

The authors have done a good job overall in addressing the previous round of reviewer comments, especially in terms of the introduction, methods/analyses and results. However, there still remain issues that need to be addressed before I can recommend the paper. In particular, the revision of the discussion is inconsistent with some suggested changes not made and some text/ideas that seem to remain from the previous version that does not fit well with the results from the new analysis.

I sent the paper back to two of the original reviewers. While one of the reviewers was happy with the changes made, the other still had concerns over various aspects of the manuscript. I've provided some additional thoughts on these comments below as well as some more specific points on my own.

Point 1: The non-independence of disease outcomes in the network is an interesting issue – individuals that are frequently found in proximity would be expected to be more likely to share similar outcomes for directly-transmitted pathogens/parasites in particular. Network autocorrelation models are certainly a good way to account for these types of pattern. However, given the focus of the study (and to some extent the likelihood that correlations between network position and infection intensity may not be related to transmission for these parasites), I think the current approach is reasonable (especially given the focus of the study is more on sampling).

Point 2: It is (inevitably) hard to judge the ability of the random effect structure to deal with clustering/non-independence, although the approach seems potentially reasonable it would be good to consider this carefully. I think the question about interactions really depends on the aims of the study, if the authors are interested in a similar relationship across all three pathogens then the current model structure seems fine, although more complex model structures could lead to more nuanced results.

Point 3: This remains an important point and I am not sure it has been adequately dealt with in the way the manuscript has been revised. In addition to the reviewer's comments about the lack of clarity in the biological rationale for the approach, makes a variety of statements related to transmission in relation to differences in the association between centrality measures and infection intensity when, given the fact that parasite is indirectly transmitted, it is not clear whether this is from social connections being a proxy for spatial proximity or because social centrality is related to health in some other way. It is fairly misleading to focus the discussion around ideas related to direct transmission (the introduction provide a much more holistic/balanced view of the relationship between social centrality and infection).

Point 4: This remains an important point to consider, but perhaps becomes less important if infection intensity is treated more as a variable trait of each node associated with network position and less as a directly-transmitted parasite (as discussed in relation to Point 3). This treatment seems feasible given the focus of the study (analyses at least) is predominantly on sampling methodology.

Point 5: I would certainly agree with the reviewer that the plot for sex (finding an alternative way to display the distribution of the data that is clearer) could be more informative. There is also a mismatch (I think) between the legend and the number of lines/confidence intervals on the plots for the non-network metric variables. It would be good to use the comments provided to tidy up the figures a little more

Point 6: I continue to agree with the reviewer here. Figure 1 looks very nice but I honestly don't feel like I learn any useful information from it. As it doesn't detract from the manuscript this is up to the authors really, but the reviewer provides some suggestions for alternatives that it may be worth considering.

Point 7: While I think I would probably also have used Spearman Rank, I think the choice of Pearson's is probably reasonable especially if the metrics have been standardized (hard to tell definitively without the data). One thing that needs to be made clearer in the methods is for which analyses metrics have been standardized – this was something I only learned from the figure legends.

In the abstract it would be good to distinguish between the two types of subsampling (that of the dataframe of metrics versus of the network data) given this finding is important.

The introduction is much improved. It's on the long side but nicely written. However, as highlighted by the reviewer the justification for studying non-directly transmitted parasites still weak in the current version.

Methods section in general is nice and clear, some minor suggestions below:

L172-173: Suggest "macaques FROM DIFFERENT GROUPS were never" for clarity

L222-223: There are typos in this sentence

L223-229: As the reviewer did, I found this rationale rather weak. I would suggest (in part at least) highlighting that the focus of the analysis is as much on the sampling effects as on examining why infection intensity is associated with network position.

L293: From the equation provided above it seems unlikely that EPGs were whole numbers – how did this factor into using negative binomial models?

L301-302: Is the problem with including them in the same model not more related to covariance between them making the interpretability of coefficients challenging (given they are typically highly correlated).

L309: One question related to statistical model design is if individuals with more samples were more likely to have higher EPGs? That could lead to potentially problematic informative cluster sizes in the mixed model.

L314-316: This text is odd here as you have already told us that you used zero-inflated models previously.

Some minor comments on the results:

L364: I would advocate for a bit more text descriptive text in this currently very short section!

Tables 4-6: Given the null models are the same model minus the effect of the centrality measure it would perhaps be informative to provide the model estimates for each term included with just the dash/slash for the centrality measure that's not in the model?

Tables 4-6: The information provided for random effects seems like it may be given incorrectly (this is worked out from the tables so may/may not be correct). It seems the authors have taken the standard deviation and variance directly from the model summary table, in which case these are providing the same information (if you square the SD then this calculates the variance). You can calculate the standard error around random effect estimates but this is done in a different way. Personally, I think it would be sufficient to provide the point estimate of the random effect variance, but the authors could provide the standard error also if preferred,

Improve the clarity of references to the supplementary material (SP1 etc. is more confusing than it needs to be)

L416-417: Looking at the supplementary tables it seems that this is written incorrectly. It looks like sub-sampling from the metrics dataframe produces results that are more similar to the original full analysis? This is a key finding and its important it is written clearly.

L434-442: It would be good to do more (either here, the discussion or both) to integrate these findings with the slightly conflicting results obtained with targeted sub-sampling (e.g. the very rapid loss of statistically significant results with random sampling the networks vs. the result for strength for females persisting even though they make up a minority of the network).

Overall the discussion was disappointing, it is very long and repetitive in places. There appeared to be left over text from the previous version that did not match well with the current results and other places where the response said changes had been made but they had not.

L450-455: These first two sentences are rather vague and also introductory in tone. The first sentence also seems at odds with both the introduction and literature in the field in not presenting that other studies have not found such a clear relationship

L487-488: This statement is not relevant given the stated mode of transmission of the parasites.

L489-491: As highlighted previously this is equally true of other social centrality measures and not specific to degree, and so is misleading to include as an argument to include specifically here.

L472-517: These sections are very focused on the association between infection intensity and network position being driven by transmission which is somewhat disingenuous with the mode of transmission of the parasites and ignores a more holistic view of the factors that may drive this relationship. It also ends up being rather repetitive and restricts space for discussion of the findings related to sampling (despite these being prominent in the title and abstract)

L524: Would suggest "non-significant" rather than "insignificant"

L531-533: I don't follow the logic of this argument

L534-547: Some of this discussion is at odds with there being no statistically significant sex effect in the current models

L551-557: This argument is incorrect as currently presented. While it is possible that sub-sampling may produce noise that impacts the correlations, simply being in a smaller group doesn't impact the correlation strengths. Imagine a degree distribution in a larger group of [10,8,6,4,2]. The same individuals are measured at another time step and still have the degree distribution [10,8,6,4,2]. However, at a third time step they are in a smaller group might have the degree distribution [5,4,3,2,1]. While the values for degree are much lower in the third group the strength of the correlation is identical. While there are reasons that sub-samples of different sizes might change the strength of correlations, the magnitude of the numbers is not one of them.

L558-560: This argument can work but needs to be adjusted to take into account the previous point.

L561-563: The topic sentence of this paragraph seems odd in the context of the new findings where strength and eigenvector centrality were more similar than strength and degree

L569-571: Seems odd to focus on females when it was zero models in juveniles?

L576-585: This paragraph is rather repetitive of the results and lacks additional discussion

L588-595: This direct comparison is a little misleading as targeted node removal was based on network position in the studies cited but a non-network trait in the current study (which could be close to random removal of nodes with respect to network position depending on the relationships between age, sex and social centrality). Another potentially relevant and interesting point related to this discussion about sub-sampling networks is that the impact on studies investigating infectious disease epidemiology may depend on the transmission mode itself (sometimes removing certain subsets may reduce noise).

In the supplementary material it would be ensure clear Figure/Table captions and check formatting to make sure it is correct (seemed to be some bolding missing at least). I found some of the current Table captions very similar and hard to distinguish from each other.