A numerical study of the Hamilton-Poisson structures of the SIR-model of epidemics evolution

Florian Munteanu, Romulus Militaru†

Abstract. Using the geometrical methods of the Hamiltonian mechanics and appropriate numerical methods we will make a study of the dynamics for two of the mathematical models of the evolution of epidemics: the Bailey $2D$ model and the classical Kermack-McKendrick $3D$ model. This three dimensional dynamical system is also known as the SIR model, where S is the number of individuals suspected of being infected, I is the number of infected individuals and R denotes the number of individuals removed.

M.S.C. 2010: 70S05, 70S10, 53D05, 65L06.
Key words: Hamilton-Poisson realization; Kermack-McKendrick model; Runge-Kutta methods.

1 Introduction

In many branches of physics, engineering and applied mathematics we find systems described by coupled ordinary differential equations. 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.

In 1927, Kermack and McKendrick ([6]) developed infectious disease models to study the Great Plague of London for the period of 1665-1666. These models served as the foundation of theoretical models in epidemiology ([2], [16]). The population is divided into three categories as susceptible, infected, and recovered ([6]) and the model is called *the SIR model*.

First of all, this study is a tribute to my best friend and colleague, Romulus Militaru (26.08.1968-20.04.2015). Secondly, this paper is a natural continuation of the work started together several years ago and materialized in papers [5], [8, 11]. Unfortunately, this collaboration could not be completed to the desired parameters.

The present study is 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. Therefore, this paper aims to present our results obtained in the

Applied Sciences, Vol.18, 2016, pp. 74-83.

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 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 models arising in many important theoretical and practical situations from mathematics, science and engineering.

In first sections we present shortly the Hamiltonian structure for Bailey model of the evolution of epidemics ([6], [6], [8, 11], [13]) and for the classical Kermack-McKendrick model of the evolution of epidemics ([6], [8, 11], [13]). Also, we will study the main size for dynamical systems associated to this mathematical models and relationship between this in the geometric framework Hamilton-Poisson structures ([8, 11]). The analysis of the systems may be used, in particular, to study the dynamics of many others models from ecology, molecular biology, ecosystems, and chemical systems. For example a model for oxygen depletion in a system of sewage could be developed ([16]).

We will present two very important examples, both represent so called *variational dynamical systems*, that is dynamical systems which are described by a system of ordinary differential equations which can be written as the Euler-Lagrange equations associated to a Lagrangian L ([12, 14]),

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

2 The Bailey model for the evolution of epidemics

In Bailey model for the evolution of epidemics ([2]) 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 facts lead us to the evolutionary dynamical system given by ([2], [13])

$$\left\{\begin{array}{ll} \dot{x} = & -kxy \\ \dot{y} = & kxy \end{array}\right. ,\ k > 0. \tag{2.1}$$

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 (2.1) can be write 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 dynamical system has also *a Hamilton-Poisson realization*

$$(\dot{x}_1, \dot{x}_2)^t = J\nabla H\,,$$

where $x^1 = x$, $x^2 = y$, $H = -k(x+y)$ and $J = \begin{pmatrix} 0 & xy \\ -xy & 0 \end{pmatrix}$.

The Bailey model for the evolution of epidemics is a simplified particular case of the classical Kermack-McKendrick model.

3 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 ([6]). 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 (or removals) z. This model is also called *SIR model* of epidemics evolution.

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 constant rate 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 ([6], [13]):

$$\left\{ \begin{array}{ll} \dot{x} = & -k_1 xy \\ \dot{y} = & k_1 xy - k_2 y \\ \dot{z} = & k_2 y \end{array} \right. , \; k_1, k_2 > 0. \tag{3.1}$$

Let us note that $x + y + z = n$, i.e., the number of individuals of the population does not change. This *conservation law* show us that this SIR model of evolution of epidemics is without demography. 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]):

$$\left\{ \begin{array}{ll} \dot{x} = & -k_1 xy \\ \dot{y} = & k_1 xy - k_2 y \end{array} \right. , \; k_1, k_2 > 0. \tag{3.2}$$

The Lagrange and Hamilton functions of the system (3.2) are

$$\begin{array}{ll} L & = \frac{1}{2}\left(\frac{\ln y}{x}\dot{x} - \frac{\ln x}{y}\dot{y}\right) + k_1(x+y) - k_2 \ln x\,, \\ H & = -k_1(x+y) + k_2 \ln x\,, \end{array}$$

and so, we have a new *conservation law* of (3.2),

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

If we get back to the Kermack-McKendrick model (3.1), then we have that the Lagrangian whose Euler-Lagrange equations are really (3.1) is $\bar{L} = L + \frac{1}{2}(\dot{z} - k_1 y)^2$, where L is the Lagrangian of the subsystem (3.2).

4 Numerical study

Between dynamical systems theory and computation analysis of dynamical systems there is a strong interplay. The theory provides a framework for interpreting numerical observations and foundations for numerical algorithms implemented in practice by the mean of a programming language ([1], [3], [7], [15], [17]).

In this section, constructing a Matlab-based numerical code, we are looking to approximate and characterize different types of invariants and also to 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 involved in the analysed problems. In the first stage we focus on the numerical solving of the initial value problem given by the ordinary differential equations with a prescribed initial conditions, 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 ([18]).

Thus we obtain the numerical solution represented by the approximate values of the solution function for a discrete set of data points. In the second stage, using this approach we perform a numerical analysis of the conservation laws and main sizes, like the Lagrangian and the Hamiltonian. Belonging to this type of systems, dynamical systems are concerned primarily with making qualitative study about the behavior of systems which evolve in time given knowledge about the initial state of the system itself.

4.1 The Bailey model

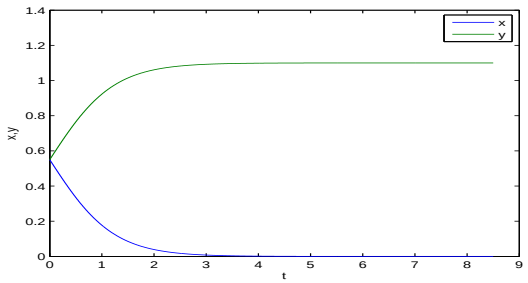

Figure 1: Graphical profile of the numerical solutions x-individuals suspected being infected and y-individuals infected, for $k = 1.5$, initial conditions $x_0 = 0.55$, $y_0 = 0.55$.

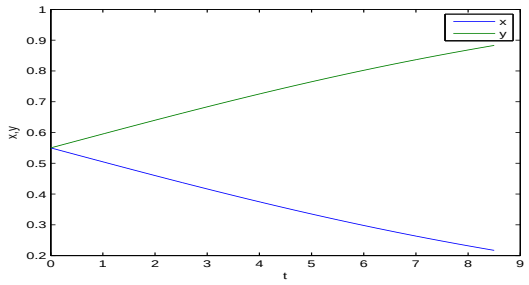

Figure 2: Graphical profile of the numerical solutions x-individuals suspected being infected and y-individuals infected, for $k = 0.15$, initial conditions $x_0 = 0.55$, $y_0 = 0.55$.

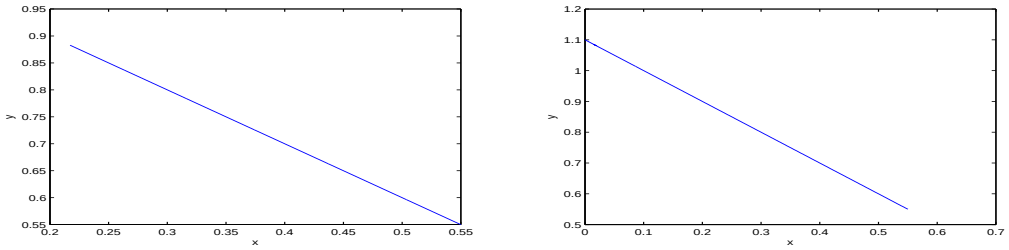

Figure 3: The phase space profile for $k = 0.15$, $k = 1.5$.

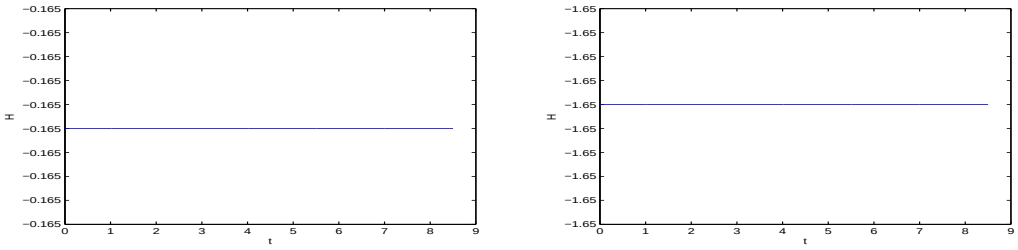

Figure 4: The profile of the Hamiltonian $H(t)$, for $k = 0.15$, $k = 1.5$ and initial conditions $x_0 = 0.55$, $y_0 = 0.55$.

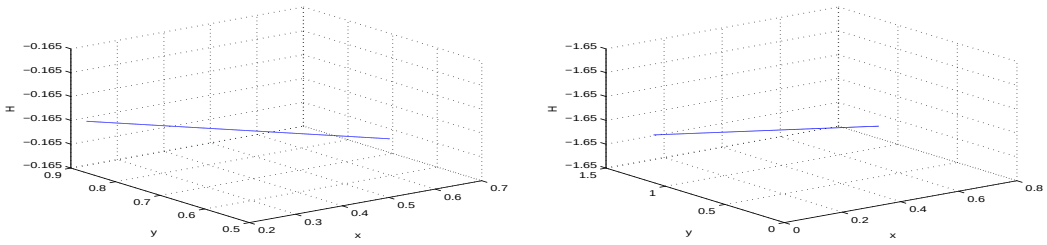

Figure 5: The profile of $H(x, y)$ for $k = 0.15$, $k = 1.5$ and initial conditions $x_0 = 0.55$, $y_0 = 0.55$.

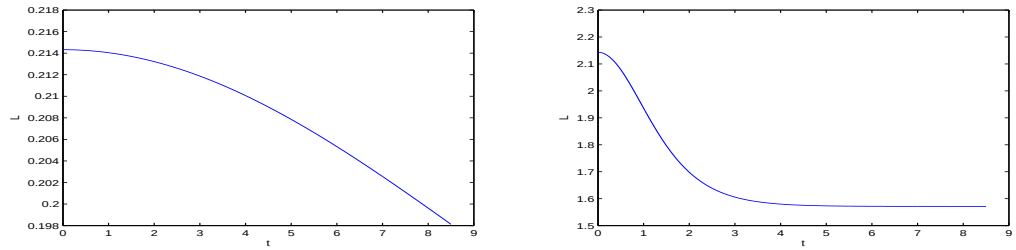

Figure 6: The profile of Lagrangian $L(t)$ for $k = 0.15$, $k = 1.5$ and initial conditions $x_0 = 0.55$, $y_0 = 0.55$.

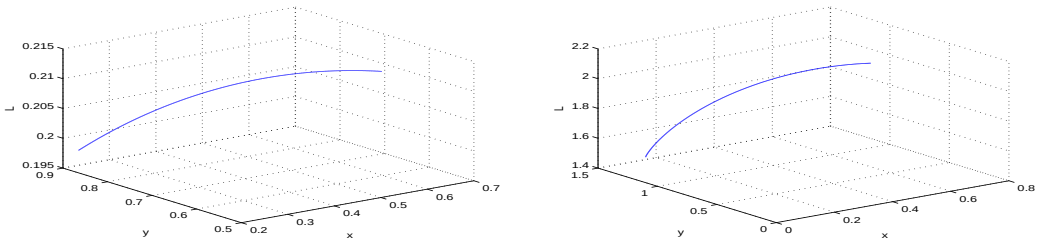

Figure 7: The profile of $L(x, y)$ for $k = 0.15$, $k = 1.5$ and initial conditions $x_0 = 0.55$, $y_0 = 0.55$.

4.2 The classical Kermack-McKendrick model

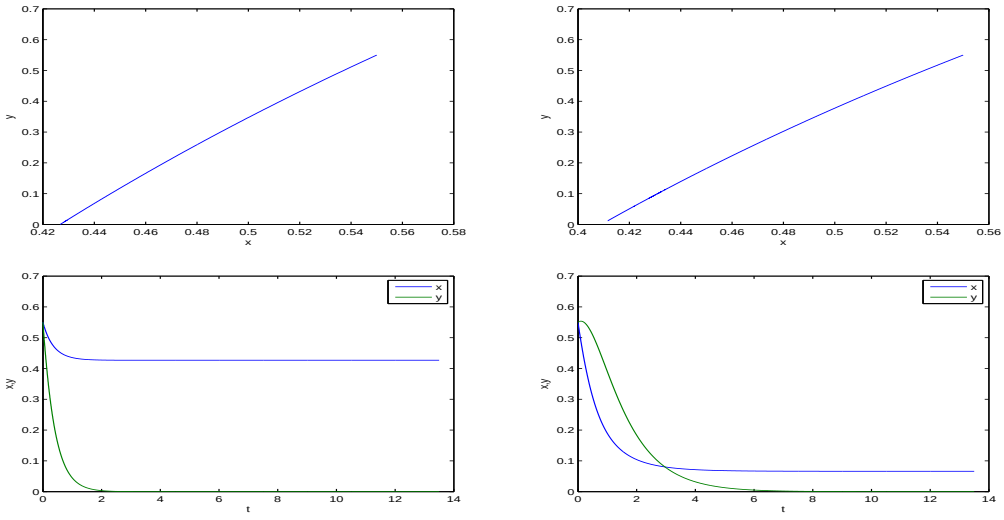

Figure 8: Graphical profile of the numerical solutions x-individuals suspected being infected and y-individuals infected carriers, for $k_1 = 0.15$, $k_2 = 0.05$, $k_1 = 0.15$, $k_2 = 0.35$, $k_1 = 1.15$, $k_2 = 3.05$, $k_1 = 2.15$, $k_2 = 1.05$ and initial conditions $x_0 = 0.55$, $y_0 = 0.55$.

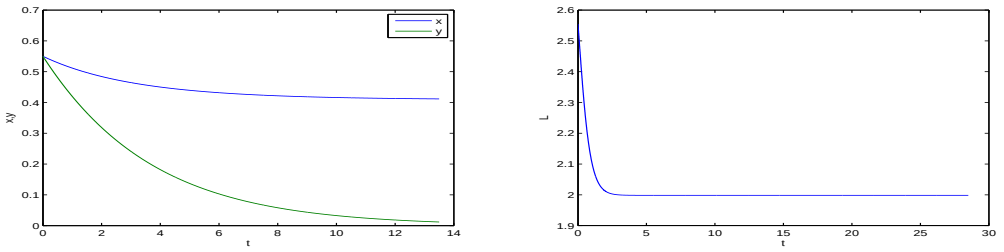

Figure 9: The phase space profile for $k_1 = 0.15$, $k_2 = 0.35$, $k_1 = 1.15$, $k_2 = 3.05$.

4.3 Final remarks

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 (Figure 1 and Figure 2).

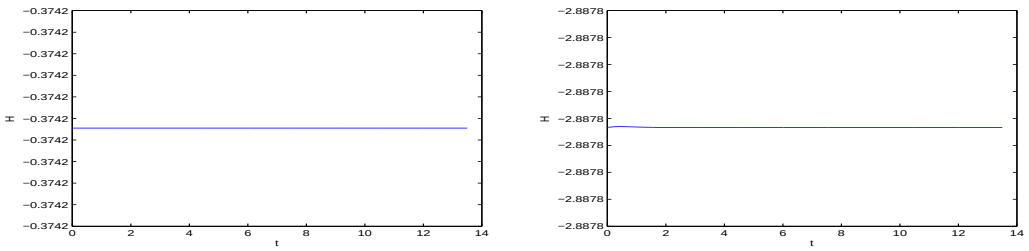

Figure 10: The profile of the Hamiltonian $H(t)$, for $k_1 = 0.15$, $k_2 = 0.35$, $k_1 = 1.81$, $k_2 = 1.5$.

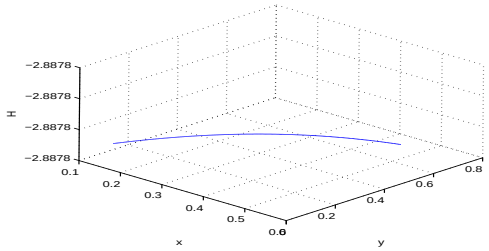

Figure 11: The profile of the Hamiltonian $H(x, y)$ for $k_1 = 1.81$, $k_2 = 1.5$, with initial conditions $x_0 = 0.55$, $y_0 = 0.55$.

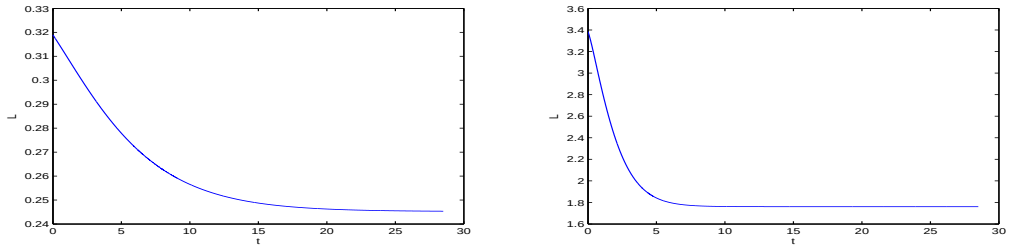

Figure 12: The profile of the Lagrangian $L(t)$ for $k_1 = 0.15$, $k_2 = 0.35$, $k_1 = 1.15$, $k_2 = 3.05$, with initial conditions $x_0 = 0.55$, $y_0 = 0.55$.

In the case of Kermack-McKendrick classical model we remark that in the corresponding case when the ratio $\frac{k_1}{k_2}$ 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 $\frac{k_1}{k_2}$ the infected population y dramatically decreases (see Figure 8), in agreement with [16].

5 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 analyzed 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.

Acknowledgements. This research was partially supported by grant FP7-PEOPLE-2012-IRSES-316338.

References

[1] U. M. Ascher, L. R. Petzold, *Computer methods for ordinary differential equations and differential-algebraic equations*, SIAM, Philadelphia, 1998.

[2] N. T. J. Bailey, *The Mathematical Theory of Infectious Diseases*, Hafner Press, New York, 1975.

[3] H. W. Broer, H. M. Osinga, G. Vegter, *Algorithms for computing normally hyperbolic invariant manifolds*, Z. Angew. Math. Phys. 48 (1997), 480-524.

[4] P. Henrici, *Discrete variable methods in ordinary differential equations*, Wiley Sons Inc., New York, 1962.

[5] A. Ionescu, R. Militaru, F. Munteanu, *Geometrical methods and numerical computations for prey-predator systems*, British Journal of Math. Comp. Sci. 10, 5 (2015), 1-15.

[6] W. D. Kermack, A. G. McKendrick, *A Contribution to the Mathematical Theory of Epidemics*, J. Royal Stat. Soc. A 115 (1927), 700-721; A 138, (1932), 55-83.

[7] R. Militaru, A. Călin, G. Călugăru, A. Georgescu, *Numerical Engineering Software* (in Romanian), Sitech, Craiova, 2011.

[8] R. Militaru and F. Munteanu , *Geometric methods for the study of biodynamical systems. symmetries and conservation laws*, Proc. of the Int. Conf. Cellular and Molecular Biology (WSEAS) Recent Researches in Medicine, Biology and Bioscience, (2013), 54-61.

[9] R. Militaru, F. Munteanu, *Symmetries and conservation laws for biodynamical systems*, Int. J. of Math. Models and Meth. in Appl. Sci. 12, 7 (2013), 965-972.

[10] R. Militaru, F. Munteanu, *Computational analysis of conservation laws for prey-predators Lotka-Volterra systems*, Proc. of Int. Conf. of Appl. and Theor. Electricity (ICATE), Craiova, October 23-25, 2014, Editor IEEE, (2014), 1-7.

[11] R. Militaru, F. Munteanu, *Geometrical methods and numerical computations for the study of mathematical models of the multi-species interactions*, BSGP 22 (2015), 51-60.

[12] F. Munteanu, *A study of the dynamical systems in the Lagrangian and Hamiltonian formalism*, Proceedings of SSMR Conference, Braşov (2001), 169-178.

[13] V. Obădeanu, *Differential Dynamical Systems. The dynamics of biological and economical processes* (in Romanian), UVT Press, Timişoara, 2006.

[14] P. J. Olver, *Applications of Lie Groups to Differential Equations*, Graduate Texts in Mathematics, 107, Springer-Verlag, New York, 1986.

[15] T. S. Parker, L. O. Chua, *Practical Numerical Algorithms for Chaotic Systems*, Springer Verlag, New York, 1989.

[16] C.R. Townsend, J.L. Harper, M. Begon, *Ecology: Individuals, Populations and Communities*, Blackwell Sci. Publ., Oxford, 1990.

[17] S. Lynch, *Dynamical Systems with Applications using Mathematica*, Birkhauser, 2007.

[18] X. Wu, *Two step Runge-Kutta methods of order five with reduced function evaluations*, Appl. Math. Comput. 155 (2004),779-811.

Authors' address:

Florian Munteanu and Romulus Militaru
Department of Applied Mathematics, University of Craiova,
13 Al.I. Cuza Str., Craiova 200585, Romania.
E-mail: munteanufm@gmail.com