

Curvature tensor and collective behavior in a population of bacteria

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Abstract

In this work, from a geometric point of view, we analyze the SET model (Schweitzer, Ebeling and Tilch) of the mobility of a bacterium. Biological systems are out of thermodynamic equilibrium and they are subject to complex external or internal influences that can be modeled in the form of noise or fluctuations. In this sense, due to the stochasticity of the variables, we study the probability of finding a bacteria with a speed v in the interval $(v, v + dv)$ or, from a population point of view, we can interpret the probability density function as associated with finding a bacterium with a speed v in the interval $(v, v + dv)$. We carry out this study from the stationary probability density solution of the Fokker-Planck equation and using the structure of the statistical manifold related with the stationary probability density, we study the curvature tensor in terms of two coordinates associated with the state of mobility of the bacteria and the environmental conditions. Taking as reference the geometric interpretations found in the framework of equilibrium thermodynamics, our results suggest that bacteria have an effective repulsive interaction that increases with mobility. These results are compatible with the behavior of populations of bacteria that form biofilms when their mobility decreases.

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I. INTRODUCTION

Nonequilibrium systems arise in a wide range of situations with very different phenomenologies. One of these situations, often called active matter, energy is dissipated at the microscopic scale in the bulk so that each constituent of the system has an irreversible dynamic. In particular, a population of bacteria is a system where each element takes energy from the environment using it in internal processes as well as to move in search of nutrients. The model that we use in this work and that contemplates these characteristics is the SET model (Schweitzer, Ebeling and Tilch) [1], which basically consists of three energy contributions, one takes into account how the bacterium take energy from the environment, a second term associated with energy invested in internal processes and a third term linked to energy dissipation due to mobility. This model considers stochastic effects, that is external noise. It has been successfully used in the study of motions of microscopic biological objects [2], such as cells or bacteria, which can be adequately described by Langevin dynamics. In this work we will focus on the problem of bacterial mobility from a population perspective.

In order to consider the stochastic effects due to fluctuations in the environment, we consider the Fokker-Plank equation (FP) for the SET model and we focus on the stationary solution $w_{s_v}(v)$ which is the probability density function that the bacterium has a velocity v in the interval $(v, v + dv)$, or from a population point of view, the probability density function associated with finding a bacterium with a speed v in the interval $(v, v + dv)$.

Our study is centered on a geometric perspective, fundamentally because this point of view allows us to link behavior of a population with microscopic aspects such as the existence of an effective interaction between mobile bacteria. [We think that this approach is particularly interesting because if, on the one hand, we have knowledge of the probability density function that describes a system out of equilibrium, and on the other hand, we take as reference the results between the microscopic and macroscopic descriptions of equilibrium, we can study and analyze the problem out of equilibrium in the context of the theoretical framework of statistical manifold \[3\].](#) For the construction of our geometric approach, we use the theoretical framework of Amari [4], associating a statistical manifold to the density function $w_{s_v}(v)$. Since $w_{s_v}(v)$ can be described in terms of two parameters, the statistical manifold associated is two-dimensional. Following this idea, we will see that by identifying a dimensionless velocity, we can write the probability density function in exponential form

[5] in terms of two parameters (θ_1, θ_2) so that by analogy with equilibrium densities we identify a macroscopic potential $\psi(\theta_1, \theta_2)$. This identification allows to calculate the geometric elements as well as being an aid in the physical interpretations of the system.

For physical interpretations we support ourselves on what we know about the geometry of systems in equilibrium. For classical systems, a non-zero scalar curvature κ is associated with the existence of an interaction potential between the constituents of the system. For example, the sign of κ gives us information about the attractive or repulsive nature of the interaction while the singularities of κ are associated with changes in the collective behavior of the system. For the two-dimensional case, the curvature tensor R has only one independent non-zero element namely R_{1212} and it satisfies the relation $\kappa = (2/\det(g_{ij})) R_{1212}$ [6, 7], where g_{ij} are the elements of the metric tensor. The method of Riemann geometry has been fruitful in equilibrium thermodynamics and we expect that differential-geometrical methods become important in non-equilibrium processes. Bearing in mind this fact, we will focus on the study of R_{1212} to analyze the collective behavior of the population of bacteria [8] as well as the character of their effective interactions. Moreover, in our particular case, the geometric elements of the two-dimensional manifold can be constructed from a macroscopic potential $\psi(\theta_1, \theta_2)$ due to the exponential form of the probability density function mentioned above.

Our work has the following structure. In the next section we will present the relevant aspects of the SET model. Section III will be dedicated to the discussion of the stationary probability density function as a solution to the FP. In section IV we present the geometric elements in the context of the SET model as well as the interpretations of the stochastic variables. Finally, in section V we present a discussion of the results in conjunction with our conclusions.

II. RELEVANT ASPECTS OF THE SET MODEL

The SET model assumes that a particle can take energy from the environment at a rate q , which is assumed to be constant. It is stored in an internal deposit $E(t)$ and then it is converted into kinetic energy at a rate $d[v, E(t)]$, which generally is a function of the velocity v . The reservoir energy $E(t)$ is dissipated at a rate $G[E(t)]$ which depends on metabolic processes and takes into account all forms of non-mechanical energy dissipation

(mainly in cellular methabolic processes). If the distribution of resources in the environment is inhomogeneous, the rate of absorption of nutrients could depend on the position. The rate of energy stored is then described by the equation.

$$\frac{dE(t)}{dt} = q - G[E(t)] - d[v, E(t)] \quad (1)$$

The total energy $E_T(t)$ of the active particle at time t is given by

$$E_T(t) = E_0(t) + E(t), \quad (2)$$

where E_0 is the mechanical energy of the active particle. In this work we consider that the interaction between bacteria is due only to collisions between them.

The balance equation for the mechanical energy reads

$$\frac{dE_0(t)}{dt} = d[v, E(t)] - \gamma v^2 \quad (3)$$

where γ is the friction coefficient of the particle.

Considering that $E_0 = mv^2/2$, we can rewrite (3) in a more explicit form

$$m\mathbf{v}\frac{d\mathbf{v}}{dt} - d[v, E(t)] + \gamma v^2 = 0, \quad (4)$$

where $v = |\mathbf{v}|$.

Based on Eq. (4), the stochastic equation of motion for the active Brownian particles take the form [1]

$$m\frac{d\mathbf{v}}{dt} = -\gamma\mathbf{v} + d_2E(t)\mathbf{v} + \mathbf{F}(t), \quad (5)$$

where we have assumed that $d[v, E(t)] = d_2E(t)v^2$. $\mathbf{F}(t)$ is a stochastic force and it have a δ -correlated time dependence [9]

$$\langle \mathbf{F}(t) \rangle = 0; \quad \langle \mathbf{F}(t)\mathbf{F}(t') \rangle = 2\gamma k_B T \delta(t - t'). \quad (6)$$

An important parameter to take into account in our mobility analysis is the mechanical efficiency σ . For the Brownian particle with an internal energy reservoir, the efficiency ratio is defined as [1]

$$\sigma = \frac{(dE_{out}/dt)}{(dE_{in}/dt)} = \left\langle \frac{d[v, E(t)]}{q} \right\rangle, \quad (7)$$

The input of energy per time interval dE_{in}/dt is given by the take-up q , while the output energy rate dE_{out}/dt is defined as the amount of mechanical energy available from the

micromotor $d[v, E(t)] = d_2 E(t) v^2$. Assuming that the energy store quickly reaches a quasi-stationary state, we have from (1) $q - G(E_s) - d(v, E_s) = 0$. If it is further assumed that the rate of energy dissipation is proportional to the energy of the deposit we have $G(E_s) = c E_s$. Under these conditions, the stationary efficiency σ_s is written as

$$\sigma_s = \left\langle \frac{d_2 v^2}{c + d_2 v^2} \right\rangle. \quad (8)$$

σ_s is a parameter that can vary between 0 and 1. When it takes the value 1 we will say that the bacterium optimizes the use of energy for mobility.

III. MOBILITY AND THE FOKKER-PLANCK EQUATION

In order to consider the stochastic effects due to fluctuations in the environment, we construct the Fokker-Planck equation (FP) for active Brownian particles. The solution of the FP equation allows us to find the probability density function $w(v, t)$ of a bacterium with a velocity between v and $v + dv$. To simplify our treatment we consider, from now on, one-dimensional description. We start the construction of the FP equation by means of the Langevin equation

$$\dot{v} = f(v) + g(v)\xi(t), \quad (9)$$

where $F(t) = g(v)\xi(t)$ represents the stochastic force.

The general expression of the FP equation for the probability density $w(v, t)$ is

$$\frac{\partial w}{\partial t} = -\frac{\partial}{\partial v} (f(v)w(v, t)) + \frac{\partial^2}{\partial v^2} (g^2(v)w(v, t)). \quad (10)$$

The stochastic force $F(t)$ in the SET model satisfies [9]

$$\langle F(t) \rangle = 0 \quad \text{y} \quad \langle F_i(t) F_j(t) \rangle = 2\gamma k_B T. \quad (11)$$

Working in one dimension, the stochastic force verifies $\langle F^2(t) \rangle = 2\gamma k_B T$.

The generalized Langevin equation in the SET model has the form

$$\dot{v} = -\frac{\gamma v}{m} + \frac{d[v, E(t)]}{m v^2} v + \frac{F(t)}{m}. \quad (12)$$

Comparing (9) with the above expression we identify the function

$$f(v) = \left(-\frac{\gamma}{m} + \frac{d[v, E(t)]}{m v^2} \right) v. \quad (13)$$

Analogously, using (11) we identify the function

$$g^2(v) = \frac{2\gamma k_B T}{m^2} = \frac{\epsilon}{m^2}. \quad (14)$$

Taking into account (10), the equation of FP for the SET model has the following expression

$$\frac{\partial w}{\partial t} = -\frac{\partial}{\partial v} \left[\left(-\gamma + \frac{d[v, E(t)]}{v^2} \right) \frac{v}{m} w \right] + \frac{\epsilon}{m^2} \frac{\partial^2 w}{\partial v^2} \quad (15)$$

In particular we are interested in the stationary solution of this equation, we noted w_{Sv} . In order to do this, we set $(\partial w / \partial t) = 0$, this is

$$\frac{\partial}{\partial v} \left[\left(\gamma - \frac{d[v, E]}{v^2} \right) \frac{v}{m} w + \frac{\epsilon}{m^2} \frac{\partial w}{\partial v} \right] = 0. \quad (16)$$

The result (16) leads us to

$$\left(\gamma - \frac{d[v, E]}{v^2} \right) \frac{v}{m} w + \frac{\epsilon}{m^2} \frac{\partial w}{\partial v} = \text{Constant}. \quad (17)$$

Taking into account (3) we have that the first term of (17) can be written as

$$\left(\gamma - \frac{d[v, E]}{v^2} \right) \frac{v}{m} w = -\frac{1}{vm} \frac{dE_0}{dt} w. \quad (18)$$

From the result (18) we can interpret the first term of (17) as a fluctuation of the inverted mechanical energy in the mobility of the bacteria. On the other hand, the second term of (17) represents the fluctuation of the stochastic force $F(t)$. In the steady state, these two terms are balanced, that is $\text{Constant} = 0$ in equation (17). Concluding that

$$\left(\gamma - \frac{d[v, E]}{v^2} \right) \frac{v}{m} w_{Sv} + \frac{\epsilon}{m^2} \frac{\partial w_{Sv}}{\partial v} = 0, \quad (19)$$

where $w_{Sv}(v)$ is the probability density function with respect to of the velocity v .

Likewise for the steady state we have (1)

$$\frac{dE}{dt} = q - d[v, E] - G[E(t)] = 0, \quad (20)$$

that together with the conditions $d[v, E] = d_2 E v^2$ and $G[E] = cE$, leads us to

$$\left(\gamma - \frac{d[v, E]}{v^2} \right) = \left(\gamma - \frac{d_2 q}{c + d_2 v^2} \right). \quad (21)$$

Returning to the equation (19) we obtained

$$\frac{\partial \ln w_{Sv}(v)}{\partial v} = \left(\frac{d_2 q}{c + d_2 v^2} - \gamma \right) \frac{mv}{\epsilon}. \quad (22)$$

Integrating the above expression respect to v

$$w_{s_v}(v) = w_0 \exp\left(-\frac{m\gamma v^2}{2\epsilon}\right) \left(1 + \frac{d_2}{c}v^2\right)^{\frac{mq}{2\epsilon}}. \quad (23)$$

Remembering that $d[v, E]$ represents the rate of energy that is converted into kinetic energy used in the mobility of the bacteria, and $G(E_s)$ represents the dissipation of energy in a non-mechanical way, we can distinguish two regimes. The first regimen is when $d/G = [(d_2v^2)/c] > 1$, we have that more energy is dissipated by the translation of the bacteria (mobility) than in methabolic processes. The second regime is given by $d/G = [(d_2v^2)/c] < 1$, more energy is dissipated by methabolic processes than by the mobility of the bacteria. The recognition of these two regimes suggests us to choose as stochastic variable for the description of the population behavior of the bacteria to

$$x = \sqrt{\frac{d_2}{c}}v, \quad (24)$$

where the variable x represents a dimensionless velocity.

In terms of the dimensionless velocity x we can be described more simply the two schemes displayed above. The first regime where the kinetic part dominates is written as $x^2 > 1$, and the second regime where methabolic processes dominate is written as $x^2 < 1$. Likewise, using the stochastic variable x , the normalized probability density (23) can be written as an exponential family [5, 10]

$$w_{s_x}(x) = \exp\left[-\theta_1 x^2 + \theta_2 \ln(1 + x^2) - \psi(\theta_1, \theta_2)\right], \quad (25)$$

where

$$\theta_1 = \frac{m\gamma c}{2\epsilon d_2} = \frac{m}{4k_B T} \frac{c}{d_2}, \quad \theta_2 = \frac{mq}{2\epsilon} = \frac{m}{4k_B T} \frac{q}{\gamma}, \quad (26)$$

and

$$\psi(\theta_1, \theta_2) = \psi(\theta) = \ln \left[\int_{-\infty}^{\infty} \exp\left[-\theta_1 x^2 + \theta_2 \ln(1 + x^2)\right] dx \right]. \quad (27)$$

The exponential form of the probability density function is the characteristic way in which the equilibrium densities are presented. In this sense, and making an analogy with equilibrium, we identify the function $\psi(\theta_1, \theta_2)$ as a non-equilibrium macroscopic potential [5].

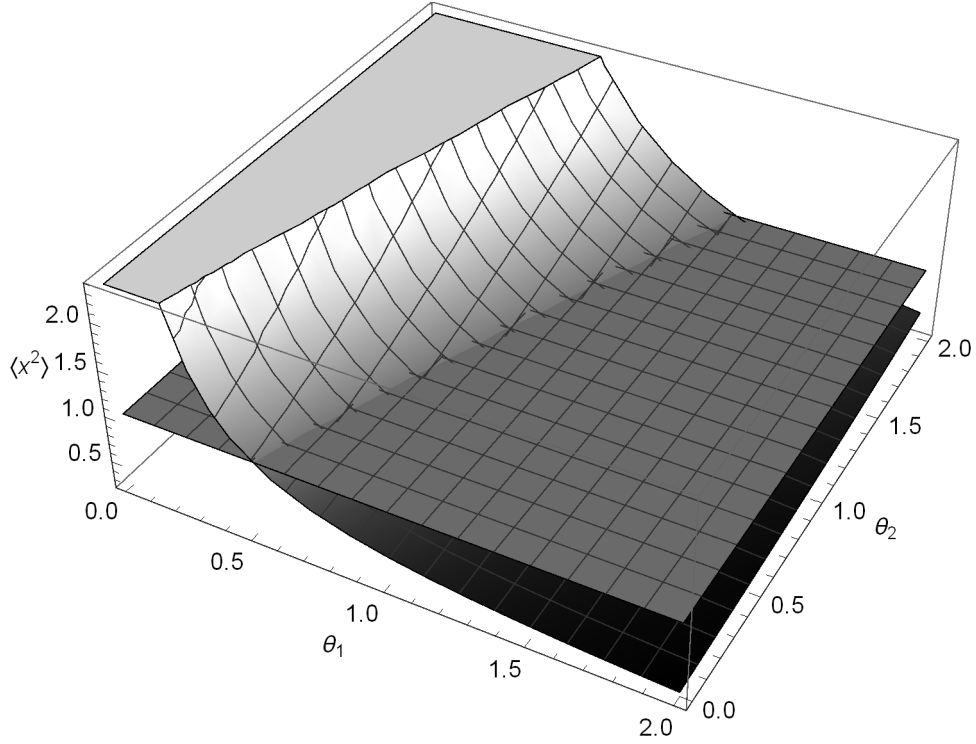


Figure 1: In this figure we show the behavior of $\langle x^2 \rangle$ as a function of (θ_1, θ_2) in conjunction with the constant function $\langle x^2 \rangle = 1$.

Taking into account the relationships (26) that indicate how the parameters θ_1 and θ_2 are defined in terms of the model variables, we can interpret that the parameter θ_1 is associated with internal processes of the bacteria and the parameter θ_2 is associated with the relationship of the bacteria with the environment.

Moreover, keeping in mind the stochastic effects and considering that the diffusion coefficient is proportional to $\langle v^2 \rangle$ [8], we can study the bacterial mobility through the diffusion coefficient using (24). In this sense, the analysis of bacterial mobility as a function of θ_1 and θ_2 can be carried out based on the behavior of $\langle x^2 \rangle$ due to (24). On the other hand, taking advantage of the fact that the probability density function (25) belongs to the exponential family, we can easily calculate the mean value $\langle x^2 \rangle$ through the macroscopic potential ψ using the relation [11]

$$\langle x^2 \rangle = -\frac{\partial \psi(\theta)}{\partial \theta_1}. \quad (28)$$

The analysis of $\langle x^2 \rangle$ in terms of θ_1 and θ_2 can be carried out by observing Figure 1 where we have represented $\langle x^2 \rangle$ depending on the parameters (θ_1, θ_2) and the plane $\langle x^2 \rangle =$

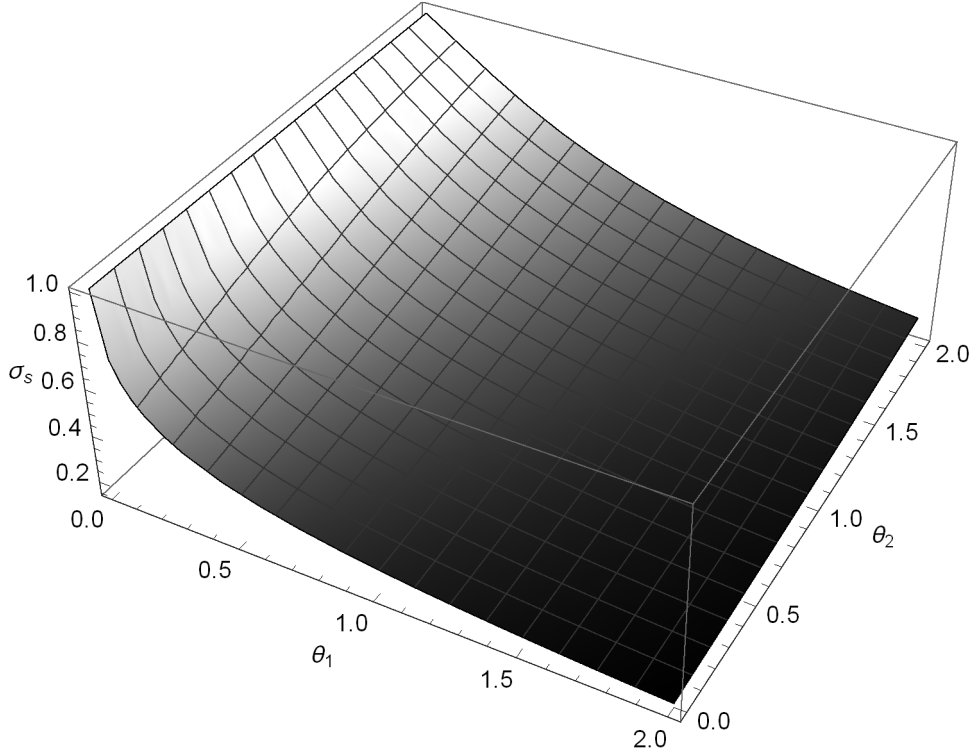


Figure 2: Stationary efficiency σ_s in terms of the parameters θ_1 and θ_2

1. We observe that for the parameters (θ_1, θ_2) there is a region where $\langle x^2 \rangle < 1$ and another where $\langle x^2 \rangle > 1$. In particular and roughly, we observe that for θ_1 values smaller than 0.5 ($\theta_1 \lesssim 0.5$) and a weak dependence on θ_2 , the mean value $\langle x^2 \rangle$ grows abruptly. We associate this behavior of $\langle x^2 \rangle$ with the fact that for low values of θ_1 , the mobility of the bacteria is high. In this analysis we do not consider that there must be a balance between the energy q taken from the medium and the energy dissipated due to the methabolic processes G and the mobility d . One way to consider this balance is to study the stationary efficiency σ_s given by the relation (8)

$$\sigma_s = \left\langle \frac{d_2 v^2}{c + d_2 v^2} \right\rangle = \left\langle \frac{d_2 v^2 / c}{1 + d_2 v^2 / c} \right\rangle = \left\langle \frac{x^2}{1 + x^2} \right\rangle. \quad (29)$$

To understand the behavior of σ_s we use the density function w_{s_x} (25), so that

$$\sigma_s = \left\langle \frac{x^2}{1 + x^2} \right\rangle = \int_{-\infty}^{\infty} \left(\frac{x^2}{1 + x^2} \right) w_{s_x}(x) dx. \quad (30)$$

In Figure 2 we show the stationary efficiency σ_s in terms of the parameters θ_1 and θ_2 . When θ_2 grows and for small values of θ_1 , we can see that the efficiency is close to unity.

Interpreting this behavior through expressions (26) we can say that the efficiency σ_s increases with the rate of energy q taken from the environment and the conversion of energy from the deposit into kinetic energy d_2 . This behavior is compatible with what we observe in the $\langle x^2 \rangle$ function, that is, the region of the domain (θ_1, θ_2) of high mobility ($\langle x^2 \rangle > 1$) is compatible with the region of high efficiency σ_s .

IV. GEOMETRIC PERSPECTIVE

In this section, we use the Amari geometric approach [4] to study a family of probability density functions (PDF) and its applications to nonequilibrium processes. Let $p(x, \theta)$ a PDF described by a random variable x and parameters $\theta = (\theta^1, \theta^2, \dots, \theta^n)$ that characterize a system. A set of PDFs

$$S = \{p(x, \theta), \theta \in \Omega \subset \mathbb{R}^n\}, \quad (31)$$

becomes an n -dimensional statistical manifold having θ^i coordinates. According to information geometrical theory, we define a metric tensor $g_{ik}(\theta)$:

$$g_{ik}(\theta) = E[\partial_i l(x, \theta) \partial_k l(x, \theta)] = -E[\partial_i \partial_k l(x, \theta)], \quad (32)$$

where $l(x, \theta) = \ln p(x, \theta)$ and $E[\cdot]$ is the expectation operation with respect to $p(x, \theta)$. The Christoffel connection coefficients are given by:

$$\Gamma_{ijk}(\theta) = \frac{1}{2} (\partial_k g_{ij}(\theta) + \partial_j g_{ik}(\theta) - \partial_i g_{jk}(\theta)). \quad (33)$$

The curvature tensor R gives a measure of the curvature of the manifold. In the case $R = 0$, the manifold is said to be flat. In this sense the covariant component R_{ijkl} plays an important role in the analysis of the curvature of the manifold:

$$\begin{aligned} R_{ijkl} &= g_{im} R_{jkl}^m = \\ &= \partial_k \Gamma_{ijl} - \partial_l \Gamma_{ijk} - \Gamma_{mik} \Gamma_{jl}^m + \Gamma_{mil} \Gamma_{jk}^m \end{aligned} \quad (34)$$

with

$$\Gamma_{jk}^i = \frac{1}{2} g^{li} (\partial_k g_{lj} + \partial_j g_{lk} - \partial_l g_{jk}) \quad (35)$$

and

$$\Gamma_{ij}^l = \Gamma_{ijk} g^{lk} \quad (36)$$

where g^{ij} denotes the inverse of the metric tensor g_{ij} .

An alternative calculation structure appears if the probability density function $p(x, \theta)$ belongs to the exponential family, that is, when it has the form

$$p(x, \theta) = \exp \left(C(x) + \sum_i^m \theta_i F_i(x) - \psi(\theta) \right), \quad (37)$$

where $C(x)$ and $F_i(x)$ are arbitrary functions of x , and $\psi(\theta)$ is a function of θ_i coordinates. In this case, the metric tensor $g_{ij}(\theta)$ defined in (32) and the covariant coefficients are straightforwardly obtained from equation [4, 12]

$$g_{ij}(\theta) = \frac{\partial^2 \psi(\theta)}{\partial \theta_i \partial \theta_j}, \quad (38)$$

$$\Gamma_{ijk}(\theta) = \frac{1}{2} \partial_i \partial_j \partial_k \psi(\theta). \quad (39)$$

In our case, it should be noted that the parameters θ_1 and θ_2 will now be the coordinates of the statistical manifold associated with the stationary probability density (25) and the macroscopical potential (27). As we commented in the introduction, in our geometric perspective we take the equilibrium results as a reference [14]. In particular we will focus on the study of the curvature tensor because for a two-dimensional manifold the information contained in the curvature tensor is equivalent to that contained in the scalar curvature. In this sense, the tensor R_{1212} gives us information about the macroscopic behavior of the system so that we interpret the singularities of the tensor as a change in bacterial mobility [8].

It is worth noting that, if we consider the equilibrium density functions, this formalism reproduces the geometric structure found by Ruppeiner for the space of equilibrium states[15]. In Ruppeiner formalism the metric elements are obtained as the second derivatives of the corresponding thermodynamic potential. The method of Riemann geometry has been fruitful in equilibrium thermodynamics and we expect that differential-geometrical methods become important in non-equilibrium processes.

The study of the behavior of the R_{1212} component as a function of θ_1 and θ_2 was carried out numerically. The strategy used was to take advantage of knowing the macroscopic potential ψ given by the relationship (27) and to calculate numerically the relationships (34), (38) and (39). In Figure 3 we graph the results of our calculations. In order to carry out a geometric study of bacterial mobility, we observe that Figure 3 has two important characteristics on

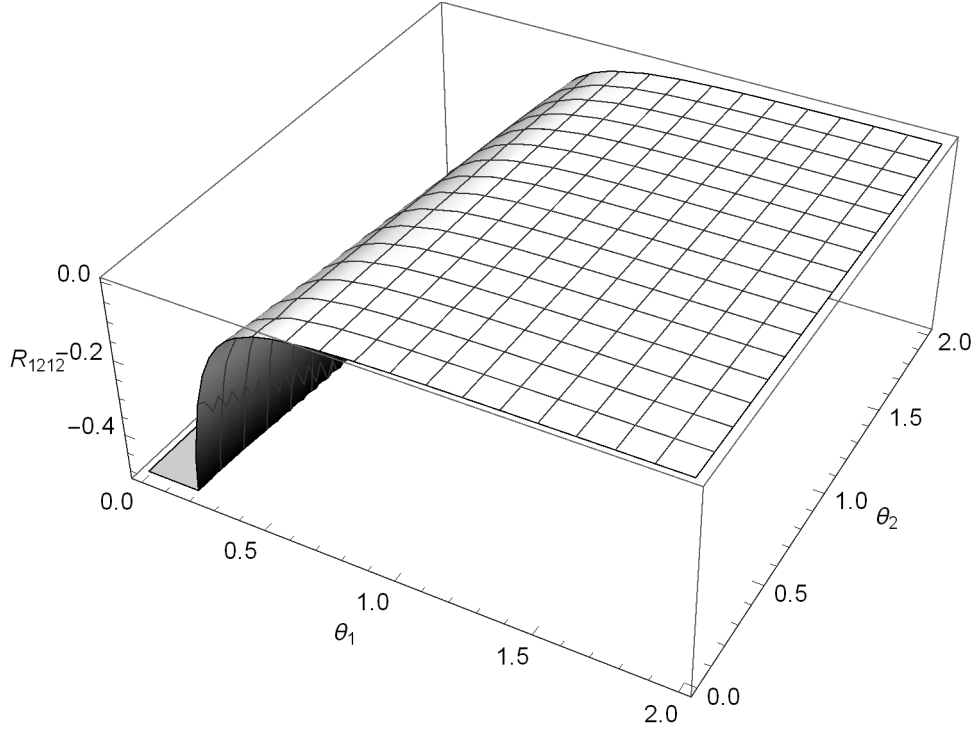


Figure 3: Element R_{1212} of the curvature tensor as a function of θ_1 and θ_2 coordinates

the behavior of the component of the curvature tensor. The first is associated with the fact that R_{1212} is always negative and close to zero for large values of θ_1 ($\theta_1 > 0.5$). The second characteristic is the singular behavior of R_{1212} for small values of θ_1 ($\theta_1 \lesssim 0.5$). It is interesting to remark that the region of the domain (θ_1, θ_2) where R_{1212} has a singular behavior is compatible with the region of greater mobility characterized with $\langle x^2 \rangle > 1$ and with an efficiency σ_s close to one.

From the perspective of the mobility of bacteria and in accordance with the results presented in the previous section, the singular behavior of R_{1212} can be interpreted as a change in the collective behavior of the bacterial population [8]. In other words, bacteria becoming more mobile in the region for which R_{1212} becomes more negative.

For a classical system, the information about the repulsive or attractive character of the interaction of its constituents is found in the sign of the scalar curvature κ [14]. If $\kappa = 0$ the interaction is zero (ideal system), if $\kappa > 0$ the interaction is attractive and if $\kappa < 0$ the interaction is repulsive [14]. For the particular case of a two-dimensional manifold and when the geometric elements can be constructed from a macroscopic potential $\psi(\theta_1, \theta_2)$, the scalar curvature κ is related to the curvature tensor R through the expression $\kappa = (2/\det(g_{ij})) R_{1212}$

[6]. Since $\det(g_{ij}) > 0$, the information about the attractive or repulsive character of the interaction will be contained in the sign of R_{1212} .

We associate the stationary probability density function $w_{s_v}(x)$ with the probability of encountering a bacterium with a speed v in the interval $(v; v + dv)$. But nevertheless, from a population point of view, the presence of other bacteria can be visualized in the model parameters. For example the presence of neighboring bacteria will modify the rate of energy q taken from the environment. Although in our representation bacteria are thought of as elements that interact only through collisions between them, within the population perspective, the sign of R_{1212} gives us information about an effective interaction between bacteria. As we mentioned previously, in classical terms, a null curvature means that there is no interaction between the constituents of the system (in our case bacteria), the positive sign is associated with an attractive effective interaction and the negative sign with a repulsive interaction. In this sense, from Figure 3 we can interpret that the interaction between bacteria is always repulsive and this interaction increases as θ_1 becomes smaller.

Related the behavior of R_{1212} with $\langle x^2 \rangle$ we can say that the increase in mobility in the population is correlated with by an increase of the effective repulsion between bacteria.

V. SUMMARY AND CONCLUSIONS

In this work we have addressed some characteristic aspects of a population of bacteria. With this target we have used the SET model (Schweitzer, Ebeling and Tilch), which allows us to think the bacterium as an energy bag that it takes from the environment and that can dissipate in two different ways, transformed into kinetic energy or by internal metabolic processes.

We have constructed the Fokker Planck equation for the SET model and have found its stationary solution w_{s_v} . Through the definition of a dimensionless velocity x we have written the probability density function w_{s_x} in exponential form and from there we have identified the macroscopic potential $\psi(\theta_1, \theta_2)$. Using $\psi(\theta_1, \theta_2)$ we have built the geometric structure. In particular we focus on the study of the curvature tensor R and, since our problem is reduced to a two-dimensional manifold, we only study the component R_{1212} .

Our geometric approach allows us to analyze the macroscopic responses of the system. In the first place we have found that the region of greatest mobility of bacteria corresponds

to the region of the domain (θ_1, θ_2) where R_{1212} has a singular behavior. This behavior of R_{1212} can be understood as a phase transition of the system [8], where it passes from a state of low mobility to another state of high mobility.

On the other hand, we observe that R_{1212} is negative and its absolute value is arbitrarily large when $\theta_1 \lesssim 0.5$. From a population point of view, we interpret the negative sign as the presence of an attractive effective interaction between the bacteria. If we take into consideration that $R_{1212} = 0$ means that the interaction is null, we can conclude that in the region where R_{1212} becomes singular, the effective interaction between bacteria becomes large in correlation with the increase in bacterial mobility.

As a final conclusion we can say that our geometric point of view allows us to conjecture the existence of an interaction between bacteria associated with the state of bacterial mobility. In summary, in a state of low mobility the effective interaction is small and in a state of high mobility the effective interaction is large.

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