Statistical inference for complicated models in ecology and evolutionary biology

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Abstract: Monte Carlo simulation has long been a widely used tool in biology, traditionally for predictive modelling, as an adjunct to more analytical approaches, and latterly for statistical inference. The predictive and inferential aspects have typically been considered separately, often by different specialisms. One reason for this is that, while it is generally easy to formulate stochastic data-generating simulations of arbitrary complexity, it may be practically impossible to obtain a likelihood function for the same problem. However, it is now becoming widely appreciated that the predictive and inferential aspects can be viewed, under the Bayesian paradigm, as simply parts of the same whole, depending on which parts of the model are regarded as fixed and which are random. A useful tool that has underpinned this conceptual change in a very practical way is the method of approximate Bayesian computation (ABC). In this talk I will outline the basic ABC approach, and how it has evolved. Using examples in ecology and population genetics I will illustrate how it can be used for Bayesian model choice, posterior predictive modelling, and prior- and posterior-model checking. The known problems of the approach are also discussed. Finally I will end by describing the use of these methods for agent-based models in ecology.