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Two-component feedback loops and deformed mechanics

David S. Tourigny

D.A.M.T.P., Centre for Mathematical Sciences, University of Cambridge, Wilberforce Road, Cambridge CB3 0WA, UK

A B S T R A C T

It is shown that a general two-component feedback loop can be viewed as a deformed Hamiltonian system. Some of the implications of using ideas from theoretical physics to study biological processes are discussed.

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1. Introduction

The physicist Eugene Wigner famously wrote on the enormous contribution that mathematical theories have made to physics [1]. By contrast, mathematics has so far had less impact on biology [2]. Biological systems can be viewed as an emergence of the laws of chemistry and the principle of natural selection, and this underlying complexity makes biological processes incredibly difficult to study mathematically. There are many instances where symmetry apparent on the level of an organism breaks down when one is to look on the molecular or cellular scale. For example, the body plans of most animals display some form of radial or bilateral symmetry, but this is not a symmetry in the exact sense as is revealed if one is to consider the arrangement of cells. Consequently, the symmetry of an organism can only be considered a symmetry 'from far away' much like the symmetries of statistical phenomena or the apparent homogeneity of the cosmos.

On the other hand, more exotic symmetries can be found in the elementary world described by the standard model of particle physics. There the concept of spontaneous symmetry breaking is well understood to play a role in hadron formation, but complications immediately arise when one is moved to consider interactions between multiple hadrons and the higher atomic nuclei. Thus, the problem of describing biological processes mathematically seems to be associated with the problem of symmetry. Whilst mathematics describes well the physics of the very large and very small it does not appear to cope well with molecular or cellular

biology, trapped, unsymmetrically, with the insufficiently large and the insufficiently small.

In classical mechanics, Noether's theorem states that for every symmetry of the equations of motion there is a corresponding conserved quantity. By a conserved quantity is meant a function of the dynamical variables that does not vary in time so that its total time derivative always remains zero. In Hamilton's formulation of classical mechanics it is the Hamiltonian representing the total energy of the system that always remains conserved, but in a typical biological process there is no analogue of the Hamiltonian and therefore no conserved quantity. Exceptions to this rule emerge when the equations governing these dynamical systems can be put into Hamiltonian form. This has been achieved for the classical Lotka–Volterra equations that govern predator-prey interactions [3,4], and simple signalling models involving constant degradation rates [5]. In these cases an analogue of the Hamiltonian immediately yields a conserved function of the dynamical variables that can be used to study Lyapunov stability and the location of equilibrium points.

In physics, scale invariance is a feature of equations or observables that does not change if the scales of certain variables are multiplied by a common factor (often forming part of a larger conformal symmetry). Scale-invariance is a typical property of critical phenomena because experimental observables are known to follow power-laws near the neighbourhood of a critical point. There is now a growing realisation that scale-invariance may be an inherent feature of many biological networks that display critical behaviour (this notion of scale-invariance is distinct from that of a network being scale-free, a topological property) [6]. For example, recent work demonstrates that pathways involved in growth

factor signalling are dependent on fold-changes in concentrations of a molecule, and not its absolute level [7]. This is an indication that certain biological processes display at least some evidence of a symmetry.

In this paper it is suggested that many scale-invariant biological processes can be viewed as a deformation of classical mechanics. In particular, the focus is on cellular signalling pathways and changes in the concentrations of their constitutive molecules. Here the symmetries present in the Hamiltonian formalism are deformed in a known way (that reflects deviation of the underlying system from being conservative) and so a conserved quantity can be recovered after reversing the deformation. This reversal relies heavily on the use of q-calculus, which is a common feature of deformed mechanics. The models considered have very general applications and the procedure for passing to conservative dynamics from a deformed system is likely to emerge as a common tool for studying near-symmetric biological processes. A detailed account of q-deformed mechanics is provided in Section 2 after a review of classical dynamics for readers not familiar with the Hamiltonian formalism. The general model and an illustrative example is considered in Section 3 prior to a higher-dimensional extension in Section 4.

2. Review of q-deformed classical dynamics in one dimension

In the Hamiltonian formulation of one-dimensional classical mechanics it is convenient to consider a two-dimensional real vector space V isomorphic to $\mathbb{R}^2$. This vector space is usually called phase space and the two components (x^1, x^2) of a vector field $x \in V$ are often referred to as position and momentum coordinates. The phase space V becomes a symplectic vector space when equipped with an anti-symmetric, non-degenerate bilinear form $\Omega : V \times V \to \mathbb{R}$. Specifically, for any $x, y \in V$ the symplectic form Ω satisfies $\Omega(x, y) = -\Omega(y, x)$ and the feature that if $\Omega(x, y) = 0$ for all $y \in V$ then $x = 0$. Viewed as a matrix acting on $\mathbb{R}^2$, Ω can be chosen to have the representation

$$\Omega = \begin{pmatrix} 0 & 1 \\ -1 & 0 \end{pmatrix}. \tag{1}$$

The symplectic form defines the Poisson bracket of two functions of the position and momentum coordinates. Writing the components of $x \in V$ as x^a ($a = 1, 2$) and the components of the symplectic form as Ω_{ab} (its inverse as Ω^{ab}), the Poisson bracket $\{f, g\}$ of any two functions $f, g : (x^1, x^2) \to \mathbb{R}$ is defined to be the function

$$\{f, g\} = \sum_{a,b} \Omega^{ab} \partial_a f \partial_b g, \tag{2}$$

where the operator ∂_a denotes partial differentiation with respect to the coordinate x^a.

In a classical physical system the total energy is a function $H : (x^1, x^2, t) \to \mathbb{R}$ called the Hamiltonian. Consider the total time derivate of a Hamiltonian that does not depend explicitly on time t:

$$\dot{H} = \sum_a \partial_a H \dot{x}^a = \partial_1 H \dot{x}^1 + \partial_2 H \dot{x}^2. \tag{3}$$

Since the system is not exchanging energy with its environment, the total energy should remain constant over time. Imposing the condition $\dot{H} = 0$ yields the relations $\partial_1 H = \dot{x}^2$ and $\partial_2 H = -\dot{x}^1$, which are precisely Hamilton's equations of motion. These can be written succinctly in terms of the inverted symplectic form

$$\dot{x}^a = \sum_b \Omega^{ab} \partial_b H. \tag{4}$$

Once the Hamiltonian has been specified the system is determined uniquely since calculating the total time derivative of any function $f : (x^1, x^2) \to \mathbb{R}$ one can show

$$\dot{f} = \{H, f\}. \tag{5}$$

For example, Hamilton's equations of motion are recovered taking f to be either of the x^a.

There is a nice symmetry of Hamilton's equations that can be most easily verified using the Poisson bracket formalism. Consider a coordinate transformation $x^a \to X^i(x^1, x^2)$ ($i = 1, 2$) with associated Jacobian matrix J. The resulting change in the Poisson bracket is

$$\{f, g\} = \sum_{a,b} \sum_{i,j} \Omega^{ab} J_a^i J_b^j \partial_i f \partial_j g, \tag{6}$$

which means the dynamics are only preserved if J satisfies

$$J \Omega J^T = \Omega \tag{7}$$

so that

$$\dot{X}^i = \sum_j \Omega^{ij} \partial_j H. \tag{8}$$

Elements of the general linear group $GL(2, \mathbb{R})$ of non-singular 2×2 real matrices that satisfy (7) form a subgroup called the symplectic group $Sp(2, \mathbb{R})$. In two dimensions the symplectic group is isomorphic to the group of non-singular 2×2 real matrices with unit determinant $SL(2, \mathbb{R})$. Consequently, Hamilton's equations remain invariant under a change of coordinates whose Jacobian is a member of $Sp(2, \mathbb{R})$. A transformation of this kind may also be called canonical since time evolution can be viewed as a one-parameter family of these generated by the Hamiltonian and taking $x^a(0)$ to $x^a(t)$.

The importance of symmetry is best demonstrated by Noether's theorem that states for every symmetry of Hamilton's equations there is an additional function of the x^a that is conserved in time. To see this, for an infinitesimal transformation

$$x^a \to x^a + \epsilon F^a(x^1, x^2) + O(\epsilon^2) \tag{9}$$

to be a symmetry the requirement (7) demands

$$\partial_1 F^1 = -\partial_2 F^2, \tag{10}$$

which is satisfied if $F^1 = \partial_2 G$ and $F^2 = \partial_1 G$ for some function $G : (x^1, x^2) \to \mathbb{R}$. Then the Hamiltonian transforms infinitesimally as

$$H \to H + \epsilon \{H, G\} + O(\epsilon^2), \tag{11}$$

but since the coordinate change is a symmetry of the Hamiltonian

$$0 = \epsilon \{H, G\} = \epsilon \dot{G} \tag{12}$$

and therefore G is also conserved. The existence of conserved quantities is useful for qualitative study of complicated isolated systems, but these are rarely present in biological processes operating far from equilibrium.

Deformations of Hamilton's equations arise when one moves to a non-commutative setting, the standard example being canonical quantisation in quantum mechanics. This deformation is on the scale of Planck's constant h and involves promoting x^1 and x^2 to operators $\bar{x}^1$ and $\bar{x}^2$ that satisfy

$$\bar{x}^1 \bar{x}^2 - \bar{x}^2 \bar{x}^1 = i\hbar, \tag{13}$$

where $i = \sqrt{-1}$ and $\hbar = h/2\pi$. A less-well-known example is the q-deformation, which involves some fixed real parameter q different than 1 and takes the form