

August 1, 2022

Dear *Journal of Infectious Diseases* editorial board,

Please find the enclosed manuscript “Epidemic time series similarity is related to geographic distance and age structure” which we submit for consideration as a research article.

The COVID-19 pandemic has had, and continues to have, clear global impacts. However, not all locations and populations were equally impacted, potentially due to the demographics of the population itself, or due to governmental intervention, testing, and vaccination efforts. It is unlikely that we will ever be able to parse these different factors apart, but understanding how differences among locations relate to epidemic similarity can provide a first step. We used COVID-19 case counts across a large set of United States counties to explore how epidemic similarity was related to geographic distance between counties, age structure dissimilarity, and differences in the basic reproduction number (R_0) and population size. The baseline assumption is that differences in R_0 will translate to differences in epidemic similarity, but we recognize that other processes may be potentially more related to epidemic similarity, as R_0 is a good measure of public health efforts, but perhaps an oversimplification in terms of explaining epidemic trajectories. To this point, we found that dissimilarity in age structure between counties was more strongly related to epidemic similarity than differences in R_0 . Together, we provide important context and highlight the role of spatial and demographic processes on SARS-CoV2 epidemics in the United States. By comparing epidemic time series directly, we present a potential path forward to estimate potential epidemic trajectories in undersampled localities based on geographic distance and age structure to other areas where data is more available.

We believe this article will be of interest to a broad range of researchers, as our manuscript takes an ecological and biogeographical approach to exploring epidemic dynamics, while leveraging non-linear time series techniques to provide novel estimates of epidemic similarity. In advance, we appreciate your consideration and assistance. Please don't hesitate to contact us with any questions.

The work has not been published previously. This manuscript is original work and not under consideration for publication elsewhere. The submission is approved by all authors.

Sincerely,
Tad Dallas