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Will the extraction of COVID-19 from wastewater help flatten the curve?

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Abstract

With the potentially fatal effect of COVID-19 and its devastating impact on economies worldwide, some environmental scientist has suggested the use of waste from household sewage to trace the movement of SARS-CoV-2, within a given country. However, this approach is not without challenges where developing countries lack proper and adequate hygiene and sanitation, resulting in widespread defecation. Limited scientific research has been done to determine how many times a recently infected person can defecate and the quantification of SARS-CoV-2 found in a single expel. On the other hand, there is no detailed research to specify where the heavy viral load of SARS-CoV-2 can be found in human excreta. In this paper, we present some obstacles that this approach could face in the absence of an intense lockdown in developing nations such as sub-Saharan countries. To achieve this, we identify some research needs that will strengthen our understanding of the transmission, occurrence, and persistence of SARS-CoV-2 in sewage and wastewater, including the lifespan that depends on temperature. A methodology to follow in the process of identifying a hotspot on a small scale using some mathematical distributions, including the normal distribution, log-normal distribution, and the most complex one known as Blancmange function, was presented with some examples. Our investigation showed that this method might have some challenges, especially in developing countries (sub-Sahara countries) where open latrine usage is very high. Some recommendations we suggested to ensure the efficiency of such a method on a small scale. However, in general, it is essential to note the
world to trace SARS-CoV-2-19 in humans.

**Keywords**, Coronavirus, SARS-CoV-2, feces, sewage, wastewater treatment, challenges, extraction method, and disadvantages.

1. **Introduction**

Coronaviruses (CoVs) belong to the large virus family Coronaviridae (Norovirus), Adenoviridae (Adenovirus), Picornaviridae (Enterovirus and Hepatitis A virus) (WHO, 2017). The virus can cause diseases ranging from the common cold to Severe Acute Respiratory Syndrome coronavirus 2 (SARS-CoV-2) and the Middle East Respiratory Syndrome coronavirus (MERS-CoV) (de Wit et al., 2016). In late December 2019, a new acute respiratory disease known as COVID-19, sustained by a novel coronavirus, SARS-CoV-2, emerged in Wuhan, China. This rapidly spread across the planet. The outbreak was declared a Public Health Emergency of International Concern on 30 January 2020. (WHO, 2020). On March 11 (2020). The world health Organization upgraded the status of the COVID-19 outbreak from epidemic to pandemic (Gorbalenya et al., 2020). Around 111 countries rapidly reported the attack (Wu et al., 2020).

The coronavirus virion is a spherical single-strand RNA, roughly with a diameter range of 60-220 nm in size. It also contains the outer viral envelope covered by a 9-12 mm projections range. (Zhu et al., 2020). The virion structure of SARS-CoV or SARS CoV-2 is shown in Fig. 1. The most common severe symptom of COVID-19 reported is related to respiratory systems.

The SARS-CoV-2 virus is excreted in the feces and found at lower concentrations in the human excreta of the infected person (Rusinol and Girones, 2017). Transmission of the virus is by direct contact, and droplets spread with sneeze and cough. The most infected stage of the virus is when a person is symptomatic, but data point to the transmission that can occur before the onset of symptoms (Chan et al., 2020). The virus can also be transmitted through
dry surfaces contamination from the self-inoculation of mucous membranes of the nose, mouth, or eye (Otter et al., 2016; Geller, 2012). Since most of the transmission in humans is characterized as a self-limiting condition, little is known about its transmission potential through the environment. COVID-19 transmission via the fecal-oral route has been mooted (Gu et al., 2020; Yeo et al., 2020) but not profoundly studied. Due to the fatality of COVID-19, transdisciplinary researchers have focused their attention on the mode of transmission, the structure of the new virus, its life-span, and mutation in the human body, its persistence on the surface, air and, water (La Rosa et al., 2020). The available literature shows the evolution of new mathematical models, which aim at understanding the spread to predict the future behavior of the virus (Atangana, 2020; Owusu et al., 2020; Danane et al., 2020). Complex statistical analysis is used to predict the future numbers of deaths, infected, and recovered to inform policy that helps to flatten the curve of COVID-19 (Atangana and Seda, 2020; Kasereka Kabunga et al., 2020; Fatmawati et al., 2020; Zhang and Liu, 2019). Biologists and chemists are working to understand the novel COVID-19 to develop methods of disruption and mitigation (Ahmed et al., 2020), and virologists are developing a vaccine.

Meanwhile, environmentalists have embraced a methodology to identify the hotspot of affected people by using wastewater. This method has been implemented in some countries, including France and Netherlands however; there is no clear indication that such will be more effective than the testing performed by medical staff worldwide (la Rose et al., 2020). In this work, further, the analysis will be presented.

This article aims to identify some research needs that will strengthen our understanding of the occurrence and persistence of SARS-CoV-2 in sewage and wastewater, including the life-span that depends on temperature and the detecting devices used. A possible procedure will be suggested to identify the SARS-CoV-2 hotspot on a small scale using some mathematical distributions, including the normal distribution, log-normal distribution, and Blancmange’s most complex one function with some examples. The fusion of the recent findings highlights
that sewage wastewater could be used to trace an infected person with the SARS-CoV-2 RNA virus.

**Fig. 1:** Virion structure of SARS-CoV/SARS-CoV-2 (La Rosa et al., 2020).

**2. Background literature**

In this section, we will discuss some areas in the study that will help strengthen our understanding of the transmission, occurrence, and persistence of SARS-CoV-2 in sewage and wastewater via temperature effect and some devices used to detect the virus.

**2.1. SARS-CoV-2 transmission via fecal-oral routes**

After the detection of SARS-CoV-2 RNA in stool/human excreta samples of infected patients, there have been many recent reports shown on the transmission via the fecal-oral route. The specific ways occur when pathogens in the fecal particles can be transmitted from one individual mouth to another. (Ahmed et al., 2020). This is due to poor hygiene and
sanitation, resulting in open defecation (Grassia et al., 2020). Humans can be infected with waterborne disease if the waters are polluted with fecal materials, resulting in some disorders such as diarrhea, typhoid, cholera, hepatitis, and polio (Wen et al., 2020). The oral-fecal follows five paths: fingers, flies, field, fluids, and food (Ahmed et al., 2020). Little information is known in the cases of COVID-19 spread via field and fluids.

At the same time, there is an argument on virus spread via fomites (surfaces and cloths), flies, and fingers (close contact) (Chen et al., 2020; Haas, 2020). Progress on the virus provides a regular inflow of new insight into its plausible transmission routes and pathogenesis (Arslan et al., 2020). There is abundant angiotensin produced by the gastrointestinal (GI) tract, which converts the ACE2 (enzyme 2) to which the virus is acknowledged to attach. Intestinal manifestation occurred mostly in the late phase of infection (Wu et al., 2020). Literature studies have reported symptoms such as nausea and diarrhea preceding fever, and respiratory symptoms usually occur from more than 10-14% of patients with GI as the only manifestation (Wu et al., 2020). It was then suggested that the SAR-CoV-2 virus might stay longer in the digested tract than the respiratory tract (Grassia et al., 2020). Clear examples of such a scenario occurred in patients excreting viral RNA through feces through several weeks of infection from when symptoms start to develop. Some instance has been reported in the literature where two positive cases of viral nucleic acid occurred in the anal swabs, after 6-14 days, negative results were obtained from respiratory specimens. Similar results were also obtained by Wu et al. (2020), where positive results were obtained from patients' fecal samples in China. Even after getting negative consequences for the respiratory samples for about 33 days (Wu et al., 2020). Another study observed a long period of 47 days before the first day of symptoms development. These cases lead us to may query concerning the virus fate and distribution into the environment via fecal route. Is it likely that most patients discharge from the hospital after treatment can excrete the virus in their feces? Back in the existences in 2003, the virus was also detected in the feces of infected patients during an outbreak in the residential complex of Amoy Garden in Hong Kong where transmission by
2.2. SARS-CoV-2 in water and wastewater

It is well known that the virus eliminated by feces can be found in wastewater, which may not be removed entirely from conventional wastewater treatment plants. It has been suggested that sewage and wastewater can trace the geographical area where there is a high risk of SARS-CoV-2 infection (hotspot). Following the outbreak in March 2003, over 3000 people were involved in a faulty untreated wastewater system that led to a high-rise housing estate in Hong Kong city (Peiris et al., 2003). Based on the scenario that the preceding SARS CoV-2 can reproduce in the enteric tract, the potential for being classified as an enteric pathogen with a potential transmission pathway via the environment (Leung et al., 2003; SARS-EWG, 2003). According to Leung et al. (2003), SARS-CoV-2 is found in both the lungs and the small intestine. For this research, the virus was cultured from patient stool/excreta about three weeks before infection. It was later observed that higher yield offer patients with the viral cultures found in the small intestine than the lung tissues (Liu et al., 2004; Chan et al., 2004). In a study done in Zhejiang provincial hospital, China, when researching a patient's stool, it was observed that SARS-CoV-2 RNA could survive for 4 days or up to about 22 days. This was much longer than the respiratory and serum samples of the same patient's sample collected, which only stay for 18 and 22 days (Zheng et al., 2020).

Some reports suggest a potential link of SARS CoV-2 to water and wastewater (La Rosa et al., 2020). One of the pioneer's works on the investigation of coronavirus traces in pure water and untreated sewage can be traced back to 2009 when the arrival of similar COVID-19 researchers investigated its potential environmental transmission (Patricia et al., 2019). The presence of coronavirus (COVID-19) was traced in both filtered and unfiltered, pure water within an interval temperature ranging from 4-23 °C and 23 °C in untreated wastewater.
The viability of coronavirus is dependent on a range defined by the daily and nightly temperature, as well as the level of inorganic matter and other antagonistic bacteria (Sobsey and Meschke, 2003). \(T_{99}\) was known to be the time required for the virus to decrease (99%) for pure water. More importantly, it was shown that coronaviruses were inactivated faster in the pure water at 23 °C in 10 days rather than 40 °C for more than 100 days (John and Rose, 2005). It has been reported that coronaviruses died off rapidly in untreated wastewater, even with a \(T_{99.9}\) value of between 2 and 4 days. While the COVID-19 may have additional properties that the one described, it is worth noting that it belongs to the coronavirus family and is likely to respond in similar ways (Melnick and Gerba, 1980).

Researcher Lisa (2015) reported on the Enveloped Surrogate Virus in the inactivation form in human sewage and fat of enveloped virus. Obtained results were used as a means to model the entrance of the Ebola virus in sewage samples. The enveloped virus in the inactivation kinetic structure in sewage uses a specific RNA bacteriophage that belongs to the Cystoviridae family, which then acts as a latent substitute of the virus enveloped human sewage. Their effects indicate in a wastewater sample that is primarily based on temperature dependence. For 3 to 7 days, the virus can ride 6 to 7 inactivation kinetic form in a pattern (Lisa, 2015).

2.3. SARS-CoV-2 detection devices

Numerous researchers in the literature have reported on the want for scientists to use paper-based device units (Mao et al., 2020); Water-Based Epidemiology (WBE) (Daugthon, 2020), nucleic acid-based polymerase chain reaction (PCR) (Casanova et al., 2009; Medema et al., 2020) to extract/detect SARS-CoV-2 immediately in wastewater. Polymerase chain reactions (PCR) had been recommended to elevate out the measurement, which was once often used in various nations (Barcelo, 2020). The above device used (Paper-based device) is known to be inexpensive, powerful, and very fast to identify the infection rate of transition and pathogens (Mao et al., 2020). Its entire surface is cover with a variety of useful surfaces, made from a
that it is susceptible and fast, which makes PCR usage for numerous infections, for instance, several pathogens and Malaria (Mao et al., 2020). Another scientist has used Water-Based Epidemiology (WBE) device to trace the COVID-19 virus in human sewage (Daugthon, 2020; Barcelo, 2020). Due to the vast infection rate of the current pandemic COVID-19, former pioneer of EPA and expert calls for all scientist to advance their research in Water-Based Epidemiology. This was called for the present COVID-19 virus and any future pandemic crises ahead. The expert explained that scientists could use sewage as an indicator to measure an infected, which can increase attention around the nation, therefore leading to more curiosity in method (Water-Based epidemiology). The expert and many different scientists accept the fact that when distributing hard work on WBE, community members are essential to acknowledge their labor to move ahead, thereby calling for an assistant in the public health sector (Daugthon, 2020). Nation across the world; Australia (Ahmed et al., 2020), Netherlands (Medema et al., 2020), Italy (La Rosa et al., 2020; Rimoldi et al., 2020), Spain (Randazzo et al., 2020), Francs and Japan (Wurtzer et al., 2020), Germany (Randazzo et al., 2020), USA (Sherchan et al., 2020; Wu et al., 2020), Ecuador (Guerrero-Latorre et al., 2020) and Indian (Kumar et al., 2020), were the first to use PCR to detect the virus in sewage, which supports the idea, implemented above, thereby using WBE was efficient to disclose the scale of the pandemic SARS-CoV-2 (Medema et al., 2020; Warish et al., 2020; Wurtzer et al., 2020).

Increasingly using wastewater as a fast and effective way to monitor and predict the spread of COVID-19 is being accepted as viable (Burger, 2020; Turton 2020). The concept has been proven by the Dutch research agency KWR and confirmed by research done in South Africa. Researcher Mallapaty suggested how sewage could reveal the coronavirus outbreak's accurate scale, and researchers from other countries are trying to implement the same procedure to trace the COVID-19 hotspot (Mallapaty, 2020). The study presents some obstacles that the extraction method could face in the absence of intense lockdown and
approach. We should also discuss if such a method can trace infected humans if one can link
the virus load found in the waste and the number of infected humans. Furthermore, some
simple mathematical models will be presented to predict the possibility of a hotspot as a viral
load function of time. Several cases could be considered starting with the possibility of
normal distribution.

3. Material and Methods

All theoretical assumptions considered for daily cases and daily tests in the manuscript were
observed from our world data.org. (Our World in Data, 2020)

In this section, we describe the normal, log-normal distribution fractional distribution
(Blancmange curve) and SIR model to trace the SARS-CoV-2 hotspot. First of all, we present
the epidemiological characteristics of SARS-CoV-2. Then, we introduce a general and
detailed description of our approach. Finally, we detail some of the distributions and model
outputs used for the numerical experiments performed later.

3.1. Epidemiological characteristics of SARS-CoV-2

We assume that each individual is in one of the following compartments (Teiji, 1901;
Cooper, 2020; Coronavirus worldometer, 2020)

According to the known characteristics of the COVID-19 pandemic, we assume that each
individual is in one of the following compartments (Coronavirus worldometer website, 2020).

- The collection of viral loads in the six different untreated wastewater treatment plants
  was done daily, denoted as \( d_1, d_2, d_3, d_4 \) (days) at a time interval \( t_0 \leq t \leq T \). Where
  \( t_0 \) is the initial time, and \( T \) is the final time
- \( P_i \) denotes a normal distribution for the viral load of SARS-CoV-2 in six different
  untreated wastewater treatment plants \( I = 1, 2, 4, 5, \ldots, N \)
\( N \) denotes the total number of untreated wastewater treatment plants.

- \( H \) denoted the log-normal distribution for the viral load of SARS-CoV-2 trace in six different untreated wastewater treatment plant.

- \( \alpha_i \) are the contribution of daily average and the deviation due to new viral load arrival of the untreated wastewater treatment plant.

- \( b_i \) is the contribution of deviation (the measure of the dispersion of the dataset) relative to the daily average viral load of the untreated wastewater treatment plant.

- \( \mu \) and \( \delta \) denote the mean and standard deviation for the six different wastewaters treatment plants.

- Blancmange curve (Blanc) represents a complex distribution, the viral load of SARS-CoV-2 in wastewater treatment plants with other Hurst parameters (\( \omega \)); 0.8, 0.85, 0.9, 0.93, 0.96 and 0.99.

- \( SIR \) model denotes Susceptible, Infectious, and recovered individuals.

I. **Susceptible individuals,** \( S(t) \): These are those individuals who are not infected, however, could become infected.

II. **Infected individuals,** \( I(t) \): These are those individuals who have been infected by the virus and can transmit it to those individuals who are susceptible.

III. **Recovered individuals** \( R(t) \): These are those individuals who have recovered from the COVID-19 virus and are assumed to be immune, \( R(t) \).

**Hotspot:** Describe the geographical area where there is a risk of many infected individual with COVID-19.

Humans rely on the collection of data for proper monitoring of given real-world problems. One of the most used procedures is perhaps the sampling, which aims to select a subset, also called a statistical sample, of persons from inside a statistical population to appraise the whole population's appearances. In the case of extraction/detection of viral load of
SARS-CoV-2 in untreated wastewater treatment plants in a given country, systematic sampling could be more appropriate. We shall recall that frequent selection is based on arranging the investigated population according to some ordering scheme; then, the next step is selecting elements at even intervals via the ordered list. Therefore, we shall stress that researchers shouldn’t rely on data collection to have a clear opinion about a given real-world problem. When data are collected, they could be plotted as a function of time, space, and space and time. Most of the time, the obtained results follow distributions, which are known as a statistical formula. In general, they are called probability as they provide the chances of different possible outcomes for collected data. Several distribution statistical functions can be obtained, for example, normal distribution, log-normal distribution, Poisson distribution, power-law distribution, and many more that cannot be listed here.

In this section, we will assume that the collected data from the different wastewater treatment plants follow either the normal distribution, log-normal distribution, or in a more complicated case, a fractal distribution, at a time interval of $t_0 \leq t \leq T$. Where $t_0$ is the initial time, and $T$ is the final time. The normal distribution is, in general, a category of continuous distribution for the real-valued random variable, which considers an average also called mean or expectation of the distribution, and the standard deviation (a proportion that describes the amount of variation or dispersion of set values). This distribution is wider used in many sciences, technology, and engineering (Park and Bera 2009; Atangana, 2020; Atangana and Seda, 2020; Doungmo Goufo et al., 2020; Khan et al., 2020; Faraz et al., 2020). In particular, in natural (Limpert and Stahel, 2011) and social science (Blanca et al., 2018), it can give real-values random variables, especially those for which the distributions cannot be identified. One of the great values of using this distribution is that the average of many observations of a random variable with a finite average and variance can be considered a random variable, particularly those distributions that are similar to the normal distribution as the number of observations accumulates. Additionally, to this advantage, it is known that
physical measures that are predictable to be an addition of many autonomous processes, like measurement errors, are most of the time following distribution that is approximately normal.

3.2. Normal distribution

This distribution possesses some uniqueness in terms of properties, which are very important in an analytic investigation, like in the case of the collection of SARS-CoV-2 traces in untreated wastewater treatment plants. Thus, if we suppose that the collected data from untreated wastewater treatment plants would follow the normal distribution, then, assuming a collection will be performed in \( N \) wastewater treatment plants. Let \( P_i(t) \) be the viral load/concentration of SARS-CoV-2 trace in the untreated wastewater treatment plant \( i = 1,2,3,4,5 \ldots \ldots \ldots N \), for four consecutive days \( d_1, d_2, d_3, \) and \( d_4 \), at time \( t \) interval range of \( t_o \leq t \leq T \). The rate of change of viral load as a function of time can be assumed to follow (equation 1).

\[
\frac{dP_i(t)}{dt} = a_i P_i(t) + b_i t P_i(t)
\]

Where \( a_i \) are the contribution of daily average and the deviation due to new viral load arrival, \( b_i \) is the contribution of deviation (the measure of the dispersion of the dataset relative to the daily average viral load of the untreated wastewater treatment plant \( i \)). Let \( \mu \) be the average viral load detected in wastewater treatment plant \( i \) (\( WWTP (i) \)) and \( \sigma_i \) the associated standard deviation, then, equation (1) becomes (equation 2).

\[
\frac{dP_i(t)}{dt} = \frac{\mu_i}{\sigma_i^2} P_i(t) - \frac{tP_i(t)}{\sigma_i^2}
\]

The exact solution of the above is given in equation (3) as:

\[
P_i(t) = \frac{1}{\sigma_i \sqrt{2\pi}} P_i(0) \exp \left( \frac{(t-\mu_i)^2}{\sigma_i^2} \right)
\]
The family of $P_i(t)$; $i = 1, 2, 3, \ldots$ can be plotted each week to evaluate a weekly density at WWTP $(i)$. From the obtained results and using the formula of the normal distribution as given in equation (3), the parameters $\mu_i$ and $\sigma_i$ can be determined. For example, by considering four consecutive days for example $d_1$, $d_2$, $d_3$ and $d_4$.

Then the average at WWTP $(i)$ is determined as (equation 4-8))

$$
\mu_i = \frac{1}{2} (d_4 + d_3)(d_4 - d_3) - \frac{\ln[P_i(d_4)]}{\ln[P_i(d_3)]} (d_2 + d_1)(d_2 - d_1)
$$

$$
\sigma_i = \sqrt{\frac{1}{2 \ln[P_i(d_3)]} \left\{ (d_1 - \mu_i)^2 - (d_2 - \mu_i)^2 \right\}}
$$

The weekly collected data from the N-wastewater plants (raw wastewater) can be plotted as functions of time (d) in the same graph.

3.3. Log-normal distribution

Alternatively, one could expect to have the following distribution at WWTP $(i)$ following a log-normal distribution, an essential statistic function to depict many natural phenomena. Various small percentage changes drive numerous regular growth processes; however, they become additive in the log scale. If these variations' effect is not significant, then the distribution of their addition is closer to normal than the acquisition. Now, when reverting to the original scale, distribution sizes convergent toward log-normal. It should be recalled, log-normal distribution is a continuous probabilistic function of a given random variable for which the logarithm is normal.

In simple terms, if we consider the random change $H$ is log-normally disseminated, then the variable $Z = \ln(H)$ has a regular spreading of the SARS-CoV-2 RNA virus. On the other hand, if $Z = \exp(H)$ follows the regular spreading, then, $H = \exp(Z)$ will follow the log-
normal spreading. This virus spreading is very convenient and very practical, for example, in measuring engineering sciences (Atangana, 2020), medicine, economics (Blanca et al., 2018), chemistry (Atangana et al., 2020), biology, and physics (Atangana, 2020), and many other fields (Limpert and Stahel, 2011). Therefore, if it is assumed that the weekly collected data would follow the log-normal spreading of the SARS-CoV-2 virus, then the following mathematical function can be considered

\[ P_i(t) = \frac{1}{\sigma_i \sqrt{2\pi}} P_i(0) \exp \left\{ \frac{(\ln(t) - \mu_i)^2}{\sigma_i^2} \right\} \tag{6} \]

In this way, by using the curve of the collected data, the following parameters can be determined using the comparison between the collected data and the mathematical formula

\[ \mu_i = \frac{1}{2} \left( \ln(d_3) + \ln(d_4) \right) - \frac{\ln \left( \frac{P_i(\ln(d_4))}{P_i(\ln(d_3))} \right)}{\ln \left( \frac{P_i(\ln(d_3))}{P_i(\ln(d_4))} \right)} \left( \ln(d_3) - \ln(d_4) \right) \tag{7} \]

\[ 1 \left( \ln(d_4) - \ln(d_3) \right) - \frac{\ln \left( \frac{P_i(\ln(d_4))}{P_i(\ln(d_3))} \right)}{\ln \left( \frac{P_i(\ln(d_3))}{P_i(\ln(d_4))} \right)} \]

While

\[ \sigma_i = \sqrt{\frac{\ln \left( \frac{P_i(\ln(d_2))}{P_i(\ln(d_3))} \right)}{2 \ln \left( \frac{P_i(\ln(d_3))}{P_i(\ln(d_4))} \right)}} \left\{ \left( \ln(d_1) - \mu_i \right)^2 - \left( \ln(d_2) - \mu_i \right)^2 \right\} \tag{8} \]

An example of such a plot is presented in Fig. 2 a and b, showing the normal and log-normal distribution for different viral loads, respectively; here, we consider that the collection was done in the six other raw wastewater treatment plant since there will be some with high trace due to the high numbers of infected persons, we choose different averages and standard distributions, then plot all in the same Fig. 2 a and b, as presented below. To perform, these plots we consider a collection of raw wastewater treatment plants for five consecutive d. For each day, it is assumed that an adequate supply of data is performed and recorded.

At the end of the five d, all collected data from the six different wastewater treatment plants are plotted as a function of time, in the same. For example, in Fig. 2 a and b, we assume that each viral load from a given wastewater plant treatment has a daily average and standard deviation to be represented with the normal distribution. In this Fig. 2a and b, we consider six
And six different standard deviation $\delta = 0.1, 0.2, 0.3, 0.4, 0.5, 2.0$

3.4. Complex distribution (Blancmange/Teiji curve)

Nevertheless, although many physical processes can follow a normal and log-normal distribution, it is essential to note that there exist many real-world problems in time and space that do not follow the conventional distribution. Therefore, more complex distributions can represent such physical problems; for example, a process curve can follow fractal features. A fractal curve or geometrical representation with the fractal quality is a curve for which each part has the same statistical character as the whole. Such features appear in many real-world problems. There is a function known as the Blancmange curve; it is also known as the Teiji Takagi curve, which was suggested in 1901. (Teiji, 1909).

Here we assume that data collected from the six different wastewater treatment plants follow the Blancmange curve (eq 9-11), with other Hurst parameters $\omega = 0.8, 0.85, 0.9, 0.93, 0.96, 0.99$.

$$Blanc(t) = \sum_{l=0}^{\infty} \frac{dist(2^l)}{2^j}, \quad t \in [0,1],$$  \hspace{1cm} (9)

Where

$$dist(z) = \min_{j \in \mathbb{N}} |z - j|, \quad z \in \mathbb{R}$$ \hspace{1cm} (10)

$$Blanc\left(\frac{t+j-1}{2}\right) = \frac{1}{2} Blanc(t) + \frac{t(-1)^j+j-1}{2}, \quad t \in [0,1] \text{ for } j = 1, 2$$ \hspace{1cm} (11)

Their results obtained, as shown in Fig. 4, 5, 6, and 7.

3.5. Susceptible infectious removed (SIR) Model

The SIR model demonstrates a system of three ordinary differential equations (ODEs), with the classic SIR model that can be easily implemented and used to gain a better understanding
of how the COVID-19 virus spread within the communities of variable populations in time, including the possibility of surges in the susceptible people (Ivorra et al., 2020). Hence the SIR here is planned to evacuate numerous of the complexities associated with the real-time advancement of the spread of the virus in a way that values both quantitatively and subjectively. It may be a dynamic framework that given by three couple ODEs that depict the time evolution of the subsequent three population;

Susceptible individuals, $S(t)$: these persons who are not infected with the SARS-CoV-2 virus could become infected. As the virus spreads from its source, more individuals will become infected. Hence the susceptible population will increase for some time, describe as the surge period.

Infected individuals, $I(t)$: These persons who are infected with the virus and can transmit the virus to others who are susceptible. An infection may remain infected in the population.

Recovered individuals, $R(t)$: those individuals who have recovered from the virus and are assumed to be immune (or have died)

A simple model of SIR is given as:

$$\begin{align*}
\frac{dS(t)}{dt} &= -IS(t)I(t) \\
\frac{dI(t)}{dt} &= IS(t)I(t) - kI(t) \\
\frac{dR(t)}{dt} &= kI(t)
\end{align*}$$

The above system (eq 12) can be solved using any numerical scheme, the numerical simulations can be presented to predict the future behavior of class $S$, $R$, and $I$, this is achieved, the above equation is converted to (eq 13):

$$\begin{align*}
\frac{S(t_{n+1})-S(t_n)}{\Delta t} &= -IS(t_n)I(t_n) \\
\frac{I(t_{n+1})-I(t_n)}{\Delta t} &= IS(t_n)I(t_n) - kI(t_n) \\
\frac{R(t_{n+1})-R(t_n)}{\Delta t} &= kI(t_n)
\end{align*}$$
From Equation 13, where the parameters $l$ and $k$ are real, positive for the infection rate and recovery, using obtained initial conditions and parameters, the number can also be obtained. It can also be predicted, as seen in Fig 5a-c below.

4. Results and Discussion

Using mathematical models normal, log-normal, and a complex distribution Blancmange curve and existing data, simulations, and MATLAB software can be used to predict SARS-CoV-2 hotspot in the six different wastewater treatment plants. The results are presented in Fig. 2a and b, Fig. 3 a-f, and Fig. 4, respectively. Also, the next hotspot predicted was considered by using the simple Susceptible, infectious, and recovered ($SIR$) mathematical model. The results obtained are depicted in Fig. 5 a-e.

In Fig 2a below, we can assume that the threshold is obtained when at $y = l$, it is possible to conclude that the hotspot (places that are at risk of a lot of COVID-19 infections) is from the raw wastewater treatment plants having the red and green curve. It can also be said that, from these two regions, on the first day, both regions had a high number of infected persons with the SARS-CoV-2 virus, while the last four areas had an endless number of infected persons. However, in Fig. 2b, the collected wastewater treatment data were assumed to be following the log-normal distribution. It is believed that the collection was performed in six different wastewater treatment plants with daily averages and standard deviation in the case of normal distribution. It can be seen that the wastewater treatment plants represented by red and green curves are considered hotspots. In particular, it can be concluded that these two regions got a high number of infected persons with the SARS-CoV-2 virus in the second and third d. So, in general, all collected data can be compared weekly, and each country can define a threshold. A wastewater treatment plant $(i)$ with a viral load above this threshold will be marked as a
hotspot. All measures could be taken to flatten the curve, including lockdown, unique deployment of medical policies, law enforcement to help with medical interventions, and security, respectively.

**Fig. 2:** (a) Possibility with normal distribution, (b) Possibility with a log-normal distribution

However, if the collected data from raw WWTP show a trend of fractal behavior, it should be recommended to use the Blancmange curve instead of log-normal and normal distribution. The mathematical formula representing the Blancmange curve is presented in equation 4-7. Again, here we considered six wastewater treatment plants. We assume that these regions’ data follow the Blancmange curve with different Hurst parameters $\omega= 0.8, 0.85, 0.9, 0.93, 0.96,$ and $0.99$, respectively. Their results are depicted in Fig. 3a-f and Fig. 4. In particular, in Fig. 4, all collected from the six different raw wastewater treatment plants are plotted. In this case, only two of the collected data are considered; it can be concluded that four regions are hotspots, as their curves are above the set thresholds.
Fig. 3: Possibility with Blancmange function for (a) \( \omega = 0.8 \) and 0.85; (b) \( \omega = 0.9 \) and 0.93 and (c) \( \omega = 0.96 \) and 0.99 respectively
Using mathematical models and existing data, simulations can predict the next hotspots of the COVID-19 virus. An example is to consider a simple Susceptible, infectious, and recovered (SIR) mathematical model (Fig. 5 a-e), which is available in the literature (Ivorra, 2020). Mathematicians called $S(t)$ the class of susceptible populations, $I(t)$ the type of infected persons, and $R(t)$ the type of recovered persons. The functions describe each class’s behavior as a function of time (see Equation 12-13 above).

It has been seen that in numerous communities, a spike within the number of infected people $I$, may happen, which results in a surge within the susceptible population, $S$, recorded within the COVID-19 datasets (Coronavirus worldometer website, 2020), which sum to a secondary wave of infections. To interpret such a possibility, $S$ within the SIR model (WHO-COVID-19, 2019). Can be reset to $s_{surge}$ at any time ($t$) that a surge happens. In this way, it can be
house different from such waves recorded within the distribution information stated in (Coronavirus worldometer website, 2020), which recognizes it from the classic SIR model.

**Fig. 5**: Numerical solutions for (a) \( l = 0.3 \) and \( k = 0.0025 \) (left), \( l = 0.4 \) and \( k = 0.0012 \) (right); (b) \( l = 0.6 \) and \( k = 0.003 \) (left) and for \( l = 0.39 \) and \( k = 0.009 \) (right); (c) \( l = 0.48 \), \( k = 0.013 \) (middle).
While all the approach mentioned above, seems to be a promising methodology to identify COVID-19 hotspots, there are some grey areas of uncertainty. Therefore we shall present some limitations of this methodology. We do not say the extraction method is useless or may not lead to better results than the testing method, but we want to show some weaknesses of this approach in developing countries (sub-Saharan countries). In the last month, many countries have relaxed their lockdown regulations to rescue the economy. There are movements from one town to another with these relaxations, from megacities to small cities, from villages to cities. The viral load contribution of traveling infected persons who were not at all in contact with residents maybe not be identified and could count as residents’ contributions. The approach could be useful during a total lockdown when there is no movement from cities to cities. On the other hand, the system may not account correctly for the release of the viral load from households as the sewage (raw wastewater) could be blocked, such as we find in Emfuleni and Harrismith, which will skew the result.

The rapid spreading of the COVID-19 virus, especially in areas where there is a risk of many infections (hotspot), has been identified positively in developing countries. Research study has identified a high risk of virus diseases in many developing nations, including sub-Saharan countries (WHO, 2020a). More attention need is required for these developing nations to mitigate the spread of the virus, especially in low-income and densely populated areas suffering from a lack of healthcare facilities and adequate hygiene and safe water (Brauer et al., 2020). Studies have shown that about 60% of sub-Saharan residents in slum conditions lack basic sanitation, including sewer collection networks. For instance, natural wetland, small-bore sewer, and latrines for used in Uganda and Nairobi for sewage treatment. Wastewater treatment methods, oxidation ditch, stabilization lagoons, activation sludge, trickling filters, coverage are very limited in Africa (Wang et al., 2014). It has been reported 51-75% of safety-treated water can be sustained to Egypt and Tunisia, 26-50% by Morocco, and either < 25% (insufficient data) is allocated to the African countries (WHO, 2018).
Majorities of these countries practiced open defecation at a very high exploring rate due to poor hygiene and sanitation practiced. In a report done by Gupta (2014), it was confirmed that open defecation is most used worldwide across the nation. About 14% of the population across the globe defecate in the open (Gupta, 2014). However, the percentage of statistics of open defecation covers a massive alteration between the countries. In Indian, about 48% of the total population defecate in the open, and this is increasingly concentrated throughout the country compared to some impoverished conflict countries such as Chad and South Sudan, which are also using open defecation (Fig. 6). Only a handful of countries across the world have a worse situation than Indians. Nearby countries such as Afghanistan, Bangladesh, and Congo are trying to reduce open defecation usage even though most of these countries still do not have improved sanitation (see Fig. 6).

According to Nakagiri et al. (2016), when assessing the performance of pit latrines in urban areas of Sub-Saharan Africa (SSA), it was found that about 52.7% (roughly 198 million) of the urban population is in use of pit latrine. Whereas in 2007, the percentage usage increases to 65%, which was approximately 162 million of the population (Banerjee et al., 2008). Although there was a decrease in the percentage of pit latrine (65 to 52.7%), the number of people in use has climbed up to the present date. More so, many individuals (about 36 million) since 2007 has adopted this sanitation technology. This number is expected to climb up since many people are in use from the previous years (Nakagiri et al., 2016). The usage of pit latrine in SSA can vary by country (Fig. 7) and the historical aspect across social-economic ranges.

Nevertheless, the majorities lie in the poor-income employees (Morella et al., 2008). These pit latrine usage within the urban areas in the different countries in SSA may also vary. Despite this, they are still in use without chucks in the urban Sub-Sahara African countries (Fig. 7). It is clear that a large percentage of the population living in urban use open pits in a
In developing countries, a pit latrine is known to be the most common form of improved sanitation. Even in leading African economies like South Africa, Tunisia and others, many communities are still using the bucket system for sanitation. The following maps indicate the percentage of open-pit latrine in the world and Africa, respectively (see Fig. 6 and Fig. 7).

Fig. 6: Map of usage of the opened pit in the world and their percentages (Gupta, 2014).
Fig. 7: Map of percentage for the urban population using pit latrines in South Sahara Africa (WHO/UNICEF, 2014).

5. Conclusion and recommendations

The suggested methodology for identifying hotspots of SARS-CoV-2 uses wastewater collected from wastewater treatment plants within a given country, city, or location. Therefore, it is essential to notice that the process starts with defecation, then these wastes have to reach the wastewater treatment plants; a collection of data follows this. These data are then processed and plot as a function of time, and then the hotspots can be identified as the wastewater with a high viral load of SARS-CoV-2 trace.

The argument presented in the study suggested that the testing method is more efficient than the claim made by researchers that SARS-CoV-2 could be extracted/detected from wastewater.
The first challenge is that not all citizens use toilets linked to the municipal wastewater treatment plant. In many countries of Sub-Saharan African, majorities of people lack proper hygiene, and sanitation resulting to open defecation remains a persistent challenge. Another deficiency of this approach is that individuals eject feces with a frequency that may vary from a few times daily to weekly. There are scientific results from a well-conducted investigation stating how many times a newly infected person defecates daily, weekly, not mention the viral load of SARS-CoV-2 in a single excel. The following recommendations can be listed to make the method useful, especially on a small scale. However, the fundamental question could be, "How will the collected be performed in all portion of the wastewater?" if all the portions are not covered, what will be the percentage of those covered, and how will we know the viral load of SARS-CoV-2 -19 in uncovered parts?

1) A scientific examination ought to be done to know how numerous times a recently tainted individual poo day by day or indeed week by week (of course, this might be another challenge owning, natural forms can vary from person excreta and numerous other components that might alter the patterns)

2) A precise examination ought to be done to recognize which canal infected individual eject more SARS-CoV-2 concentration (Butt-centric or urinal)

3) A precise examination ought to be done to know how much concentration of SARS-CoV-2 can be found in a single expel of defecation or urine

4) During the process, all sewage must be unblocked

5) The legitimate checking framework can be introduced at the wastewater treatment plants to guarantee the fair collection of everyday data

6) Inter-cities travelers ought to be prohibited from guaranteeing the collected information come from an inhabitant of the area

7) All inhabitants ought to have their toilettes connected to regions sewages (A circumstance exceptionally outlandish indeed in developed nations)
A legitimate examination ought to be done to compare the fetched of utilizing this approach with the current in utilize that comprises of testing and segregating.

On a small scale, if these suggestions are not watched, the strategy will be futile and diversion for the battle of following SARS-CoV 2 utilizing testing and confinement. This strategy has been found productive in numerous nations where the numbers of day by day modern diseases at nearly reaching zero.

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Declaration of competing Interest

Authors declare that there is no conflict of interest

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Fig. 1: Virion structure of SARS-CoV/SARS-CoV-2 (La Rosa et al., 2020).

Fig. 2: (a) Possibility with normal distribution, (b) Possibility with a lognormal distribution.
Fig. 3: Possibility with Blancmange function for (a) \( \omega = 0.8 \) and 0.85; (b) \( \omega = 0.9 \) and 0.93 and (c) \( \omega = 0.96 \) and 0.99 respectively.
Fig. 4: The plot of the six different wastewater treatment plants
Fig. 5: Numerical solutions for (a) $l = 0.3$ and $k = 0.0025$ (left), $l = 0.4$ and $k = 0.0012$ (right); (b) $l = 0.6$ and $k = 0.003$ (left), and for $l = 0.39$ and $k = 0.009$ (right); (c) $l = 0.48$, $k = 0.013$ (middle).
Fig. 6: Map of usage of the opened pit in the world and their percentages (Gupta, 2014).
Fig. 7: Map of percentage for the urban population using pit latrines in South Sahara Africa (WHO/UNICEF, 2014).
Highlights

- We review the spread of COVID-19 in wastewater under temperature effect
- We examine COVID-19 extracted from wastewater will be useful to trace the hot spots
- Lognormal distributions and Blancmange function methods to identify hot spots.
- Restraint of COVID-19 extracted from sewage in nations open pits are mostly used
- Testing method are endorsed since the extraction may be costly and inept worldwide
All authors are aware of the submission, rules and regulations of the journal
Declaration of interests

☒ The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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