

Population ecology modelling with R: a comparison of object oriented approaches

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The R system with the underlying S programming language is well suited for the development, implementation and analysis of ecological models and it is increasingly accepted among ecologists. Existing applications already cover a range from small conceptual process and teaching models up to large coupled models on the ecosystem scale. Small models can be implemented very easily in pure R. For larger ones, R is primarily used as an environment for data management, simulation control and data analysis, while the model cores are usually implemented in other languages like C++ or Fortran. This works perfectly at the extremes, but problems appeared with medium-sized models:

- non-trivial ecological models are based on more or less modular building blocks (submodels), which are either the underlying base equations or complex models themselves.
- both, data and procedural code (submodels) are highly variable. A typical example is the comparison of similar models with identical data, but with slightly different submodels.

The `simecol` package was developed in order to provide an open and minimally standardized structure to implement and run ecological models; however, the S3 list-based structure of the first version had to be extended to organize more complex applications. Different object oriented approaches (S3 lists, proto, R.oo, S4) were evaluated using the example of a typical and yet simple Lotka-Volterra type model. The implementations were compared with respect to usability, flexibility, conformity to common standards and performance. A larger model¹ for the genus *Daphnia* is presented to demonstrate some of the object oriented approaches. This model represents a more complex and computation intensive simulation, a bioenergetic model which accounts for demographic population structure.

With the examples used here we found it advantageous to use OOP and the difference between using OOP and not using OOP was more significant than which OOP framework was used. If one OOP implementation exists it is relatively easy to transform it to one of the other versions, but distinctive differences and specific features of the packages remain. The purpose of this presentation is to compare the technical frameworks available in the R environment according to their suitability to organize ecological models. Reference applications are provided that can help ecologists to structure their work. Moreover, the examples demonstrate that it would be feasible to use R and OOP as a medium for the distribution and share of ecological modelling code.

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¹Rinke, K. & Vijverberg, J. (2005) A model approach to evaluate the effect of temperature and food concentration on individual life-history and population dynamics of *Daphnia*. *Ecological Modelling*, 186, 326-344