supported hypothesis

Version: 1 Date: 25 Jul 2018

Reviewer: James Moody

Reviewers report:

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This is a very nice review of the role of network structure and dynamics on STI and potential BV variation across populations. I've only one minor quibble, which is that I think the notion of connectivity you end up using (partner degree and concurrency) are all local and not really getting at the level of global network connectivity necessary to assess spread. You'd be better off, in my opinion, looking at things like size of the largest connected component, bicomponent, or forward-reachable-path (in the dynamic case). All of these are of course difficult to measure without global network data, but can be estimated in the simulation tools. That is, use the local collected degree and concurrency data to estimate/simulate global networks, allowing you to assess connectivity per se, rather than these local features by themselves.

Are the methods appropriate and well described?
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