

County Level Predictors for Covid-19 Prevalence During the Introduction of Omicron

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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 ([New York 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 2021a](#)). 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-19 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 R_0 to calculate R_t in its current state. Using these current R_t values, I then infer predicted R_t values for Omicron for each county to highlight at-risk counties.

Methods

All code and graphs were written using the programming language R and maps of the United States were modeled using the package USmaps([Lorenzo 2021](#), [R Core Team 2021](#)). For data on Covid-19 cases by county, I used the time series data provided by the New York Times ([New York Times 2021](#)). For total population estimates, I used US Census data predictions for 2021

([United States Census Bureau 2021a](#)). Total cases were mapped out as the number of cases in each county divided by the total population to get the total percentage of infections (Figure 1). Rolling averages were mapped out based on reported cases within the last 30 days (Figure ??). Mask mandate data used was collected in July of 2020([Wright et al. 2020](#)). Data from the early infection was chosen and graphed to show how early responses to Covid-19 have led difference in the total percentage of cases (Figure ??). A t-test was performed to test the significance between the two groups and bar graph was made for visualization (Figure ??). Rural data was graphed using two criteria, based on HRSA classifications and the census Bureaus classifications of urban and rural areas ([HRSA 2021](#), [United States Census Bureau 2021b](#)). Both were graphed as a map of the US to show county classification as well as a bar graph to compare the average total case percentage (Figure ??; Figure ??). An ANOVA test was performed on the data classified based on the Census Bureau Data distinction of urban and rural to test for significance. A t-test was performed on the data classified based on the HRSA distinction of urban and rural to test for significance. R Vaccine data was collected from the CDC to calculate the proportion of susceptible individuals ([CDC 2021b](#)).

The effective reproductive number (R_t) was calculated using basic reproductive values(R_0) for each county predicted in a previous studies (Figure 3) ([Ives and Bozzuto 2021](#)) . Using previous models and calculations of R_0 , the formula

$$R_0 = \frac{\beta * \lambda}{(\gamma + \mu + \epsilon + \sigma) * (\tau + \mu)}$$

was used to calculate the β value, or the transmission rate, per county (see Table S1 for parameter descriptions) ([Ahmed et al. 2021](#)). Beta values were than used to calculate using the formula

$$R_t = (1 - p) * \frac{S}{N} * \frac{\beta * \lambda}{(\gamma + \mu + \epsilon + \sigma) * (\tau + \mu)}$$

where S represents individuals Suscpetible to the disease and N represents the total population size in that count. Parameter p represents the proportion of vaccinated individuals per county ([CDC 2021b](#)). The effective reproductive number for the Omicron was then calculated using the same formula, with higher overall transmission rates and lower mask mandate usage to reflect the increase in Ro seen when the Delta variant of Covid-19 was first introduced into the United

States ([Liu and Rocklöv 2021](#)).

Results

Figures Insert figure by code chunk. And cross-ref it back as Figure 1.

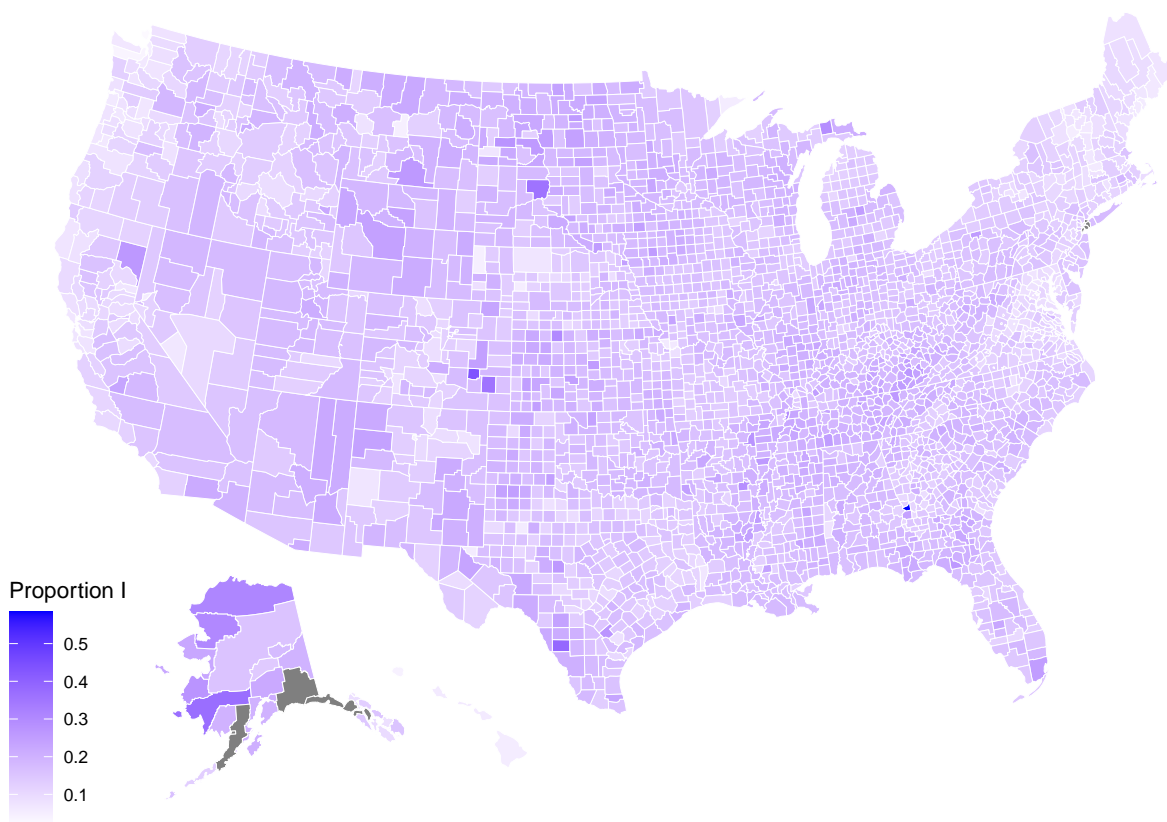


Figure 1. No - or _ in the caption ref. No space at the end of this line!

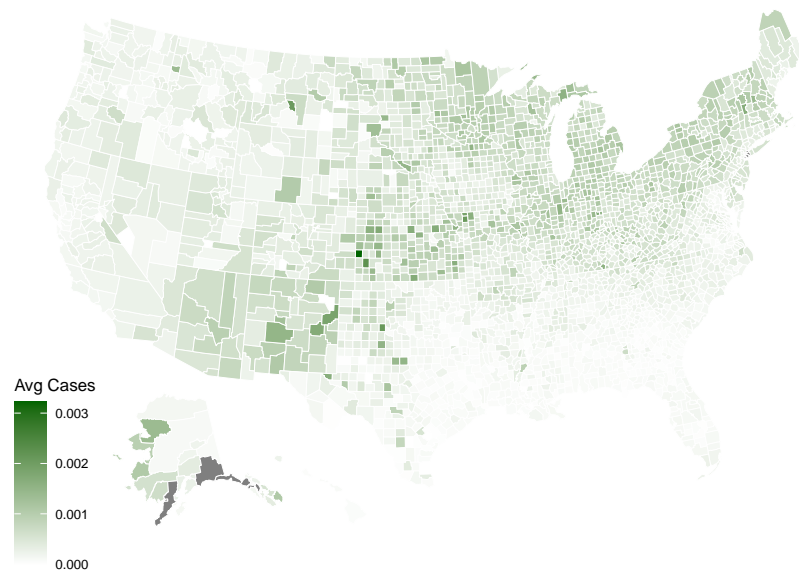


Figure 2. No - or _ in the caption ref. No space at the end of this line!

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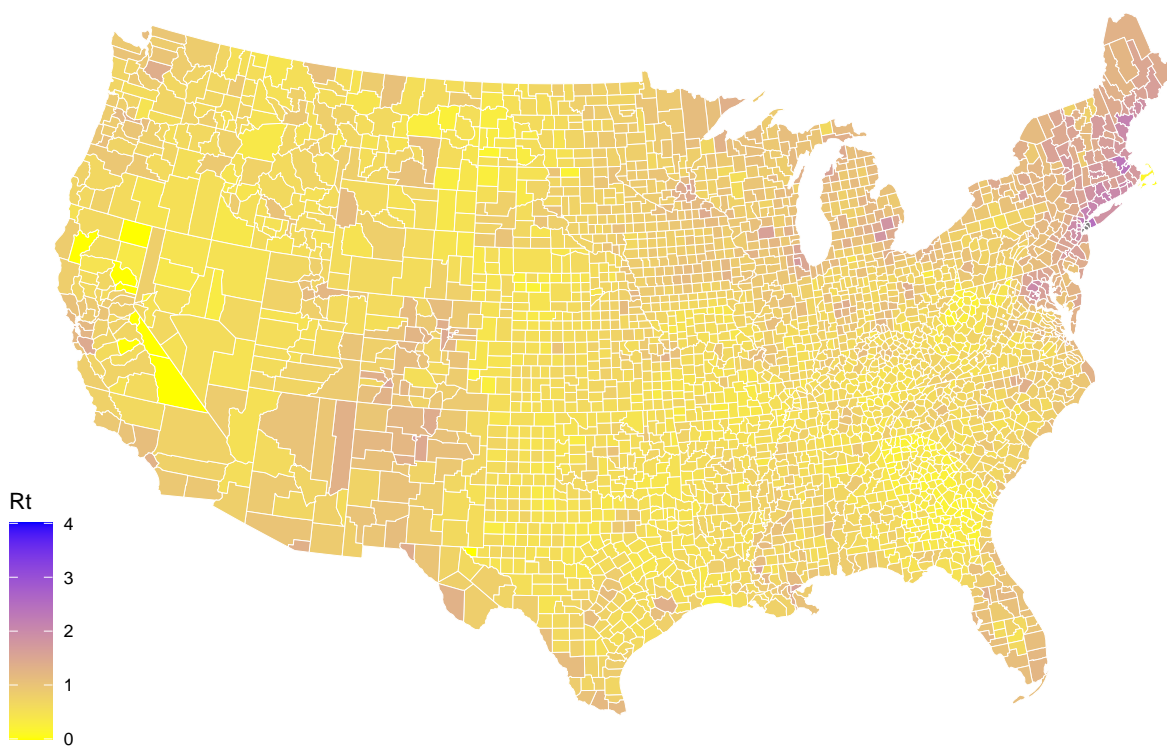


Figure 3. No - or _ in the caption ref. No space at the end of this line!

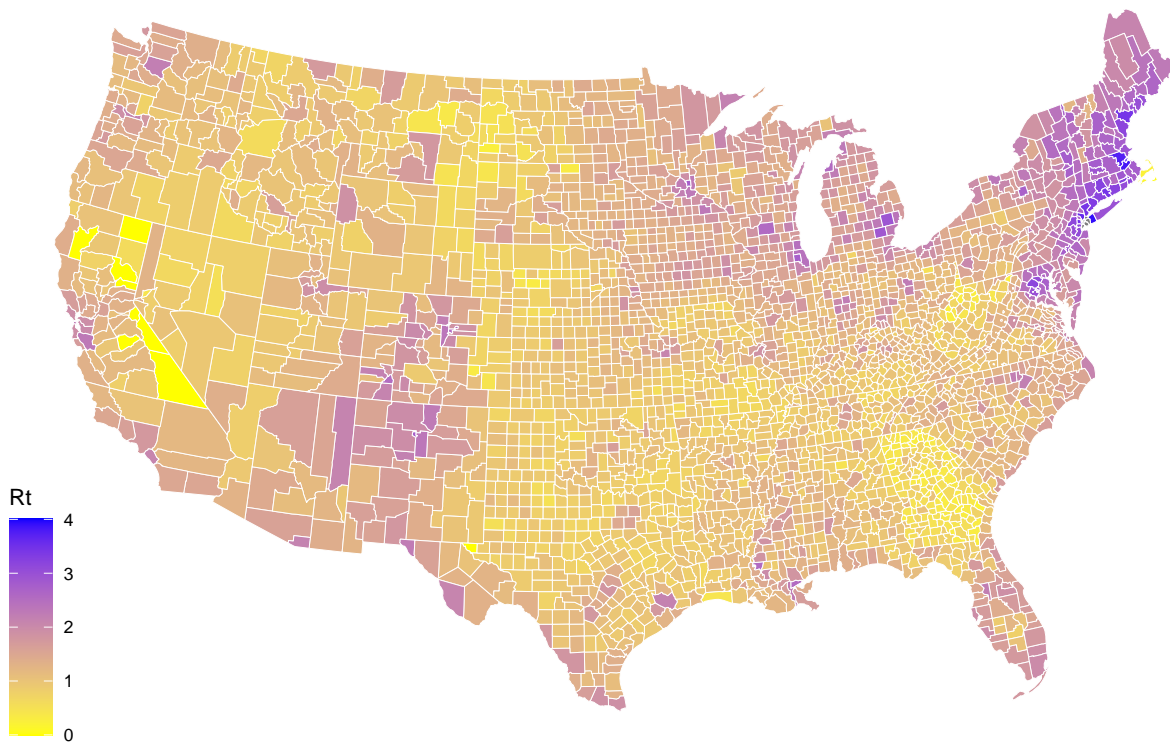


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Discussion

I used current data on Covid-19, effective

Focus on these counties

Masks do work.

Vaccine data all over the place.

Potential error

Conclusion

References

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Supporting Information

Tables

Table S1. Parameter descriptions and values used to calculate R_0 ([Ahmed et al. 2021](#)).

Parameter	Value	Description
β	Varies	Transmission rate
λ	.0025	Births into system
γ	$2.01 * 10^{-4}$	Transfer from the exposed class to the quarantined class
μ	.0015	Natural Mortality Rate
ϵ	.45	Transfer from the exposed class to the symptomatic infected class
σ	.067	Transfer from the exposed class to the asymptomatic infected class
τ	$2 * 10^{-4}$	Transfer from the susceptible class to the quarantine class
p	Varies	Proportion vaccinated