Your Awesome Title

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Running headline: Environment and species richness

Abstract: Your awesome abstract here.

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Introduction

The first case of Covid-19 was recorded in the United States in January 22, 2020 according to the CDC. As of December 5, 2021, the United States has reported more than 780000 deaths due to Covid-19, more than any other country (Times 2021). Initially, non-pharmaceutical methods were used to help stop the spread of Covid-19, including the closing of many public spaces, encouraging social distancing, and encouraging the use of masks to help reduce transmission rates. Through time, social distancing and mask mandate policies changed as Covid-19 became the new norm, leading to patterns of increasing and decreasing Covid-19 rates in the United States (Rebeiro et al. 2021). The current widespread availability of vaccines helping to fight Covid-19 has also helped to reduce the overall transmission and resulting mortality (Haas et al. 2021). Transmission and Covid-19 rates have increased post vaccination due to mutations in spike proteins that have allowed for new variants of COVID-19 to spread Monajjemi et al. (n.d.). As of December 5th, 2021, the Delta variant, is the most common strain of COVID-19, representing more than 99 percent of cases (CDC 2020).

Mask mandates, social distancing, and vaccination have all been proven to reduce the transmission of Covid-19 (Ferguson et al. 2020, Lyu and Wehby 2020, Nguyen 2021, Haas et al. 2021). Areas that adopted the use of masks early tended to have lower overall COVID-19 rates compared to those that did not. Given the efficacy of masks preventing transmission as well as the high-availability to everyone, masks have been one of the best tools in fighting the spread of Covid-19 (Rebeiro et al. 2021). Despite the clear benefits, masks have been met with much opposition across the United States, especially in politically conservative leaning counties (Kahane 2021, He et al. 2021). These counties tend to be more rural and more against mask mandates than their urban counterparts (Pro et al. 2021).

Spatial Heterogeneity, or the uneven distribution of populations across space, is important for predicting disease dynamics in pathogens like Covid-19. Areas with low spatial heterogeneity tend to be better environments for a disease to persist when compared to high spatial heterogeneous environments (Hagenaars et al. 2004). Populations with higher densities tend to have higher disease spread assuming the disease transmission is not based on frequency of contact (Scott 1988). Density dependent disease like Covid-19 should therefore have a

harder time spreading in rural areas with higher heterogeneity and lower population densities. However, with resistance to preventative measures such as masks and vaccines, cases may be higher in rural areas than their urban counterparts (Sun and Monnat 2021).

With changes in population density and spacial spread, the basic reproductive number, R_0, should change as a result. The basic reproductive number represents the number of predicted infections that can result from one infection (Delamater et al. 2019). While studies have already looked into how R_0 changes by county, no recent studies have looked at the effective reproductive number on a county level (Ives and Bozzuto 2021). More importantly, not much is yet known about the new Omicron variant first introduced into the US on December 1, 2021. The Omicron variant is predicted to be more infectious than previous variants of Covid-19 and is predicted to be more resistant to the vaccines we currently have available (CDC 2021). The Reproductive number of the Omicron variant is not calculable at such a low prevalence due to the lack of data.However, predictions on how the new variant will spread provides vital information on preventing new infections and reducing overall mortality.

While data is presented on county-level Covid rates, few studies have taken this further to investigate the how the infection rates in urban and rural areas compare. With the Omicron variant just recently emerging, no studies have yet to be published examining the predicted rate of spread. In this study, I seek to investigate the total infection prevalence per county. I also compare the prevalence per county in rural and urban areas, as well as those with and without mask mandates. Finally, I seek to use previous predictions of Ro to calculate Rt in its current state. Using these current Rt values, I then infer predicted Rt values for Omicron for each county to highlight at-risk counties.

Methods

Here is the method section. You can include equations easily. For inline equations, use $\text{var}(X) = p(1-p)$. For display equation, use

$$\text{var}(X) = p(1-p)$$

Results

Tables Insert tables by kable in knitr package in R. Then cross-reference it back with: see Table **??**.

Put results inline, e.g. the mean species richness is.

Figures Insert figure by code chunk. And cross-ref it back as Figure **??**.

Or if you already have the figure:

And cite it as Figure **??**.

More details can be found at here[2].

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Supporting Information

Figures