Is SARS CoV-2 a Multifractal?—Unveiling the Fractality and Fractal Structure

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Received: 17 September 2020 / Accepted: 9 December 2020 / Published online: 15 January 2021
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Abstract
A first report of unveiling the fractality and fractal nature of severe acute respiratory syndrome coronavirus (SARS CoV-2) responsible for the pandemic disease widely known as coronavirus disease 2019 (COVID 19) is presented. The fractal analysis of the electron microscopic and atomic force microscopic images of 40 coronaviruses (CoV), by the normal and differential box-counting method, reveals its fractal structure. The generalised dimension indicates the multifractal nature of the CoV. The higher value of fractal dimension and lower value of Hurst exponent \( H \) suggest higher complexity and greater roughness. The statistical analysis of generalised dimension and \( H \) is understood through the notched box plot. The study on CoV clusters also confirms its fractal nature. The scale-invariant value of the box-counting fractal dimension of CoV yields a value of 1.820. The study opens the possibility of exploring the potential of fractal analysis in the medical diagnosis of SARS CoV-2.

Keywords Fractality · SARS CoV · Coronavirus · Fractal dimension · Multifractal

1 Introduction
At the outset of the outbreak of coronavirus disease 2019 (COVID 19), caused by the novel coronavirus reported from Wuhan, China, the world addresses the pandemic disease multi-dimensionally [1–3]. A glimpse of the recent literature can reveal the contribution of all realms of knowledge to science and social science [1, 2, 4]. Because of the interconnection and interdependence of diversified fields of knowledge, every spark in it can kindle the minds of hundreds and extend a helping hand in achieving the goal. Through this paper, we would like to expose the fractality and fractal nature exhibited by the severe acute respiratory syndrome coronavirus (SARS CoV-2). Investigation of the embedded signature of self-similarity in animate and inanimate objects through fractal analysis is capable of revealing intriguing mystery [5–8]. A non-integer dimension quantifies the spatiotemporal self-similarity (having the same details under various levels of magnification), called the fractal dimension \( D \), and can be used as a parameter to analyse the object. Today, we can see applications of fractal analysis in medical diagnosis [8–10] apart from its technological applications [11]. Of various methods for finding the value of \( D \)-like power spectrum, box-counting, prism counting, walking-divider, and Brownian motion—a particular method is selected depending on the nature of the problem [12, 13]. This paper is the first report of disclosing the fractality and fractal nature of coronaviruses (CoV) through the box-counting method. Among the different box-counting methods, the model proposed by Chaudhuri and Sarkar in 1995 [14], known as differential box-counting (DBC) technique, has emerged as the most popular method for the analysis of greyscale images. The analysis of greyscale images can efficiently be executed with DBC method, without the process of converting the images into binary, overcoming the limitations of normal box-counting method [15]. When a fractal is characterised by a single number \( D \), a multifractal is defined by the generalised dimension \( D(Q) \) containing more number of dimensions, like information, correlation, and box-counting dimension [16, 17], that adds more information of that same object.

Coronaviruses belong to the Nidovirales order, which are the largest group of viruses. The Nidovirus family members differ chiefly in the type, size, and number of the structural proteins that cause alterations in their morphology and structure of the virions and nucleocapsids. CoVs exhibit a typical morphology of spherical geometry with club-shaped spikes on the surface,
prompting fractal analysis. These characteristic protein spikes, resembling solar corona, gave the name coronavirus and enabled its binding to the membrane of human cells [1, 18]. Reports say that SARS-CoV-2 has a binding capacity more than ten times than the SARS CoV. Considering the epidemic due to human-to-human transmission of CoV, the World Health Organization declared COVID 19 a pandemic, causing severe acute respiratory syndrome coronavirus (SARS CoV-2) [1]. Since the outbreak of SARS in Southern China (SARS CoV) [19] in 2002, the scientific community is well aware of its structure as an enveloped, positive-sense, single-stranded RNA viruses with diameter ranging between 80 and 130 nm, usually causing respiratory tract illness [18, 19]. Intense research is going globally to understand deeply about the origin, cause, structure, and medicine for curing this deadly disease.

2 Materials and Methods

To unveil the fractality and fractal nature exhibited by the CoV and to facilitate medical image analysis, the fractal dimension of CoVs is determined by the box-counting method. In the present study, the scanning electron microscopic (SEM), transmission electron microscopic (TEM), and atomic force microscopic (AFM) images of coronaviruses, taken from the article of Ng et al. 2004 [19], Centers for Disease Control and Prevention’s Public Health Image Library [20, 21], www.sciencephoto.com [22], and www.doherty.edu.au [23], are subjected to box-counting fractal analysis. The algorithmic approach for finding the box-counting fractal dimension is [5, 7, 12].

i. Select the photograph to be analysed.
ii. Convert it into an 8-bit image using ImageJ.
iii. Suitably threshold to get a clear image of the boundary.
   (For the analysis, all the images are brought to same resolution of 600 dpi. The images are converted to 8-bit grey scale images in which 256 different shades are present, where 0, 255, and 127 indicate black, white, and grey respectively. Then the images are threshold to get the binary equivalent, which is subjected to box-counting fractal analysis.)
iv. Overlay the image with square grids of size, ‘s’.
v. Count the number of grids (N(s)) containing the image.
vi. Repeat the steps iv and v with different value of s and count N(s).

\[ N(s) \propto s^{-D} \]

Taking logarithm we get

\[ \ln(N(s)) = -D \ln(s) + \text{constant} \]  

\[ \lim_{s \to 0} \frac{\ln N(s)}{\ln(s)^{Q}} = -D \]  

\[ Q \text{ vs. } \ln(s) \text{ graph.} \]

\[ \text{Perform linear curve fitting to the } \ln N(s) \text{ vs. } \ln(s) \text{ graph.} \]

\[ \text{Calculate the slope of the fitted line.} \]

\[ \text{The negative of the slope of the fitted line gives the fractal dimension (D) whose value lies between 1 and 2 for two-dimensional cases like the images.} \]

\[ H \text{ is an another indicator of self-similarity} \]

\[ \text{More insights into the details of the images can be obtained from the multifractal analysis, which is an extension of fractal technique. The DBC method is the most suitable method for finding the multifractal dimension of the greyscale SEM and TEM images [15]. In DBC, the signal or image is divided into boxes of sizes (s) and the difference between the maximum and minimum grey levels in the (i,j)th box, N(s), is calculated. By repeating this procedure for all boxes, the FD is calculated as in Eq. (3). In the present work, the multifractal analysis is done using the Fraclac plugin in ImageJ software. A monofractal object possessing a unique scaling property is defined by a single value of D [25]. But nature consists of complex set of multifractals, where the scaling characteristics can be quantified only by a spectrum of generalised fractal dimensions } D(Q) \text{. When a complex system is distorted by an amount } Q, \text{ then the change in its probability distribution is given by } D(Q). \text{ For heterogeneous systems, the greyvalue probability distribution of each box is given by Eq. (4)} \]

\[ P_{ij}(s) = \frac{M_{ij}(s)}{\sum_{i,j=1}^{N} M_{ij}(s)} \]

where \( M_{ij}(s) \) is the grey value of the box (ij). After Q amount of distortion, the greyvalue probability distribution and generalised dimensions are given by Eqs. (5) and (6) [16].

\[ I(Q,s) = \sum_{i,j=1}^{N} P_{ij}(s) \]

\[ D(Q) = \lim_{x \to 0} \frac{\ln I(Q,s)}{\ln s_{x}^{Q}} \]

The multifractal spectrum generated using the values of } D(Q) \text{ gives three essential dimensions—capacity/box-counting (Dc) dimension, information dimension/Shannon entropy (Dh), and correlation dimension (Dc). At } Q = 0, 1, \text{ and } 2, \text{ we get } D_{h}, D_{c}, \text{ and } D_{c} \text{ respectively. Generally, for a multifractal object, } D(Q) \text{ is a decreasing function with a sigmoidal around 0, where } D_{Q=0} \geq D_{Q=1} \geq D_{Q=2} \geq \text{, whereas for a monofractal or non-fractal object, it is a straight line. When the } D_{h} \text{ gives the number of boxes} \]
containing the portion of the pattern, $D_I$ gives the density of distribution of points completely enclosing the pattern, and $D_C$ reveals the extend of correlation of the neighbouring points through the power law relating the number of image pixels within the range $s$ of a given pixel [16]. $D_I$ is also a measure of the disorder in a system. Thus, the multifractal analysis helps in characterizing the variability and heterogeneity of the objects.

Univariate numerical data are most commonly visualised in the form of scatter plots. But, overplotting of a large set of data makes this plot confusing and complex. This is overcome by introducing a plot, called as Notched Box Whisker/Notched box plot (NBP), which shows only extreme values of the full data individually through their quartiles. From the NBP of a set of data, we get a lot of information at a glance. The median point indicates the location, whereas the orientation of the box tells about the correlation. The position of the outliers and median point gives the skewness, and the size of the box gives the spread of data. The plot contains lines extending from the boxes termed as whiskers that denote the variability outside the upper and lower quartiles. This type of graphical representation of univariate data makes the visualisation and analysis of data simple and easier. The NBP contains four regions, the box, the whiskers, the line, and the notch. Fifty percent of the total data points are contained in the box region, the whiskers mark 99.3% of the data of a normal distribution, a line gives the median, and the notch interval indicates the 95% confidence interval around the median [26].

### 3 Result and Discussion

The fractal dimension of TEM, SEM, and AFM images of more than 40 coronaviruses represented at different scales—1 μm, 5 μm, 100 nm, 200 nm, and 500 nm—is found out by the box-counting method. The superimposition of grids of varying dimension on to the TEM, SEM, and AFM images of CoVs and counting the number of boxes $N(s)$ of dimension ‘s’ required to cover the image, and the fractal dimension $D$ is calculated using Eq. 3. Some representative images of CoVs, their threshold images, the ln-ln plot, and the obtained $D$ values are shown in Fig. 1a. The NBP of $D$ values obtained is shown in Fig. 2a, and it gives the average value of $D$ as 1.816. The

![Fig. 1](image-url) Electron microscopic images of CoV [19–22]—a, b, and c with their respective threshold images, ln-ln plot, and fractal dimension. Credit: CDC/Fred Murphy

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**Fig. 1** Electron microscopic images of CoV [19–22]—a, b, and c with their respective threshold images, ln-ln plot, and fractal dimension. Credit: CDC/Fred Murphy

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A higher value of $D$ close to 2 suggests the complexity of the system, CoVs. The value of $H$ calculated from the value of $D$ can also give information about the surface morphology of the virus. When a higher value of $H$ indicates a smooth surface, the lower value indicates rough surface [24]. The analysis of CoVs shows a low value of $H = 0.184$, as shown in the NBP (Fig. 2b) indicating a rough surface as evidenced by the SEM, TEM, and AFM images. The various elements in the NBP of $D$ and $H$ are given in Table 1.

The generalisation of a fractal system is called a multifractal system and the corresponding dimension is referred to as the generalised dimension $D(Q)$, which is calculated by the DBC method using the software FracLac. For a pattern, $D(Q)$ gives information about the distortion of the mean of the distribution. For a multifractal system, the plot of $Q$ vs. $D(Q)$ exhibits sigmoidal nature. From a representative multifractal spectrum given in Fig. 3, it can be confirmed that the CoV is a multifractal. When $Q = 0$, $D(0)$ gives the box-counting fractal dimension and the NBP with the $D_B$ values for all samples analysed is shown in Fig. 4a with a mean value 1.806. This shows that the normal box-counting method and the DBC method yields the same value for fractal dimension.

The drawback of $D_B$ is that it is independent of the density of points in a system. Therefore, for a system having non-uniform distribution of points, another dimension, called as information dimension ($D_I$), gives more accurate information. Thus, for $Q = 1$, we get $D_I$, which indicates the fractal dimension of a probability distribution. From the NBP of $D_I$ given in Fig. 4b, it can be understood that the mean value is 1.784. The difference in the values of $D_B$ and $D_I$ makes clear that the CoVs are a complex system with a non-uniform density of points. The correlation dimension is a type of fractal dimension which describes the dimensionality of the space enclosed by a collection of random points. It is obtained when the value of $Q = 2$. The NBP of the values of $D_C$ acquired from the multifractal spectrum, shown in Fig. 4c, has a mean value of 1.790, which shows the high correlation of measures in the complex multifractal system. From literature [17], it is evident that only for a monofractal object with exact self-similarity and homogeneity, all the values of dimensions are equal. The average values of dimensions from the NBP plot show a slight difference in values of $D_B$, $D_I$, and $D_C$, which is

![Fig. 2](image2)

The notched box plot showing the value of $D$ (a) and $H$ (b) of 40 CoV images

![Fig. 3](image3)

Sigmoidal plot of $Q$ vs. $D(Q)$ indicating the multifractal nature of a CoV image

| Table 1 | The various elements in the NBP of $D$, $H$, $D_B$, $D_I$, and $D_C$ |
|---------|---------------------------------------------------------------|
| $D$     | $H$  | $D_B$  | $D_I$  | $D_C$  |
| Upper whisker | 1.895 | 0.300 | 1.916 | 1.903 | 1.908 |
| 75th percentile | 1.857 | 0.230 | 1.859 | 1.853 | 1.855 |
| Notch | 0.043 | 0.043 | 0.045 | 0.069 | 0.064 |
| Median | 1.823 | 0.177 | 1.816 | 1.805 | 1.78 |
| Mean | 1.816 | 0.184 | 1.806 | 1.784 | 1.790 |
| 25th percentile | 1.77 | 0.142 | 1.769 | 1.628 | 1.733 |
| Lower whiskers | 1.70 | 0.105 | 1.684 | 1.628 | 1.623 |
evident from the various elements given in Table 1. This confirms the multidimensionality nature of CoVs.

The fundamental principle of fractal nature is self-similarity. Hence, it is essential to investigate whether CoVs give the same fractal dimension upon clustering. Figure 5 shows some representative clusters of CoVs, threshold image, and the average $D$ value (1.840). Figure 6 shows clusters of CoV-infected cells. It is observed that just as individual CoVs and clusters, clusters of infected cells also yield nearly the same value of $D$ (1.800), thus giving information about the infection to cells.

4 Conclusion

Thus, the scale-invariant value of fractal dimension confirms that COVID 19 viruses have a fractal structure with an average box-counting fractal dimension equal to 1.820. The multidimensional characteristics of CoVs are evident from the multifractal spectrum, showing sigmoidal nature, carried out through DBC method. $D_B \neq D_I \neq D_C$ confirms that CoVs are not monofractals. Also, the higher value of fractal dimension close to 2, obtained from normal box counting and multifractal analysis, depicts the
complexity of the system. The lower value of $H = 0.184$ suggests the roughness as justified by the SEM, TEM, and AFM images. The statistical analysis of $D, H, D_B, D_I,$ and $D_C$ of the 40 CoVs is represented through the notched box plot. We hope that, like the application of fractal methods in the analysis of medical images, the fractal analysis of COVID-19 viruses also can contribute to understanding its replication, propagation, and infection.

Acknowledgements The authors thank the Editor-in-Chief of the Journal, Emerging Infectious Diseases, CDC, Fred Plapp, the pathologist, and Dr. Julian Druce, Head of Virus Identification Library, the Peter Doherty Institute for Infection and Immunity for granting permission to reproduce the images.

Authors’ Contributions All the authors have equally contributed.

Compliance with Ethical Standards

Competing Interests The authors declare that they have no competing interests.

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