Biomolecules and Brownian Motion

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***Abstract*—Structures and different life functions of microorganisms, like motion, are based on molecular biology processes, which comprise molecular and submolecular particles. It is very important to determine relation between molecular and microorganisms levels. The aim of our research is the analysis of Brownian motion as a general phenomenon and the consequence of structures hierarchy from molecular to microorganisms level. If we approach this idea from the aspect of biomimetic correlations at the level of the alive and nonalive matter system particles, the condensed matter particles could be considered as a part of micro, nano and molecular microorganisms structures. In this research we used the experimental results of bacterial motion influenced by different energy impulses. The important goal of this research paper is to obtain significant data regarding Brownian motion in the frame of fractal nature similarities, as an integrative property of living and nonliving systems particles processes. This opens new frontiers for submicroelectronics relations within the integrated supermicro biophysical systems. This is a potential new trend in nowadays advanced research, where we integrate the knowledges of complex relations between the electrons or other particles and their clusters as joint structures in alive and condensed matter, what could be a possible direction for new microelectronics complex biodevices and integrations.**

***Index Terms*—molecular biology; microorganisms; Brownian motion; biomimetic; fractals.**

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I. Introduction

Phenomena that exist in both living and nonliving matter, as electron and molecular motion, are to be considered from different aspects and they require a multidisciplinary approach. Molecular biology, as a life science, studies various processes in alive organisms at the molecular level. Thus, electron motion in biomolecules as well as molecular motion, belong within the molecular biology and molecular bioelectronics research field.

Electron motion is based on the same principles in alive organisms and in condensed matter, so it should be observed as a joint property to get the complete insight into this fundamental process. Based on our current knowledge and possibilities, we are not able to determine electron motion. However, we can determine motion of the molecules that contain those electrons. Every molecule which is moving, carries an electron cluster making it move as well. Within molecules as parts of biosystems, existing atoms and electrons „are not aware of“ whether they are a part of an alive organism or condensed matter. That is very important because it distinguishes the molecule as the significant integrative factor between living and nonliving systems.

The idea of biomimetic correlation between molecular and submolecular particles of alive and nonalive matter, in the frame of the Brownian motion fractal nature characterization, implies the entire new possibility of considering these particles motion as the biunivocal phenomenon. Microorganisms and viruses demonstrate biomimetic similarities with condensed matter particles motion because of their dimensions and motion patterns [1]. Bacteria motility behavior, which implies velocity, direction and trajectory, is also influenced by environmental changes like temperature, pH, or different energetic impulses [2].

We used Brownian motion fractal nature, as a general characteristic of both alive and nonalive systems, to establish the relation between these two different systems, but consisting of identical particles. Also, we plan to develop the biophysical-mathematical asymptotic approaching model for living organisms and condensed matter particles, as they are biunivocaly correspondent.

One of the objectives of our research is to explain the Brownian motion as the joint characteristic of biomolecule and physical system particles. Controling particles motion and predicting their trajectories [3] in this kind of biomimetic approach [4], provides new perspectives for

further microelectronics miniaturization and electronics parameter integrations [5,6].

So, our goal is to characterize the molecular motion based on Brownian motion within the combination of the experimental and the theoretical experiment results.

II. EXPERIMENTAL METHODS AND PROCEDURES

We performed real experiments with diverse bacteria in a liquid phase under the influence of variant energy impulses [7], among which were some different music impulses (Figure 1). In that sense, we got some data from which we generated the two and three dimensional diagrams [2,7].

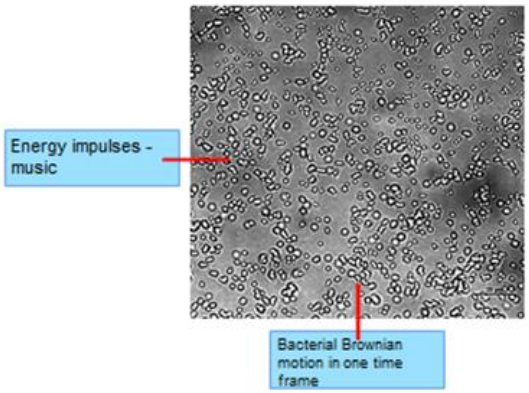

Fig. 1. The bacterial motion experiment diagram.

Now, our intension is to generate the analytical forms. Also, we used some other available research results which are based on molecular motions [8]. In this case we treat the molecules like clusters of electrones in different matter organizations from atomic to molecular level. This way we avoid the lack of worldwide research recorded electron motions. Hence, we now observe the molecules as "packages" of electrons or other particles. From the other hand, we also analyze all of these molecules as a part of alive bacterial matter. At the end, we can jointly understand the biophysical integrated systems with one important characteristic and that is just the Brownian motion.

A. *Mathematical Background*

It is well known that it is possible to create some mathematical model describing the relationship between several quantities. By using one of them, called the dependent variable (we will denote it by y) and one or more quantities, called the independent variables (we will denote them by $x_1, x_2 \dots x_n$,), we can obtain a model which represents a linear relationship between the dependent variable and independent variables in the form:

$$y = a_1x_1 + a_2x_2 + \cdots + a_nx_n + b, \quad (1)$$

where $a_1, a_2 \dots a_n$, b are real (or complex) numbers. If the value of the variable y depends only on one independent variable x, then (1) has a form:

$$y = ax + b. \quad (2)$$

This formula could be obtained by applying various numerical approximation models. One of very useful approximation models is the least square approximation.

The least squares method (also called discrete mean square approximation [9]) belongs to the so-called best approximations, i.e. approximation methods in which the criterion is the minimization of the error according to one of the norms. Specifically, this is the norm L^2, ie. the total sum of the squares of the errors in the approximation nodes is minimized [9,10]. Some of the interesting applications of those methods are already given in [11-13].

B. *Main Results*

We applied the technique to the data in Table I, which describes the coordinates of bacteria locations, during movement through coordinate system [7].

TABLE I
BACTERIA LOCATIONS COORDINATES

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

Based on the data from Table I, we obtained the 3D diagram presented in Figure 2.

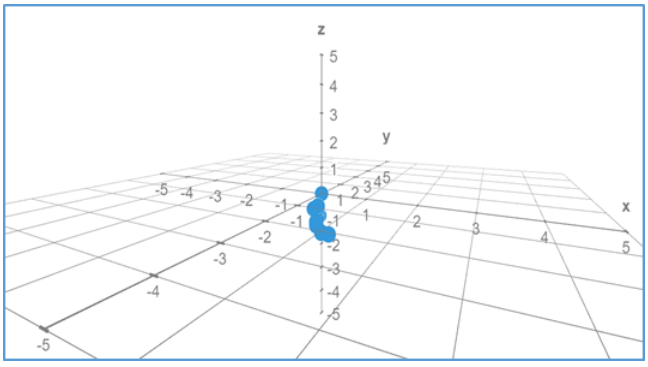

Fig. 2. The points of the bacteria locations in 3D.

Next, we considered four molecule location points in 3D given in Table II and presented in Figure 3.

TABLE II
MOLECULE LOCATIONS 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

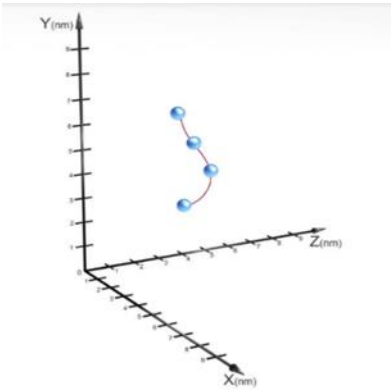

Fig. 3. 3D diagram of molecule motion in different time intervals.

III. RESULTS AND DISCUSSION

We applied multiple linear regression, to determine the mutual dependence of the coordinates and to obtain explicit formula for predicting and calculating positions.

Based on the data from Table I, we will apply the procedure of forming an approximation function

$$\varphi(x, y) = ax + by + c, \tag{3}$$

by using the least squares method. Thus, by applying the least square approximation (the operational software was statistical package in Excel) on the given data sets, we obtained next results considering the best linear fit for the presented model: the coefficients of the resulting linear function are respectfully a=–1,47999912, b=–0,02844679 and c=–0,36733904 and the estimated regression function is of the form:

$$\varphi(x, y) = -0.746871x - 0.421536y - 0.306160 \tag{4}$$

We can compare values and precision of dependent variables $\boldsymbol{z_i}$ in given points and results obtained by formula trough the absolute and relative error (Table 3).

TABLE III
COMPARISON BETWEEN REAL AND APPROXIMATE COORDINATES, ABSOLUTE AND RELATIVE ERROR

x_i	y_i	z_i	φ_i	Δ	%
0	0	0	-0.3061600	0.3061600	
0.1043	-0.3698	-0.2869	-0.5399426	0.2530427	-88.20%
0.0521	-0.4622	-0.3641	-0.5399059	0.1758059	-48.29%
0.0521	-0.2773	-0.4809	-0.4619639	0.0189361	-3.94%
0.0521	-0.2773	-0.7842	-0.4619639	0.3222361	-41.09%
0.0521	-0.1849	-0.7605	-0.4230139	0.3374860	-44.38%
0.1564	-0.5547	-0.7709	-0.6567966	0.1141034	-14.80%
0.2607	-0.7396	-0.7757	-0.8126373	0.0369373	-4.76%
0.5213	-0.7396	-1.0163	-1.0072718	0.0090281	-0.89%
0.4170	-0.8320	-0.9330	-0.9683232	0.0353232	-3.79%
0.3649	-0.8320	-0.9349	-0.9294112	0.0054888	-0.59%

The plot (4) obtained with the least squares method is presented in Figure 4.

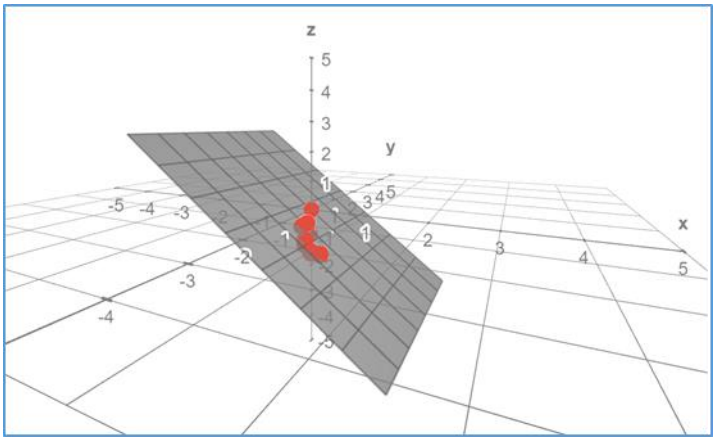

Fig. 4. The approximation plot with marked red points from Table III.

Similarly, as in previous procedure applied on bacterial motion experimental data, we obtained next results for molecule motion in different time intervals, considering the best linear fit for the presented model: the coefficients of the resulting linear function are respectfully a=1.4685067, b=0.0035386 and c=0.973673 and the estimated regression function is of the form:

$$\varphi = 1.4685067x + 0.0035386y + 0.973673. \tag{5}$$

Next, by using the estimated regression function (5) and by implementing the 2D coordinates we obtained the estimated dependent values of the z-coordinates, presented in the Table IV, together with the evaluated absolute and relative error of this approximation:

TABLE IV
Z- COORDINATES WITH THE ABSOLUTE AND RELATIVE ERROR

x_i	y_i	z_i	φ_i	Δ	%
0	0	0			
2	5.8	4	3.9312102	0.0687898	1.72%
2.2	2	4.2	4.2114649	0.0114649	0.27%
2.5	4.4	4.5	4.6605095	0.1605096	3.57%
2.8	3.2	5.2	5.0968150	0.1031850	1.98%

The plot (5) obtained with the least squares method is presented in Figure 5.

If we observe alive and nonalive matter particles as a hierarchical phenomenon, we can consider an atom as a

cluster of electrons and other particles, a molecule as a cluster of atoms with already mentioned particles which are penetrating each other from their orbitals in interatomic relations within the molecule, and a microorganism as a cluster of molecules. Nowadays fundamental research and science do not have high-tech and also resolution possibilities to recognize, separately, the electron motion. We can consider only the indirect effects. Here, we must stress the complexity in the matter based on quantum mechanical principles and Heisenberg uncertainty principle, as well, in all of these considerations.

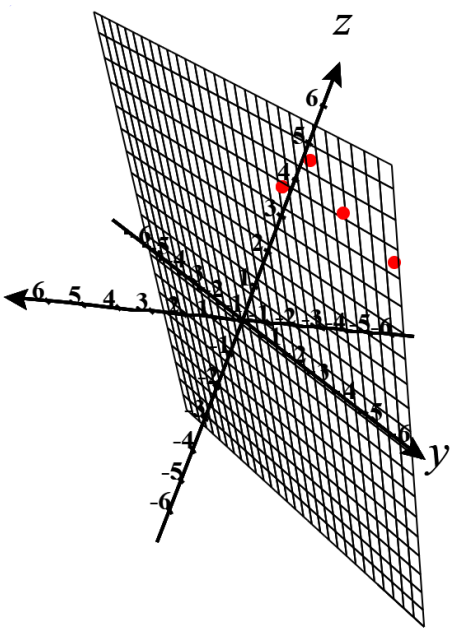

Fig. 5. The approximation plot with marked red points from Table IV.

Each bacterial cell comprises 2 – 4 millions of protein molecules [14], which implies that the total number of molecules per bacterial cell is much higher. This is just one comparison. We can observe the effect of electron motion at the molecular and microorganisms level. So definitely, the particles motion based on Brownian motion fractals effects, is the base for deeply understanding all of these processes within the submicro scale sizes with the joint characteristic which we can nominate as "actio in distans" in motion.

In this paper we introduced two mathematical analytical forms: one for bacterial and second for molecular motion, which are characterized by Brownian motion. In that sense we would like to establish a relation between these two mathematical analytical forms considering molecule number ratio. In this way we could determine asymptotic approaching of two mathematical functions towards fractals biomimetical self-similarity. This is the idea for our further research.

IV. OUTLOOK

All of these results and innovative methods in mathematical analysis and discussions are just the original start in this field. In the next step we plan to develop a method by which we can establish the relation between the analytical mathematics and asymptotic approaching of alive and nonalive matter particles, with an idea to do it by fractal similarities.

V. CONCLUSION

In this paper we performed the results regarding molecular and bacterial motion. Regarding molecular motion, comprising electron motion, we provided mathematical analytical forms, in order to substantially characterize this motion. We analyzed bacterial motion influenced by different energy impulses, like music, and presented obtained data, showing random bacterial trajectories based on Brownian motion, in mathematical analytical forms, as well. Thus, in this stage we fulfilled and satisfied the idea of "electron clusters" in biomolecules which are also a part of microorganisms. Here, we define just a beginning of the joint integration in biophysical systems with general characteristic which is the Brownian motion.

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REFERENCES

[1] V.V.Mitic,G.Lazovic, D.Milosevic, E.Ristanovic, D.Simeunovic,S.-C. Tsay, M.Milosevic and B.Vlahovic, "Brownian fractal nature Coronavirus motion," *Mod. Phys. Lett. B*, vol. 35, no. 04, pp. 2150076, Jan. 2021.

[2] V.V. Mitic, G. Lazovic , D. Milosevic, C.-A. Lu, J. Manojlovic, S.-C. Tsay, S. Kruchinin and B. Vlahovic, "Brownian motion and fractal nature," *Mod. Phys. Lett. B*, vol.34, no. 19n20, pp. 1-11, July, 2020.

[3] Z. B. Vosika, V. V. Mitić, G. Lazović, V. Paunović and Lj. Kocić, "Meso-kinetics of one time relaxation electrical processes in BaTiO3 ceramics—modified Boltzmann-Poisson model," *Ferroelectrics*, vol. 531, pp. 38–50, Nov, 2018.

[4] J. Mei, X. Peng, Q. Zhang, X. Zhang, T. Liao, V.V. Mitic and Z, Sun, "Bamboo-membrane inspired multilevel ultrafast interlayer ion transport for superior volumetric energy storage," *Adv. Funct. Mater*, May, 2021.

[5] V.V. Mitic, S.Ribar, B.Randjelovic, C.-A. Lu, I. Radovic, A. Stajcic, I.Novakovic and B.Vlahovic, "Neural networks and microelectronics parameters distribution measurements depending on sintering temperature and applied voltage," *Mod. Phys. Lett. B*, vol.34, no. 35, pp. 2150172, Dec, 2020.

[6] V. V. Mitic, G. Lazovic, S. Ribar, C.-A. Lu, I. Radovic, A. Stajcic, H. Fecht and B. Vlahovic, "The artificial neural networks applied for microelectronics intergranular relations determination," *Integr. Ferroelectr*, vol. 212, pp. 135–146, Nov, 2020.

[7] V.V. Mitic, G. Lazovic, D. Milosevic, J. Manojlovic, E. Ristanovic, D. Simeunovic, S.-C. Tsay, M. Milosevic, M. Sokovic and B. Vlahovic, "Brownian motion fractal nature frontiers within the matter," in *Biocompatible and Biomimetic Features of Materials for*

Biomedical Applications – New Insights, Switzerland, Springer, 2021, ch. 10.

[8] S. Bhunia, A. Rana, P. Roy, D. J. Martin,M. L. Pegis, B. Roy and A. Dey, "Rational design of mononuclear iron-porphyrins for facile and selective 4e-/4H+ O2 reduction: activation of O-O bond by 2nd sphere hydrogen bonding," *J. Am. Chem. Soc,* vol. 140, no.30, pp. 9444-9457, July, 2018.

[9] G.V.Milovanović, *Numerical analysis II*, 3rd ed. Belgrade, Serbia, Naucna Knjiga,1991, VIII+210 pp.

[10] G.V.Milovanović and M.A.Kovačević, *A collection of solutions for problems in numerical analysis*, 3rd ed. Belgrade, Serbia, Naucna Knjiga,1991, IV+278 pp.

[11] B.Ranđelović, I.Radojković and B.Gajić, "One Application of Discrete Mean Squere Approximation For Prediction of Voluntary Pension Fund Development," *Appl. Math. and Comp. Science*, vol 5, no. 1, University of Nis, Faculty of Science, pp.7-15, 2020.

[12] I.D.Radojkovic**,** B.Gajic and B.M.Randjelovic, "Predicting the Development of Voluntary Pension Funds in Serbia by Applying The Mathematical Method of Linear Regression," *J. of Economic and Social Development – Resilient Society*, vol. 8, no. 1, pp. 2-13, 2021.

[13] I.D.Radojkovic, B.M.Randjelovic and I.D.Ilic, "Modelling Development of Volontary Pension Fund Using Mathematical Model Of Approximation with Lagrange Interpolation Polynomials," *Ekonomske teme*. vol. 59, no.2, pp.243-257, 2021.

[14] R. Milo, "What is the total number of protein molecules per cell volume? A call to rethink some published values," BioEssays, vol.35, no. 12, pp. 1050-1055, Dec. 2013.