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Delay differential systems. A generalization of the Lotka-Volterra model

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Abstract
The first mathematical laws used in the theory of survival were introduced by *Th. Malthus* (1798-*Principle of population*; 1803-*The theory of population*), *B. Gompertz* (1860), and *W. Makeham* (1874). They proposed different exponential laws to describe the intensity of death, which then formed the basis for the biometric functions of survival. In the twentieth century, the development of demographic research, as well as the study of various epidemics affecting populations, led to the emergence and evolution of new methods for solving problems in survival theory. *Lotka-Volterra* (in their Predator-Prey model) described the differential equations of population growth (in humans, microorganisms, and other species). These models were later improved by *E. M. Wright* and *P. J. Wangersky* (1978), who more plausibly assumed that the phenomena of immigration-emigration could represent the biological reaction of self-regulation of a population, and that this factor acts with a certain delay. The use of random processes and, later, stochastic differential equations contributed to the evolution and diversification of mathematical models in biological systems. In this article, we have developed a variational functional framework for the description of problems associated with delayed differential systems. We have thus made a generalization of the *Lotka-Volterra model*.

Keywords: Delay Differential Equations, Lotka-Volterra model, Variational problems

1. INTRODUCTION. CLASSICAL MODELS IN SURVIVAL THEORY

We assume that in an isolated environment live two biological species, prey and predators (much like how numerous fish species coexist in a sufficiently large and yet isolated habitat such as an ocean, where species are divided into these two categories). Similar examples can also be found in the case of populations of microorganisms or human communities subject to natural or controlled phenomena of immigration-emigration.

We denote with $x(t)$ and $y(t)$, respectively, the number of individuals in the two species at time t. *Malthus*' model of homogeneous population growth assumes that, at any given time, the rate of growth (the difference between the birth rate and the death rate) is directly proportional to the size of the population at that moment. In other words,

$$x'(t) = a\,x(t)\,, \quad t \geq t_0 \;\; (a > 0 \text{ and } t_0 \geq 0 \text{ are fixed}). \tag{1.1}$$

P.F. Verhulst (1841) finds the so-called *logistic equation* more plausible (*Verhulst-Pearl* model),

$$x'(t) = a\,x(t) \cdot \left(1 - \frac{1}{p}x(t)\right), \; t \geq t_0 \;\; (a, p > 0 \text{ and } t_0 \geq 0 \text{ are fixed}). \tag{1.2}$$

This model assumes that the growth rate (velocity) of an isolated biological population decreases as the population size $x(t)$ increases due to agglomeration phenomena and limited food resources. The factor $\left(1-\frac{1}{p}x(t)\right)$ is called the biological reaction of self-regulation of the population.

However, subsequent demographic research suggests that the self-regulating biological reaction factor needs to be improved because it acts with a certain $h>0$ delay. This is what the *Wright* model looks like (1878),

$$x'(t)=a\,x(t)\cdot\left(1-\frac{1}{p}x(t-h)\right),\ t\geq t_0\ \ (a,p>0 \text{ and } t_0\geq 0 \text{ are fixed}). \quad (1.3)$$

With double changes, one of variable $t\to s$, and the other of function $x\to z$ represented by,

$$t=hs \text{ and respectively, } z(s)=\frac{1}{p-1}\cdot x(hs)$$

and with the notation $ah=c$ we get the equation

$$z'(s)=-\,c\,z(s-1)\cdot\left(1-\ z(s)\right),\ s\geq\frac{1}{h}t_0\ \ (c>0 \text{ and } t_0\geq 0 \text{ are fixed}). \quad (1.4)$$

Over time, several mathematical models have been proposed for the study of the growth (or destruction ≡ extinction) of an isolated population, taking into account both delay effects and the average lifespan.

Returning to the study of two-species populations, we will have to consider a differential system with unknown functions $t\to x(t)$ și $t\to y(t)$ represented by,

$$\begin{cases} x'(t)=a_1\,x(t)-b_1\,x(t)y(t) \\ y'(t)=-\,a_2\,y(t)+b_2\,x(t)y(t) \end{cases},\ (a_1,a_2,b_1,b_2>0) \quad (1.5)$$

starting from the following physical aspects: predators consume part of the prey, and the rate of prey depletion is proportional to $x(t)y(t)$; if the prey population decreases significantly, then the predator population also declines exponentially.

This is the classical *Lotka-Volterra model*. In 1957, *Wangersky-Cuningam* proposed an improvement to this model by also considering it necessary to incorporate the influence of delay in the biological, natural or controlled self-regulation of the two species' populations , i.e. the substitution of the $x(t)y(t)$ by $x(t-h)y(t-h)\,,h>0$. In other words,

$$\begin{cases} x'(t)=a_1\,x(t)\cdot\left(1-\frac{1}{p}x(t)\right)-b_1\,x(t)y(t) \\ \quad y'(t)=-\,a_2\,y(t)+b_2\,x(t-h)y(t-h) \end{cases},\ (p,a_1,a_2,b_1,b_2>0). \quad (1.6)$$

In 1931 *Vito Volterra* published an article that inspired the European academic communities to introduce *Feller-Kolmogorov delayed stochastic differential equations* as more accurate models for describing the growth of biological populations, or of some populations of microorganisms (viruses, bacteria, spores, tumor cells), also starting from the diversification of the fields in which this research became a necessity.

Volterra thus proposed the introduction of control functions, which allow populations to maintain a certain growth rate, or on the contrary, to achieve controlled extinction:

$$\begin{cases} x'(t) = [\,a_1 - b_1\, y(t) - \int_{-h}^{0} g_1(s)\; y(t+s)ds\,] \cdot x(t) \\ y'(t) = [-\,a_2 + b_2\, x(t) + \int_{-h}^{0} g_2(s)\; x(t+s)ds\,] \cdot y(t) \end{cases}, \tag{1.7}$$

where $g_1, g_1 : [-h, 0] \to \mathbb{R}$ are continuous and non-negative functions that will be determined based on certain *conditions of optimality*.

2. Variational functional framework of delayed differential equations

Let $h > 0$ be a real number, and let $n \in \mathbb{N}^*$ be fixed. By $W^{1,p}(-h, 0;\ \mathbb{R}^n)$, $p \in [1, +\infty]$ we denote the *Banach* space of all functions $\varphi : [-h, 0] \to \mathbb{R}^n$ that are absolutely continuous with derivatives in $L^p(-h, 0;\ \mathbb{R}^n)$. The norm in this space $W^{1,p}(-h, 0;\ \mathbb{R}^n)$ is given by,

$$\|\varphi\|_p = (\,|\varphi(-h)|^p + \int_{-h}^{0} |\varphi'(\theta)|^p d\theta\,)^{\frac{1}{p}}, \text{ for } p < +\infty \tag{2.1}$$

$$\|\varphi\|_\infty = |\varphi(-h)| + \underset{\theta \in [-h, 0]}{essup}\, |\varphi'(\theta)| \quad , \text{for } p = +\infty\,. \tag{2.2}$$

The duality between *Sobolev* spaces $W^{1,p}(-h, 0;\ \mathbb{R}^n)$ and $W^{1,q}(-h, 0;\ \mathbb{R}^n)$, where $\frac{1}{p} + \frac{1}{q} = 1$ will be further denoted with $\langle\langle \cdot\,,\ \cdot \rangle\rangle$ and is defined by the equality

$$\langle\langle\, \varphi\,, \psi \rangle\rangle = \big(\varphi(-h)\,, \psi(-h)\big) + \int_{-h}^{0} (\varphi'(\theta)\,, \psi'(\theta))d\theta \tag{2.3}$$

where I obviously noted with $(\cdot\,,\ \cdot)$ the inner product on $\mathbb{R}^n$.

We also recall that the duality between the spaces $L^p(0, T;\ \mathbb{R}^n)$ and $L^q(0, T;\ \mathbb{R}^n)$ by $\frac{1}{p} + \frac{1}{q} = 1$ will be further denoted with $\langle\cdot\,,\ \cdot\rangle$ and defined by equality,

$$\langle u\,,\ v\rangle = \int_0^T |u(t)|^p \cdot |v(t)|^q dt\,. \tag{2.4}$$

The delayed equation of a controlled biological system can, for now, take the form of the following *Cauchy problem*,

$$\begin{cases} x'(t) = A_0 x(t) + A_1 x(t-h) + B(t)u(t)\,,\ a.p.t.\ \ t \in [0\,, T] \\ \qquad\qquad x_0 = \varphi\,,\ pe\ \ [-h\,, 0] \end{cases} \tag{2.5}$$

where A_0 și A_1 are, for now, constant matrix of $n \times n$ type , where again $B(t)$ is a functional matrix of $n \times m$ type with the elements in $L^\infty(0, T)$.

The initial data φ in the problem described above has been considered by those who studied it (J.K. Hale [4], [5], M.C. Delfour [2], H.T. Banks [1], K. Kunisch, W. Schappacher [8]) to belong to spaces (reflective or not) of the type $L^p(-h, 0;\ \mathbb{R}^n)$, or $W^{1,p}(-h, 0;\ \mathbb{R}^n)$, or even $C(-h, 0;\ \mathbb{R}^n)$.

Next, we will select the known hereditary state $\varphi \in W^{1,1}(-h, 0;\ \mathbb{R}^n)$ and the control function (or command) $u \in L^1(0, T;\ \mathbb{R}^m)$, for the enhancement of the chosen model, in order to establish results concerning the existence and uniqueness of the optimal trajectory for the state of the biological population $x(t;\, \varphi, u)$. At the same time, we will introduce a cost functional that will have to be minimized, given in the form:

$$I_{l,L}(\varphi,u) \;=\; l(\varphi,x_T) \;+\; \int_0^T L(t,x_t\,,u(t))\,dt\;, \tag{2.6}$$
$$\text{with } x_t(s) = x(t+s)\,,\;\; (\forall)s \in [-h\,,0]\,,\;\; (\forall)t \in [0\,,T]\,.$$

The results obtained by J.K. Hale [5], were based on the reflectivity properties of the spaces from which the data of the problem were taken $\varphi \in W^{1,2}(-h,0;\ \mathbb{R}^n)$ and $u \in L^2(0,T;\ \mathbb{R}^m)$, but on sufficiently general properties for the functions of l and L.

In our more general hypotheses $\varphi \in W^{1,1}(-h,0;\ \mathbb{R}^n)$ and $u \in L^1(0,T;\ \mathbb{R}^m)$ We will choose a simple form for $l\colon W^{1,2}(-h,0;\ \mathbb{R}^n) \times L^2(0,T;\ \mathbb{R}^m) \to \mathbb{R}$ and $L\colon [0,T] \times \mathbb{R}^n \times \mathbb{R}^n \to (-\infty,+\infty]$, as well as simpler cost functionality,

$$I_{l,L}(\varphi,u) \;=\; l(\varphi,x_T) \;+\; \int_0^T L(t,x(t)\,,u(t))\,dt\,. \tag{2.7}$$

Lemma 2.1 (V. Popescu, [7])

For anything $(y,v) \in W^{1,\infty}(-h,0;\ \mathbb{R}^n) \times L^\infty(0,T;\ \mathbb{R}^m)$ they exist and are unique, $P(y,v) \in W^{1,\infty}(-h,0;\ \mathbb{R}^n)$ and $Q(y,v) \in L^\infty(0,T;\ \mathbb{R}^m)$ so,

$$\langle\langle\, y\,,x_T\rangle\rangle \;+\; \langle v,x\rangle \;=\; \langle\langle\, P(y,v)\,,\varphi\rangle\rangle \;-\; \int_0^T (Q(y,v)(t)\,,u(t))\,dt\,. \tag{2.8}$$

■

Theorem 2.2 (G. Morosanu, V-M Hokkanen [6])

The pairs,
$(\varphi,u) \in W^{1,1}(-h,0;\ \mathbb{R}^n) \times L^1(0,T;\ \mathbb{R}^m)$ and $(y,v) \in W^{1,\infty}(-h,0;\ \mathbb{R}^n) \times L^\infty(0,T;\ \mathbb{R}^m)$ satisfy the conditions of optimality in the variational problem (2.8) if and only if

$$\begin{cases} (\,P(y,v)\,,y\,) \in \partial l(\varphi,x_T)\;, \\ (\,v(t)\,,Q(y,v)\,) \in \partial L\big(t,x(t),u(t)\big)\,,\;\; a.p.t.\;\; t \in [0\,,T] \end{cases}. \tag{2.9}$$

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