

Approximate Aggregation Methods and Applications to Population Dynamics

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Abstract

When modelling biological systems, in particular ecological ones, we usually find very complex systems that we should try to manage to get some insights. A first approach to do this consists in building an abstract model describing the real system in detail. This leads to a family of models involving a very large number of variables. The complexity of the system is included in the model and computer simulation becomes the only available tool to carry out its study. At the other extreme we can find those models avoiding almost every detail in order to be mathematically tractable. These models of ecological communities only deal with a few variables, assuming that the internal structure of the population has no important effect and so can be neglected. This assumption corresponds to an approximation of the total system by means of a reduced one that should be checked. However, in most cases, simplified models are used and few arguments are given to justify them. A tool trying to fill the gap between these two approaches is approximate aggregation.

Approximate aggregation consists in describing some features of the dynamics of a general system in terms of the dynamics of a reduced system governed by a few number of global variables. We think of a hierarchically organized population, thus subdivided into sub-populations, which allows distinguishing two processes of a general nature and whose corresponding time scales are very different from each other. Results will be presented showing that, under quite general conditions, the asymptotic behaviour of the general system can be known in terms of the corresponding behaviour of the reduced system.

We present a review ([1],[2],[3]) of aggregation methods for different kinds of discrete dynamical systems linear and non-linear, deterministic and stochastic.

References

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