Abstract differential equations that arise in various biological contexts provide an example of infinite dimensional nonlinear dynamical systems, which aim to describe simultaneously ecological and evolutionary processes. In many cases the analysis of such systems is highly non-trivial. It turns out, however, that an additional assumption on the specific birth rates in the models allows to significantly reduce the dimensionality of the problem, ending up with a system of ordinary differential equations. In my talk I will introduce such heterogeneous mathematical models and present some non-obvious consequences of the key simplifying assumption. The problem of systems identification, i.e., inferring parameter values from the available data, will be discussed. (Received July 06, 2017)