A Geometrical and Numerical Study of the Main Sizes of the Lotka-Volterra Models

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Abstract—The blend of geometry and numerical analysis that is taking place in the present material produces a subject with can gives a lots of detail and richness for the case of dynamical models arising in mathematics, science and engineering. The goal of this paper is the geometrical and numerical study of the main sizes of the mathematical models of the multispecies interactions which are important in determining long-time dynamics, based on the application of various notions from the theory of dynamical systems to the numerical approximation of initial value problems over long-time intervals. The numerical methods are widely used for the study of complicated temporal behavior of dynamical systems, in order to approximate different types of invariants sets or invariant manifolds and also to extract statistical information on the dynamical behavior in the computation of natural invariant measures or almost invariants sets. The present study is a interplay between dynamical systems geometrical theory and computational calculus of dynamical systems, knowing that the theory provides a framework for interpreting numerical observations and foundations for efficient numerical algorithms. We perform a computational study for the case of four important examples: prey-predator 2D Lotka-Volterra system, Bailey model for the evolution of epidemics, classical Kermack-McKendrick model of evolution of epidemics and the prey-predator 3D Lotka-Volterra system.

I. INTRODUCTION

In many branches of physics, engineering and applied mathematics we find systems described by coupled ordinary differential equations. The interest in chaotic systems bursted with one decade delay after the publication of Lorenz's 1962 seminal paper. Rather similarly, only after 2 years after construction of Chua's 3rd order nonlinear electrical circuit in 1982, it was observed by Matsumoto that the Chua's circuit exhibits(for some parametrization and wild nonlinearity) may be chaotic behaviour, and only in 1986 it was proved by Chua-Komuro-Matsumoto that the behavior (even for a slight nonlinearity) is really chaotic [15]. Belonging to this type of systems, dynamical systems are concerned primarily with making qualitative study about the behaviour of systems which evolve in time given knowledge about the initial state of the system itself.

This paper is devoted to studying conservation laws for Volterra-Lotka type systems and others systems arising from biology and relationship between this in the geometric framework of Classical Mechanics. The Lotka-Volterra model indeed may be the simplest possible predator-prey model. Nevertheless, it is a useful tool containing the basic properties of the real predator-prey systems, and serves as a robust basis from which it is possible to develop more sophisticated models. The Lotka-Volterra model is very important in population modeling. The analysis of the system may be used, in particular, to describe the dynamics in models from ecology, molecular biology, ecosystems, and chemical systems (for example a model for oxygen depletion in a system of sewage could be developed), and also in the detection of failures in civil structures.

The viewpoint is geometric and we also compute and characterize objects of dynamical significance, in order to understanding the mathematical properties observed in numerical computation for dynamical systems.

We will present four very important examples. First three examples represent so called *variational dynamical systems*, that is dynamical systems described by a system of ordinary differential equations which can be written as the Euler-Lagrange equations associated to Lagrangian L,

$$\frac{d}{dt}\left(\frac{\partial L}{\partial y^i}\right) - \frac{\partial L}{\partial x^i} = 0 \tag{1}$$

These examples are: prey-predator 2D Lotka-Volterra system ([9], [13], [18], [19]), Bailey model for the evolution of epidemics ([2], [7], [13]), classical Kermack-McKendrick model of evolution of epidemics ([7], [13]). This dynamical systems are included in the presymplectic case because the 2-form ω_L associated to the corresponding Lagrangian is degenerate. Finally, we present different versions of the well-known prey-predator 3D Lotka-Volterra system. This system is not a variational dynamical system. However, we can give more Hamilton-Poisson realizations of this bi-Hamiltonian system like in the 2D case.

II. THE PREY-PREDATOR 2D LOTKA-VOLTERRA SYSTEM

Let us consider the system of ordinary differential equations ([11]):

$$\begin{cases} \dot{x} = ax - bxy \\ \dot{y} = -cy + dxy \end{cases}, \ a,b,c,d > 0 \tag{2}$$

This system is called *Lotka-Volterra system* and represents a complex biological system model, in which two species x and y live in a limited area, so that individuals of the species y (predator) feed only individuals of species x (prey) and they feed only resources of the area in which they live. Proportionality factors a and c are respectively increasing and decreasing prey and predator

populations. If we assume that the two populations come into interaction, then the factor b is decreasing prey population x caused by this predator population y and the factor d is population growth due to this population x. The evolution system (2) can be written in the form of Euler-Lagrange equations (1), where the Lagrangian L is

$$L = \frac{1}{2}\left(\frac{\ln y}{x}\dot{x} - \frac{\ln x}{y}\dot{y}\right) + c\ln x - a\ln y - dx + by$$

and the corresponding Hamiltonian H is

$$H = \frac{\partial L}{\partial \dot{x}}\dot{x} - \frac{\partial L}{\partial \dot{y}}\dot{y} - L = -c\ln x + a\ln y + dx - by$$

Let us remark that the total energy $E_L = H$ is a *conservation law* for prey-predator system (2) and the Lagrangian L is singular.

If we consider the Cartan forms associated to L,

$$\theta_L = \frac{\partial L}{\partial \dot{x}}dx + \frac{\partial L}{\partial \dot{y}}dy \quad \text{and} \quad \omega_L = -d\theta_L, \text{ then has a}$$

constant rank, equal with *2*, and so, we will obtain a pre-symplectic system $\left(TR^2, \omega_L, dE_L\right)$.

According to [12] and [14] the Lotka-Volterra equations (2) has the following *Hamilton-Poisson realization*

$$\dot{x}^i = J\nabla H, \text{ where } H = c\ln x + a\ln y - dx - by \text{ is}$$

the Hamiltonian and $J = \begin{pmatrix} 0 & xy \\ -xy & 0 \end{pmatrix}$ is the Poisson

bracket.

III. THE BAILEY MODEL FOR THE EVOLUTION OF EPIDEMICS

In Bailey model for the evolution of epidemics are considered two classes of hosts: individuals suspected of being infected, whose number is denoted by x and individuals infected carriers, whose number we denote by y. Assume that the latency and average removal rate is zero and then remain carriers infected individuals during the entire epidemic, with no death, healing and immunity.

It is proposed that, in unit time, increasing the number of individuals suspected of being infected to be proportional to the product of the number of those infected them.

These considerations lead us to the evolutionary dynamical system given by ([13]):

$$\begin{cases} \dot{x} = -kxy \\ \dot{y} = kxy \end{cases}, \quad k > 0 \qquad (3)$$

The model is suitable for diseases known animal and plant populations and also corresponds quite well the characteristics of small populations spread runny noses, dark, people such as students of a class team

First of all, let us remark that we have a conservation law, $x + y = n$. That means that n, the total number of individuals of a population, does not change during the evolution of this epidemic. The equations (3) can be written as Euler-Lagrange equations, where the Lagrangian L is

$$L = \frac{1}{2}\left(\frac{\ln y}{x}\dot{x} - \frac{\ln x}{y}\dot{y}\right) + k(x + y)$$

and the corresponding Hamiltonian H is

$$H = \frac{\partial L}{\partial \dot{x}}\dot{x} - \frac{\partial L}{\partial \dot{y}}\dot{y} - L = -k(x + y).$$

This particular case of Lotka-Volterra system (2) has a *Hamilton-Poisson realization* with the Hamiltonian $H = -k(x + y)$ and the Poisson structure defined by J from above.

IV. THE CLASSICAL KERMACK-MCKENDRICK MODEL OF EVOLUTION OF EPIDEMICS

The classical model of evolution of epidemics was formulated by Kermack (1927) and McKendrick (1932) as follows. Let us denote the numerical size of the population with n and let us divide it into three classes: the number of individuals suspected of x, the number of individuals infected carriers y, and the number of isolate infected individuals z.

For simplicity, we take zero latency period, that all individuals are simultaneously infected carriers that infect those suspected of being infected. Considering the previous example we note the rate constant k_1 of disease transmission. Changing the size of infected carriers depends on the rate k_1 and also depend on k_2, the rate that carriers are isolated. In this way, we have the system ([11]):

$$\begin{cases} \dot{x} & = & -k_1 xy \\ \dot{y} & = & k_1 xy - k_2 y, k_1, k_2 > 0 \\ \dot{z} & = & k_2 y \end{cases} \qquad (4)$$

Let us note that $x + y + z = n$, i.e. the number of individuals of the population does not change. This conservation law tells us not cause deaths epidemic.

The evolution of a dynamic epidemic begins with a large population which is composed of a majority of individuals suspected of being infected and in a small number of infected individuals. Initial number of isolated infected people is considered to be zero.

So, we can consider the subsystem ([13])

$$\begin{cases} \dot{x} & = & -k_1 xy \\ \dot{y} & = & k_1 xy - k_2 y \end{cases}, k_1 > 0, k_2 > 0 \qquad (5)$$

The Lagrangian and Hamiltonian of the system (5) are

$$L = \frac{1}{2}\left(\frac{\ln y}{x}\dot{x} - \frac{\ln x}{y}\dot{y}\right) + k_1(x + y) - k_2\ln x$$

$$H = -k_1(x + y) + k_2\ln x$$

and so, we have a new *conservation law* of (5)

$$H = E_L = -k_1(x + y) + k_2\ln x.$$

If we get back to the Kermack-McKendrick model (4), then we have that the Lagrangian whose Euler-Lagrange equations are really (4) is $\overline{L} = L + \frac{1}{2}(\dot{z} - k_1 y)^2$,

where is the Lagrangian of the subsystem (5).

The corresponding Hamiltonian is given by

$$\overline{H} = -k_1(x+y) + k_2 \ln x + \frac{1}{2}\dot{z}^2 - \frac{1}{2}k_1^2 y^2.$$

Let us observe that the associated Lagrangian $\overline{L}$ is singular and $\omega_{\overline{L}}$ has a constant rank, equal with 1, and so, we will obtain a presymplectic system $(TR^3, \omega_{\overline{L}}, dE_{\overline{L}})$. $E_{\overline{L}} = \overline{H}$ is *the energy* of $\overline{L}$ and $E_{\overline{L}}$ is a conservation law for (4).

V. THE 3D LOTKA-VOLTERRA SYSTEM

In [5] was discussed the next three-dimensional Lotka-Volterra system which models the evolution of competition between three species:

$$\begin{cases} \dot{x} &=& x(cy + z + \lambda) \\ \dot{y} &=& y(x + az + \mu) \\ \dot{z} &=& z(bz + y + \nu) \end{cases} \quad (6)$$

where $a, b, c \in R, \lambda, \mu, \nu > 0$.

Following [5], if $abc = -1$ and $\nu = \mu b - \lambda ab$, then the 3D Lotka-Volterra system (6) admit two conservation laws $H_1 = ab \ln x - b \ln y + \ln z$ and

$H_2 = abx + y - az + \nu \ln y - \mu \ln z$, because (6) is a particular case of a *bi-Hamiltonian system*. The dynamics of (6) has two distinct Hamilton-Poisson realizations $\dot{x}^i = J_1 \nabla H_2$ and $\dot{x}^i = J_2 \nabla H_1$, where

$$J_1 = \begin{pmatrix} 0 & cxy & bcxz \\ -cxy & 0 & -yz \\ -bcxz & yz & 0 \end{pmatrix},$$

$$J_2 = \begin{pmatrix} 0 & cxy(az+\mu) & cxz(y+\nu) \\ -cxy(az+\mu) & 0 & xyz \\ -cxz(y+\nu) & -xyz & 0 \end{pmatrix}.$$

From $J_1 \nabla H_1 = 0$ and $J_2 \nabla H_2 = 0$ we have that H_1, H_2 are Casimir functions of J_1, J_2, ([12]).

VI. NUMERICAL STUDY

Between dynamical systems theory and computation analysis of dynamical systems there is a strong interplay.

Numerical integration is a important, actual and active subject due to the today high computer efficiency (speed and memory), being analysed by extensive theory and a vast range of software, platforms or libraries, [1], [3], [10]. Taking into account that even for the simplest 2D Lotka-Volterra system, the analytical solution is useless:

root of a polynomial with an integral plus the special function Lambert, we must resort to numerical methods in order to have information about the trajectories. Thus, constructing a Matlab-based numerical code, we approximate and characterize different types of invariants and also extract informations on the dynamical behavior and perform comparisons for both different initial conditions associated to the considered problem and for different values of the parameters. In the first stage we focus on the numerical solving of the initial value problems by appropriate numerical methods, such as Runge-Kutta methods (for the 2D case we use a fourth order Runge-Kutta method, [4], and for the 3D case we used a fifth order Runge-Kutta method, [20]). We obtain the numerical solution represented by the approximate values of the solution function for a discrete set of data points. Using this approach we perform a numerical analysis of the conservation laws and main sizes.

A. 2D Lotka-Volterra System
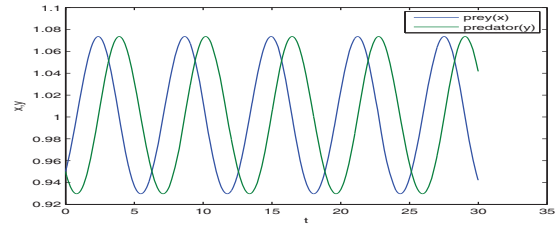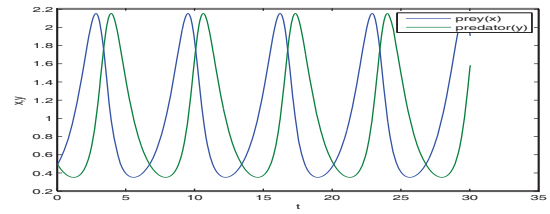
Fig. 1. Profile of the numerical solution (x(t), y(t)), for a = b = c = d = 1 and initial conditions (x0 = 0.5, y0 = 0.5) and (x0 = 0.95, y0 = 0.95)
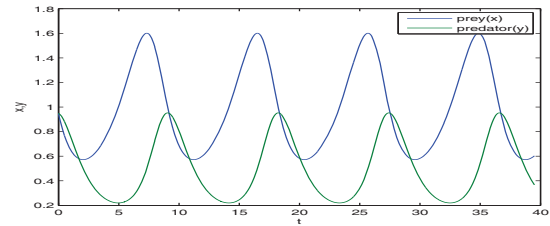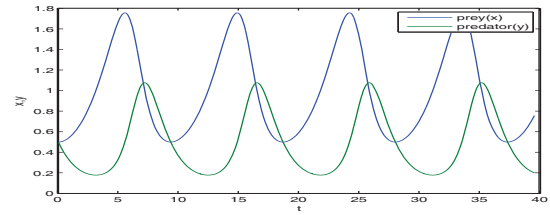

Fig. 2. Profile of the numerical solution (x(t), y(t)), for a = 0.5, b = c = d = 1 and initial conditions (x0 = 0.5, y0 = 0.5), (x0 = 0.95, y0 = 0.95)

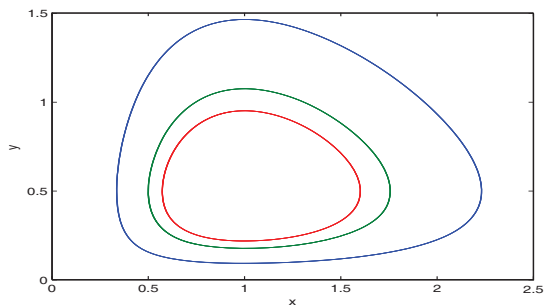Fig. 3. Phase space portrait for a = 0.5, b =c = d = 1 and initial conditions (x0 =0.35, y0 = 0.35), (x0 = 0.5, y0 = 0.5), (x0 =0.95, y0 = 0.95) listed in order from outermost trajectory to innermost trajectory.
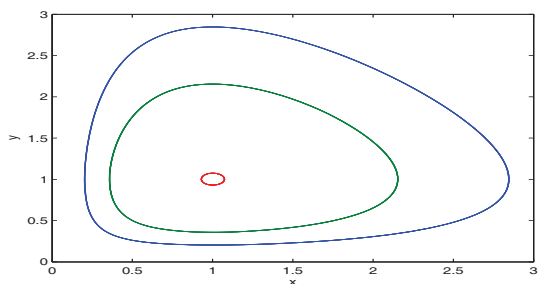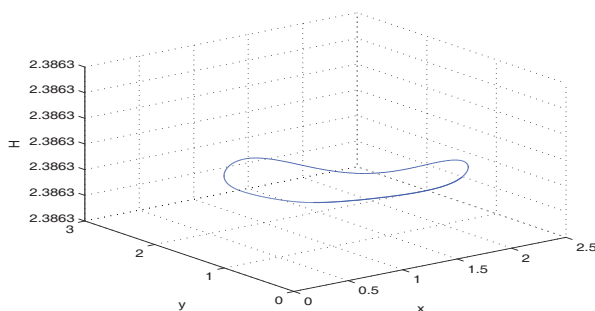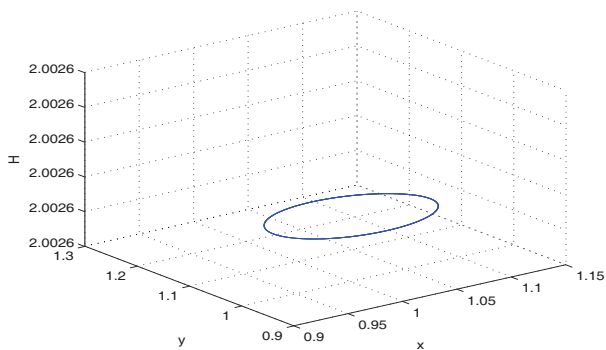

Fig. 4. Phase space portrait for a = 0.5, b =c = d = 1 and initial conditions (x0 = 0.35, y0 = 0.35), (x0 = 0.5, y0 = 0.5), (x0 =0.95, y0 = 0.95) listed in order from outermost trajectory to innermost trajectory.

Fig. 6. The profile of H(x, y) for a = 0.5, b =c = d = 1 and initial conditions (x0 = 0.5, y0 =0.5), and (x0 = 0.95, y0 = 0.95) respectively.
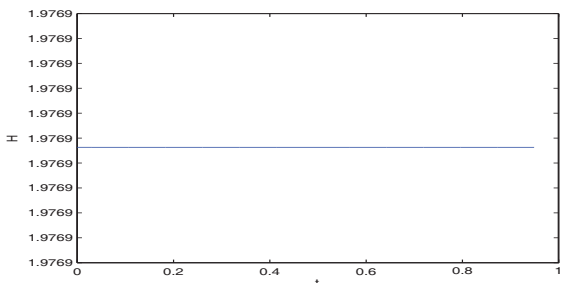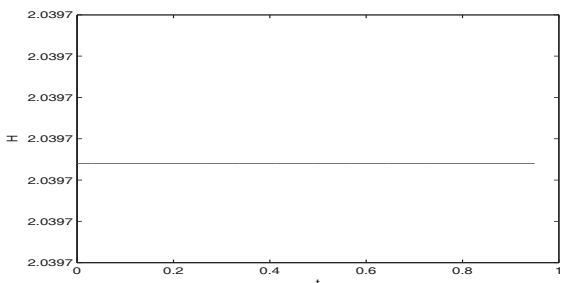
Fig. 5. The profile of the Hamiltonian H as function of t, for a = 0.5, b = c = d = 1 and initial conditions (x0 = 0.5, y0 = 0.5), and (x0 = 0.95, y0 = 0.95) respectively.
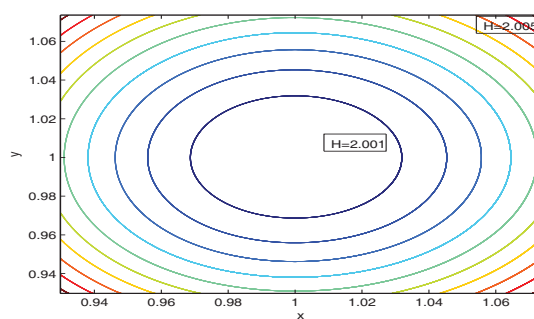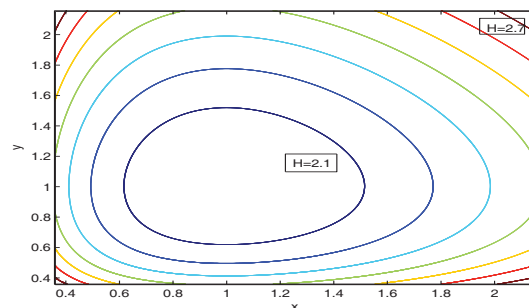
Fig. 7. Some level courves of H(x, y) for a = b = c = d = 1 and initial conditions (x0 = 0.5, y0 = 0.5), and (x0 = 0.95, y0 = 0.95) respectively.
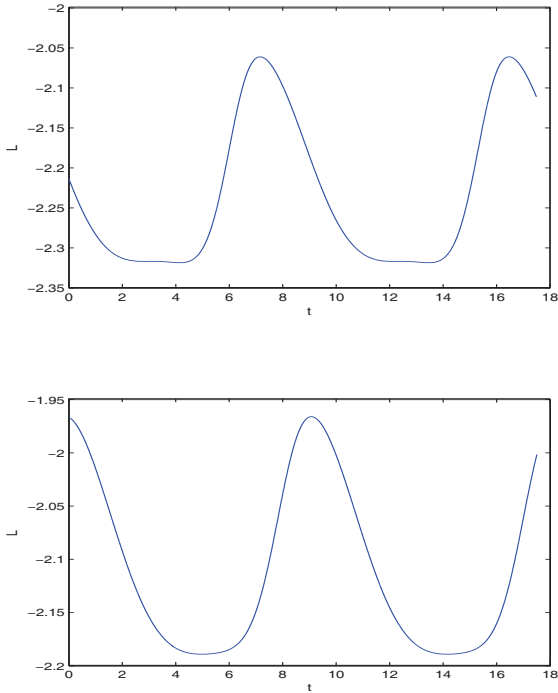
Fig. 8. The profile of the Lagrangian L as function of t for a = 0.5, b = c = d = 1 and initial conditions (x0 = 0.5, y0 = 0.5), and (x0 = 0.95, y0 = 0.95) respectively.

B. The Bailey Model
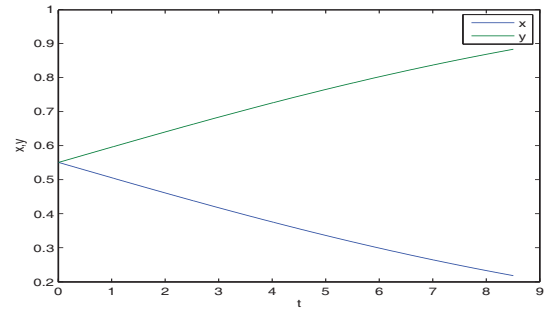
Fig. 10. Graphical profile of the numerical solutions x- individuals suspected being infected and y- individuals infected carriers, for k=1.5, initial conditions x0=0.55, y0=0.55
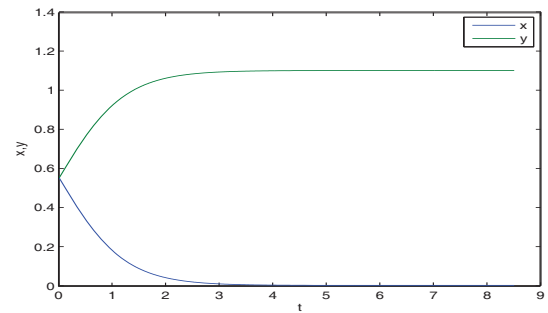
Fig. 11. Graphical profile of the numerical solutions x- individuals suspected being infected and y- individuals infected carriers, for k=0.15, initial conditions x0=0.55, y0=0.55

Fig. 9. The profile of L(x, y) for a = 0.5, b =c = d = 1 and initial conditions (x0 = 0.5, y0 = 0.5) and (x0 = 0.95, y0 = 0.95) respectively.
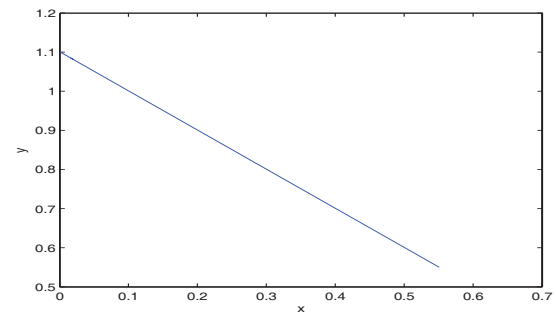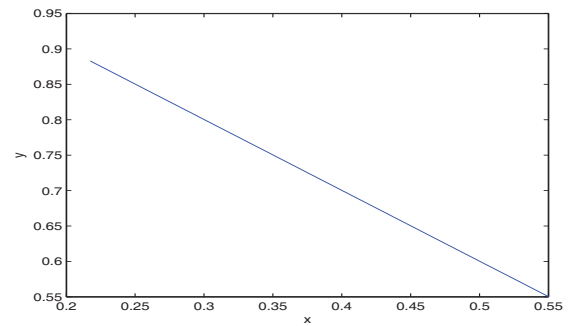
Fig. 12. The phase space profile for k=0.15, k=1.5
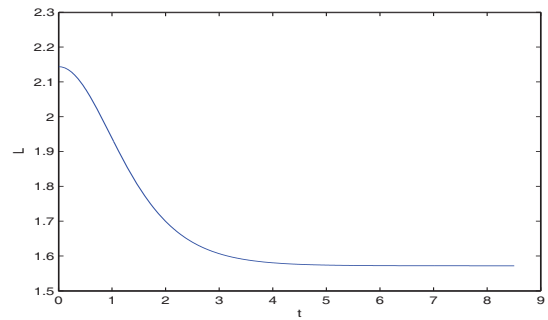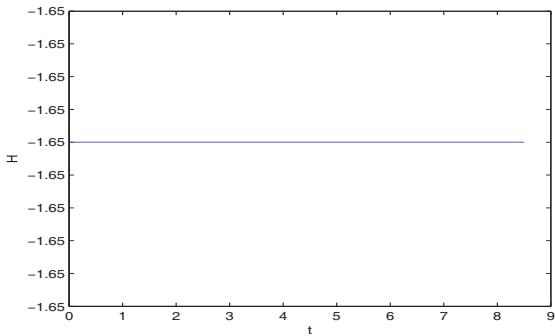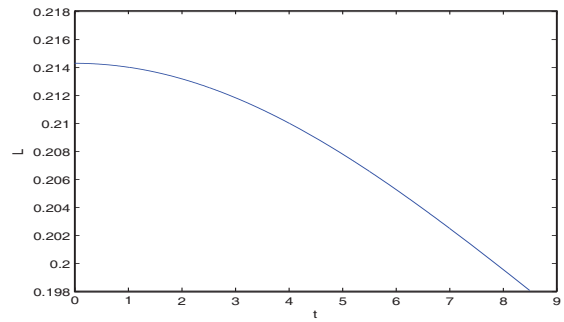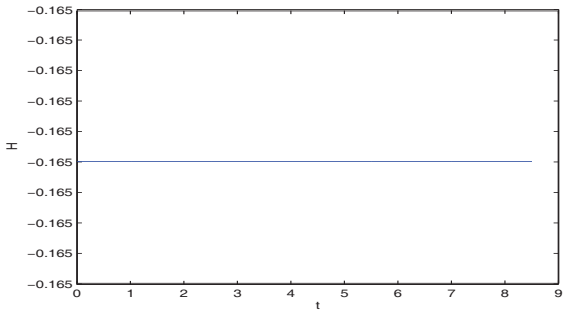
Fig. 13. The profile of the Hamiltonian H as function of t, for k=0,15, k=1.5 and initial conditions x0 = 0.55, y0 = 0.55.

Fig. 15. The profile of the Lagrangian L as function of t for k=0.15, k=1.5 and initial conditions x0=0.55, y0 =0.55.
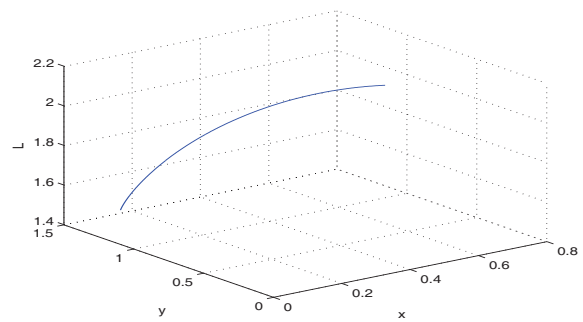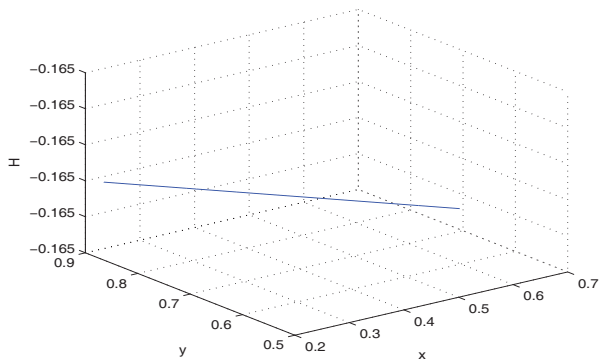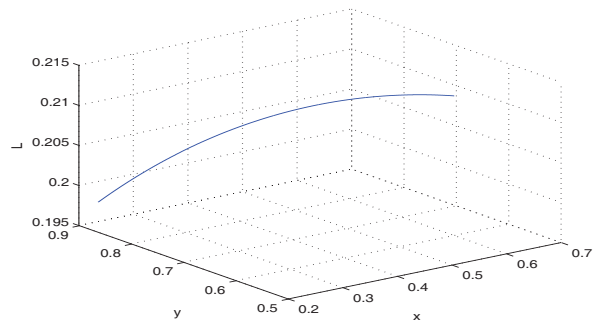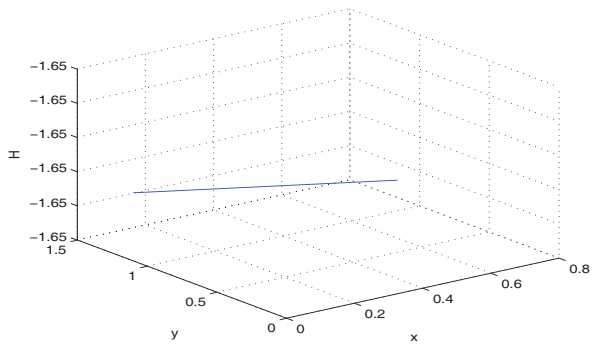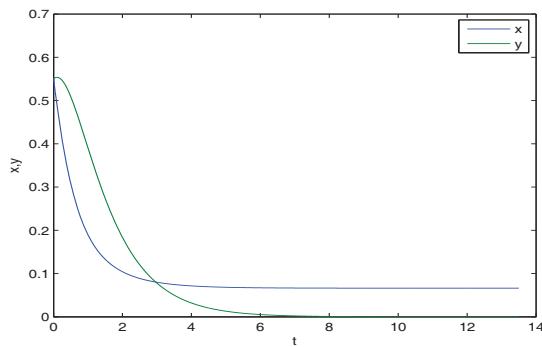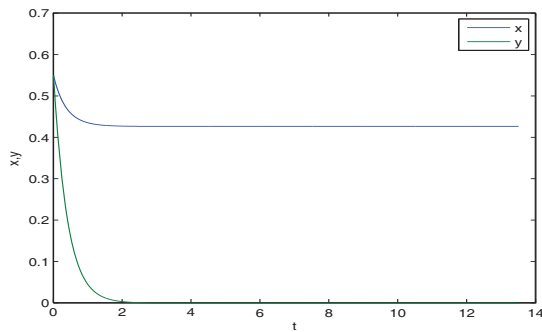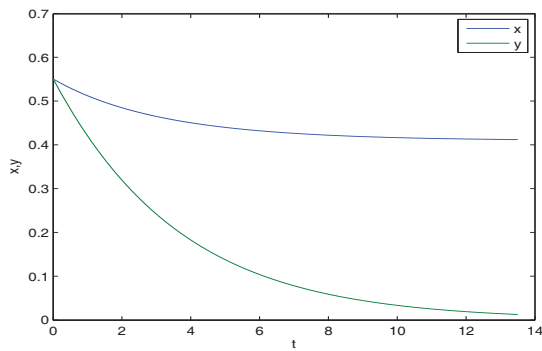

Fig. 14 The profile of H(x, y) for k=0,15, k=1.5 and initial conditions x0 = 0.55, y0 = 0.55.

Fig. 16. The profile of L(x, y) for for k=0.15, k=1.5 and initial conditions x0=0.55, y0 =0.55.

C. The Classical Kermack-McKendrick Model

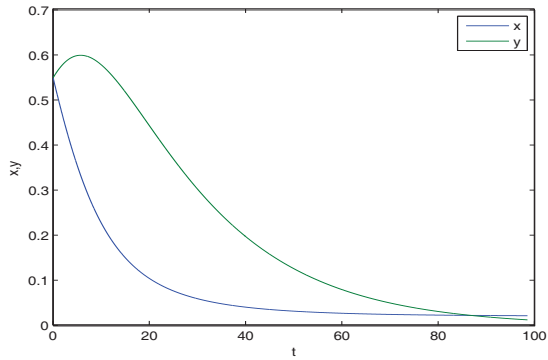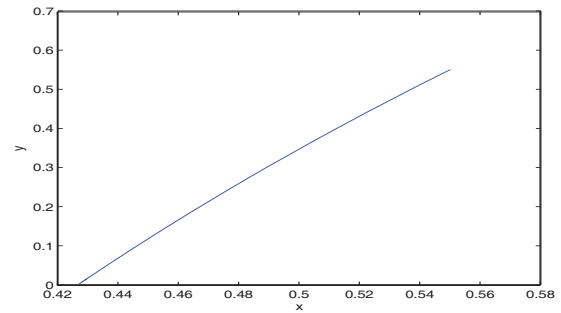Fig.18 The phase space profile for k1=0.15, k2=0.35, resp. k1=1.15, k2=0.35

Fig. 17 Graphical profile of the numerical solutions x- individuals sus-
pected being infected and y- individuals infected carriers, for k1=0.15,
k2=0.05, k1=0.15, k2=0.35, k1=1.15, k2=3.05, resp. k1=2.15, k2=1.05
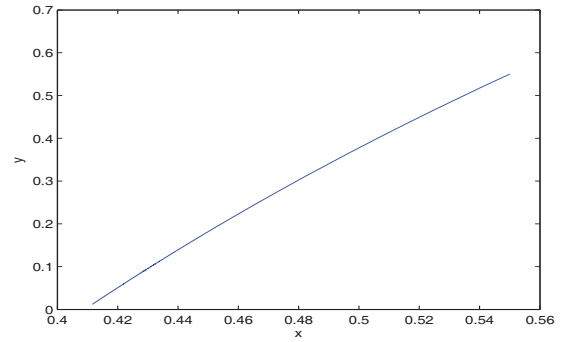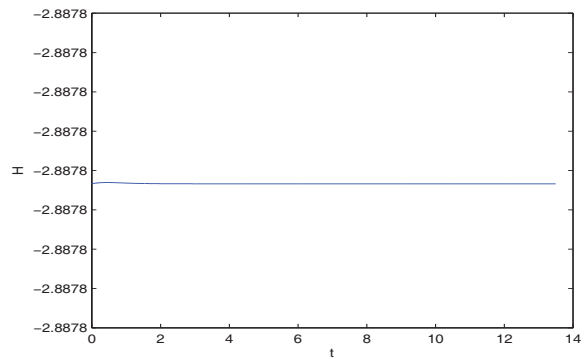and initial conditions x0=0.55, y0=0.55.
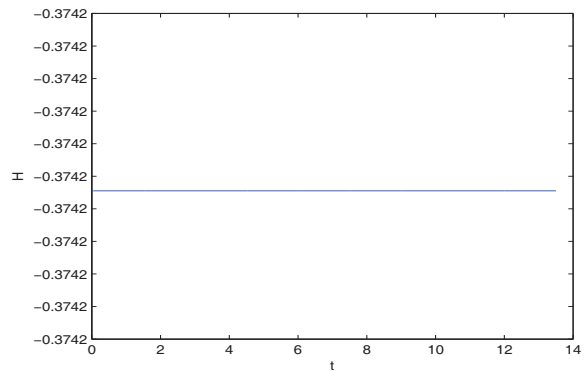
Fig.19 The profile of the Hamiltonian H as function of t for k1=0.15,
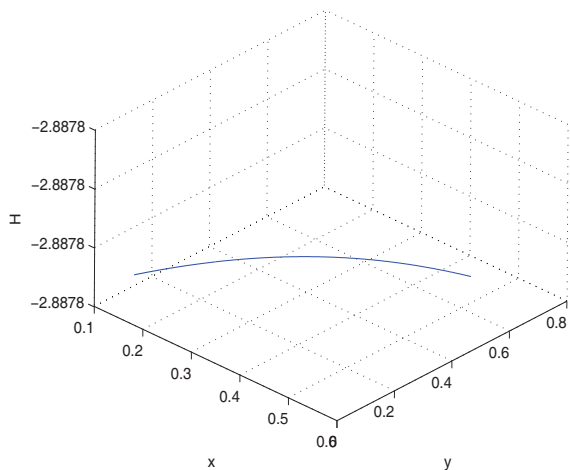k2=0.35, resp. k1=1.81, k2=1.5.

Fig.20 The profile of H(x, y) for k1=1.81, k2=1.5 and initial conditions
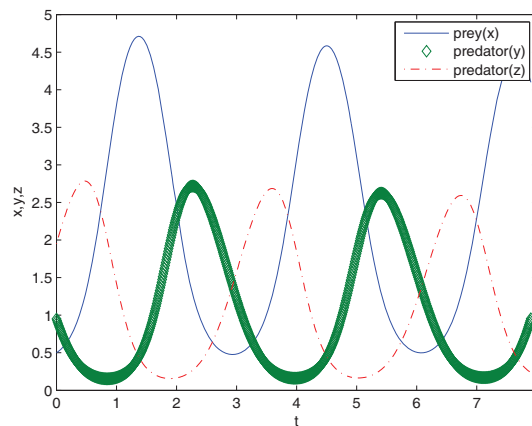x0 = 0.55, y0 = 0.55.

Fig. 22. The profile of the numerical solution (x(t), y(t), z(t)), for the
initial conditions (x0 = 0.5, y0 = 1, z0 = 2).

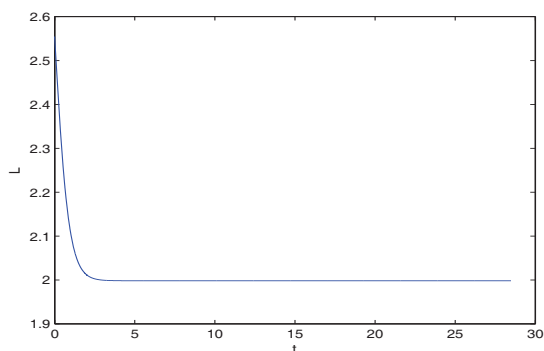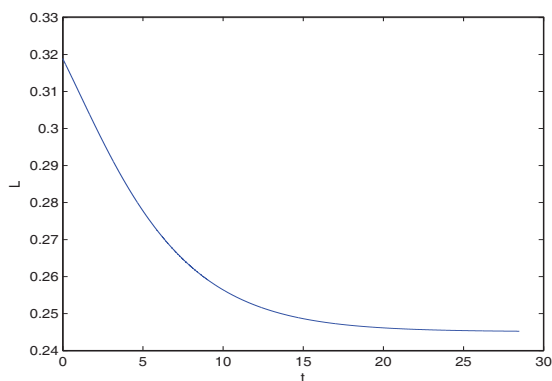Fig. 21 The profile of the Lagrangian L as function of t for k1=0.15,
k2=0.35, resp k1=1.15, k2=3.05 and initial condtions x0=0.55, y0=0.55
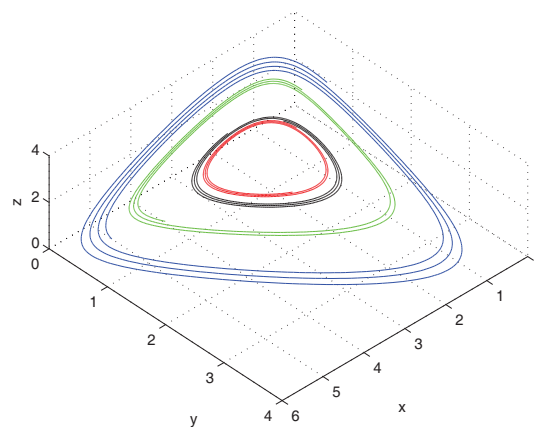
Fig. 23. Phase space portrait for the initial conditions (x0 = 0.5, y0 =
0.95, z0 = 2.95), (x0 = 0.5, y0 = 0.5), z0 = 1.95), (x0 = 1, y0 = 0.75, z0
= 1.25), (x0 = 2.1, y0 = 0.35, z0 = 1.55) listed in order from outermost
trajectory to   innermost trajectory.

Fig. 24. Phase space for the initial conditions (x0 = 1, y0 = 0.25, z0 =
2.5) The numerical solution presents a graphical profile given by
downward spirals.

D. 3D Lotka-Volterra System

We consider the case $abc = -1$, $v = \mu b - \lambda ab$.

We set $a = b = c = -1$ and $\mu = 1$, $\lambda = 0$, $v = -1$.

Fig. 25. The profile of the Hamiltonian H1 as a function of t, for the initial conditions (x0 = 2.1, y0 = 0.35, z0 = 1.55).
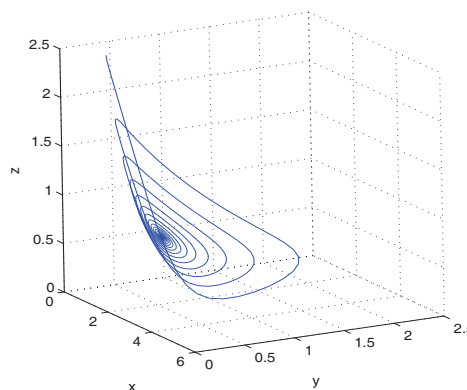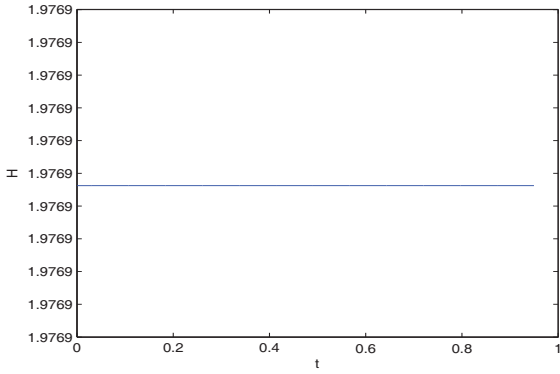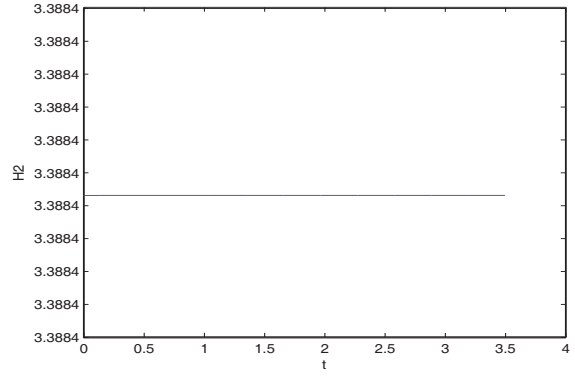

Fig. 28. The profile of the Hamiltonian H2 as a function of t, for the initial conditions (x0 = 2.1, y0 = 0.35, z0 = 1.55).

Fig. 26. The profile of the Hamiltonian H1 as a function of (t, x), (t, y) and (t, z), and for the initial conditions (x0 =2.1, y0 = 0.35, z0 = 1.55).

Fig. 29. The profile of the Hamiltonian H2 as a function of (t, x), (t, y) and (t, z) , for the initial conditions (x0 = 2.1, y0 = 0.35, z0 = 1.55).

Fig. 27. The profile of the Hamiltonian H1 as a function of (x, y), (x, z) and (y, z), for the initial conditions (x0 = 2.1, y0 = 0.35, z0 = 1.55).
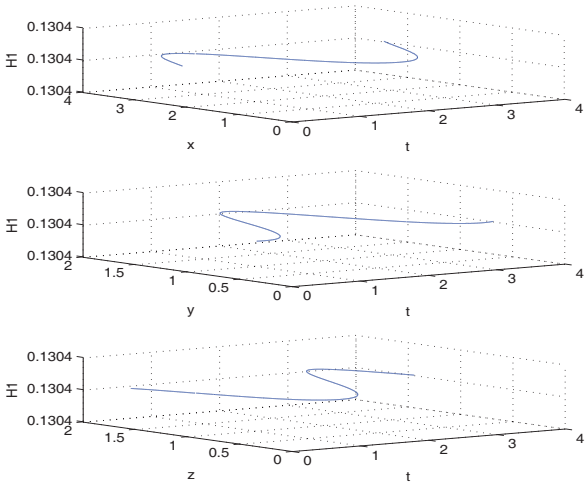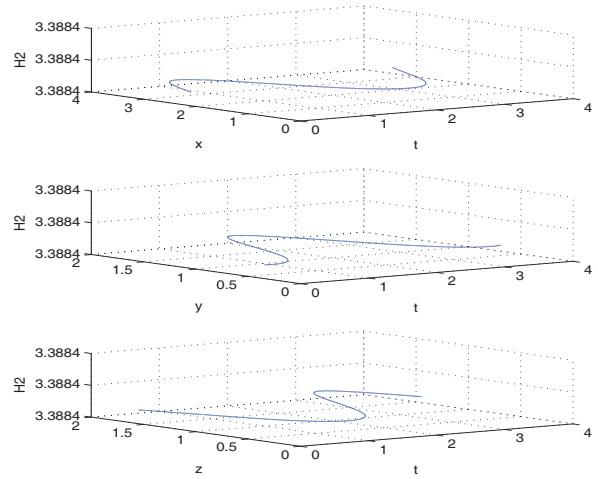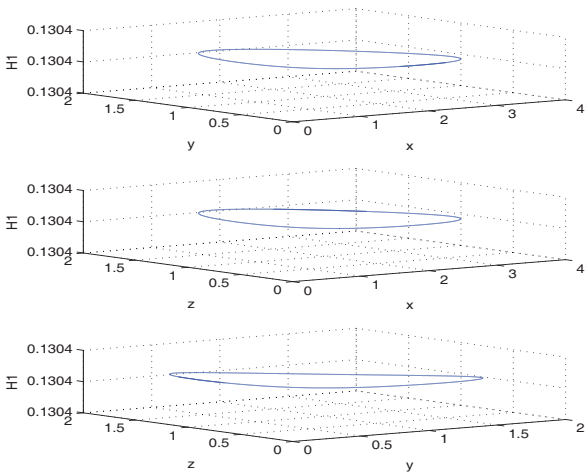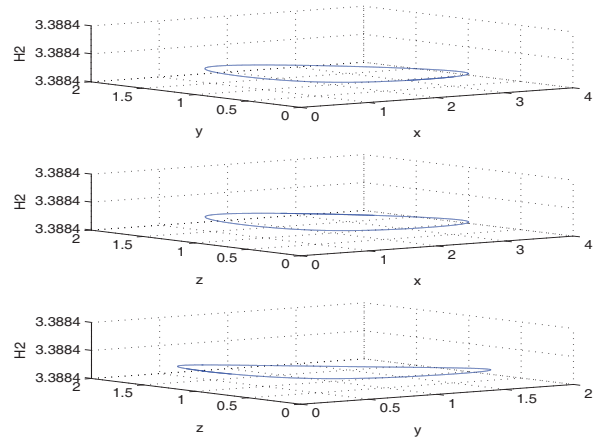

Fig. 30. The profile of the Hamiltonian H2 as a function of (x, y), (x, z) and (y, z) , for the initial conditions (x0 = 2.1, y0 =0.35, z0 = 1.55).

E. Observations

The predator population begins to decline shortly after the prey population starts to decrease. Then after the prey population begins to recover, the predator population also starts to recover, in agreement with [18]. They share a common period, Fig. 1, Fig. 2.

The total energy H takes constant values for different values of parameters a, b, c, d and different initial conditions, as we presented in Fig. 5, Fig. 6. Thus we are in agreement with the property to be a conservation law.

For the Bailey model of epidemics, in the case when the rate k of disease transmission is smaller than 1, we can observe a rapid stabilization of the two main sizes x and y, while in the case when k is greater than 1 the variation is more pronounced (Fig. 10 and Fig. 11).

In the case of Kermack-McKendrick classical model we remark that in the corresponding case when the ratio k_1 / k_2 is greater than 1 the stabilization of the two main sizes x and y became to appear after relative long interval, which contains a peak of infected population y. For a smaller ratio k_1 / k_2 the infected population y dramatically decreases (Fig. 17), in agreement with [16].

In the 3D case displaying the graph of x, y and   z across time t, one observes the periodic behavior of the system. Each predator population also peaks and then begins to decrease shortly after its respective prey population peaks and begins to decrease, Fig. 22.

The two Hamiltonians H_1 and H_2 associated to the 3D case of Lotka-Volterra system are characterized through our numerical study by constant values, for different initial conditions, as we presented in Fig. 25 - Fig. 30.

VII. CONCLUSIONS

We perform a computational analysis of these mathematical models, in order to approximate different types of invariants and main sizes, through numerical codes based on appropriate numerical calculus techniques for numerical integration of these type problems. Thus, starting from certain initial value problems associated to our models, we obtain the numerical solution and we develop the numerical characterization of the main sizes previously analysed from the geometrical point of view. Thus we are able to make different comparisons between these studied quantities for different values of parameters, for different initial conditions etc. Taking into considerations that the predator and prey populations display a variety of dynamic patterns, we emphasize that the present study can be useful also to make certain adjustments for the parameters involved in the differential equations in order to calibrate more precisely the models to better predict some realistic situations and take account for the differences from one example to the next.

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