many of these underlying drivers of estimated R_0 may potentially change over time or with different intervention strategies (Islam et al., 2021).

The SARS-CoV-2 pandemic has created a situation where it may be possible to start to disentangle the role of different factors on resulting epidemic trajectories. For one, county-level data on infectious case counts provide a means to compare how epidemics progressed at the county scale, and to compare epidemic trajectories between counties. At a basic level, this allows for the comparison of epidemic trajectories to differences in R_0, as the larger difference in R_0 would suggest that the epidemics should be quite dissimilar in their trajectories. For one, R_0 may be estimated from the epidemic time series itself, such that epidemics with similar R_0 would naturally have similar dynamics. However, R_0 is a simple composite measure estimated from a time series that may belie the influence of mitigation efforts and fluctuating epidemic dynamics (e.g., COVID-19 case counts appeared in distinct waves, while R_0 estimates do not use all waves (Ives & Bozzuto, 2021)). Apart from similarity in R

constant. The goal is to find an alignment which minimizes the overall dissimilarity between the two time series. We use the `dtw` R package (Giorgino, 2009

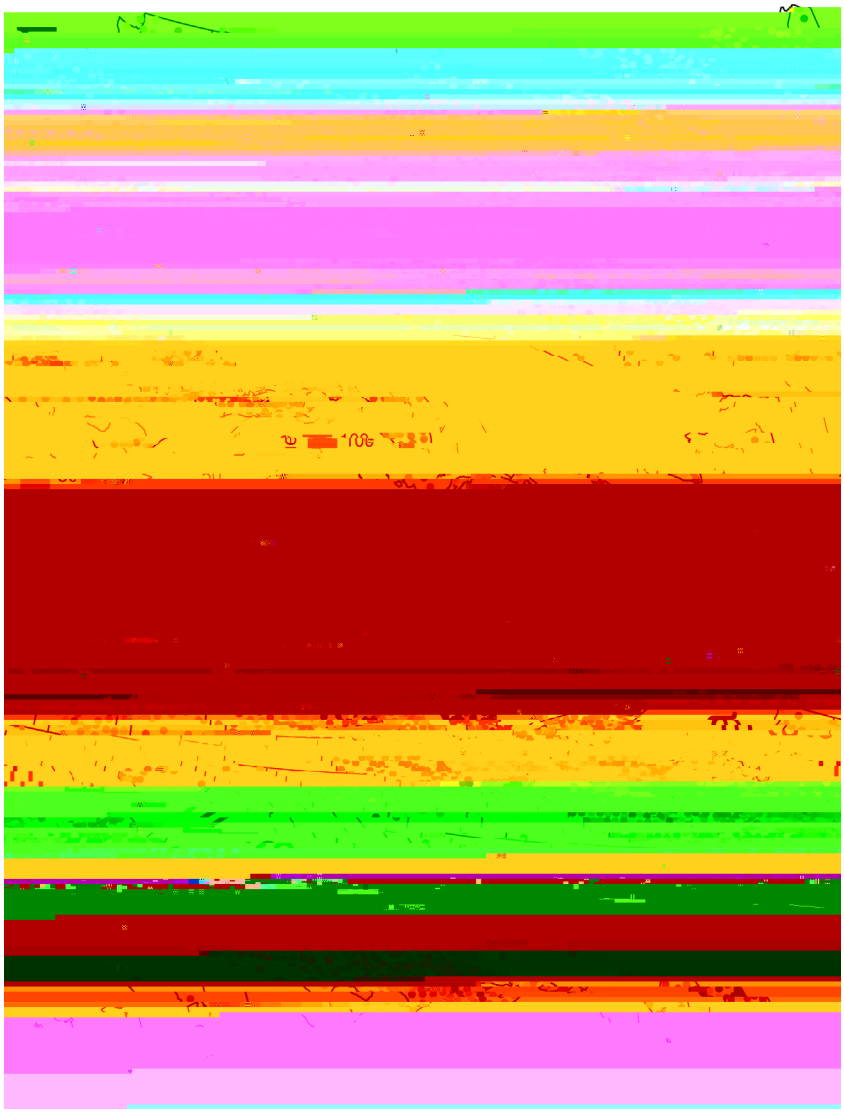
dimensional space, more traditional regression techniques can be used. The results of both analyses are qualitatively similar (see Supplementary Materials for further discussion).

2.4. Reproducibility

R code and data to reproduce the analyses is provided at https://doi.org/10.6084/m9.figshare.19782406.v1.

3. R

Pairwise epidemic time series similarity was calculated using dynamic time warping (DTW). These pairwise estimates of similarity were weakly related to Euclidean distance in epidemic time series, suggesting that the DTW approach was able to capture additional information relative to a more simple distance measure (see Supplemental Materials). The matrix of pairwise DTW values were reduced to two axes using t-SNE (Gisbrecht et al., 2015). This low-dimensional representation of site-level epidemic similarity showed clear spatial patterns for the first two t-SNE axes (Fig. 2). Interestingly, the spatial patterns adhere to geopolitical (i.e., US state) boundaries in some instances, a phenomenon which may be due to differences



F . 2. The spatial distribution of epidemic trajectory similarity (t-SNE decomposition of the pairwise dynamic time warping matrix). In this geographic projection of the t-SNE values, there are clearly some states which cluster, suggesting similar mitigation efforts, sampling/reporting biases, and/or epidemic trajectories.

4. D

Here, we explored how geographic space, demographics, and R_0 influence differences in epidemic trajectories for over 3000 United States counties. We expected — and found — that counties with similar R_0 values tended to have similar epidemics. Independent of this, we found clear effects of geographic distance between counties and dissimilarities in county age structure on resulting epidemic trajectories, suggesting that R_0 estimated from case or mortality data (Ives & Bozzuto, 2021) may not capture the full potential of the epidemic in a given location. Together, we highlight the importance of considering population demographics, age-specific contact network structure, and geographic distance when attempting to estimate epidemic trajectories. While we approach the problem as one of pairwise dissimilarity in epidemics, it may be possible to use similar approaches to recreate an expected epidemic time series for an unsampled location given information on geography and demography.

Spatial structure in both age structure and population sizes precludes the attribution of any form of causal link between age structure or geographic distance and resulting epidemic trajectories. However, our findings, based on the entire epidemic time, broadly agree with similar studies which focused on components of the transmission process or summary statistics such as R_0. Further, the analyses can be updated as the epidemic progresses, or using different time windows to explore how time series clustering changes temporally. It is recognized that both parts of the transmission process — encounter and susceptibility — vary with individual age (Covid et al., 2020; Jones et al., 2021; Kerr et al., 2021; Magpantay et al., 2019), suggesting that for some pathogens including SARS-CoV-2, considering the age structure is quite important to epidemic forecasting (Kerr et al., 2021). Additionally, geographic patterns in R_0 (Ives & Bozzuto, 2021), non-pharmaceutical interventions initiation and compliance (Amuedo-Dorantes et al., 2021; Yang et al., 2021), and vaccine hesitancy (Zuzek et al., 2022) have emerged as potential drivers for spatial variation in epidemic progression (Richards et al., 2022). By comparing epidemic trajectories directly, using a fl

(Foster et al., 2022). But it seems relevant to use approaches such as the one we do here to understand how epidemic trajectories differ, both within the same pandemic and potentially for different pathogens (e.g., how dissimilar are temporal patterns in seasonal flu epidemics in a given location?). The comparison of epidemic trajectories — especially along moving windows as the epidemic progresses — can provide insight into the relative effects of different mitigation and control efforts. Finally, while many approaches to forecasting epidemics rely on a single time series, this work alludes to the possibility of incorporating information on nearby or similar time series, creating the possibility of joint epidemic forecasts.

F

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E

The present study used publicly available data compiled by the Center for Systems Science and Engineering at Johns Hopkins University (Dong et al., 2020).

A

TAD performed the analysis. All authors contributed to manuscript writing.

D

R code is available on figshare at
https://doi.org/10.6084/m9.figshare.19782406.v1 .

D

2031196). The authors have no conflicts a432-doi.org/10.86.4.17.01k-1-2.6TJ.4(t)-299.5(wdof)-327.424

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