Counting equilibria of an ODE using algebraic methods: application to problems originating from biology

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The number of equilibrium states of a dynamical system is considered as one of the most important sources of information about its qualitative behaviour. This is because the appearance or disappearance of an equilibrium under the variation of model parameters drastically changes the geometric structure of the phase portrait. Solutions of dynamical systems possessing several equilibria may be characterized by more diverse asymptotic behaviours.

In particular, in population dynamics, multistability may lead to the formation of a heterogeneous structure from the same type of individuals. As an example, we may take adipose cells, the main component of adipose tissue. The size distribution of adipocytes within a single depot is observed to have two modes [3]. One of the hypothesis explaining this phenomenon is the bistability of an individual adipocyte. This idea was reflected in the ordinary differential equation governing adipocyte size evolution proposed in [4]. A careful selection of parameter values results in a bistable model. However, identifying the analytical conditions for which two stable equilibria exist is a very demanding task, that was beyond our capabilities using standard analytical tools.

We present here a method developed in [1], exploiting a special property of the so-called Hermite quadratic form [2]. The proposed method is designed to find a number of equilibrium states for a broad class of ordinary differential equations in the form of rational/polynomial equation. To our best knowledge, such an approach has not been yet used in the domain of mathematical biology. However, it proves to be especially useful in the case of a large parameter space, which is common in this area. By using as an example the logistic equation describing population growth, we demonstrate how the method explores efficiently the parameter space to establish the number of stationary states. Next, we present the results of the algorithm applied to the model describing adipocyte size dynamics. What is more, we show that the algorithm results are in agreement with the numerical solutions of the model.

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