

# COVID-19 Surveillance Project Update

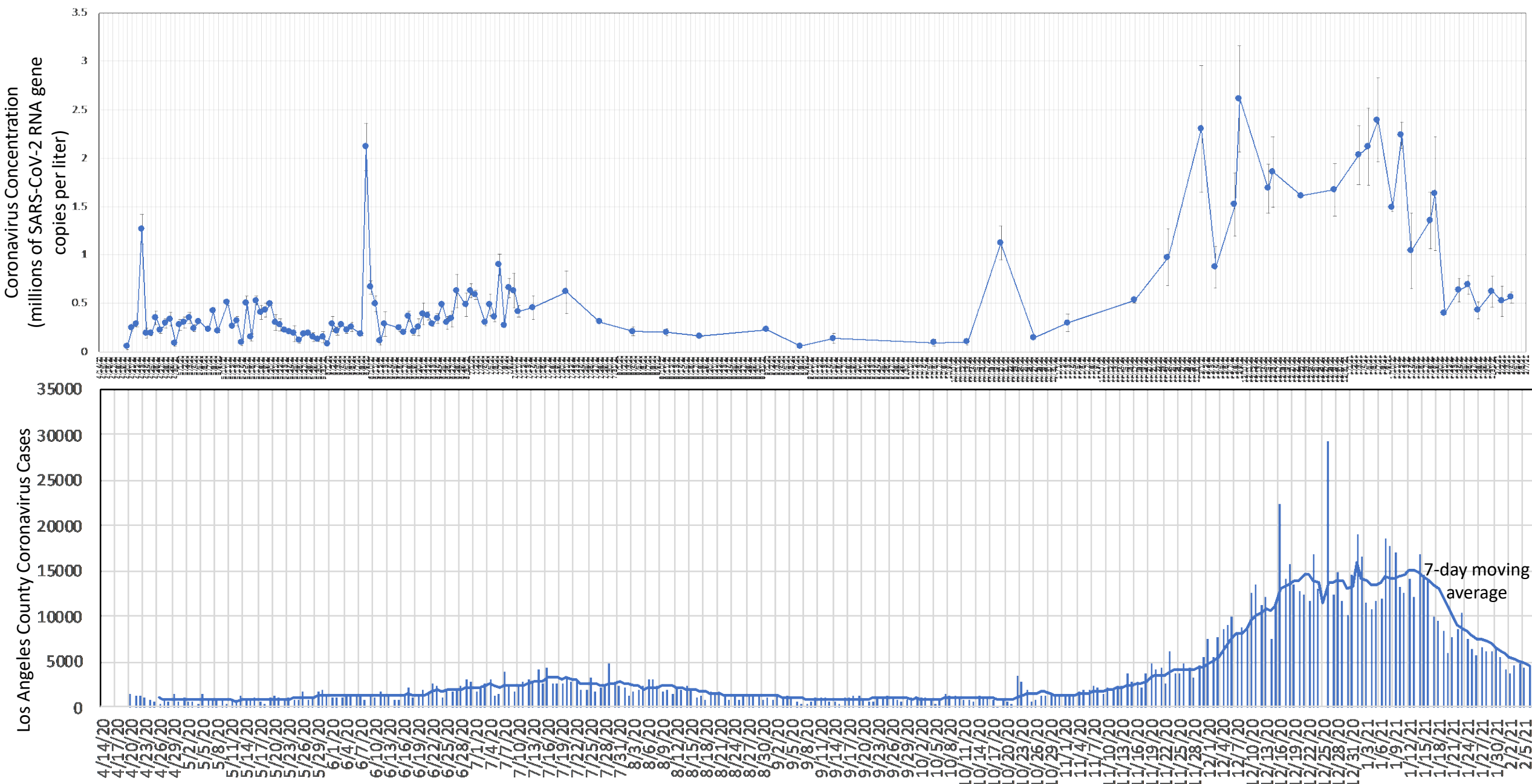
Presentation to the SCCWRP Commission  
March 5, 2021

John F. Griffith

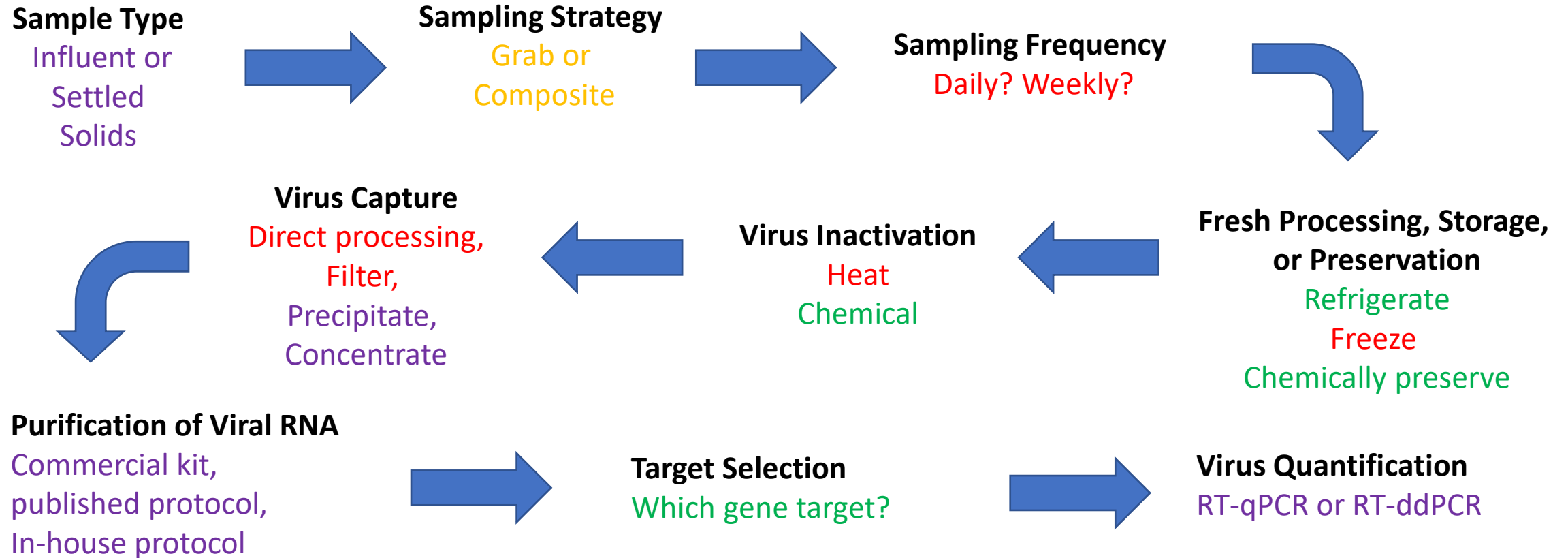
# Background

- Wastewater epidemiology is a great concept
  - Allows for tracking population levels of the SARS-CoV-2 virus
  - None of the drawbacks of individual testing
- Differences in methods lead to lack of compatibility of results across labs, plants, and regions
  - Comparison studies show wide variability across methods
- Our focus is on the relationship between variability and methodological choices

# Coronavirus Concentration in HTP Influent and Case Counts 4/20-2/21



# Potential Sources of Variability



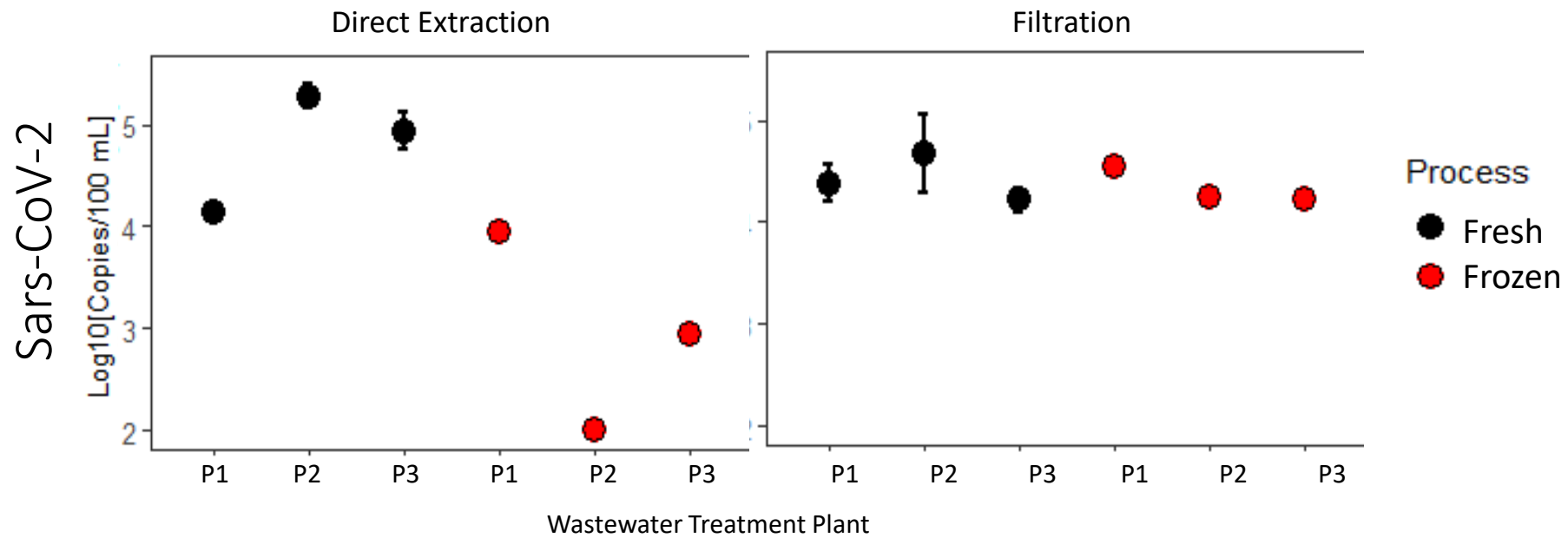
- Large Effect (> 1 order magnitude)
- Moderate Effect (0.5 - 1 order magnitude)
- Inconsequential Effect (0 – 0.5 order magnitude)
- In Progress

# Biggest Sources of Variability

- Freezing and thawing
  - Reduces sensitivity by up to 4 orders of magnitude
- Heat Treatment (Pasteurization)
  - Reduces sensitivity by up to 3 orders of magnitude

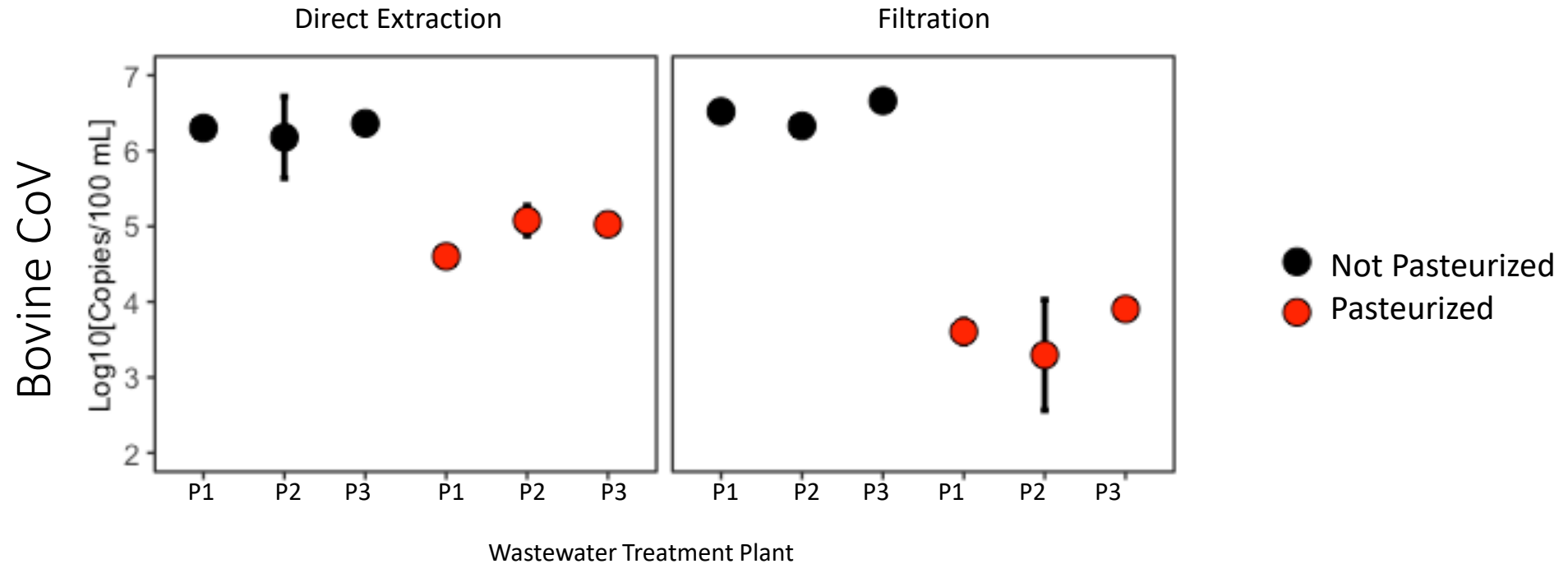
# Effect of Freezing

- When you can - minimize freeze thaws



# Heat Treatment

- ~1 to 3 log reduction in concentrations in pasteurized sample



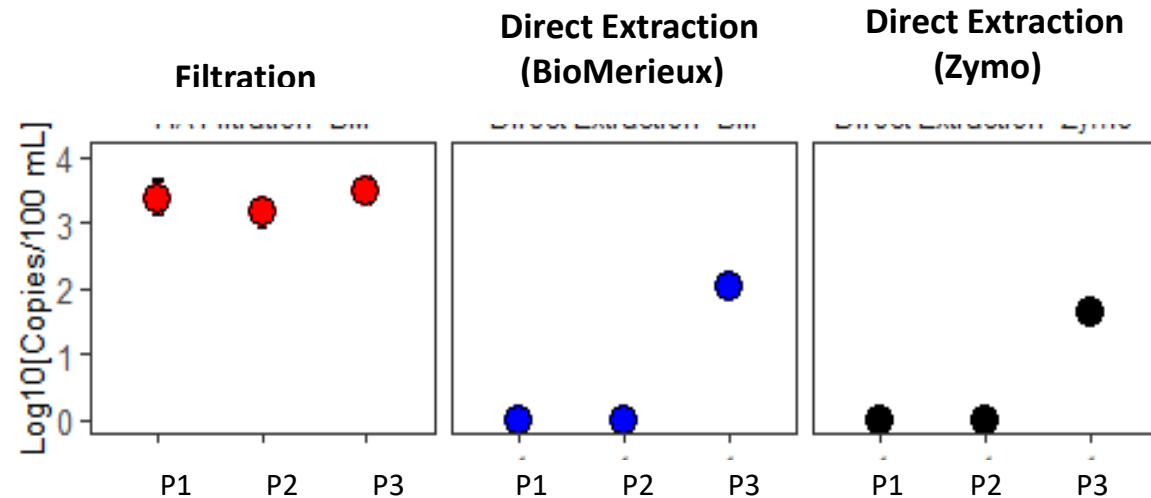
# Two other critical things we learned

- Direct extraction vs. filtration
  - Trade-off between expediency and method sensitivity when virus titers are low
- Frequency matters
  - Sampling once per week is inadequate



# Direct Extraction vs. Filtration

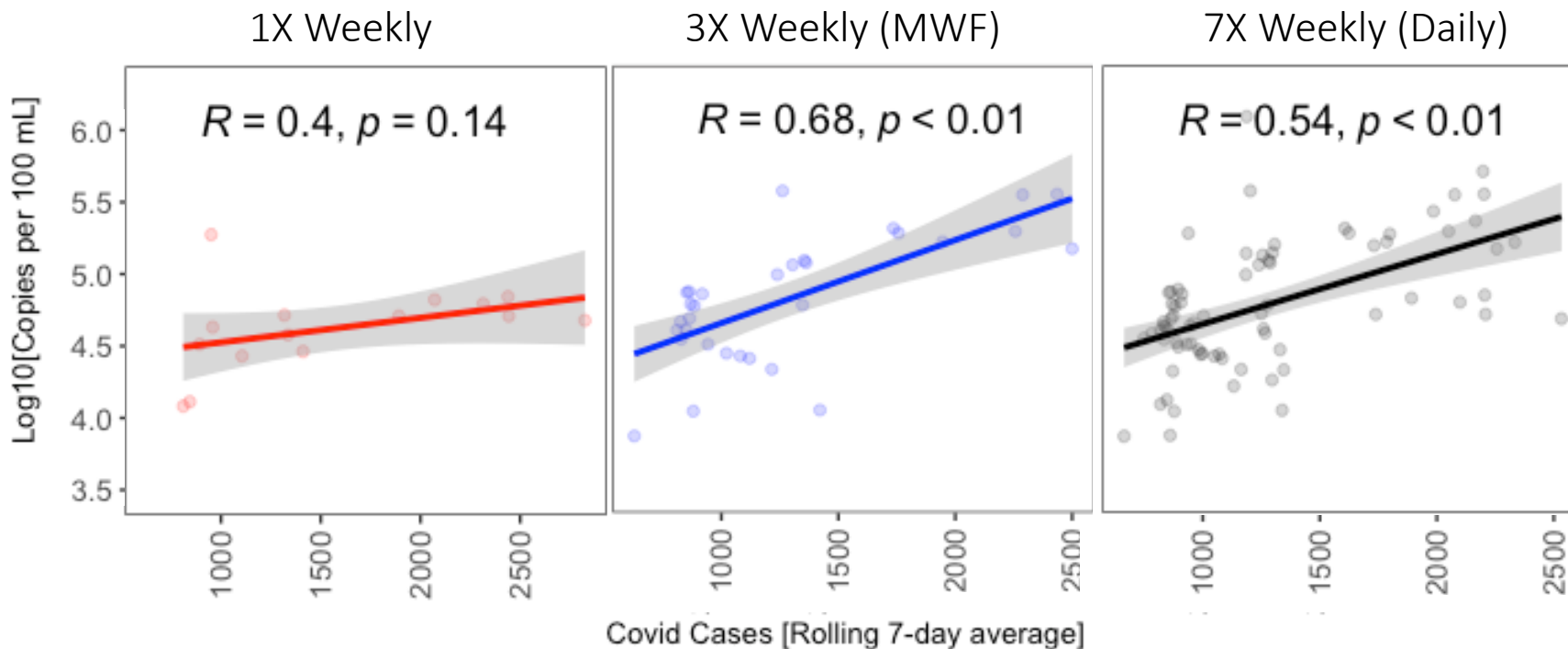
- Direct extraction more expedient
- BUT- trade off with limit of detection and method sensitivity
- Direct extraction may not be best option with lower SARS-CoV-2 concentrations



Sars-CoV-2

# How frequently to sample?

- No significant relationship between Covid-19 case counts and **weekly** wastewater samples
- Significant relationship with **3X** or **daily** samples



# Work in Progress

- Items remaining in Flow Chart
  - Comparison between paired influent and settled solids samples
  - Comparison of virus purification methods
  - Comparison of RTqPCR vs. RT-ddPCR
- Sequencing of SAR-CoV-2 in influent to track spread of variants
  - Collaboration with Stanford and UCI