The Feynman Path Integral to Characterize and Anticipate Bacteria Chemotaxis in a Host Healthy Body

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Abstract. In this paper the idea of Feynman’s path integral is introduced inside a nano biological system such as bacteria population where due to their property of chemotaxis, a stochastic modeling might be drawn to describe their mobility due essentially to electrical interactions among them as a recurrent resource to protect themselves against antibacterial agents such as macrophages. Due to composition of K+, Cl- and Na+ exists there a net charge along the internal and external phospholipid membrane of bacteria. The model of path’s integration invented by Richard Feynman has been extensively used to tackle crucial problems in quantum mechanics for various decades essentially in atomic physics and nano physics. The idea of the path’s integral assumes a space-time pathway where the space-time bacteria displacements are governed by physics interactions that gives rise to changes of position in the space-time plane in a fully accordance to biological and physics laws. We worked out the idea of the Feynmans path integral to describe space-time dynamics of aggregations of bacteria trying to host a healthy body. We assumed that the bacteria interactions is governed by electric fields and potentials. While the net charge is predominantly positive due to the high concentrations of Cl+, there are clearly external electric fields and potentials that might seriously affect the behavior of bacteria space-time dynamics. In this manner this phenomenology would fit the path integral theory. Therefore the change of the net charge in bacteria due to the presence of others charged nano organisms would affect their translational dynamics by being vulnerable to macrophages. Thus the knowledge of the pathway of these bacteria populations is seen as an advantage to tackle the beginning of diseases inside the framework of Internet of Bio-nano Things that targets to anticipate infections using electromagnetic pulses through advanced software-hardware interfaces. In order to assess possible advantages and disadvantages of this theory we use the Machine Learning algorithm.

1. Introduction
Although the theory of path integral invented by Feynman was conceived inside the framework of elementary particles interactions. This theory has had a wide spectrum of applications because their robustness to carry out predictions about the space-time trajectories. This theory has its grounds in the model of propagator by which any particle characterized by physical properties exhibits space-time displacements as consequence by interactions and change of energy along its trajectory.
It is well-known key properties of bacteria that show capabilities of motility, mobility,
competence and cheating each other. Starting from the fact that most of their spatial and temporal displacements are done in a random manner [1][2] since there is not a fully deterministic law that make predictions about the spatial evolution of a single or aggregation of bacteria in a host body. Clearly this opens a plethora of ways to model them and understand them their intrinsic properties. The accurate understanding of bacteria dynamics might be advantageous from the point of view of the Microbiology in the sense that by knowing the bacteria dynamics is possible to formulate a firm biochemical strategy to abate or anticipate them in a sustainable manner.

**Computational Test of the Feynman’ Theory**

In order to test the Feynman theory we use Machine Learning from the fact that bacteria have capabilities to communicate each other the learning factor might be a cause of their fast growth and exhibit an aggressive behavior to colonize spaces. By following the Mitchell’s criteria we assign a dynamic action as to (i) task, (ii) performance and (iii) experience. Thus Machine Learning theory [3] is associated as an algorithm that would fit the stochastic meaning of the Feynman path integral as well as from the fact of the random behavior of most bacteria.

Under the assumption that Machine Learning theory [3] the Feynman path integral so that it fits well the random behavior of most bacteria. Using the nomenclature of Mitchell’s any action that is dictated by a Machine Learning process would consists essentially in up to three criteria: (i) the task of the process, (ii) the performance to accomplish that task, and (iii) the gained experience to achieve the task. All these three points can be well adjusted to the behavior of certain types of bacteria. Apart from the fact that bacteria can execute tasks and social interaction in order to led them to guarantee an eventual wellness and their nutrition for large periods as well as to colonize new spaces. Most of their dynamics is dictated by a random mobility fact that might be well described by the Brown motion or stochastic laws.

Therefore the applicability of the Feynman theory [4][5] would fit well to describe the dynamics of bacteria even when most of them are under interaction each other. We have focused concretely in the prospective role that the future upgrade versions of Internet such as the Internet of Nano things (IoNT) [6]. To this end the understanding of the translational dynamics of a bacteria aggregation [7] might be an advantageous to any nano device whose end is the sensing and intervention to abate them in cases of a rapid propagation in a healthy host [8-10].

Since the fact that bacteria dynamics is characterized by having a dynamics based in a random evolution [11-12] such a pure Brownian movement then their space-time propagations would fit formulations based on stochastic theories as Quantum Mechanics where the observables are measured in terms of probabilities. In this work we paid attention to the technique of path integral that is build in the knowledge of the state equation (or commonly called the system’s Lagrangian). In this work we use the knowledge of the physical interaction among bacteria that use charged units of transmission of information: plasmid. The electric composition of these basic units represent a window to model bacteria interactions based entirely on electric signals. With the advent of the novel technologies such as the Internet of Nano Things which might implement nano networks aimed to anticipate bacteria dynamics would demand to know within a certain range of precision the bacteria spatial translations and associate properties. Therefore we can project the behavioral characteristics of a bacteria population such as: aiming to achieve a task, evaluate by themselves their performance and to acquire capabilities for learning as a key mechanism to anticipate antibacterial organism such as macrophages or other microbiological species that would abate them successfully.

Therefore the precise modeling of bacteria dynamics would serve as input for schemes of bacteria communications inside the framework of Internet of Nano Things. Second part of this paper presents the essentials of the Feynman path integral. Once the theoretical formulation in third part we pass to use the Mitchell’s criteria to implement a Machine Learning algorithm based on the knowledge of the dynamics and translational behavior when bacteria colonizes a healthy
Figure 1. Sketch of a dynamics of various bacteria achieving space-time displacements. As illustration a single bacteria performs space-time changes depending on their physical or chemical interactions that allow it to perform successive space-time displacements.

host. Last section present the conclusion of paper.
The computational results of this paper are seen as a tool to anticipate and tackle down the sustainable growth of bacteria population inside a framework of Internet of the Nano Things.

2. Essentials of the Feynman Propagator
In Fig 1, is shown a space-time trajectory of one bacterium under an event of Chemotaxis. Thus for this example this single bacterium is passing up to for 4 gates given in \((x_1, y_1), (x_2, y_2), (x_{N-1}, y_{N-1})\) and \((x_N, y_N)\): the first two ones and the last two ones, without any obstruction or stoppable situation. Such trajectory would represent the optimal in terms of space, time and resources. Therefore the theoretical formulation that governs these space-time displacements is done through the well-known Green's functions:

\[
\frac{1}{tt(r_2, r_1)} = \int_{-\infty}^{\infty} dr_{1} r_{1} dr_{2} r_{2} tt(r_1, r) tt(r_2, r)
\]  

which are playing the role of space-time propagators [4][5] for a single bacterium. Inspired in that representation of space-time propagation, we can project the idea of Fig. 1 in the full formulation of Feynman:

\[
W(x, t|x_0, t_0) = \int_{-\infty}^{\infty} dx' W(x, t|x', t') W(x', t'|x_0, t_0)
\]

that is done considering the space-time plane as seen in Fig.1. Since we need to make estimates associated to the bacterium space-time displacements we write down a proposition 1 and 2, and therefore we formulate the respective theorem.

2.0.1. Proposition 1 Any single bacterium is following a space-time displacement given by the Gaussian-like profile

\[
w(x, t) = \frac{1}{4\piDt} \frac{e^{-\frac{x^2}{4Dt}}}{4Dt}
\]
2.0.2. **Proof** By assuming that the biological species movement is dictated by the diffusion’s equation then
\[
\frac{\partial w(x, t)}{\partial t} = D \frac{\partial^2 w(x, t)}{\partial x^2}
\]
where the more generalized has the form
\[
\frac{\partial w(x, t)}{\partial t} = D \Delta^{(\delta)} w(x, t)
\]
where the operator in the right side is given by the multidimensional Laplacian
\[
\Delta^{(\delta)} = \frac{\partial^2}{\partial x_1^2} + \frac{\partial^2}{\partial x_2^2} + \ldots + \frac{\partial^2}{\partial x^n^2}
\]
so the case when is 1-dimension the closed-form solution of Laplacian gives (3).

2.0.3. **Proposition 2** The displacements of a single bacterium is governed by the Green’s function that satisfies Eq.2.

\[
W(x_0, t_0 \to x_0, t_0) = \sqrt{\frac{1}{4\pi D(t - t_0)}} \exp \left( -\frac{(x_1 - x_0)^2}{4D(t - t_0)} \right)
\]

2.0.4. **Proof** In order that \( W(x_0, t \to x_0, t_0) \) is conceived as a space-time propagator, this has to satisfy the diffusion’s equation

\[
\frac{\partial W(x, t)}{\partial t} = D \frac{\partial^2 W(x, t)}{\partial x^2} + \delta(t)\delta(x)
\]

2.0.5. **Theorem 1** The space-time propagation of a single bacterium is governed by the Feynman path integral [4][5]

\[
w(x, t) = \int_{-\infty}^{\infty} dx_0 W(x_0, t_0 \to x_0, t_0) w(x_0, t_0)
\]

2.0.6. **Proof** In order to demonstrate the validity of this theorem we need to demonstrate that the continuity of the displacements of the bacterium is governed by the Gaussian-like profile from the beginning until the end of its path in the space-time plane. If \( w(x, t) \) is seen as a probability density then the probability for a space-time movement between the point \( A \) and \( B \) is written as

\[
P(\chi(t) \in [AB]) = \int_B^A dx w(x, t).
\]

By using preposition 1 and 2 together we can write down that this probability for a transition from the space-time \( (x, t) \) to \( (x_N, t_N) \) is:

\[
P = \int_{B_1}^{B_2} \cdots \int_{B_{n-1}}^{B_n} \int_{A_1}^{A_n} \frac{1}{4\pi D(t^2 - t_1)} \frac{1}{4\pi D(t^3 - t_2)} \cdots \frac{1}{4\pi D(t^N - t_{N-1})} \exp \left( -\frac{(x_1 - x_0)^2}{4D(t^2 - t_1)} \right) \exp \left( -\frac{(x_2 - x_0)^2}{4D(t^3 - t_2)} \right) \cdots \exp \left( -\frac{(x_N - x_0)^2}{4D(t^N - t_{N-1})} \right).
\]
To note that despite of the fact that we are working in a territory entirely stochastic we use the Gaussian profiles that tacitly indicates that the diffusion equation would govern the space-time propagation for an aggregation of bacteria. Fact that supports the usage of these Gaussian forms for a single bacterium. In this manner we proceed with the integration per space-time slide, so we arrive to

$$\exp \left[ -\sum_{i=1}^{\infty} \frac{(x_i - x_{i-1})^2}{4D(t_i - t_{i-1})} \right] \sum_{i=1}^{\infty} \frac{dx_i}{4\pi D(t_i - t_{i-1})}$$

In the case of instantaneous interaction among single bacteria the propagator can be seen as a pure Dirac-Delta function, thus from Eq.(2) we arrive

$$\lim_{t \to 0} W(x_t, t|x_0, 0) = \delta(x_t - x_0)$$

and

$$W(x_t, t|x_0, o) = \sqrt{\frac{1}{4\pi Dt}} \exp \left[ -\frac{(x(t) - x(o))^2}{4Dt} \right]$$

On the other hand la successive integration of functionals given by Gaussian profiles as seen in Eq.12

$$\int \psi d\tau x(\tau) F[x(\tau)] = \int \psi \frac{dx(\tau)}{4\pi D\tau} \text{Exp}(-\int_{\tau=0}^{t} x(\tau) d\tau) F[x(\tau)]$$

allows us to write down the full product of probabilities in the same manner as a Markov chain,

$$\mathcal{P} = \prod_{i=1}^{N} W(x_i, t_i|x_{i-1}, t_{i-1})$$

where each element of this chain is a solutions of the diffusion’s equation [6] for all space-time points where a single bacterium is crossing fact that demonstrates the theorem 1.

2.1. Bacteria Interactions

Consider the successive propagators written as

$$tt(s, t) = \int_{-\infty}^{\infty} tt_1(x''', s) tt_2(x'''', t) dx'''$$

that again, it satisfies

$$\frac{\partial tt(s, t)}{\partial t} = D \frac{\partial^2 tt(s, t)}{\partial s^2}$$
It should be noted that in the same manner as microscopic physics laws are given, the movement of a single bacterium very independent of its own or group interests would depend in most part of its expended energy or physical interactions based on fundamental laws along its path in space and time. As it is well known in most cases bacteria are composed by ions fact that becomes an advantage as to make a precise description of their translational dynamics. This leads to write down that the interaction between two single bacterium is also governed by the sign which has each one of the individual bacterium,

\[
\int_{-\infty}^{\infty} Q_1 Q_2 t t_1 (x^{\mu \nu}, s) Q_2 t t_2 (x^{\mu \nu}, t) dx^{\mu \nu}
\]

(19)

where the product of the charges \(Q_1 Q_2\) defines the electric state of a single bacterium interaction due to plasmid exchange [7]. Consider now the Green's function at \(t_0 = 0\) given by

\[
W(x, t|x_0, 0) = \sqrt{\frac{1}{4\pi Dt}} \exp\left(-\frac{(x - x_0)^2}{4Dt}\right) \sum_k
\]

(20)

when \(x \to x(t)\) then

\[
W(x(t), t|x(0), 0) = \sqrt{\frac{1}{4\pi Dt}} \exp\left(-\frac{|x(t) - x(0)|^2}{4Dt}\right) \sum_k
\]

(21)

Consider an finite aggregation of bacteria whose entire body is governed by the diffusion's equation so that the solution of the dynamics of this aggregation under a cylinder coordinate system is given by

\[
\rho_\lambda(r, t) = \rho_0 \exp[-\lambda (t - t_0)] \times
\]

\[
\sum_{n_1, n_2} \sin \frac{n_1 x_0}{z_1} \sin \frac{n_2 \pi \theta}{\theta_1} J_1(kr),
\]

(22)

now we treat the case where \(x(t) \to r(t)\) so that a more simplified form of (22) is given by

\[
\rho_\lambda[r(t)] = \rho_0 \exp[-\lambda (t - t_0)] J_1[kr(t)],
\]

(23)

that is valid when the product of \(\sin \frac{n_1 x_0}{z_1} \sin \frac{n_2 \pi \theta}{\theta_1} \approx 1\). Thus the space-time evolution of the compound \(\rho_\lambda(r, t)\) is governed by the Green’s function

\[
w = \int_{-\infty}^{\infty} dr \rho_\lambda[r(t)] W(r(t), t|r(0), 0).
\]

(24)

2.2. Diffusion equation and path integral describing bacteria random behavioral

In order to numerically estimate space-time bacterium displacements we proceed to use the derivate of probability of density, thus when we insert each components in (24) we arrive to

\[
\frac{d\omega}{dt} = \frac{\exp (-\lambda D t \frac{\Delta x}{\sqrt{4\piDt}}) J_0[kr(t)]}{4\pi Dt} \sum_k \exp (-\frac{|x(t)|^2}{4Dt} \sum_k
\]

(25)

denoting the change in time of the probability density. Clearly we have used the fact that the electric interactions governs the space-time translational changes. Fact that is explained by the presence of a Bessel function that is commonly derived from a Laplace equation in electrodynamics.
3. Computational Test of the Feynman’s Theory
Under the assumption that the bacteria aggregation dynamics is governed by the Green’s function (25) then we can assign a well-defined trajectory to the movement law \[ x(t) \]. Thus we start a linearity given by \[ x(t) = x_0 + vt \] where \( x_0 \) is a random point.
Thus we write down the Mitchell’s criteria [3] that would accomplish to tackle down the sustainable progress of an aggregation of bacteria. Thus we write down these criteria:

**Task** Bacteria dynamics has an end: to guarantee the wellness of their society so any space-time displacement should end in earnings and not lost. For this is know that bacteria carry out well defined actions of:

- Chemotaxis [8][9]
- Motility [10][11]
- Mobility [12]

**Performance** Bacteria is said that have accomplished a certain performance when an important fraction of them remains the same after of time \( T \). indeed, the colonization of spaces guaranteeing their nutrition for large periods is also seen as a kind of performance.

**Experience** Once the bacteria population have reached their “planned” objectives without any discount and damage in their aggregation even in an eventual facing with antibacterial agents is said that bacteria have gained a certain experience.

We turn back to Fig.1 where we have associated the elements of the translational displacement of a single bacterium as seen in task bacterium opt by a random path to reach a objective. In this manner **Performance** is actually perceived as the fact by which bacterium has not has no any event against its wellness, **experience** where bacterium has reached its objective and back to its safety place because he learned that the pathway is safety. All these ideas are projected in the algorithm below:

### 3.1. Results
In Fig. 2 are plotted up to 4 different numerical evaluations of the \( \frac{\partial w}{\partial t} \) Eq. 25 when an aggregation of bacteria performs space-time displacements. Space variables is given by the radial part expressed in nm whereas time in units of 0.01 s. In (A) we see the case where there are aggregation while the agglomeration prefers to be in a radius of 0.4 nm. A similar case is seen in (B) but a small part of the aggregation performs translation from 0.1 nm to 1 nm. In (C) the bacteria aggregation makes a pure radial translation, but again only a small fraction of the total population achieved such translation.

**The Machine Learning Explanation**
Plot (D) can be explained in terms of the Mitchell’s criteria: once the bacteria population have skipped their obstacles and reached their objective, from the angle of the Internet of Nano Things is possible to anticipate the dynamics since bacteria have been able to travel various space-time points. Therefore by knowing these points the deployment of antigen agents would have adverse effects on the bacteria population. Thus in plot (D) we can see the asymmetric form of the distribution of bacteria in space and time. Therefore by assuming that the bacteria have experienced unstoppable translations it gives confidence to the expected nano devices as to to tackle down them in an efficient manner.

**Algorithm Explanation** The Machine Learning Algorithm 1 presents a simulation of the pathway of a random aggregation of bacteria in the plane X-Y. The algorithm contains up to three loops, one is to perform all possible tasks that bacteria might carry out. Next loop has as target the performance of bacteria to make a spatial displacement. A third loop targets to determine the variation of the probability in time. All this allows us to estimate the best performance. Thus the information is saved in slides lying in the X-Y plane. last lines of
Machine Learning Algorithm 1

1 SET FREE PARAMETERS
2 define the \((X, Y)\) space-time objective
3 DO \(k=1, K\) TASKS
4 \(x_ky_k = x_{k-1}y_{k-1} + x_ky_k\)
5 DO \(n=1,N\) performances
6 DO \(q=1,Q\)
7 \(\frac{dx}{dt}\) probability
8 IF \(q=Q\) THEN
9 selects best estimates best PERFORMANCE
10 saves \(x_ky_k\) space-time safety slides
11 END IF
12 END DO
13 END DO
14 IF \(x_ky_k = (X, Y)\) THEN
15 save trajectory
16 end task EXPERIENCE gained
17 ENDF
18 ENDDO
19 next task \(k = k + 1\)
20 END

algorithm is reserved to save trajectories and gain experience looking next task as seen in \(k = k + 1\).

Figure 2. Smooth contour plots [13] for Eq.25 for different bandwidth. The usage of this technique of plotting allows us to distinguish the effect of the Feynman path integral as a model to describe bacteria communications.
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