

Five-week warning of COVID-19 peaks prior to the Omicron surge in Detroit, Michigan using wastewater surveillance

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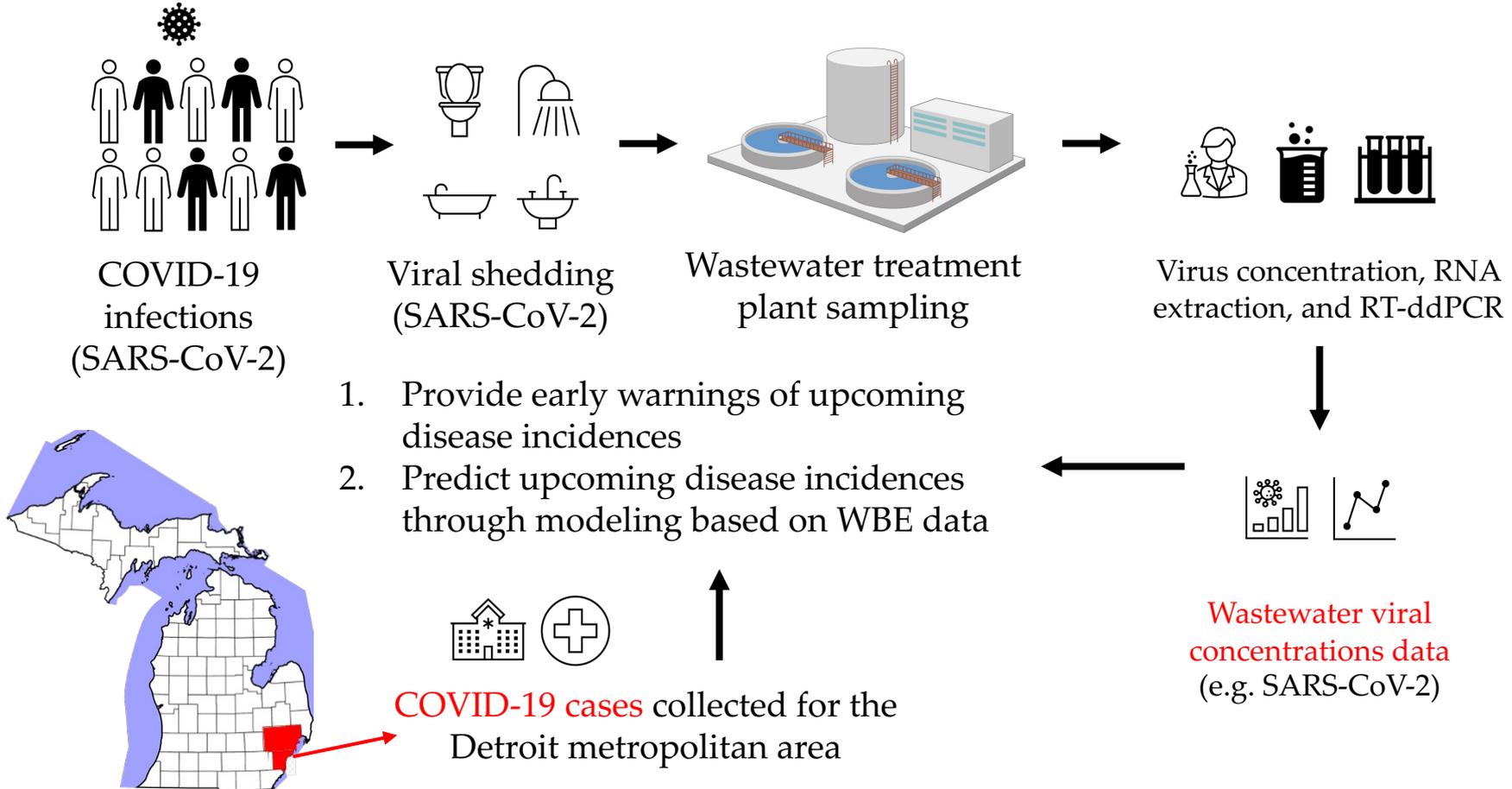
Introduction & research objectives

Lag time of wastewater signals preceding clinical cases

Methods & experiments

Prediction of COVID-19 cases based on wastewater data

Conclusions & future work



1

- To **monitor SARS-CoV-2 fluctuations** in wastewater of the Detroit metropolitan area.

2

- To analyze the **correlation** between COVID-19 incidences in the Detroit metropolitan area and measured SARS-CoV-2 concentrations in wastewater.

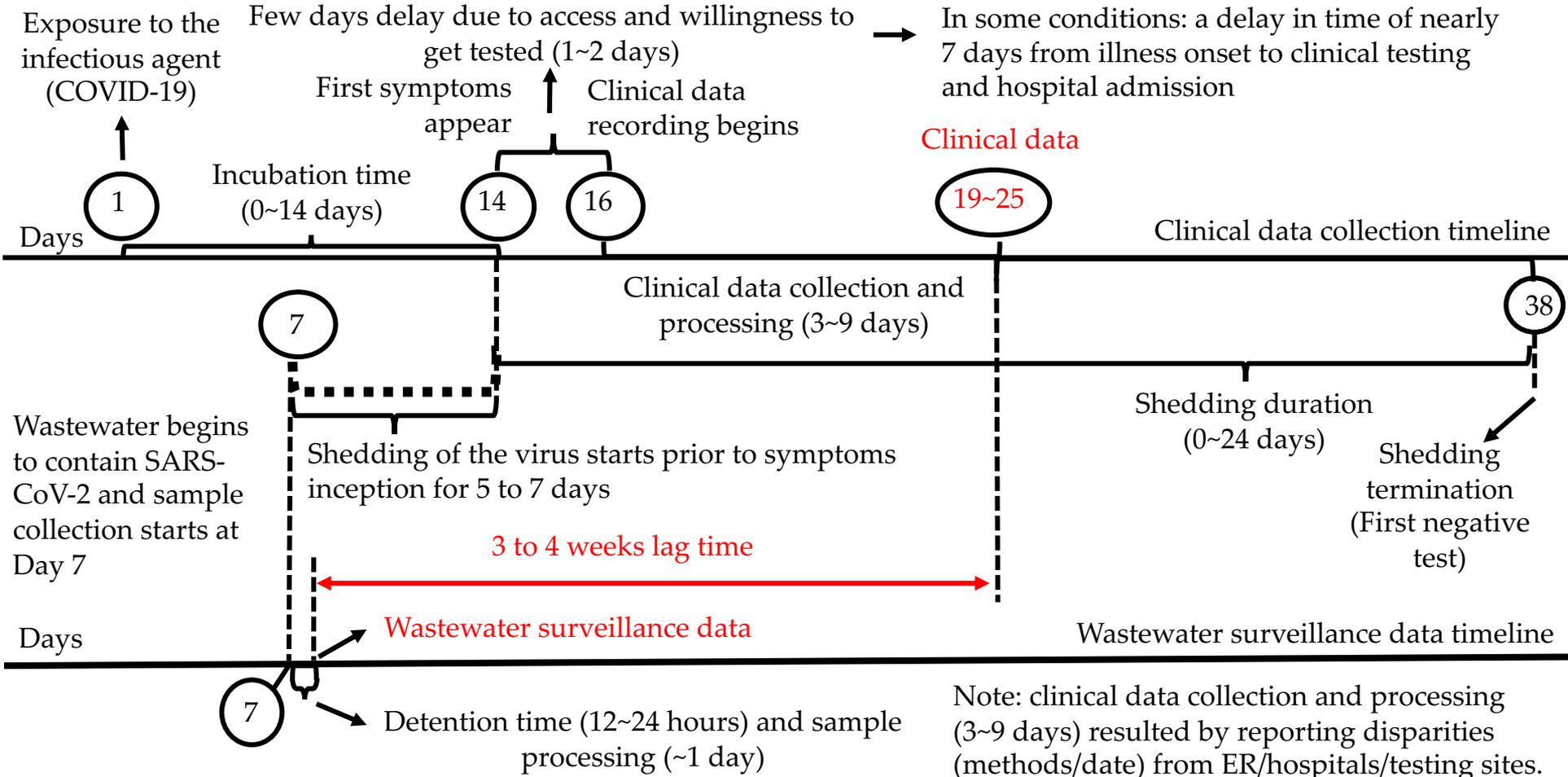
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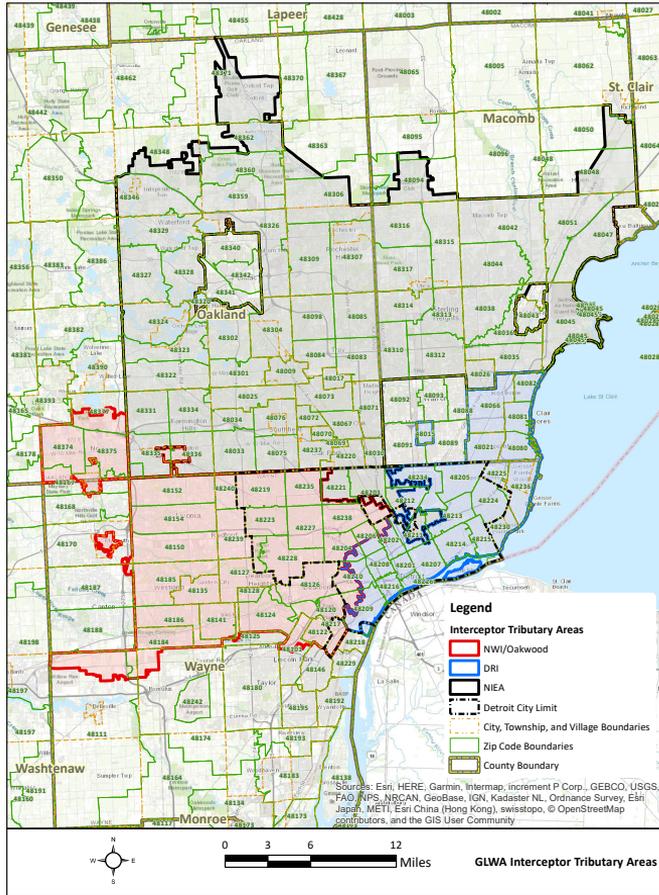
- To estimate the **lag time** between measured SARS-CoV-2 concentrations in wastewater and COVID-19 incidence in the corresponding communities.

4

- Based on the lag time of wastewater signals ahead of clinical cases, provide early warnings of future pandemics and reference for improving public health policy.

Lag time for early warning





Interceptor tributary area



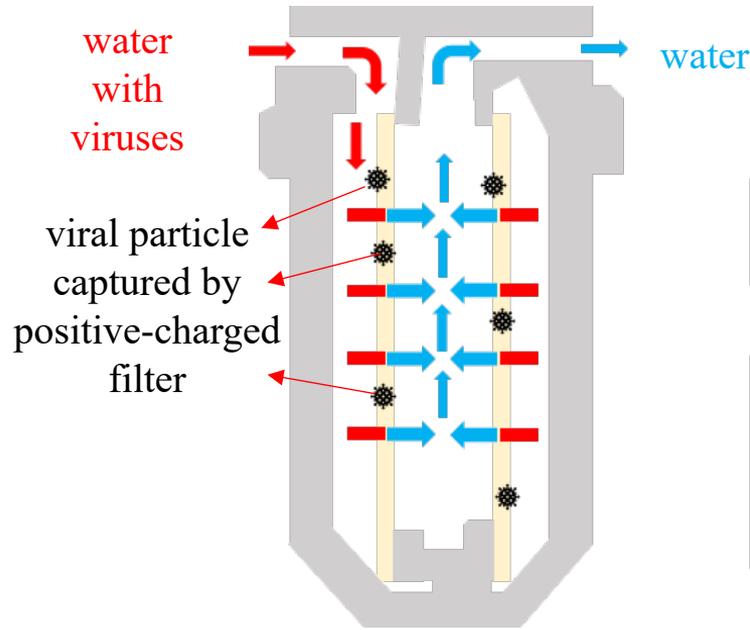
Sampling onsite

1. Untreated wastewater samples were collected from three main interceptors: Detroit River Interceptor (**DRI**), North Interceptor-East Arm (**NIEA**), and Oakwood-Northwest-Wayne County Interceptor (**ONWI**) in southeast Michigan.
2. We used NanoCeram column filters based on the EPA Virus Adsorption-Elution (**VIRADEL**) method to collect wastewater.

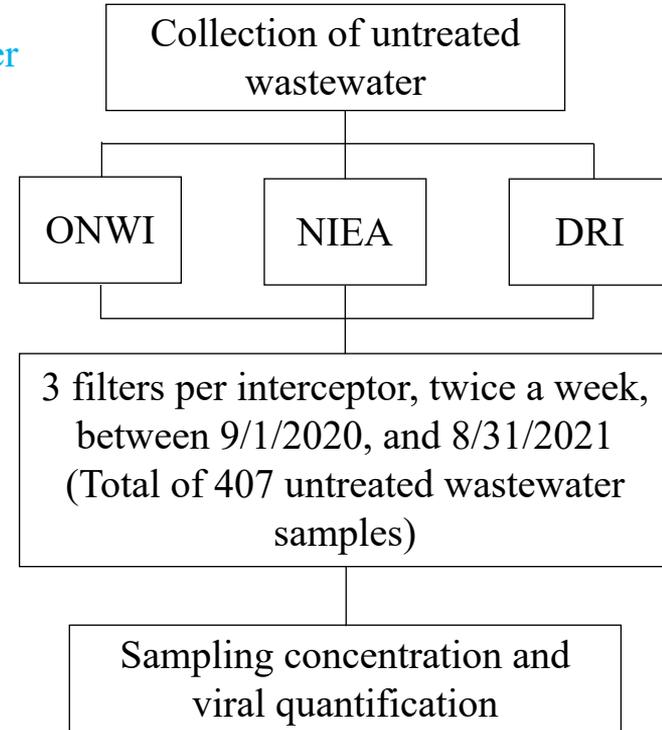
Sampling



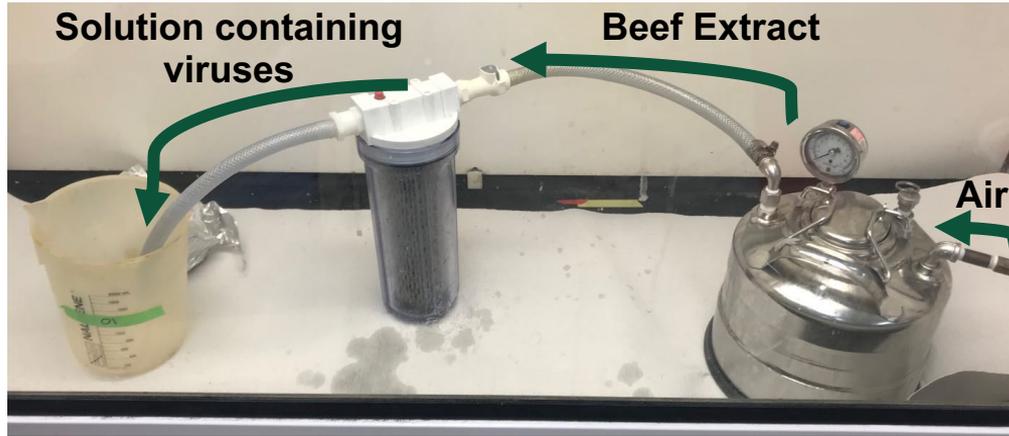
Sampling apparatus



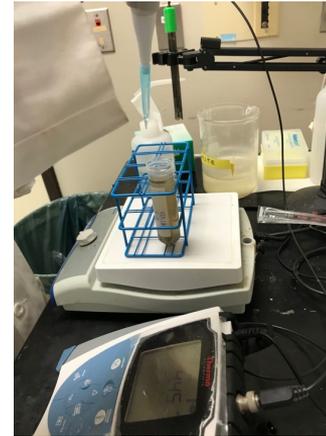
Sampling mechanism



Sample processing



Virus elution with beef extract



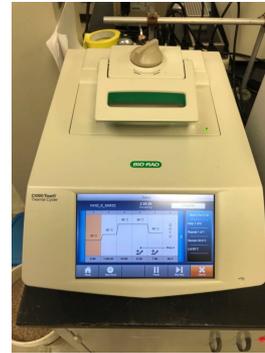
pH adjustment



Vortex during RNA extraction



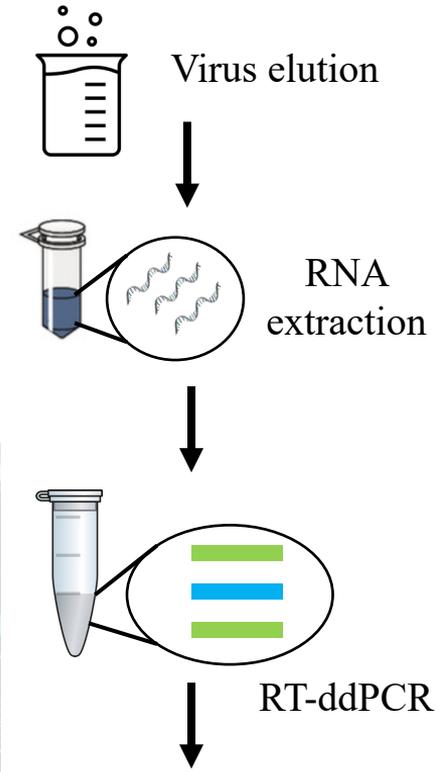
Droplet generator for RT-ddPCR



Thermocycler for RT-ddPCR

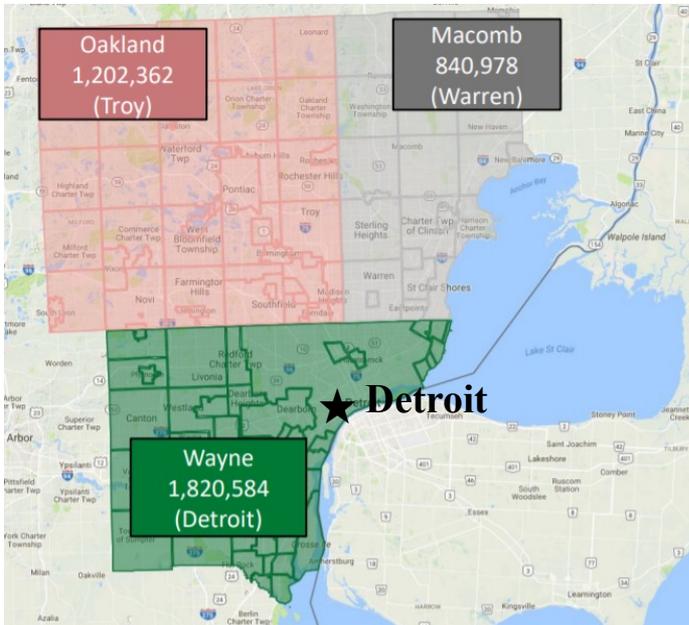


Droplet reader for RT-ddPCR

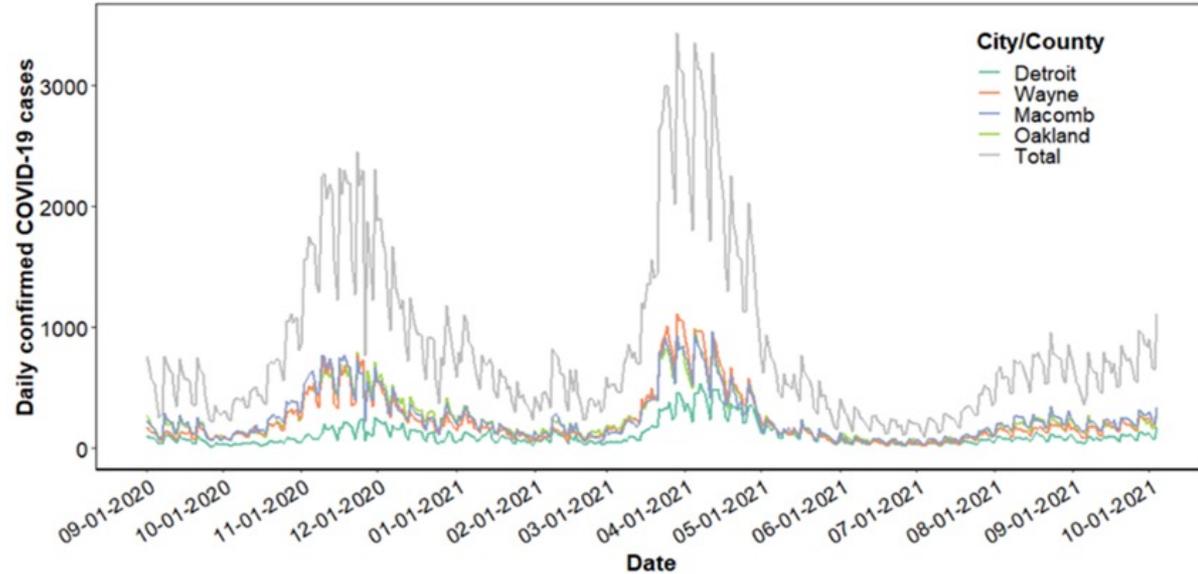


Viral concentration

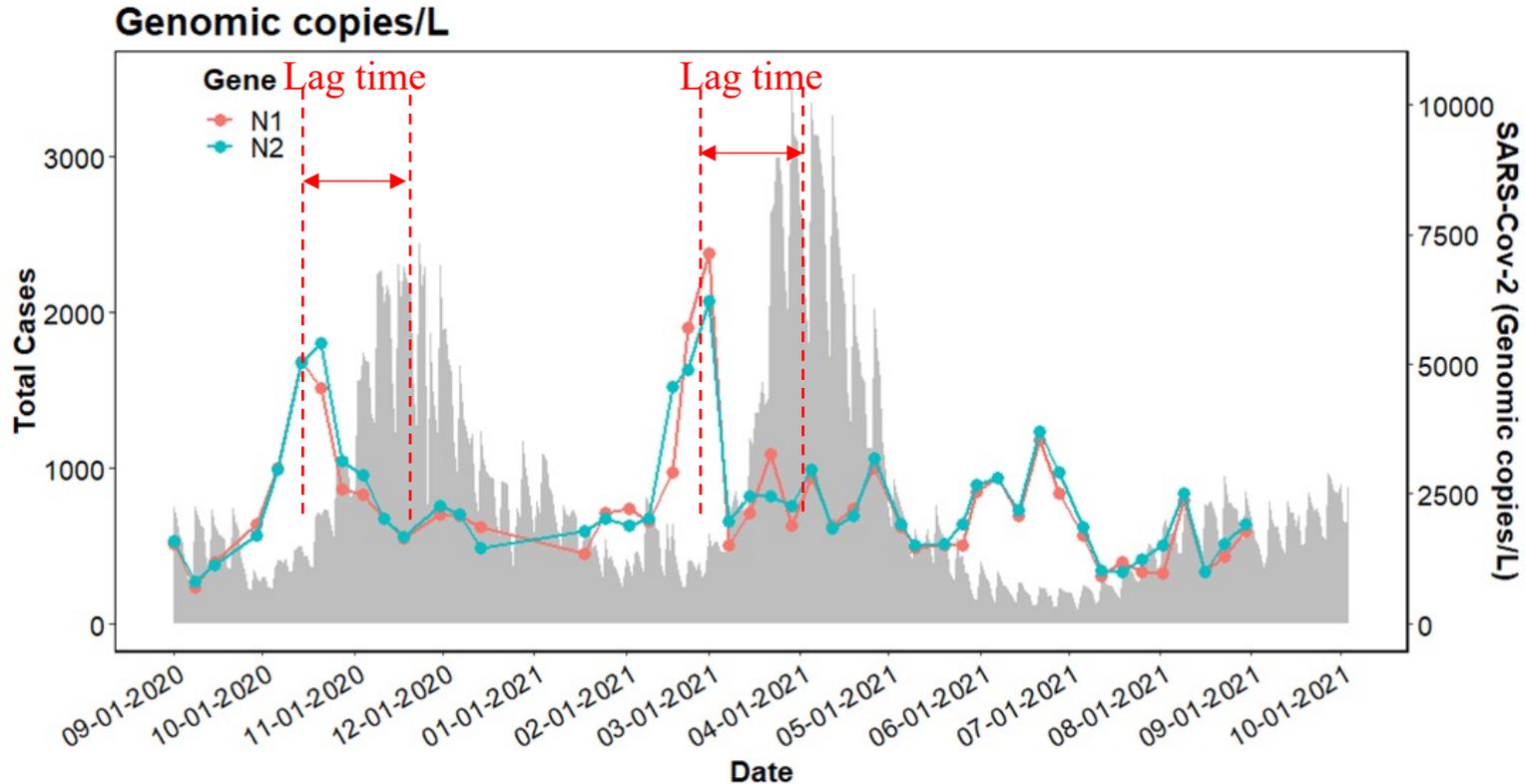
Collection of COVID-19 cases



Study Area: Three Largest Counties in Michigan



COVID-19 cases collected for the City of Detroit, as well as Wayne, Macomb, and Oakland counties



Total N1 and N2 gene concentrations in gc/L for the three interceptors and total confirmed COVID-19 cases in the study areas (gray area)

Pearson's correlation between **N1 and N2 gene concentrations** (in different units) and **total COVID-19 cases** in city of Detroit, as well as Wayne, Macomb, and Oakland counties with lag times

Lag time	Unit	N1 vs. total cases	N2 vs. total cases
3 weeks	gc/l	0.27	0.28
	gc/d	0.11	0.11
	gc/l of sanitary flow	0.10	0.09
4 weeks	gc/l	0.51	0.52
	gc/d	0.29	0.26
	gc/l of sanitary flow	0.28	0.25
5 weeks	gc/l	0.62	0.64
	gc/d	0.34	0.31
	gc/l of sanitary flow	0.33	0.30

Lag time

ARIMA, SARIMA, VAR modeling



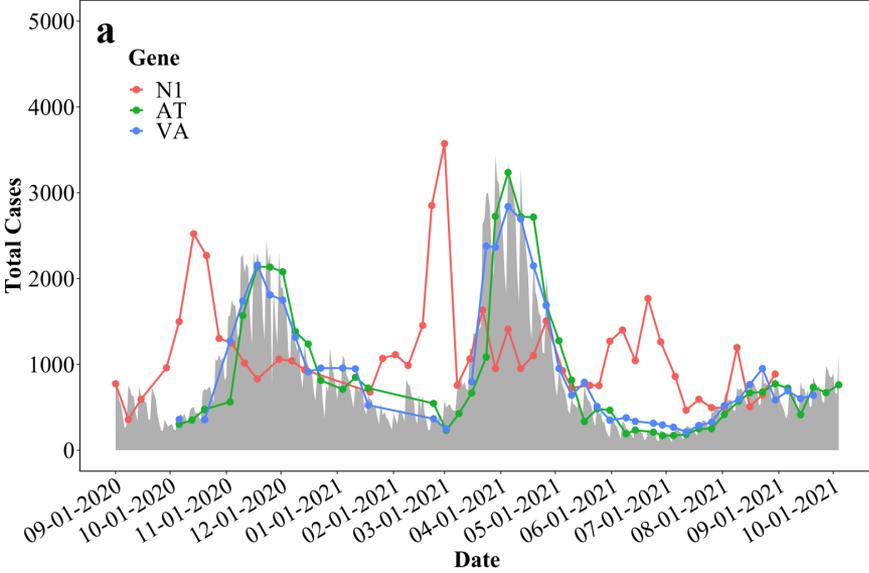
Lag time	Model	Equation (N1, gc/L)	RMSE	Pearson r
3 weeks	Linear	$y_{t(3)} = 0.015 x_{t(3)} + 534.96$	7.22	0.26
	Autoregression	$y_{t(3)} - 0.2928y_{t(3)-1} - 0.3741 y_{t(3)-2} = 0.015(x_{t(3)} - 0.2928x_{t(3)-1} - 0.3741x_{t(3)-2}) + 534.96$	135.65	0.07
	Autoregression+ time effect	$y_{t(3)} = 1052 - 1.7923t(3) - 0.044dx_{t(3)}$ $y_{t(3)}^* = y_{t(3)} + 0.5857y_{t(3)-1}$	10.18	0.76
	Vector Autoregression	$y_{t(3)} = 1.30y_{t(3)-1} + 0.12 y_{t(3)-2} - 0.49 x_{t(3)-1} - 0.01x_{t(3)-2} - 73.46$	8.32	0.72
4 weeks	Linear	$y_{t(4)} = 0.29 x_{t(4)} + 227.04$	7.26	0.51
	Autoregression	$y_{t(4)} - 0.1706y_{t(4)-1} - 0.2799 y_{t(4)-2} = 0.29(x_{t(4)} - 0.2354x_{t(4)-1} - 0.2799x_{t(4)-2}) + 227.04$	182.92	0.50
	Autoregression+ time effect	$y_{t(4)} = 1730 + 6.78t(4) + 0.06dx_{t(4)}$ $y_{t(4)}^* = y_{t(4)} + 0.59y_{t(4)-1}$	7.50	0.92
	Vector Autoregression	$y_{t(4)} = 1.42y_{t(4)-1} + 0.20 y_{t(4)-2} - 0.61 x_{t(4)-1} + 0.004x_{t(4)-2} + 109.89$	8.00	0.86
5 weeks	Linear	$y_{t(5)} = 0.35 x_{t(5)} + 93.13$	1.83	0.62
	Autoregression	$y_{t(5)} - 0.2362y_{t(5)-1} - 0.0785 y_{t(5)-2} = 0.35(0.2362x_{t(5)-1} - 0.0785x_{t(5)-2}) + 93.13$	105.81	0.67
	Autoregression+ time effect	$y_{t(5)} = 1337 + 20.20t(5) - 0.011dx_{t(5)}$ $y_{t(5)}^* = y_{t(5)} + 0.64y_{t(5)-1}$	1.47	0.95
	Vector Autoregression	$y_{t(5)} = 1.54y_{t(5)-1} - 0.02 y_{t(5)-2} - 0.68 x_{t(5)-1} - 0.04 x_{t(5)-2} - 191.18$	0.35	0.96

Modeling results of N1 gene in gc/L for September 2020 to August 2021

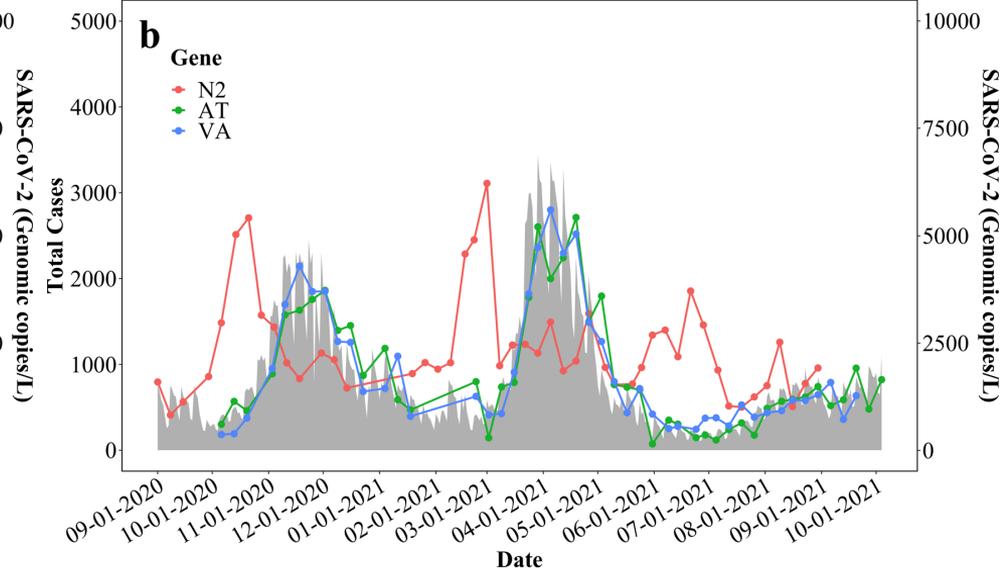
Lag time



Genomic copies/L, 5-week lag time, AT and VA, best N1 prediction scenario



Genomic copies/L, 5-week lag time, AT and VA, best N2 prediction scenario



Best prediction models based on (a) N1 gene concentrations (gc/L) and (b) N2 gene concentrations (gc/L) with a 5-week lag time

1

- The total N1 and N2 gene concentrations measured by RT-ddPCR ranged from 714.85 to 7145.98 gc/L and 820.47 to 6219.05 gc/L, respectively.

2

- A **5-week lag time** was estimated between September 1, 2020, and August 31, 2021.

3

- **Autoregression** with a seasonal pattern model and a **vector autoregression model** are more effective in predicting clinical COVID-19 cases.

4

- The lag time could provide early warnings for the upcoming fluctuations of COVID-19 cases, therefore, better assist to prepare the **public health policies**.



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Thank you!

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