Aggregation and emergence in systems of ordinary differential equations.

Aggregation and emergence in population dynamics.


In modeling biological systems, many variables and parameters are often used to describe the dynamics of the system. With too many variables and parameters, a rigorous analysis of the system may be either unfeasible or impossible.

Aggregation is the process of deleting some of the variables, keeping only as many as are needed to describe the relevant dynamics of the system. Restated, aggregation is a process of extracting from a micro-system (a mathematical model for a large scale system involving many micro-variables) a macro-model, or aggregated model, with fewer variables.

As a result of aggregation, one can compare the dynamics of the original micro-system with the dynamics of the aggregated macro-model. Being less than precise, we say that an emergence from the micro-dynamics to the macro-dynamics exists if the dynamics of the micro-model and the macro-model are topologically different. The authors give more precise definitions of functional emergence and dynamical emergence.

As noted in the paper’s abstract, the aim of the study is to present aggregation methods for a system of ordinary differential equations involving two time scales. The system of ODEs considered is composed of the sum of fast parts and a perturbation. Using biological terms, the ODEs are written in a form which considers separate interactions between subpopulations within the same population (an internal fast part), and interactions between subpopulations of different populations (an external slow part). The fast dynamics are assumed to be conservative. The authors discuss strategies and methods of aggregation where the macro-variables are chosen as first integrals of the fast parts. The aggregated system then models the macro-variables at the slower time scale. Emergence is discussed and illustrated.

{For the collection containing this paper see MR1608869}