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## **Difference and differential equations in population biology: History and modelling**

Difference equations have been used to model population growth at least since Fibonacci's work in 1202. With the seminal work in the early 20th century by Lotka and independently by Volterra on biological interactions, differential equations began to play a more prominent role. In the 1970s when Robert May, George Oster and others pointed out to biologists that simple difference equations may show complicated behaviour, the popularity of using difference equations as a modelling tool in population biology grew.

In my talk I will give a short historical and critical account of the use of difference and differential equations in population biology

To every differential equation one can associate a difference equation by Euler's method and use this to numerically approximate the solution of the differential equation. This approach has been used in the literature to derive discrete time population models from established continuous time models. In this talk I will show that, as a rule, this method does not lead to biologically relevant models.

On the other hand, difference equation description of population growth occur naturally from mechanistic modelling because in nature reproduction in many species happen at short and limited time periods during the year. Other processes such as foraging and death happen continuously and therefore one is often led to hybrid models in which the dynamics during the season is described by a differential equation and the reproduction event is modelled as a jump.

In my talk I will give mechanistic derivations of some well-known and some less well-known population models that ultimately take the form of a difference equation (or systems of difference equations).