Monitoring COVID-19 has required continuous testing that has often failed to capture the substantial asymptomatic population. A cheaper, less invasive way of determining the virus’s impact on populations may exist in wastewater-based epidemiology (WBE) – an approach that seeks to learn about a community’s health by monitoring their collective sewage. From July to December of 2020, our lab collected weekly samples from the local OWASA and Pittsboro wastewater treatment plants (WWTPs) and tracked the concentration of SARS-CoV-2 RNA over time using droplet digital PCR (ddPCR). These data mirrored the trends seen in local COVID-19 cases, particularly during the return of UNC students to campus in August 2020. For further WBE, I will use these samples for surveillance of antimicrobial resistance (AMR). This rapidly spreading ability of microbes to resist antibiotics can be monitored in the environment. However, because antimicrobial resistance genes (ARGs) in the environment are not automatically human health threats, a reliable method for assessing the risk posed by environmental AMR is needed. Wastewater brings varied microbes together in a nutrient-rich environment, providing an excellent opportunity for ARGs to pass from human-indifferent microbes to human pathogens. The OWASA WWTP is valuable because it receives wastewater from the UNC Chapel Hill hospital, a potent source of antimicrobials. Even more, the occasional need for antibiotics to treat secondary bacterial infections in COVID-19 patients may have increased antibiotic use during the pandemic. This seminar will 1) illustrate risk-focused AMR surveillance by determining trends in ARG presence, mobility, and possession by pathogens in wastewater from July to December 2020 using long-read DNA sequencing, and 2) assess if and how antibiotic use varied over this period (using data provided by the UNC Chapel Hill hospital) and how this correlates with the AMR metrics in 1).

The learning objectives for this seminar are to:
1. Understand the concept of WBE and how we used it to track COVID-19.
2. Recognize the factors impacting the health risk of an antimicrobial resistance gene.
3. Understand how long-read sequencing can avoid the pitfalls of AMR surveillance.