Poisson geometry and disease spread

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Abstract

This is a very brief introduction to Poisson geometry and the geometrical formalism of dynamical systems. We will explore how differential geometry can be used to study the Lotka–Volterra equations, which is a system of equations used in the study of predator-prey interactions, economics and disease spread.

1 Introduction

Any physics student that had studied the Hamiltonian formalism of classical mechanics encountered the *Poisson bracket* and how it is related with the dynamics of the system. Poisson geometry appeared from the mathematical, and hence rigorous, formulation of classical mechanics, when Siméon Poisson was studying the dynamics of particles [CFM21]. Some years later, Jacobi continued to study this mathematical formalism, discovering the Leibniz and Jacobi identity, which influenced Lie to discover what we now call Lie groups.

One of the principal characteristics of science is its great ability to predict new phenomena using mathematical models. However, there are some more experimental sciences, as biology, where these models are not so well received by the community [Wan78]. The Lotka-Volterra model is one of those mathematical models that tries to study the dynamics of the interactions of different biological species. More recent studies, had used this model to study this interaction but when some disease is considered [Ven94].

2 Poisson geometry

In classical mechanics, the state of the system is described by the functions $(q(t), p(t)) \in \mathbb{R}^{2n}$, corresponding to position and momentum[1] respectively. These functions live in the *phase space*, $\mathbb{R}^{2n}$, and the dynamics of the system is governed by a scalar function, $H : \mathbb{R}^{2n} \to \mathbb{R}$ called the *Hamiltonian*, via the equations,

$$\begin{cases} \dot{q}^i = \frac{\partial H}{\partial p_i} \\ \dot{p}_i = -\frac{\partial H}{\partial q^i} \end{cases} \tag{1}$$

called the *Hamilton's equations* [Fer07]. Note the simplicity and power of this formalism, unlike Newton's formalism, where one has to draw all the forces and put them in the right place, here we just need to write a scalar function, which typically is the energy of the system, and get the equations of motion. We can simplify it further by introducing the main object of this article, the Poisson bracket.

Definition 1. ([CFM21]) A *Poisson bracket* on the space $C^\infty(M)$, with M a smooth manifold, is a Lie bracket,

$$\{\cdot,\cdot\} : C^\infty(M) \times C^\infty(M) \to C^\infty(M)$$

satisfying the Leibniz identity:

$$\{f, gh\} = g\{f, h\} + \{f, g\}h, \qquad \forall f, g, h \in C^\infty(M).$$

A smooth manifold M equipped with a Poisson bracket is called a *Poisson manifold*. As always, we need to define what are the maps between Poisson manifolds that preserve this new structure.

Definition 2. ([CFM21]) A *Poisson map* between Poisson manifolds $(M_1, \{\cdot,\cdot\}_1)$ and $(M_2, \{\cdot,\cdot\}_2)$ is a smooth map $\varphi : M_1 \to M_2$ which is also a Lie algebra homomorphism:

$$\{f \circ \varphi, g \circ \varphi\}_1 = \{f, g\}_2 \circ \varphi, \qquad \forall f, g \in C^\infty(M_2).$$

In our case, $M = \mathbb{R}^{2n}$, and in local coordinates, (q^i, p_i), the Poisson bracket is given by,

$$\{f_1, f_2\} = \sum_{i=1}^{n} \left(\frac{\partial f_1}{\partial p_i}\frac{\partial f_2}{\partial q^i} - \frac{\partial f_1}{\partial q^i}\frac{\partial f_2}{\partial p_i} \right). \tag{2}$$

With this Poisson bracket, the Hamilton's equations reduce to a simple and elegant form,

$$x^i = \{H, x^i\}, \qquad (i = 1, \dots, n) \tag{3}$$

with x^i any of the functions q^i, p_i [Fer07]. We can now use this elegant form, and the fact that the Poisson bracket is a derivation[2] on the algebra $C^\infty(M)$, to define the Hamiltonian vector field

$$X_H(f) = \{H, f\}$$

so we get $\dot{x}(t) = X_H(x(t))$ [CFM21, Fer07].

[1] In classical mechanics, the momentum of a particle is the mass of the particle times its velocity, $\vec{p} = m\vec{v}$.

[2] A derivation, D, on $C^\infty(M)$ is a linear map satisfying the Leibniz rule, i.e., $D(fg) = fD(g) + D(f)g$ [Fer24].

3 Lotka-Volterra equations

In the beginning of the twentieth century, Volterra introduced the system of differential equations

$$\dot{x}_j = \varepsilon_j x_j + \sum_{k=1}^{n} a_{jk} x_j x_k \tag{4}$$

with $j = 1, \ldots, n$, to model the interaction of n biological species [FO95]. We first need to understand how this equation works. The functions $x_j(t) > 0$ represent the number of elements of species j at time t, the a_{jk}'s coefficients are the interaction coefficients between different species and ε_j determines if the species j can survive in the no interaction scenario.
Let us assume that the interaction matrix is skew-symmetric, $a_{jk} = -a_{kj}$.

Example 1. *Consider the simple Lotka-Volterra system for $n = 2$, $\varepsilon_j = 0$ and the interaction matrix skew-symmetric with no entries in the diagonal. We obtain the system,*

$$\begin{cases} \dot{x} = ayx \\ \dot{y} = -axy \end{cases} \quad \longrightarrow \quad \dot{x}(t) + \dot{y}(t) = 0$$

with $a \in \mathbb{R}$, giving a conservative system.

With this assumption[3], Volterra noticed that he could rewrite his system of equations in the Hamiltonian formalism. To do that, he introduced new variables, called Volterra quantity of life, defined by $Q_j = \int_0^t x_j(s)ds$. With these new variables, one can rewrite the equations,

$$\ddot{Q}_j = \varepsilon_j \dot{Q}_j + \sum_{k=1}^{n} a_{jk} \dot{Q}_j \dot{Q}_k \tag{5}$$

and define the Hamiltonian $H = \sum_{j=1}^{n} (\varepsilon_j Q_j - \dot{Q}_j)$, which is a conserved quantity ($\dot{H} = 0$). Remember that in the Hamiltonian formalism we had two different functions, the position and momentum. We already have one type of function, Q_j, so we need one more type and this will be given by[4] $P_j = \log \dot{Q}_j - \frac{1}{2}\sum_{k=1}^{n} a_{jk} Q_k$. With these new variables, one can show that the original system is equivalent to

$$\begin{cases} \dot{P}_j = \frac{\partial H}{\partial Q_j} \\ \dot{Q}_j = -\frac{\partial H}{\partial P_j} \end{cases} \tag{6}$$

with $H = \sum_j \varepsilon_j Q_J - \sum_j \exp(P_j + \frac{1}{2}\sum_k a_{jk} Q_k)$, which is similar to Eqn. 1. In this way we were able to write the Lotka-Volterra system in the Hamiltonian formalism and, as we saw, we can use the machinery of Poisson geometry to study this system due to the simple formula Eqn. 3.

[3] It is also possible, in some cases, to write the system in the Hamiltonian formulation for non skew-symmetric cases, see [FO95].

[4] This function is well defined since $\dot{Q}_j = x_j(t)$ is always positive.

3.1 Equilibrium situation

Now we want to study the equilibrium solution for the system (4) in a way that we do not need to extend the number of variables in the system to get the Hamiltonian formalism. We first need to introduce the Poisson bracket on $\mathbb{R}^n$,

$$\{f_1 f_2\} = \sum_{j<k} a_{jk} x_j x_k \left(\frac{\partial f_2}{\partial x_j}\frac{\partial f_1}{\partial x_k} - \frac{\partial f_1}{\partial x_j}\frac{\partial f_2}{\partial x_k} \right) \tag{7}$$

which one can check that it is indeed a Poisson bracket. If there is an equilibrium $(y_1, \ldots, y_n)$ satisfying $\varepsilon_j + \sum_k a_{jk} y_k = 0$ and if we define $H = \sum_j (x_j - y_j \log x_j)$ we can write the system (4) in the form $\dot{x}_j = \{H, x_j\}$. Again, we were able to get an Hamiltonian system, but this time with only n variables instead of $2n$. This process is called *geometric reduction*.

Theorem 1. *([FO95]) The map $\Psi : (Q_i, P_i) \mapsto x_j$ defined by*

$$x_j = \exp(P_j + \frac{1}{2}\sum_k a_{jk} Q_k)$$

is a Poisson map from $\mathbb{R}^{2n}$ with the bracket 2 to $\mathbb{R}^n$ with bracket 7. Moreover, if $(y_1, \ldots, y_n)$ is an equilibrium as above, then this maps reduces the system 6 to the original system 4.

3.2 Disease spread

The system (4) can be used for epidemiological models, like the SI (Susceptible-Infectious) and SIS (Susceptible-Infectious-Susceptible) models, where we have two species, susceptibles and infectious [Ven94, KM27]. The simple SIS model is given by

$$\begin{cases} \dot{S} = -\mu S + \gamma I - \lambda IS + \mu \\ \dot{I} = -(\gamma + \mu) I + \lambda IS \end{cases} \tag{8}$$

with $S + I = 1$ by conservation of population. The γ coefficient represents the recovery rate and μ the mortality rate. If we set $\gamma = 0$, then once we are infected we will remain always infected until death, we get the SI model [Ven94]. Notice that in both cases the interaction matrix is skew-symmetric, and we can explore the formalism presented in last section to study these systems.

4 Conclusion

In this article we were able to introduce some basic concepts of Poisson geometry and how they are related with the Hamiltonian formalism. We then present the famous Lotka-Volterra equations and how can they be written as an Hamiltonian system, in the skew-symmetric case. We also explored a process called reduction, where we do not need to extend the number of variables of our system to get the Hamiltonian.

At the end, we present how these equations are related with the epidemiological models to study diseases propagation. We focused on the SI model, which is a particular case of the SIS model.
To sum up, we formalized the bridge between differential geometry, in particular Poisson geometry, and dynamical systems, used to study disease spread (and more), so that one can now use the machinery of geometry to get qualitative properties of those systems like conserved quantities as the Hamiltonian.

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