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Interpolation Methods Applied on Biomolecules and Condensed Matter Brownian Motion*

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Biophysical and condensed matter systems connection is of great importance nowadays due to the need for a new approach in microelectronic biodevices, biocomputers or biochips advanced development. Considering that the living and nonliving systems' submicroparticles are identical, we can establish the biunivocally correspondent relation between these two particle systems, as a biomimetic correlation based on Brownian motion fractal nature similarities, as the integrative property. In our research, we used the experimental results of bacterial motion under

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the influence of energetic impulses, like music, and also some biomolecule motion data. Our goal is to define the relation between biophysical and physical particle systems, by introducing mathematical analytical forms and applying Brownian motion fractal nature characterization and fractal interpolation. This work is an advanced research in the field of new solutions for high-level microelectronic integrations, which include submicrobiosystems like part of even organic microelectronic considerations, together with some physical systems of particles in solid-state solutions as a nonorganic part. Our research is based on Brownian motion minimal joint properties within the integrated biophysical systems in the wholeness of nature.

Keywords: Microorganisms; organic microelectronics; nonorganic microelectronics; solid state; Brownian motion; fractal interpolation.

1. Introduction

Molecular biology, as a life science with vast fields of interest, is closely related to biochemistry, biophysics, bioelectronics and biotechnology, and is always present in multidisciplinary research. It is of great importance to elucidate and predict the essential biological processes at the molecular and submolecular levels because it provides the possibility to interfere with and control them.

At the basis of all microorganisms' life functions, including bacterial motility as well, lie various molecular biology processes, which on the molecular and submolecular levels determine the occurrences at the microorganism level. These processes are based on particles' motion, which is identical in both living and nonliving systems. Molecular and submolecular particles' motion affects the entire bacterial organism's motion and therefore, it is very important to establish the relation between molecular, submolecular and microorganism levels.

The intrinsic property of every molecule in both living and nonliving matter systems is its energy state layout, as a self-inherent spectrum, which in itself provides all the important information about the molecule. Due to the fact of constant and overall exposure to the influence of internal and external electromagnetic fields, the molecule's energy state and the molecular spectrum, as well, are being changed. Thus, electrons cross over the energy levels from one molecule to another, as well, being influenced by Brownian motion all the time, resulting also in electromagnetic induction.

Regarding ceramic grains or grain clusters, collision effects of electrons on the grain boundaries affect the grains' shape, size, orientation and microcapacitive structure and distribution,[1] and because of that, it is very important to control the consolidation of ceramic materials' microstructure and properties.[2] If we apply Brownian motion characterization and fractalization on electron trajectories on the grain boundaries (Fig. 1), we can predict and design appropriate dielectric, ferroelectric and remaining other microelectronic properties, which will open new frontiers for further microelectronic circuits' miniaturization and integration.

If we take into consideration that atomic and subatomic particles have the same properties and energy state layouts in biosystems and condensed matter systems, we

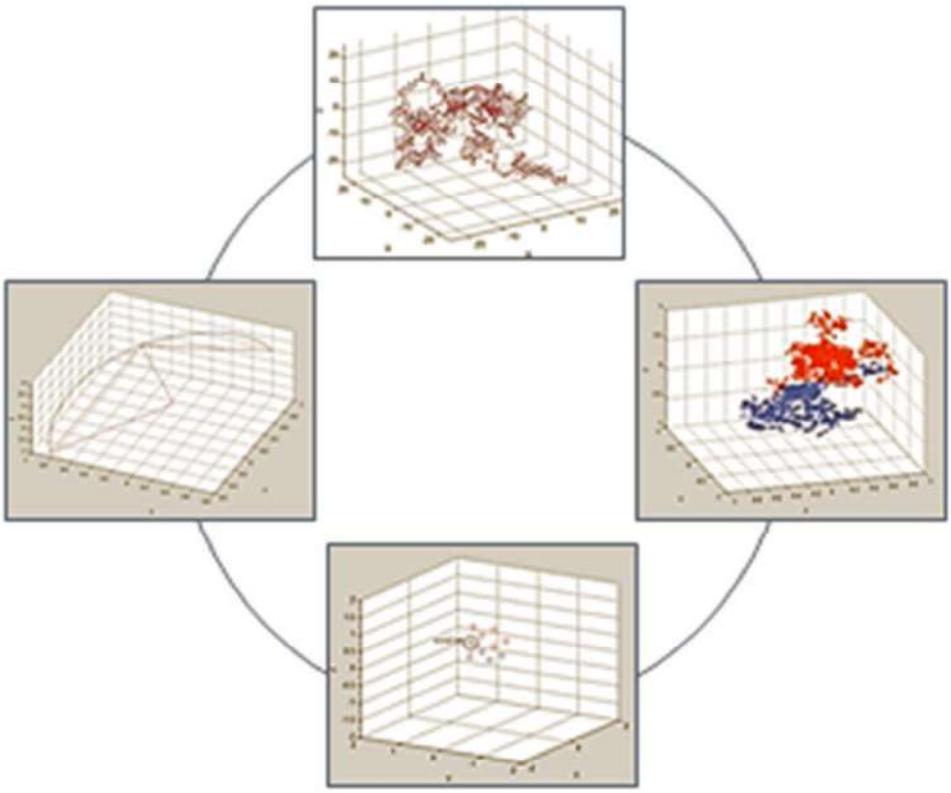

Fig. 1. Electrons' Brownian motion trajectories on the grain boundary.[3]

can also introduce a biomimetic approach[4] which can provide new perspectives for bionics, nanotechnology or microelectronics development.

Dimensions and motion patterns of bacteria and viruses, as well, allow us to consider condensed matter particles' motion and these organisms' motion to be having biomimetic similarities. As the microorganisms are small enough, their motion could be jointly considered with condensed matter particles. Regarding the bacterial motion patterns, there are several of them, like run-and-tumble, run-and-flick, bend-and-rotate, tumble-and-rotate, etc. Bacterial trajectories are stochastic and, thus, unpredictable[5] because these microorganisms collide with each other and with the surrounding molecules, which characterize the Brownian motion influence. Random collisions cause sudden changes in their direction, so bacteria move in a zigzag or rotational manner. The main parameters that characterize bacterial motion are trajectory and velocity, which are specific for each bacterial species. These characteristics could be affected by different environmental factors, like temperature, pH, light, nutrients, energetic impulses, etc.

All of these considerations consistently open the gate for research advancement in the direction of biophysical subsystems, like circuit integrations in nature. This is like the idea of complex joint subsystems within the living and nonliving matters. Also, it is an important direction to very subtle integrations which stress the advancement in biophysical information systems.

2. Mathematical Background of the Fractal Interval

Approximation theory deals with the problem of replacing one function with another. One of the most commonly used forms of the approximation function is the polynomial form,

$$f(x) = a_1 x^n + a_2 x^{n-1} + \cdots + a_{n+1} . \tag{1}$$

The parameters $a_i, i = 1, \ldots, n+1$, are determined so that some conditions are fulfilled. In our paper, we use the condition that the function passes through predefined points in three dimensions. This type of approximation is called interpolation, and the function itself is called an interpolation function.

Suppose that the points $\mathbf{p}_i = (x_i, y_i, z_i)$, $i = 1, \ldots, n+1$, are given, through which we want the interpolation function to pass. We get the interpolation function in parametric form:

$$\mathbf{f}(t) = \sum_{k=0}^{n} \mathbf{p}_k \frac{\mathbf{g}(t)}{(t - \mathbf{p}_k)\mathbf{g}'(t)} , \tag{2}$$

where

$$\mathbf{g}(t) = \prod_{k=0}^{n} (t - \mathbf{p}_k) . \tag{3}$$

In addition to the polynomial form, we will also use the Fractal Interpolation Curve (FIC). Fractal is a subset of the complete metric space, which is invariant in relation to the union of contractive mappings

$$W(F) = F . \tag{4}$$

In order to obtain the FIC curve in three dimensions, we used the Iterative Function System (IFS) which is a finite set of contraction mappings $\{w_1, w_2, \ldots, w_n\}$ of the complete metric space $(\mathbb{R}^3, d)$ onto itself. Let X be a bounded set from $\mathbb{R}^3$, then

$$W(X) = \bigcup_{i=1}^{N} w_i(X) \tag{5}$$

is the Hutchinson operator over $\mathbb{R}^3$. The Hutchinson operator over $\mathbb{R}^3$ is a contraction in metric space $(H(\mathbb{R}^3), h)$, where h is the Hausdorff distance. The fixed

point of the Hutchinson operator

$$W(A) = A \tag{6}$$

is called the IFS attractor and it has at least one attractor.[6]

Let us turn back to the points $\mathbf{p}_i, i = 1, \ldots, n+1$, through which we want the FIC curve to pass. Over these points, we will define the IFS $\{\mathbb{R}^3; w_1, w_2, \ldots, w_n\}$ with affine transformations

$$w_k \begin{bmatrix} x \\ y \\ z \end{bmatrix} = \begin{bmatrix} a_k & 0 & 0 \\ c_k^1 & d_k^{1,1} & d_k^{1,2} \\ c_k^2 & d_k^{2,1} & d_k^{2,2} \end{bmatrix} \begin{bmatrix} x \\ y \\ z \end{bmatrix} + \begin{bmatrix} e_k^1 \\ e_k^2 \\ e_k^3 \end{bmatrix} \tag{7}$$

and constraints

$$w_k \begin{bmatrix} x_1 \\ y_1 \\ z_1 \end{bmatrix} = \begin{bmatrix} x_{k-1} \\ y_{k-1} \\ z_{k-1} \end{bmatrix} \quad \text{and} \quad w_k \begin{bmatrix} x_n \\ y_n \\ z_n \end{bmatrix} = \begin{bmatrix} x_k \\ y_k \\ z_k \end{bmatrix}. \tag{8}$$

In each affine transformation, $w_1, w_2, \ldots, w_n$, there are 10 parameters $a_k, c_k^1, c_k^2, e_k^1, e_k^2, e_k^3, d_k^{1,1}, d_k^{1,2}, d_k^{2,1}$ and $d_k^{2,2}$. Since two conditions with three equations each exists, four parameters are free. We choose the parameters $d_k^{1,1}, d_k^{1,2}, d_k^{2,1}$ and $d_k^{2,2}$ to be free. These four parameters make the matrix

$$A = \begin{bmatrix} d_k^{1,1} & d_k^{1,2} \\ d_k^{2,1} & d_k^{2,2} \end{bmatrix}. \tag{9}$$

For affine transformations to be a contraction, it is sufficient that the norm of matrix A is less than one. If all affine transformations $w_1, w_2, \ldots, w_n$ are contractions, then the attractor of IFS represents the graph of a continuous function passing through the interpolation points $\mathbf{p}_i, i = 1, \ldots, n+1$. The obtained FIC is self-affine because each affine transformation $w_i, i = 1, 2, \ldots, n$, maps the whole function to the part between the interpolation points $\mathbf{p}_i$ and $\mathbf{p}_{i+1}$, for each $i = 1, 2, \ldots, n$.

When ordinates of the interpolation points $\mathbf{p}_i, i = 1, \ldots, n+1$, are not in strictly ascending order, FIC cannot be obtained by the direct use of IFS. In that case, we have to define the reversible transformations

$$T(x_i, y_i, z_i) = (u_i, v_i, w_i), \quad i = 1, \ldots, n+1, \tag{10}$$

where

$$u_i = x_0 + \sum_{j=1}^{i} (|x_j - x_{j-1}| + t) = u_{i-1} + (|x_i - x_{i-1}| + t), \tag{11}$$

$$v_i = y_i, \tag{12}$$

$$w_i = z_i, \tag{13}$$

achieving that the ordinates u_i have been arranged in ascending order. The constant $t > 0$ is necessary only in the case when all interpolation points have the same ordinates. In all other cases, it can be taken that $t = 0$.

Finally, we apply the following inverse transformation to the obtained FIC curve:

$$T'(u', v', w') = (x', y', z'), \tag{14}$$

where

$$x' = x_{i-1} + (x_i - x_{i-1}) \frac{u' - u_{i-1}}{u_i - u_{i-1}}, \quad u' \in [u_{i-1}, u_i], \tag{15}$$

$$y' = v', \tag{16}$$

$$z' = w', \tag{17}$$

to each point of the obtained attractor (u', v', w').

3. Experimental

We performed some experiments[7] regarding the influence of various energetic impulses on bacterial motility behavior (Fig. 2). Different bacterial species (*Staphylococcus aureus* and *Pseudomonas aeruginosa*) were introduced into a liquid phase, and we analyzed their trajectories under energetic — music — impulses. In order to characterize random Brownian motion bacterial trajectories, we compared two different bacteria with and without music. Based on this experiment, we obtained significant data regarding bacterial motion and accordingly established the mathematical analytical forms and 3D diagrams.

In our theoretical experiments regarding molecular motion, we obtained the results and established mathematical equations and 3D diagrams, as well, based on some available research results.[8]

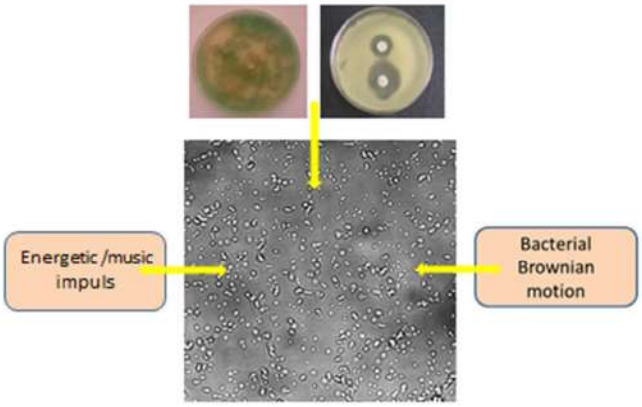

Fig. 2. Schematic diagram of the experiment on bacterial motion influenced by music impulses: *Staphylococcus aureus* (left) and *Pseudomonas aeruginosa* (right).

3.1. *Experimental results*

Based on the experiments, we obtained important bacterial positions data which are presented in Tables 1–4.[7]

Molecule positions in three dimensions were determined based on the theoretical experiments and are presented in Table 5.[9]

Table 1. Coordinates of the first bacterium positions without music.

i	x_i	y_i	z_i
1	0	0	0
2	0.1043	−0.3698	−0.2869
3	0.0521	−0.4622	−0.3641
4	0.0521	−0.2773	−0.4809
5	0.0521	−0.2773	−0.7842
6	0.0521	−0.1849	−0.7605
7	0.1564	−0.5547	−0.7709
8	0.2607	−0.7396	−0.7757
9	0.5213	−0.7396	−1.0163
10	0.4170	−0.8320	−0.9330
11	0.3649	−0.8320	−0.9349

Table 2. Coordinates of the first bacterium positions with music.

i	x_i	y_i	z_i
1	0	0	0
2	0.1043	0.1849	−0.1822
3	−0.2607	0	−0.1127
4	−0.3649	0.3698	−0.0791
5	−0.3128	0.4623	−0.1107
6	−0.2607	0.2774	−0.0054
7	−0.3128	0.1849	−0.1336
8	−0.2607	0.1849	−0.1031
9	−0.2607	0.1849	−0.0806
10	−0.2607	0.0092	−0.0581
11	−0.3649	0.3698	−0.1685

Table 3. Coordinates of the second bacterium positions without music.

i	x_i	y_i	z_i
1	0	0	0
2	−0.3127	0.4622	−0.8545
3	−0.6776	−0.4622	−1.7845
4	−1.1989	−0.5547	−2.1152

Table 3. (*Continued*)

i	x_i	y_i	z_i
5	−0.9383	−0.2773	−2.6437
6	−0.9904	0.1849	−2.9061
7	−1.0425	−0.0092	−3.662
8	−0.8862	−0.2773	−3.4277
9	−1.1989	0.4622	−3.8249
10	−1.0947	−0.2773	−3.8952
11	−0.8862	0.3698	−4.4158

Table 4. Coordinates of the second bacterium positions with music.

i	x_i	y_i	z_i
1	0	0	0
2	−0.0521	0.1849	0.5398
3	0.2607	0.7396	0.811
4	0.2085	0.5547	0.9604
5	0.2085	0.9245	1.012
6	−0.1564	0.6471	1.7786
7	0.1043	0.4623	1.9442
8	0.4171	0.4623	2.3245
9	0.5213	0.4623	2.3744
10	0.5213	1.0169	2.7151
11	0.5213	1.5716	2.1193

Table 5. Molecule position coordinates.

i	x_i	y_i	z_i
1	2	5.8	4
2	2.2	2	4.2
3	2.5	4.4	4.5
4	2.8	3.2	5.2

4. Results and Discussion

The bacterial motion experiments and the theoretical experiments with molecule motion are the basis for our further research, which implied the creation of mathematical analytical equations, generating adequate 3D interpolating diagrams, and applying the fractal interpolation method for designing 3D fractal interpolating diagrams of bacterial and biomolecule motions.

Based on the data from Table 1 (the first bacterium positions without music), we obtained the following analytical equations:

$$\begin{aligned} x(t) = {} & 18.7129 - 55.2529t + 66.3847t^2 - 43.3618t^3 + 17.2814t^4 - 4.4358t^5 \\ & + 0.748566t^6 - 0.0825332t^7 + 0.00571969t^8 - 0.000225966t^9 \\ & + 3.87861 * 10^{-6}t^{10}\,, \end{aligned} \tag{18}$$

$$\begin{aligned} y(t) = {} & -100.479 + 285.098t - 327.188t^2 + 203.865t^3 - 77.5513t^4 + 19.0238t^5 \\ & - 3.07207t^6 + 0.324507t^7 - 0.0215696t^8 + 0.000818207t^9 \\ & - 0.0000135009t^{10}\,, \end{aligned} \tag{19}$$

$$\begin{aligned} z(t) = {} & -69.5243 + 197.979t - 228.023t^2 + 142.468t^3 - 54.2881t^4 + 13.3306t^5 \\ & - 2.15519t^6 + 0.228139t^7 - 0.0152186t^8 + 0.000580324t^9 \\ & - 9.64145 * 10^{-6}t^{10}\,. \end{aligned} \tag{20}$$

The adequate spatial bacterial motion is presented as the 3D interpolating diagram in Fig. 3.

In Fig. 4 is presented the 3D fractal interpolating diagram obtained after applying the fractal interpolation on the bacterial trajectory.

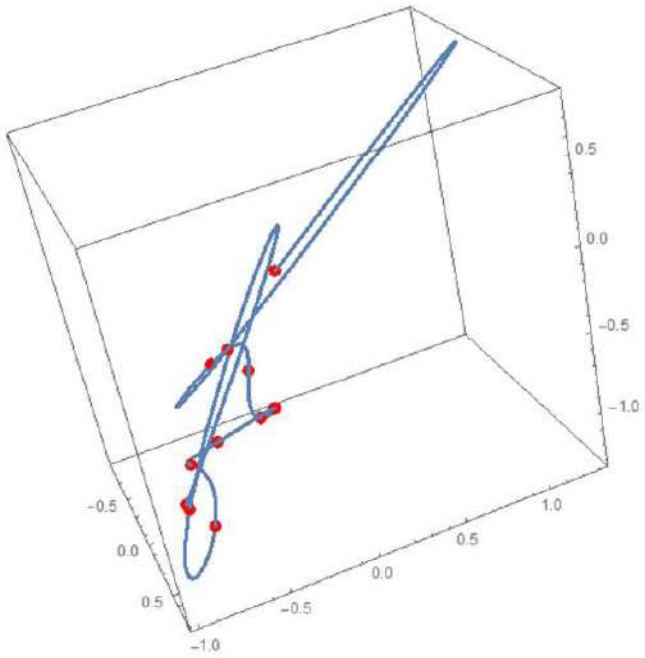

Fig. 3. The 3D interpolating diagram of the first bacterial motion without music.

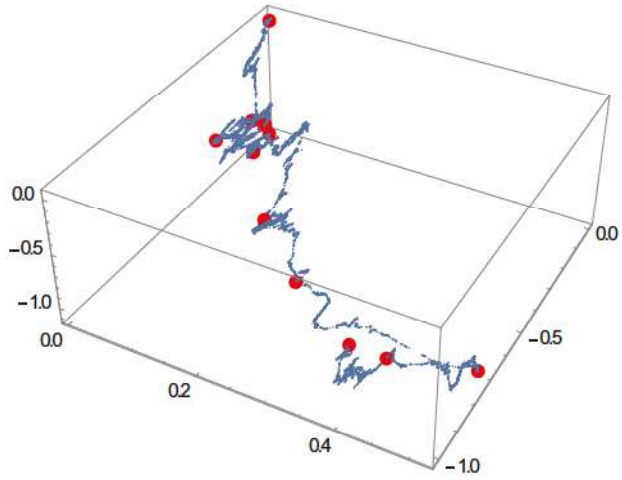

Fig. 4. Bacterial motion's (the first bacterium motion trajectory without music) 3D fractal interpolating diagram.

Based on the data from Table 2 (the first bacterium positions with music), we obtained the following analytical equations:

$$x(t) = -24.4494 + 67.194t - 75.0942t^2 + 46.2836t^3 - 17.6857t^4 + 4.40531t^5 - 0.727088t^6 + 0.0787646t^7 - 0.00537635t^8 + 0.000209451t^9 - 3.54704 * 10^{-6}t^{10}, \quad (21)$$

$$y(t) = -5.8331 + 9.43531t - 1.64148t^2 - 4.52017t^3 + 3.60785t^4 - 1.27716t^5 + 0.258226t^6 - 0.0317402t^7 + 0.00235233t^8 - 0.0000968886t^9 + 1.70649 * 10^{-6}t^{10}, \quad (22)$$

$$z(t) = -62.159 + 178.622t - 208.148t^2 + 131.792t^3 - 50.9074t^4 + 12.6652t^5 - 2.07194t^6 + 0.221514t^7 - 0.0148915t^8 + 0.00057099t^9 - 9.5189 * 10^{-6}t^{10}. \quad (23)$$

The spatial bacterial motion with music is presented as the 3D interpolating diagram in Fig. 5.

After applying the fractal interpolation on bacterial motion, the 3D diagram presenting bacterial trajectory, shown in Fig. 6, is obtained.

Based on the data from Table 3, regarding the second bacterial motion without music, we established the following analytical equations:

$$x(t) = 72.5157 - 196.258t + 212.062t^2 - 122.976t^3 + 42.9447t^4 - 9.54724t^5 + 1.38096t^6 - 0.129201t^7 + 0.00751896t^8 - 0.000246545t^9 + 3.46398 * 10^{-6}t^{10}, \quad (24)$$

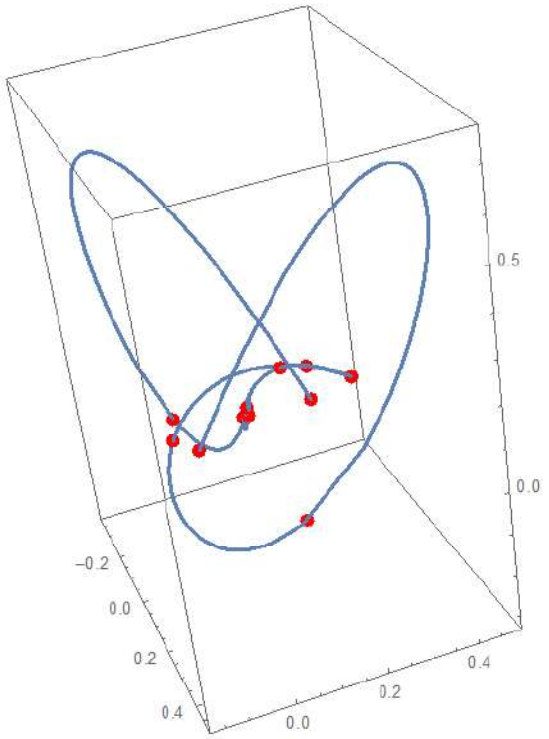

Fig. 5. Bacterial motion's 3D interpolating diagram (the first bacterium positions with music).

$$y(t) = -60.6098 + 159.254t - 167.228t^2 + 95.3259t^3 - 33.1614t^4 + 7.39731t^5 - 1.07329t^6 + 0.0999718t^7 - 0.00570623t^8 + 0.000179092t^9 - 2.31454 * 10^{-6}t^{10}, \quad (25)$$

$$z(t) = -243.028 + 691.829t - 798.683t^2 + 502.32t^3 - 193.506t^4 + 48.1848t^5 - 7.91272t^6 + 0.851038t^7 - 0.0576426t^8 + 0.00222896t^9 - 0.0000374927t^{10}. \quad (26)$$

The 3D diagram in Fig. 7 represents the spatial bacterial motion of the second bacterium.

After applying the fractal interpolation on the second bacterial motion without music, the 3D diagram is obtained (Fig. 8).

Regarding the second bacterial motion, with music, based on Table 4, we obtained the following analytical equations:

$$x(t) = 134.716 - 377.973t + 429.189t^2 - 265.261t^3 + 100.224t^4 - 24.4295t^5 + 3.92017t^6 - 0.411493t^7 + 0.0271835t^8 - 0.00102513t^9 + 0.0000168232t^{10}, \quad (27)$$

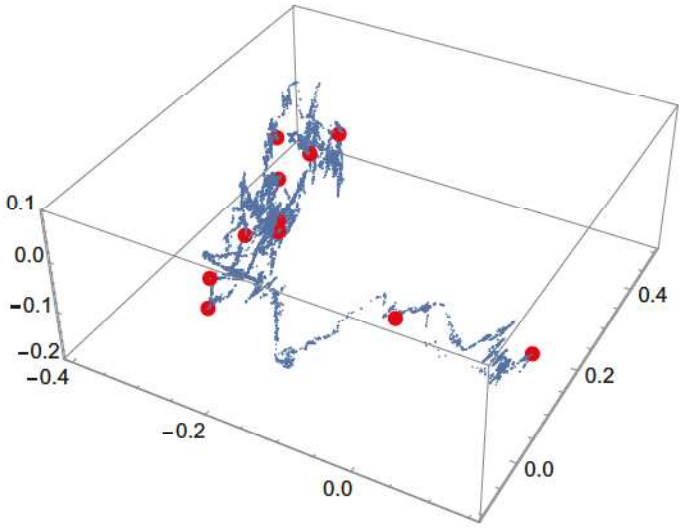

Fig. 6. The 3D fractal interpolating diagram of the first bacterium motion trajectory with music.

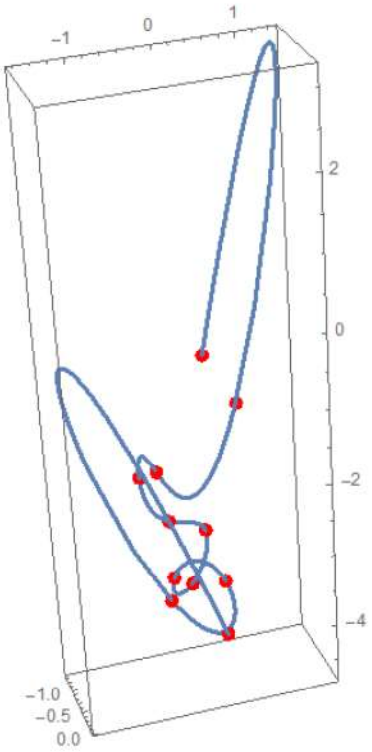

Fig. 7. Bacterial motion's 3D interpolating diagram (the second bacterium positions without music).

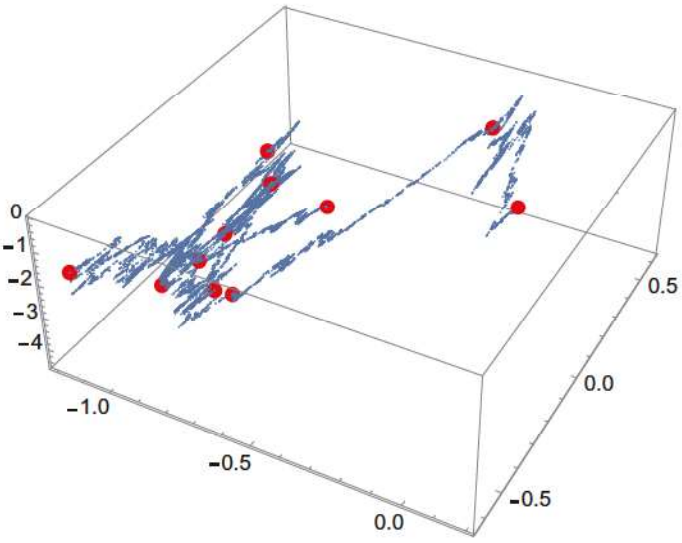

Fig. 8. The 3D fractal interpolating diagram of the second bacterium motion trajectory without music.

$$y(t) = 149.064 - 410.619t + 454.682t^2 - 272.539t^3 + 99.5592t^4 - 23.432t^5 + 3.63071t^6 - 0.368318t^7 + 0.0235467t^8 - 0.000860675t^9 + 0.0000137119t^{10}\,, \tag{28}$$

$$z(t) = -206.087 + 584.869t - 674.022t^2 + 423.528t^3 - 162.661t^4 + 40.2841t^5 - 6.56588t^6 + 0.699926t^7 - 0.0469524t^8 + 0.00179779t^9 - 0.0000299493t^{10}\,. \tag{29}$$

The 3D representation of the spatial second bacterium motion was obtained and is presented in Fig. 9.

After applying the fractal interpolation on bacterial motion, the 3D diagram in Fig. 10 is obtained.

Regarding the molecular motion with the position coordinates given in Table 5, there are also associated mathematical equations:

$$x(t) = 2 - 0.133333t + 0.15t^2 - 0.0166667t^3\,, \tag{30}$$

$$y(t) = 25.6 - 31.0667t + 12.9t^2 - 1.63333t^3\,, \tag{31}$$

$$z(t) = 3.6 + 0.6t - 0.25t^2 + 0.05t^3\,. \tag{32}$$

The corresponding 3D diagram is presented in Fig. 11.

The fractal interpolation 3D diagram regarding molecular motion is presented in Fig. 12.

We use the fractal interpolation mathematical method in our research in order to find and establish the relation between biophysical and condensed matter particle

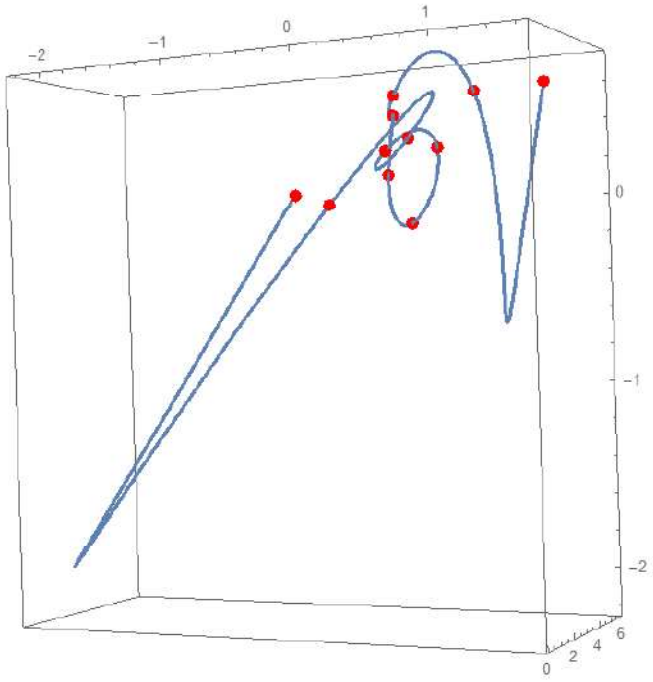

Fig. 9. The 3D interpolating diagram of the second bacterium motion with music.

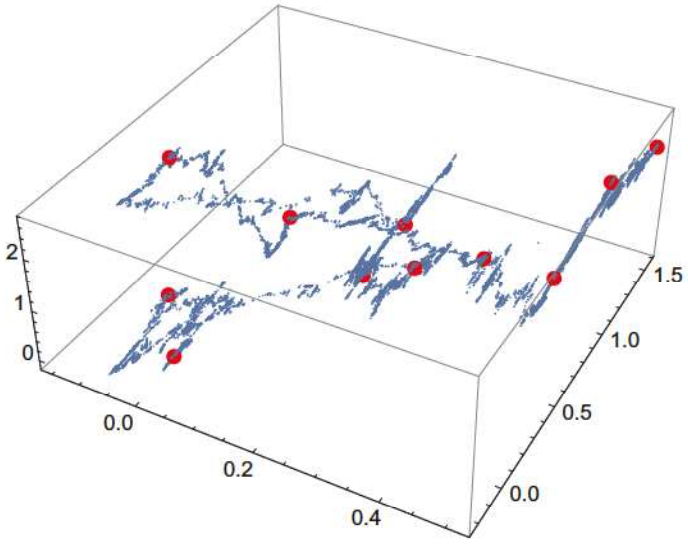

Fig. 10. Bacterial motion's 3D fractal interpolating diagram (the second bacterium motion trajectory with music).

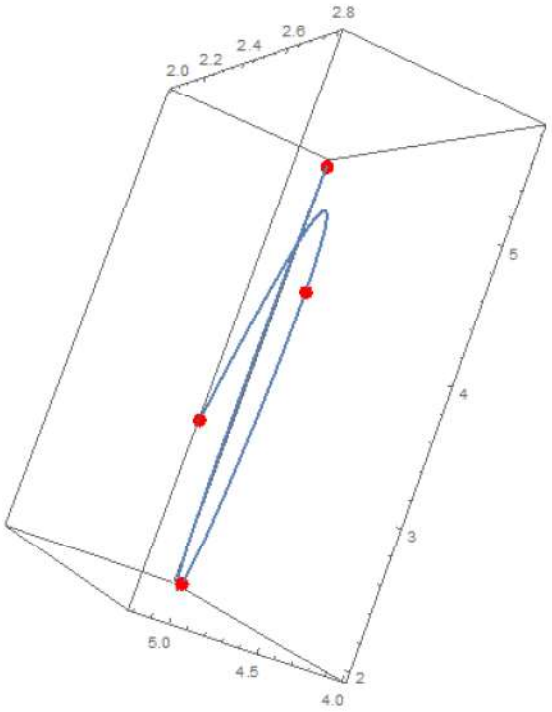

Fig. 11. Molecular motion's 3D interpolating diagram.

systems and to connect them in an asymptotic way. The substantial integrative characteristic of these systems is Brownian motion with its fractal nature, which is the basis of the biomimetic motion similaritics.

We understand that electrons and other similar particles in orbitals, and their motion from one orbital to another, and also in the complex of molecules with different orbitals where the electrons could be like joint particles in the molecule systems, do not recognize their location within the irrespective of living and nonliving matter. So, electrons existence and their motion are the evident minimum required point and also their motion, like Brownian, is important as a bridge between biomatter and condensed matter, especially for the solid-state solutions in microelectronic applications. In this way, there are no limitations for biophysical systems in advanced submicroelectronic solutions and designs.

The whole idea of our research work is to open new perspectives for interconnecting biophysical and physical systems, as they are the biunivocal correspondents, which is very significant from the aspect of living and nonliving matter structure integrations towards designing new materials and technologies.

The research data is very rich, including several scientific information about the molecule, bacteria and also the impacts of energetic impulses even in the form of

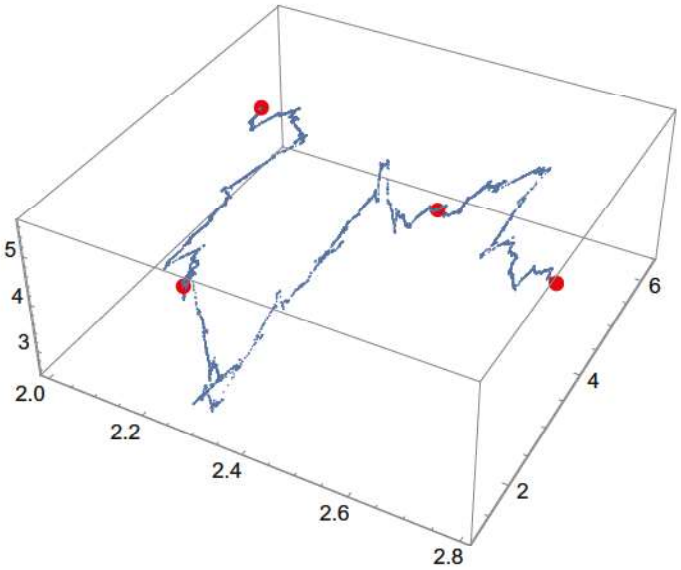

Fig. 12. Molecular motion's 3D fractal interpolating diagram.

different music waves on their motion through experiments. This diversity of experimental results enriches the concluding data for different representations disposed to fractal interpolation method. This is a very rare and quite a new application in the Brownian motion fields. The results on a molecule's motion are based on the incorporation of the motion like "clusters" of electrons in atoms and molecules. This motion does not recognize in which material in nature the electrons are. So, now, we continue further to analyze this motion within bacterial motion as the global motion, because there are some experimental results indicating that the total number of protein molecules per bacteria is 2–4 million. Our experimental and theoretical analysis results in the figures previously presented confirm that the motion of submicroparticles in a molecule is a subset of the general bacterial Brownian motion. By this method, we are on the right way to approach the asymptotical biunivocality of these systems, which upgrades the results on the level of joint properties, expressed through Brownian motion, between biophysical subsystems. This is because we understand the asymptotic approaching between two point sets or geometric shapes that is very important to be applied as a relation system in living and nonliving matters. There are existing self-similarities of the morphological shapes and structures in nature in general. If we like to use a similar structure in nature within the biosystems and apply that in condensed matter, especially solid states, it is very important to recognize self-similarities in the aspect of fractals and biomimetic phenomena. So, if we use fractal self-similarities as a bridge from the biomimetic structures and shapes to our higher-level and even submicroelectronic hybrid

integrations, it is necessary to provide an approach for biunivocal relation of living and nonliving biophysical systems. In this sense, *asymptotic* means the way by which the above-mentioned systems could correspond, i.e., how could the infinitesimal point process provide the matching of different systems and structures.

All of these complex considerations between biophysical subsystems within nature open new perspectives and shed light on advanced microelectronic structures which connect different particle systems within the totality of nature and matter.

5. Conclusion

Modern microelectronics is very important for different advanced applications within high-level integration circuits, microdevices and also in computer field. In these areas and especially in IT, there is a growing interest which includes complex integrations of different microcircuits and devices and also some high-tech hybrid solutions for computers. Nowadays, modern science and technological developments demonstrate very important advancement in biosystems and condensed matter particles, including even quantum-level integration in computers and high-level integrations for joint information and telecommunication applications. From this point of view, the fundamental research which includes different phenomena related to particles in biophysical and condensed matter systems is of great importance. Our research and reporting in this paper come up to the level of investigations of particles' motion as a joint characteristic in biophysical and condensed matter subsystems. The fractal analysis of particle trajectories in living and nonliving systems under different conditions was applied not only on bacteria, but also on coronavirus[10] or other potential virus motions. In our research, based on the real and the theoretical experiments, we established mathematical analytical forms regarding the electron motion in biophysical and condensed matter systems, providing new perspectives for their asymptotic approaching, based on a single but essential joint characteristic, which is Brownian motion in the frame of fractal nature of particles' motion similarities. As an integrative research result in our paper, we confirmed the asymptotic approach between the motion of electron sets in molecule and that in bacterial structures, where we have similar particle motion as well which does not have a sense as to where the motion happens, i.e., living or nonliving systems. The idea of joint examination and linking of living and nonliving systems, as a biomimetic approach, is of great importance for further microelectronic miniaturization and integration, and also for developing new advanced technologies for complex biodevices.

6. Outlook

In future research, there is a plan to develop more experiments on bacterial and viral motions and behaviors. In this way, we expect to provide additional data to prove the above-mentioned effects in Sec. 4.

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