



PIMS Mathematical Biology Seminar



**Monday, February 4, 2007
3 pm - 657 CAB**

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Data cloning: easy maximum likelihood estimation for complex ecological models using Bayesian Markov chain Monte Carlo methods

We introduce a new statistical computing method, called data cloning, to calculate maximum likelihood estimates and their standard errors for complex ecological models. Although the method uses the Bayesian framework and exploits the computational simplicity of the Markov chain Monte Carlo (MCMC) algorithms, it provides valid frequentist inferences such as the maximum likelihood estimates and their standard errors. The inferences are completely invariant to the choice of the prior distributions and therefore avoid the inherent subjectivity of the Bayesian approach. The data cloning method is easily implemented using standard MCMC software. Data cloning is particularly useful for analyzing ecological situations in which hierarchical statistical models, such as state space models and mixed effects models, are appropriate. We illustrate the method by fitting two non-linear population dynamics models to data in the presence of process and observation noise.

*This is joint work with Brian Dennis and Fritjof Lutscher.
The paper appeared in Ecology Letters (July 2007).*

Join us for refreshments in CAB 549 immediately following the seminar

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