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LETTER TO THE EDITOR

**Bi-Hamiltonian structure of the Kermack–McKendrick model for epidemics**

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**Abstract.** The dynamical system proposed by Kermack and McKendrick to model the spread of epidemics is shown to admit bi-Hamiltonian structure without any restrictions on the rate constants. These two inequivalent Hamiltonian structures are compatible.

Various phenomena in biology are modelled by dynamical systems. We refer to the recent book by Murray [1] for an interesting discussion of such systems. Some of these dynamical systems are still of interest from a mathematical point of view; namely, they admit bi-Hamiltonian structure. There are a number of advantages in recognizing the existence of bi-Hamiltonian structure in a dynamical system. In particular, this makes it possible to discuss the stability of relative equilibria by the energy-Casimir method [2].

We have recently pointed out [3] that a special class of 3-species Lotka–Volterra equations admits bi-Hamiltonian structure. The purpose of this letter is to point out that the Kermack–McKendrick model [4] for epidemics also admits bi-Hamiltonian structure which is very similar to that of the Lotka–Volterra equations.

The model proposed by Kermack and McKendrick for epidemics is a three-dimensional dynamical system which is also known as the *SIR* model. The equations of motion are given by

$$\begin{aligned} \dot{S} &= -rSI \\ \dot{I} &= rSI - aI \\ \dot{R} &= aI \end{aligned} \tag{1}$$

where *S* stands for the number of susceptibles, *I* for those infected and *R* denotes the removals. The constants *a*, *r* determine the infection and removal rates of infectives respectively. This has proved to be the basic model for describing epidemics because it contains the essential features of the phenomenon in a very simple way and adequately describes some simple epidemics. In this model the population size

$$H_1 = S + I + R \tag{2}$$

is constant and it is also well known that

$$H_2 = R + \frac{a}{r} \log S \tag{3}$$

is another conserved quantity associated with the system (1).

The Kermack-McKendrick equations can be formulated as a Hamiltonian system [5] in two distinct ways. If we let  $x^i$ ,  $i = 1, 2, 3$  stand for  $S, I, R$  respectively, (1) can be written as

$$\dot{x}^i = J_1^{ik} \nabla_k H_2 = J_2^{ik} \nabla_k H_1 \quad (4)$$

where the structure functions are given by

$$J_1^{ik} = rSI \begin{pmatrix} 0 & 1 & -1 \\ -1 & 0 & 1 \\ 1 & -1 & 0 \end{pmatrix} \quad (5)$$

and

$$J_2^{ik} = \begin{pmatrix} 0 & -rSI & 0 \\ rSI & 0 & -aI \\ 0 & aI & 0 \end{pmatrix}. \quad (6)$$

It can be readily verified that they satisfy the Jacobian identities

$$J^{m[i} J^{jk]},_{m} = 0 \quad (7)$$

with square brackets denoting antisymmetrization. Furthermore any linear combination of  $J_1$  and  $J_2$  also satisfies the Jacobi identities, thus they are compatible. Finally, we find that

$$J_1^{ik} \nabla_k H_1 = 0 \quad J_2^{ik} \nabla_k H_2 = 0 \quad (8)$$

that is, the Hamiltonians  $H_1$  and  $H_2$  act as the Casimirs of  $J_1$  and  $J_2$  respectively.

The general result that emerges for the Hamiltonian structure of the Kermack-McKendrick equations is the same as that for the 3-species Lotka-Volterra equations that we had studied earlier. However, no restrictions had to be imposed on the rate constants  $a, r$  in order to show the bi-Hamiltonian structure of (1). So, unlike the case of the Lotka-Volterra equations, the bi-Hamiltonian structure of the Kermack-McKendrick equations is true quite generally.

## References

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