The Contagion of Vaccine Hesitancy:

Bivariate cluster and multivariate global weighted regression analysis of COVID-19 vaccination rates on Polio vaccination rates in New York City

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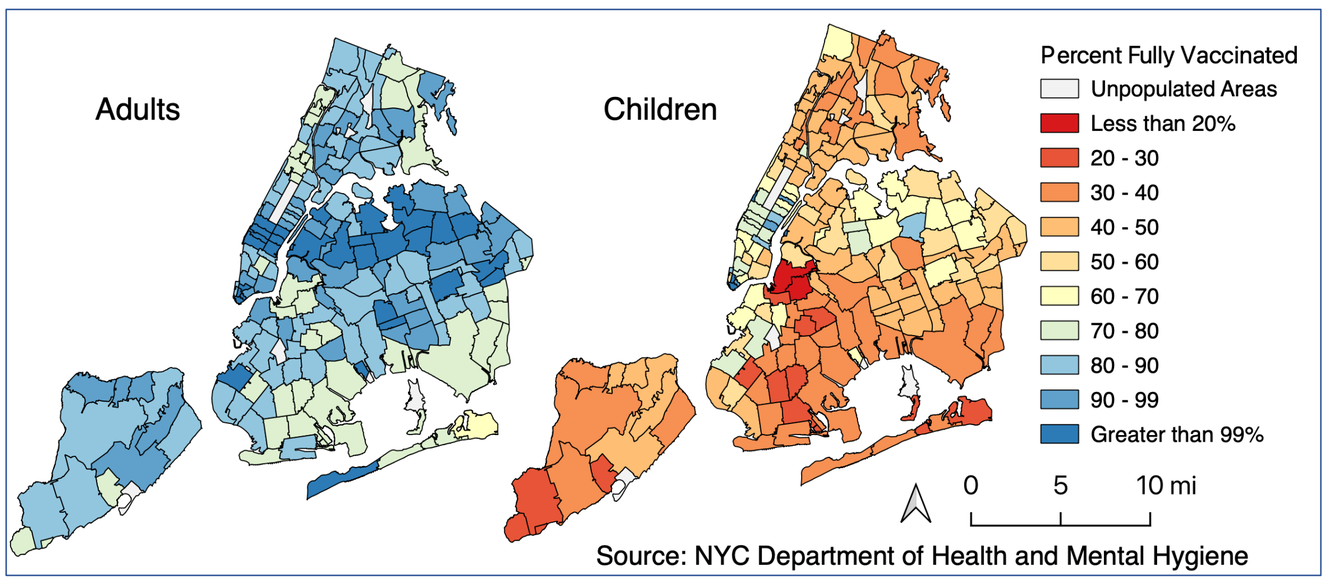
Background

COVID-19 vaccination rates have lagged behind the high coverage rates initially thought possible. At the same time, outbreaks of vaccine-preventable disease (VPD) have become more prevalent, including an ongoing outbreak of polio in New York[1]. Community spread of these diseases is thought to be driven by low vaccination rates. As vaccination has become more controversial socially and politically, it is important to investigate whether vaccine hesitancy is socially contagious, and to understand the predictors of the spatial variation of hesitancy.

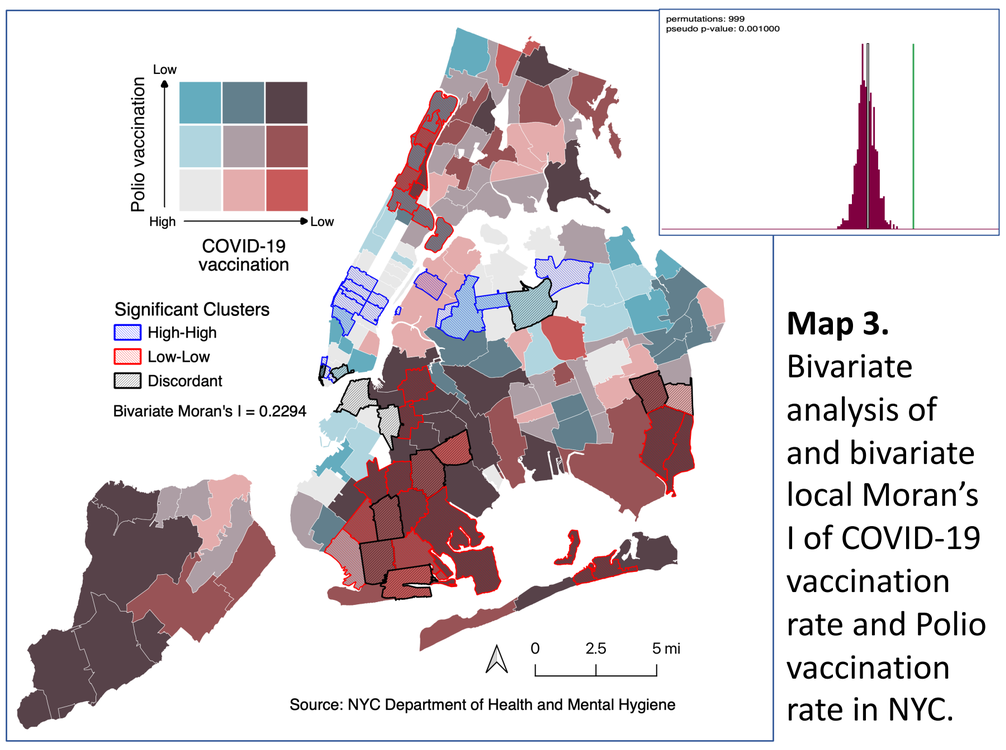
Research question: Do rates of COVID-19 vaccination coverage predict rates of polio vaccination coverage among children?

Methods

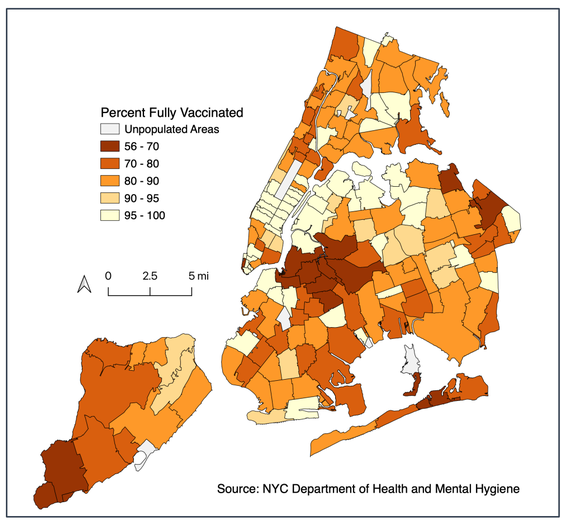
- Data obtained from New York City Department of Health and Mental Hygiene for all 177 zip codes in NYC[2].
- Bivariate map created with QGIS to visualize the spatial clustering of vaccination rates for COVID-19 and poliovirus.
- Bivariate local Moran's I analysis using GeoDa with 1st order Queens contiguity used to quantify statistically significant clusters of low, high, and discordant vaccination rates.
- Global weighted regression analysis run with R to determine the predictive effect of COVID-19 vaccination in conjunction with minority status, poverty, education, and household age, using variables obtained from CDC/ATSDR[3].



Map 1. Percent of population by age group in NYC receiving full primary COVID-19 vaccine series, 2022.



Map 3. Bivariate analysis of and bivariate local Moran's I of COVID-19 vaccination rate and Polio vaccination rate in NYC.

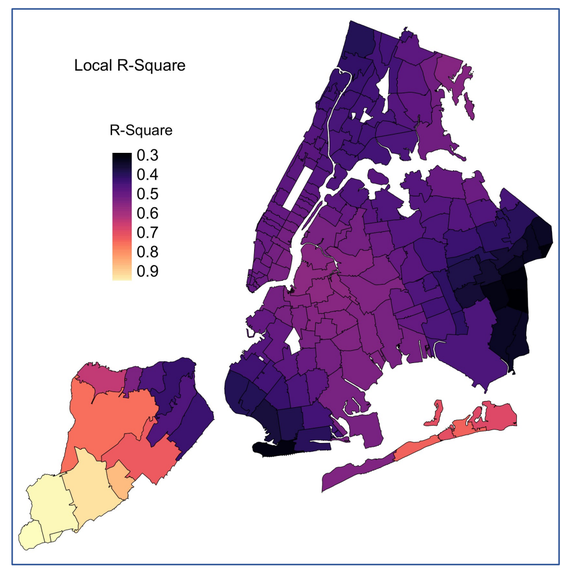


Map 2. Percent of children in NYC aged 6 months–5 years receiving full Poliovirus vaccine series, 2022.

Variable	Coefficient	t value	Pr(>|t|)
intercept	0.5400		
COVID-19 vaccination	0.0035	6.822	1.49e-10*
poverty	-0.0001	-0.248	0.8045
education	-0.0013	-2.086	0.0384*
age 65+	0.0013	2.188	0.0300*
minority status	0.0002	0.561	0.5755
Quasi-global R^2	0.5411	F=12.46	2.553e-10*

** denotes statistically significant result*

Table 1. Global weighted regression model. Outcome = polio vaccination rate, COVID vaccination=% of adults aged 18+ receiving full primary COVID-19 vaccine series, poverty=% below 150% of poverty line, education=% without high school diploma, age 65+=% over age 65, minority status=% identifying as non-White race or ethnicity



Map 4. Local R^2 of the correlation between Polio vaccination rate and all covariates included in regression model in NYC.

Results

- Rates of COVID-19 vaccination coverage are much lower among children than adults in New York City (Map 1).
- Polio vaccination rates are much lower in some zip codes than 80% coverage needed for herd immunity[4] (Map 2).
- Bivariate analysis shows that the spatial distribution of Polio vaccination with respect to COVID-19 vaccination is non-random (p-value=0.001) with several significant clusters (Map 3).
- 54.11% of the variation in polio vaccination rates can be attributed to the covariates in this model (Table 1), with areas of stronger and weaker correlation shown by mapping the local R^2 measure (Map 4). COVID-19 vaccination is a significant predictor (p-value<0.0001).

Discussion

- Polio vaccination rates are used as a proxy in this analysis for overall vaccine hesitancy among parents for all childhood VPDs due to data availability. Rates of vaccination for other childhood VPDs may vary for other reasons not captured in these results,[5,6] and therefore this model may not be generalizable to vaccine hesitancy overall among parents for routine childhood vaccinations.
- Other covariates such as housing type, insurance status, and partisan division across states have been found to be associated with COVID-19 vaccine hesitancy,[7,8,9] but the predictive power of these more recent trends has not been investigated in relation to childhood VPDs.
- Quantifying the concept of social contagion is not well-defined, emphasizing the need for spatial analysis in epidemiology to understand the distribution and spread of predictors and causes.

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