Bayesian Modeling in R with JAGS

Martyn Plummer International Agency for Research on Cancer

JAGS is a C++ library for analyzing Bayesian hierarchical models using Markov Chain Monte Carlo. It is not wholly unlike WinBUGS (Bayesian inference Using Gibbs Sampling) [1] and has many of the same features, with the notable exception of a graphical user interface.

JAGS takes a description of a model in the highly flexible BUGS language and a data set defining the observed variables. It then provides a sequence of samples from the posterior distribution of the unobserved variables which can be used for approximate Bayesian inference. The capabilities of JAGS can be extended with dynamically loadable modules. A module can extend the modeling language by defining new functions and distributions, or it can improve performance by defining new samplers for specific modeling situations, such as mixture models or generalized linear models.

This talk will review the JAGS package for R which is currently under development. The package uses R's simple interface to external references [2]. A JAGS model object in R contains an opaque pointer to an external C++ object. JAGS model objects therefore have a mutable state, which makes them different from the more familiar "fitted model" objects, such as those created by the glm() function, and requires an object-oriented user interface.

References

- Spiegelhalter D, Thomas A, Best N, Lunn D. WinBUGS User Manual, Version 2.0, June 2004. http://mathstat.helsinki.fi/openbugs/
- [2] Tierney L. Simple References with Finalization. http://www.stat.uiowa.edu/~luke/R/ simpleref.html