Analysis of sampling strategies for pulse loads in sewer catchments

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Highlights

- A deterministic packet-routing engine that includes dispersion and decay in a postprocessing step was developed for water quality modelling of pulse loads
- Artificial sampling was done on multiple probabilistic timeseries to analyse different sampling strategies
- A sensitivity analysis was performed to inform the development of local wastewater-based epidemiology sampling strategies

Introduction

Wastewater-based epidemiology (WBE) has been found to be a useful tool to monitor and trace the extent of SARS-CoV-2 transmission in communities (Kitajima et al., 2020). It allows for large-scale monitoring of viral infections, which is particularly useful if clinical monitoring is limited and/or if asymptotic cases are predominant in the community (Kitajima et al., 2020). WBE involves the continued sampling and analysis of wastewater for faecal matter with the goal of isolating remnants of SARS-CoV-2 viral RNA that is shed from the gastrointestinal tract of infected individuals (Kitajima et al., 2020). Often sampling is conducted at wastewater treatment facilities, however, sampling can also be conducted upstream in the collection system providing more targeted caseload data about the community (Ahmed et al., 2021).

Currently, sampling campaigns are often comprised of grab samples (Betancourt et al., 2021), time-weighted composite samples (Ahmed et al., 2020) or flow weighted composite samples (Weidhaas et al., 2021), that were designed to inform on daily loads of either distributed, continuous sources or high-frequency point sources. However, WBE is particularly relevant during low SARS-CoV-2 transmission periods when small clinical caseloads dominate (sparse point sources of pulse loads) and try to inform on the number of sources instead of the overall load. The application of stochastic wastewater modelling could provide catchment-specific sampling strategies targeted towards identifying trends in the community with spatially and temporally sparse point-pulse-loads. The objectives of research presented in this paper were to develop a modelling approach to represent the transport and transformation of pulse loads (e.g. faecal matter from toilet flushes) in sewer systems, and apply the developed approach to analyse and inform the sampling protocol at sites currently being monitored for SARS-CoV-2. Research outcomes will result in a decreased risk of failure to detect cases of infected individuals leading to a lower public health risk.

Methodology

Study site

To analyse the suitability of different sampling strategies a simulation approach was chosen. A neighbourhood in Toronto, Ontario Canada with a population of approximately 60,000 and a separated sewer system was chosen for this modelling exercise. The 11.3 km^2 of serviced area is comprised of 84.2 km of sanitary pipes, 1363 maintenance holes, and is dominated by medium density residential land cover (39%), 4% of the land being commercial 4% industrial, and the remainder in the open space category.

Composite model

Using asset and attribute information obtained directly from the City of Toronto a calibrated dry-weather-flow model was built in PCSWMM (CHI Water). Using the calibrated hydraulic model as a base, a deterministic water-quality model (swmmPulse) was developed and added to simulate pulse loads of SARS-CoV-2 and fecal matter from toilet flushes. SwmmPulse routes input loads, defined as packets, through the sewer network and calculates dispersion and decay in a postprocessing step. This allows the creation of temporally high resolution timeseries of water quality data.

Input parameters and sensitivity analysis

The input-timeseries of packets were created stochastically at 10 second time steps for all nodes within the catchment area, and distributed according to their serviced population. The node populations were derived from census data and building information. These packets were classified as healthy (containing only fecal matter) or infected (containing fecal matter and SARS-CoV-2 RNA). The probability density function used, here on called the *Bristol distribution*, was obtained from Cummings et al. 1992. This distribution is influenced by behaviour, that may change due to lockdown or stay at home measures. To evaluate the sampling regimes sensitivity to these measures, two more distributions were investigated in the sensitivity analysis: A *homogeneous* defecation pattern to represent potential disease related diarrhea, and an updated version of the Bristol Distribution, hereon called the *Adapted Bristol* which was informed by a discrete, high-resolution field sampling campaign at the monitoring site.

The influence of non-local input parameters, were investigated and included particulate dispersion (0.05 m^2s^{-1} to 0.36 m^2s^{-1}, selected 0.16 m^2s^{-1} (Rieckermann et al., 2005)) and the decay rate of SARS-CoV-2-RNA (0.083 d^{-1} to 0.144 d^{-1}, selected 0.114 d^{-1} (Ahmed et al., 2020)), as Indicated in Table 1.

Table 1. Parameters varied in the sensitivity analysis. If two are given, the first parameter concerns the healthy population and the second one the infected.

	Scenario 1/4/7	Scenario 2/5/8	Scenario 3/6/9
Flushing distribution	Bristol/Homogeneous	Adapted Bristol/Adapted Bristol	Adapted Bristol/Homogenous
Decay rates [d^{-1}]	0.144	0.083	0.144
Dispersion rates [m^2s^{-1}]	0.16	0.05	0.36

Simulation

For each scenario, 1000 stochastic variations with uniform distribution were created and simulated with varying fractions of infected population to yield mean diurnal curves of the constituent concentrations along with an estimate of their variability. Since all packets were tagged with their node of origin and the travel time to the sampling node determined by the model, the distribution of spatial origins of samples taken at time T was derived. Simulated samples for each scenario's variations are created by averaging the calculated concentrations of fecal matter and SARS-CoV-2 RNA within the sampling time-window. The suitability of different sampling times and regimes was then evaluated using the correlation of the sampling campaign to the simulated fraction and variability of infected individuals, along with the over- or underrepresentation of cases within different areas of the catchment.

Results and discussion

Preliminary results suggests that sampling campaigns that focus on collection efforts after a morning peak correlate best to the fraction of infected individuals in the catchment (Figure 1a). To calculate correlation coefficients, the simulated samples were grouped by the fraction of infected population and sampling hour. Correlation coefficients were then calculated for each hour between the fraction of infected population and the mean measured concentration of SARS-CoV-2-RNA copies (Figure 1b). However, this analysis is ongoing the results are not yet available.

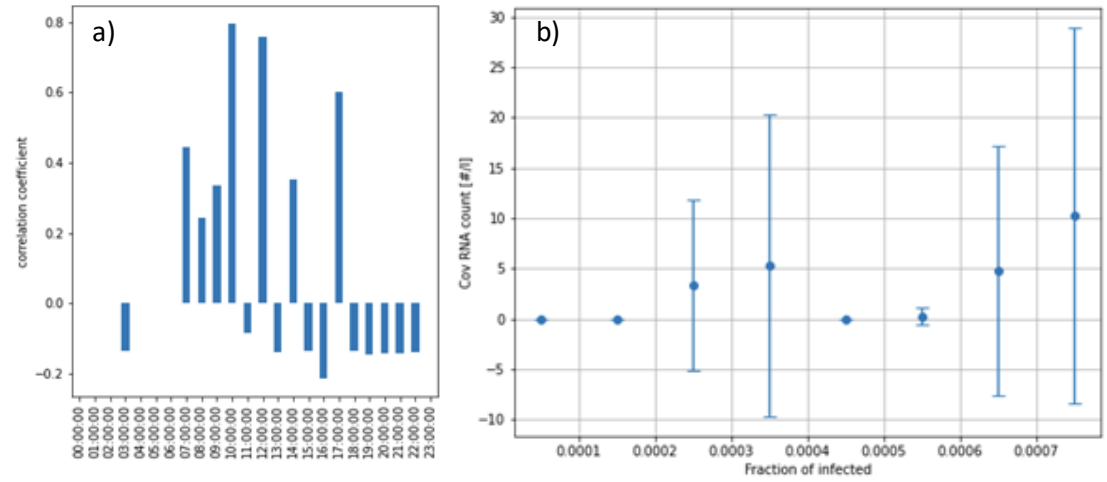

Figure 1: a) Correlation coefficients of preliminary results showing different sampling hours to the fraction of infected packets, b) mean concentrations and standard deviation for samples collected at 10 am.

The spatial over- or underrepresentation of infected individuals at given sampling times will be derived. The accuracy of the spatial representation is influenced by the decay rate of SARS-CoV-2 and can be accommodated for in sampling campaigns by adjusting the sampling frequency and volume collected.

Conclusions and future work

It has been demonstrated that that optimized sampling regimes lead to a significant increase in overall sample representativeness. Since knowledge of local defecation patterns is necessary, a high-resolution sampling campaign regarding fecal matter is recommended. The impact of the different input variables on suitable sampling regimes will help to eliminate uncertainty in WBE monitoring.

References

Ahmed, W., Bertsch, P. M., Bibby, K., Haramoto, E., Hewitt, J., Huygens, F., Gyawali, P., Korajkic, A., Riddell, S., Sherchan, S. P., Simpson, S. L., Sirikanchana, K., Symonds, E. M., Verhagen, R., Vasan, S. S., Kitajima, M., & Bivins, A. (2020). Decay of SARS-CoV-2 and surrogate murine hepatitis virus RNA in untreated wastewater to inform application in wastewater-based epidemiology. *Environmental Research*, *191*, 110092. https://doi.org/10.1016/j.envres.2020.110092

Ahmed, W., Bivins, A., Bertsch, P. M., Bibby, K., Gyawali, P., Sherchan, S. P., ... & Korajkic, A. (2021). Intraday variability of indicator and pathogenic viruses in 1-h and 24-h composite wastewater samples: Implications for wastewater-based epidemiology. Environmental Research, 193, 110531.

Betancourt, W. Q., Schmitz, B. W., Innes, G. K., Prasek, S. M., Brown, K. M. P., Stark, E. R., ... & Pepper, I. L. (2021). COVID-19 containment on a college campus via wastewater-based epidemiology, targeted clinical testing and an intervention. Science of The Total Environment, 779, 146408.

CHI Water. (n.d.). *SWMM5 modeling with PCSWMM*. Www.pcswmm.com. Retrieved August 20, 2021, from https://www.pcswmm.com/

Cummings, J. H., Bingham, S. A., Heaton, K. W., & Eastwood, M. A. (1992). Fecal weight, colon cancer risk, and dietary intake of nonstarch polysaccharides (dietary fiber). *Gastroenterology*, *103*(6), 1783–1789. https://doi.org/10.1016/0016-5085(92)91435-7

Kitajima, M., Ahmed, W., Bibby, K., Carducci, A., Gerba, C. P., Hamilton, K. A., ... & Rose, J. B. (2020). SARS-CoV-2 in wastewater: State of the knowledge and research needs. Science of The Total Environment, 739, 139076.

Rieckermann, J., Neumann, M., Ort, C., Huisman, J. L., & Gujer, W. (2005). Dispersion coefficients of sewers from tracer experiments. *Water Science and Technology*, *52*(5), 123–133. https://doi.org/10.2166/wst.2005.0124

Weidhaas, J., Aanderud, Z. T., Roper, D. K., VanDerslice, J., Gaddis, E. B., Ostermiller, J., ... & LaCross, N. (2021). Correlation of SARS-CoV-2 RNA in wastewater with COVID-19 disease burden in sewersheds. Science of The Total Environment, 775, 145790.