

Data Cloning: A Simple Approach to Likelihood Inference for Dynamical Systems

Subhash R. Lele
Department of Mathematica & Statistical Sciences
University of Alberta
Edmonton, AB T6G 2G1
CANADA
ionides@umich.edu

Abstract

Dynamical systems are useful for developing understanding of the structure and general behavior of the biological systems. However, confronting these models with real data has proved to be a challenging problem because of the presence of unobservable states and reporting biases. Recently Lele (2007) and Lele et al. (2007) have developed a new computational algorithm called data cloning that uses Bayesian Markov Chain Monte Carlo approach to conduct full likelihood based inference for general hierarchical models. Data cloning provides ML estimators without ever explicitly evaluating or maximizing the likelihood function. Aside from providing the point estimators, this method also provides asymptotic standard errors in a very simple fashion. Furthermore, if the parameter space is compact, it guarantees location of the global maximum. In this talk, I will provide an overview of the data cloning algorithm and illustrate its use for conducting likelihood based inference for dynamical system models with applications in ecology and epidemiology.

References

- Lele, S.R. (2006) Data Cloning: A simple approach for computing maximum likelihood estimates for mixed models. *Biostatistics* (under review).
- Lele, S.R., B. Dennis and F. Lutscher (2007) Data cloning: Easy maximum likelihood estimation for complex ecological models using Bayesian Markov Chain Monte Carlo methods. *Ecology Letters* (in press).