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Brownian fractal nature coronavirus motion

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The goal of our research is to establish the direction of coronavirus chaotic motion to control corona dynamic by fractal nature analysis. These microorganisms attaching the different cells and organs in the human body getting very dangerous because we don't have corona antivirus prevention and protection but also the unpredictable these viruses motion directions what resulting in very important distractions. Our idea is to develop the method and procedure to control the virus motion direction with the intention to prognose on which cells and organs could attach. We combined very rear coronavirus motion sub-microstructures images from worldwide experimental microstructure analysis. The problem of the recording this motion is from one point of view magnification,

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but the other side in resolution, because the virus size is minimum 10 times less than bacterizes. But all these images have been good data to resolve by time interval method and fractals, the points on the motion trajectory. We successfully defined the diagrams on the way to establish control over Brownian chaotic motion as a bridge between chaotic disorder to control disorder. This opens a very new perspective to future research to get complete control of coronavirus cases.

Keywords: Coronavirus; Brownian motion; fractals; time interval method.

1. Introduction

The global coronavirus disease (COVID)-19 pandemic caused by the deadly and highly transmissible severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) virus almost took the lives of about 800,000 people all over the world provoking besides medical, also serious economic, socio-political, psychological impacts that would change the world forever. Thus it is necessary to understand COVID-19, its molecular structure, target receptors, molecular pathogenesis to know how to treat it best and prevent its spreading. Although many experts around the world are devoted to this job, many unknowns remain, including the one why it is so highly transmissible in comparison to its other relatives such as SARS and Middle East respiratory syndrome (MERS) who were more deadly but less transmissible staying in China and the Middle East. There is strong evidence, especially in Chinese studies conducted this year, that many infected and ill individuals, even around 79%, who required hospital treatment having even severe pulmonary manifestations were primarily infected from persons who were fully asymptomatic without any coughing or sneezing but could transmit COVID-19.[1–4]

This means that direct or indirect contact or aerosol transmission stay the main possible modes of COVID-19 transmission. Media and public health attention in the first time focused primarily on the importance of personal hygiene and physical distance in different communication, while less attention was paid to aerosol transmission although van Doremalen *et al.* demonstrated that aerosolized SARS-CoV-2 remains viable and infectious in aerosols for hours and on surfaces up to days.[5] Previous influenza researchers have found that viable virus can be emitted in significant quantities from an infected individual by breathing or speaking.[6] Asadi *et al.* considered a 10-minute normal conversation with an infected, asymptomatic super emitter talking in a normal volume thus would yield an invisible "cloud" of approximately 6,000 aerosol particles that could potentially be inhaled by the close persons.[7] The minimum infectious dose for COVID-19 has not been definitively established, although for other viral respiratory illnesses a single virus can initiate infection. Thus, many questions about aerosol transmission and COVID-19 must be answered. The virology, epidemiology, molecular biology, as well as aerosol science community, need to tackle the challenge presented by COVID-19, and also to help the community to prepare better for future pandemics. One notification, what is also remarkable, is the fact that aerosol inhalation pathways is the best way of transmission of potential biological weapons that will become more and more important in the security architecture of the modern world that rapidly changes.

So, the possible terroristic aspects of this virus are very realistic, dangerous, and important. In that case, the anti-terrorist methods are very important, and there is a need to be developed in advance. Regarding this consideration, there is great importance for getting the different knowledge of additional negative infects.

Our research is a contribution to help in solving and protecting from coronavirus phenomena. In that sense, the results reporting in this paper are on the way to provide more understanding about this virus motion direction, which has the character-like Brownian motion, which is important for advanced prognosis the attaches on the cells and body organs.[8–11]

1.1. *Short intro in coronavirus motion by iterative function system*

Based on the localization of the COVID-19 virus position in discrete moments, we will construct a fractal interpolation curve (FIC) that simulates the trajectory of the virus movement.[12–20] To obtain the FIC curve, we will use the iterative function system (IFS).[15,17,19]

Let $\{w_1, w_2, \ldots, w_N\}$ be a set of contractive mappings of the metric space $(\mathbb{R}^2 d)$ into itself. We call these mappings with the space in which they operate a hyperbolic iterative functional system. The prefix hyperbolic indicates that all mappings are contractive and are usually implied, and not explicitly stated. Over IFS, we will define the Hutchinson operator. Let X be a bounded set from $\mathbb{R}^2$, then

$$W(X) = \bigcup_{i=1}^{N} w_i(X) \tag{1}$$

is Hutchinson operator over $\mathbb{R}^2$ It can be proven that the Hutchinson operator over $\mathbb{R}^2$ is also a contraction in metric space $(H(\mathbb{R}^2), h)$, where h is the Hausdorff distance. The fixed point of the Hutchinson operator $W(A) = A$ is called the IFS attractor.

Suppose that a set of points $\left\{(x_i, y_i) \in \mathbb{R}^2, i = 0, 1, \ldots, N\right\}$ is given, and abscissas of these points are been arranged in ascending order. This means that multiple inequalities $x_0 < x_1 < \cdots < x_N$ hold. Over these points, we will define IFS $\{\mathbb{R}^2; w_1, w_2, \ldots, w_N\}$ with affine transformations

$$w_i \begin{bmatrix} x \\ y \end{bmatrix} = \begin{bmatrix} a_i & 0 \\ c_i & d_i \end{bmatrix} \begin{bmatrix} x \\ y \end{bmatrix} + \begin{bmatrix} e_i \\ f_i \end{bmatrix} \tag{2}$$

and constraints

$$w_i \begin{bmatrix} x_0 \\ y_0 \end{bmatrix} = \begin{bmatrix} x_{i-1} \\ y_{i-1} \end{bmatrix} \quad \text{and} \quad w_i \begin{bmatrix} x_N \\ y_N \end{bmatrix} = \begin{bmatrix} x_i \\ y_i \end{bmatrix}. \tag{3}$$

In each affine transformation, $w_1 w_2, \ldots, w_N$ there are five parameters a_i, c_i, d_i, e_i, and f_i. As four conditions have given for each of them, we conclude that one parameter is free. For free parameter, we will select parameter d_i

The reason for this choice is found in the geometric interpretation of the parameter d_i. The transformation w_i maps the lines parallel y axes to the lines parallel y axes. This means that straight length l, which is parallel the y axis maps to the straight length $w_i(l)$ which is also parallel the y axis. The quotient of their lengths is exactly equal $|d_i|$.

Regarding the understanding of the parameters a_i, c_i, d_i, e_i, and f_i we can provide some more precise definitions and listed parameters and their relation. Parameter a_i is a factor of scaling of coordinate x and on that way has a direct influence on image $w_i(x)$. Parameter c_i is, also, a factor of scaling of coordinate x and in that way has a direct influence on image $w_i(y)$. The meaning of the parameter d_i is already discussed in a previous paragraph. The parameters e_i and f_i defined translation in x and y ordinates. All of these parameters are important in a process of characterization and analyzing the creating coronavirus trajectories.

For the affine transformation to be a contraction, it is sufficient for free parameter $|d_i| < 1$. If all affine transformations $w_1 w_2, \ldots, w_N$ are contraction, then the attractor G of IFS

$$W(G) = \bigcup_{i=1}^{N} w_i(G) \tag{4}$$

is a graph of a continuous function passing through interpolation points.[13] We will call this function the Fractal Interpolation Function (FIF). It is self-affine because each of affine transformation w_i maps the whole function to the part between the interpolation points (x_{i-1}, y_{i-1}) and (x_i, y_i) for every $i = 1, 2, \ldots, N$

In the case when interpolation points $\{ (x_i, y_i) \in \mathbb{R}^2,\ i = 0, 1, 2, \ldots, N\}$, does not satisfy the condition that their ordinates are in a strictly ascending order, that is, that the condition

$$x_0 < x_1 < x_2 < \ldots < x_N, \tag{5}$$

holds, then, in this way, using FIF, we would not be able to get an interpolation curve that would pass through all the interpolation nodes.

For condition (5) to be fulfilled, we can introduce additional coordinates in place of the ordinate, for example, we can assume that the ordinate is $x_i = i$, for each $i = 0, 1, \ldots, N$ Another way of ensuring the validity of condition (5) comes down to the use of a reversible transformation, which achieves that the ordinates have arranged in ascending order.[4]

Let the interpolation points $\{ (x_i, y_i) \in \mathbb{R}^2,\ i = 0, 1, 2, \ldots, N\}$ have given. We will apply the transformation

$$T(x_i, y_i) = (u_i, v_i), i = 0, 1, \ldots, N \tag{6}$$

where

$$u_i = x_0 + \sum_{j=1}^{i} (|x_j - x_{j-1}| + p) = u_{i-1} + (|x_i - x_{i-1}| + p). \tag{7}$$

The constant $p > 0$ is necessary in the case when all interpolation points have the same ordinate. In other cases, it can assume that $p = 0$. The coordinate y do not change with the transformation T, therefore, $v_i = y_i$.

Obtained points $\{(u_i, v_i), i = 0, 1, \ldots, N\}$ satisfy condition (1), that is, for them hold inequality $u_0 < u_1 < u_2 < \ldots < u_N$.

It is worth noting to point out that the transformation T preserves the distances between adjacent interpolation points. So, equalities

$$d\left((x_i, y_i), (x_{i-1}, y_{i-1})\right) = d\left((u_i, v_i), (u_{i-1}, v_{i-1})\right), \quad i = 1, \ldots, N \tag{8}$$

hold. The introduction of the transformation T enables the attractor obtained by IFS to represent a graph of a continuous function that interpolates points (u_i, v_i) $i = 0, 1, \ldots, N$.

In the last step, it is necessary to apply the inverse transformation T' to each point of the obtained attractor $\left(u^{'}, v^{'}\right)$ Applying the inverse transformation, we obtain the ordinate $x^{'}$ is equal to

$$x^{'} = x_{i-1} + (x_i - x_{i-1}) \frac{u^{'} - u_{i-1}}{u_i - u_{i-1}}, \quad u^{'} \in [u_{i-1}, u_i] \tag{9}$$

The other coordinate remain unchanged, $y^{'} = v^{'}$ In this way, we get a graph of the function that interpolates the starting points $\{\ (x_i, y_i) \in \mathbb{R}^2,\ i = 0, 1, 2, \ldots, N\}$.

2. Experimental Part

We have developed an experiment, related to coronavirus within the liquid in one chamber what is presented on the diagram (Fig. 1). The goal of this experimental

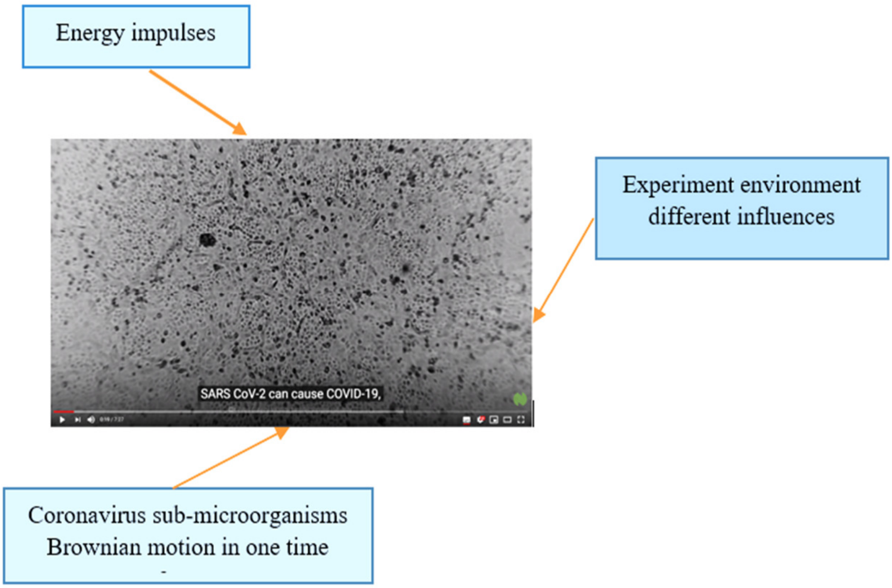

Fig. 1. The principle diagram of coronavirus motion experiment.

presentation is to develop and demonstrate the Brownian motions, alive organisms in the liquid.

These experimental parameters influence within the environment the experiments that are very real experiment conditions. Regarding the gray–blue box with energy, notification makes the precise observation that we have different energy impulses from the environment, which could not be isolated from the very fine interactions coronavirus has in aerosol motions and liquid medium in the experiment. Coronavirus, as we discussed, is very super-microorganism. So, without additional recorded images of virus trajectories, we could not analyze all of these very fine interactions, which could be even on the level of the Heisenberg principle of indeterminism. This question with being analyzed in the next step of the research paper.

Regarding the outer box, we just registered possible outer influences from the environment on our experiment, which have a character of micro-vibration and outer influences that could be discussed in the frame of energy impulses influences, as we already mention.

The third blue box practically treats the Brownian motion as a very specific characteristic of the meter and analyses contributions in this paper, which are in the direction of this very important influence for trajectories creation.

For sub-microorganisms' dynamic, we selected four and disposed of their complex trajectories. Furthermore, we gave some results regarding the fractal interval nature analysis applied to the previous Brownian motion diagrams.

In our experiments, we formed a trajectory of the coronavirus motion. We started with the six pictures of the COVID-19 virus obtained in the successive time interval of 0.1 sec[21–23] given in Fig. 2.

Four coronavirus have randomly selected, and changes in their position have observed in six given figures. The observation of this virus and related conclusions are also applicable for this virus on its different modifications.

In the pictures given in Fig. 2, we singled out four COVID-19 viruses and recording their x and y coordinates as given in Table 1.

These numerical values are available for any proportion regarding the microscopic characterization, especially for magnification and resolution. This comment is very important from the point that we have very rear microscopic results applied to register as a video the coronavirus trajectory motion. Also, there is evidence protection of the results regarding the microstructure characterizations, which are generated within some worldwide laboratories, research centers, institutes, and hi-tech companies. The real problem in all of these researches is the fact that the size of this virus is a minimum 10 times less than the dimension of the bacteria where are the results about the trajectories are more present.

We used the numerical data based on the scaled dimension from the microscopy generated images. Practically speaking, the values in Table 1 are applicable on any scaled different size depend on the results on the microscope.

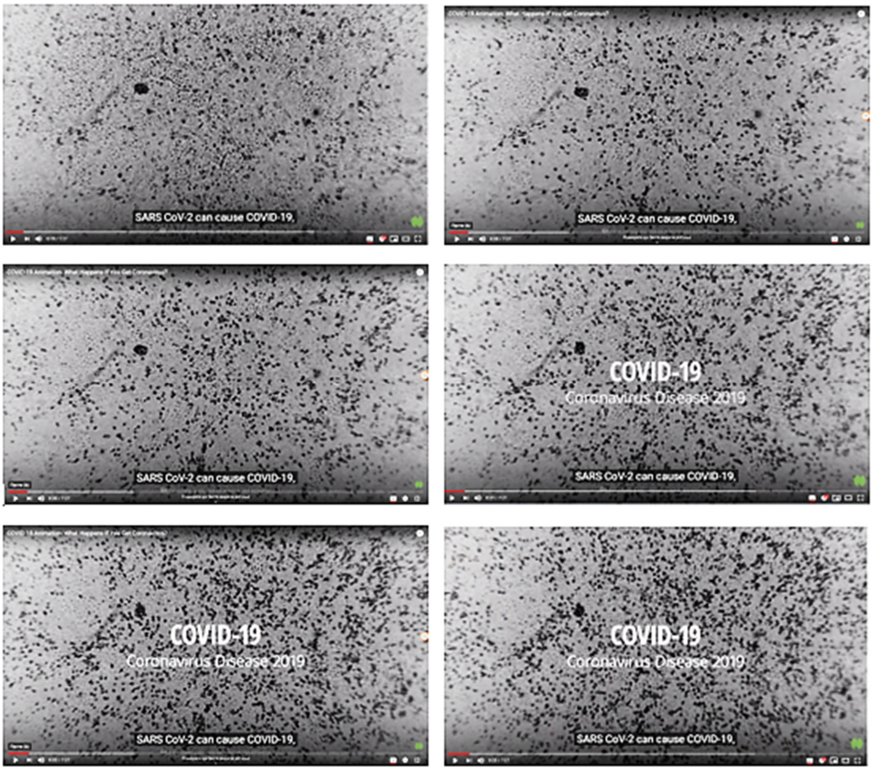

Fig. 2. Picture of COVID-19 virus recorded in successive time moment.

Table 1. Coordinates of the COVID-19 virus position.

x_1	0	0.560	0.9156	1.6157	0.6509	0.7868
y_1	0	−0.0705	0.2018	−0.1645	−0.0893	−0.1336
x_2	0	−0.2549	−0.5679	−1.171	−0.0706	−0.1155
y_2	0	−0.3407	0.6103	−0.176	0.365	−0.661
x_3	0	−0.0888	−0.90794	−1.93617	−1.2926	−1.7911
y_3	0	−0.1462	0.0513	−0.5102	0.197	−0.0833
x_4	0	−0.56757	−0.84831	−1.58725	−1.2254	−1.6697
y_4	0	0.9122	0.9588	0.7453	1.5856	1.2978

3. Results and Discussion

Using the interval method presented in the introduction, based on the obtained data as interpolation data presented in the experimental part, the fractal interpolation function has constructed for each virus, for the various scaling factors. The resulting fractal interpolant has represented the reconstructed motions of the viruses in the observed time interval. In this way, the trajectories of the virus motion have obtained. These trajectories are shown in Figs. 3–6.

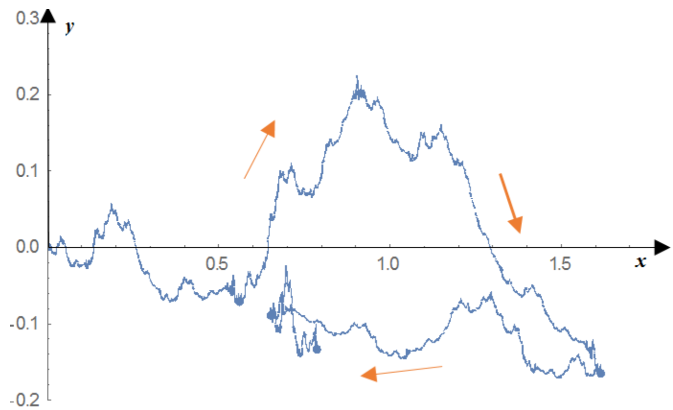

Fig. 3. The trajectory of the first coronavirus with scaling factors $d_i = 0.3, i = 1, 2, \dots, 6$.

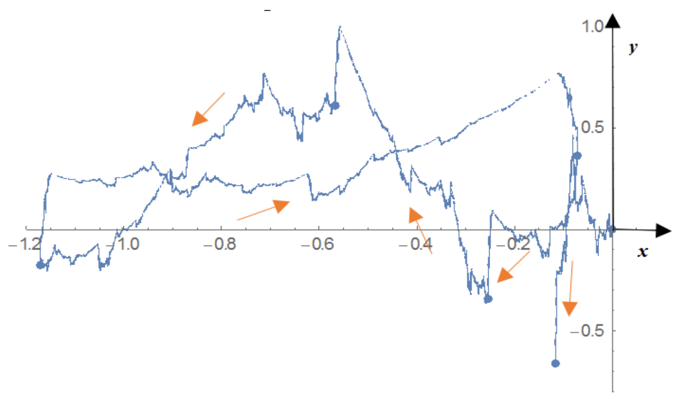

Fig. 4. The trajectory of the second coronavirus with scaling factors $d_i = 0.3, i = 1, 2, \dots, 6$.

Because of the very short intervals in which we analyzed the sub-microorganisms Brownian motion, we have extracted six figures that are representing phase cross-section in this dynamic motion process.[16] Video trajectories motion record lent is 7.27 sec. Regarding the intention to connect micro-motions in fractalized Brownian motion and the coronavirus world with also specific Brownian motion, we specified the Brownian motion as a dominant evident kinetic, which is concluded from the experimental data images. From the previous research results, based on experiments with alive microorganisms, especially bacteria, we also recognized the fractal nature in Brownian motion of such a case, what could be somehow concluded as a general characteristic of the motions in the sub-microorganism world.

Based on the extracted coordinates of the experimental results, by using the algorithm presented in the short intro Subsec. 1.1, we obtained motion trajectories given in the Fig. 3.

The coordinates x and y are notified on the diagram as constructive parameters for the points on the trajectory.

By observing the trajectory of the first virus given on the Fig. 3 and its Brownian chaotic motion, the application of interval fractal analysis, shows that in the interval of 0.5 seconds virus form a chaotic loop.

The obtained trajectory of the second virus from Fig. 4 and its Brownian chaotic motions indicates its disordered circular motion and return to a point very close to the starting point after 0.4 sec.

Observing the trajectory of the third virus on Fig. 5 application of the interval fractal analysis shows that in this virus there is no return to the starting position in the interval of 0.5 sec, so the motion of the virus is evidently progressive.

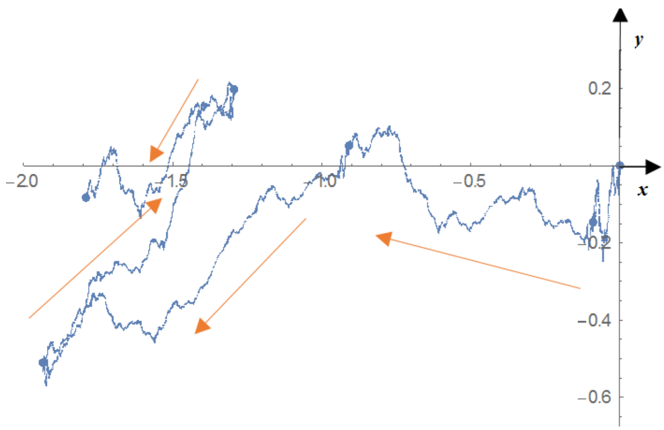

Fig. 5. The trajectory of the third coronavirus with scaling factors $d_i = 0.3, i = 1, 2, \ldots, 6$.

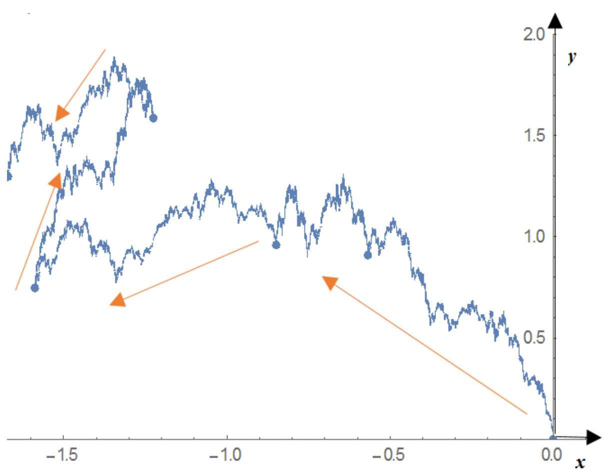

Fig. 6. The trajectory of the fourth coronavirus with scaling factors $d_i = 0.4, i = 1, 2, \ldots, 6$.

Based on the obtained trajectory of the fourth virus from Fig. 6, its chaotic motion is observed, which shows that this virus has a progressive motion without returning to the starting point in the interval of 0.5 sec. Practically, virus continue in direction as progressive motion.

This is the first time, which in the biophysics published results on the coronavirus case, by mathematical–physical interval fractal analysis we provide the reconstruction of the viruses' trajectories. So, this is the exact experimental result from the real procedure, which is not simulation and modeling. We understand that it is not so easy to establish transformation from virus Brownian motion chaotic dynamic to complete control non-chaotic order. So, for up to this stage of this presented results, we satisfy the conditions of the original scientific approach by which we can establish over fractalized Brownian motion, through the interval mathematics, as a next face, somehow, gust method of the chaotic dynamic-controlled chaos dynamic. In the next step, we practically recognize the possibility to introduce, over fractal analysis, the order transformed from the chaotic motion. In the future research, our intention is to grow with the coronavirus samples, what could be helpful to define possible domination of one from the two evident results: concluded results cyclic return to the beginning point on the loop or direction of the progressive motion.

Also, there is a very interesting possibility to continue the research and analysis on very fine waving motions shown in all curves between the mark dots. These very fine local waving motions are probably and mostly results of specific relaxation processes with the coronavirus motion. Our next stage research could be on a direction in which biomimeticaly compares the micro-particles and microorganisms' kinetics that we already reported within our reference.[20]

4. Conclusion

In this research, we open one quite new approach within sub-microorganisms' motion processes characterized by fractal nature as just general Brownian motion in the alive matter like only one existing. We demonstrated the collection from deferent experimental results and methods to see the real world of coronavirus motion. Based on experimental results with viruses we recognize the transformation of the trajectories as a cyclic and progressive dynamic. So, we opened a new frontier to understand and predict coronavirus the real Brownian motion nature case.

Our results could be very helpful to further analysis of the level microbiology and clinical analyses in infective medicine and epidemiology, how to recognize the goals in kinetic directions of the virus within organ cells. This mathematical–physical–biological multi-disciplinary dimension in experimental results opens the new prospective on the field of completing the results in understanding the complexity of coronavirus, which could be treated as a possible constructed and designed one.

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