

CRAN Task View: Bayesian Inference

Maintainer: Jong Hee Park

Contact: jongheepark at snu.ac.kr

Version: 2015-09-30

Applied researchers interested in Bayesian statistics are increasingly attracted to R because of the ease of which one can code algorithms to sample from posterior distributions as well as the significant number of packages contributed to the Comprehensive R Archive Network (CRAN) that provide tools for Bayesian inference. This task view catalogs these tools. In this task view, we divide those packages into four groups based on the scope and focus of the packages. We first review R packages that provide Bayesian estimation tools for a wide range of models. We then discuss packages that address specific Bayesian models or specialized methods in Bayesian statistics. This is followed by a description of packages used for post-estimation analysis. Finally, we review packages that link R to other Bayesian sampling engines such as [JAGS](#), [OpenBUGS](#), [WinBUGS](#), and [Stan](#).

Bayesian packages for general model fitting

- The [arm](#) package contains R functions for Bayesian inference using `lm`, `glm`, `mer` and `polr` objects.
- [BACCO](#) is an R bundle for Bayesian analysis of random functions. [BACCO](#) contains three sub-packages: `emulator`, `calibrator`, and `approximator`, that perform Bayesian emulation and calibration of computer programs.
- [bayesm](#) provides R functions for Bayesian inference for various models widely used in marketing and micro-econometrics. The models include linear regression models, multinomial logit, multinomial probit, multivariate probit, multivariate mixture of normals (including clustering), density estimation using finite mixtures of normals as well as Dirichlet Process priors, hierarchical linear models, hierarchical multinomial logit, hierarchical negative binomial regression models, and linear instrumental variable models.
- [bayesSurv](#) contains R functions to perform Bayesian inference for survival regression models with flexible error and random effects distributions.
- [DPpackage](#) contains R functions for Bayesian nonparametric and semiparametric models. `DPpackage` currently includes semiparametric models for density estimation, ROC curve analysis, interval censored data, binary regression models, generalized linear mixed models, and IRT type models.
- [MCMCpack](#) provides model-specific Markov chain Monte Carlo (MCMC) algorithms for wide range of models commonly used in the social and behavioral sciences. It contains R functions to fit a number of regression models (linear regression, logit, ordinal probit, probit, Poisson regression, etc.), measurement models (item response theory and factor models), changepoint models (linear regression, binary probit, ordinal probit, Poisson, panel), and models for ecological inference. It also contains a generic Metropolis sampler that can be used to fit arbitrary models.
- The [mcmc](#) package consists of an R function for a random-walk Metropolis algorithm for a continuous random vector.

Bayesian packages for specific models or methods

- [abc](#) package implements several ABC algorithms for performing parameter estimation and model selection. Cross-validation tools are also available for measuring the accuracy of ABC estimates, and to calculate the misclassification probabilities of different models.
- [AdMit](#) provides functions to perform the fitting of an adaptive mixture of Student-t distributions to a target density through its kernel function. The mixture approximation can be used as the

importance density in importance sampling or as the candidate density in the Metropolis-Hastings algorithm.

- The [BaBooN](#) package contains two variants of Bayesian Bootstrap Predictive Mean Matching to multiply impute missing data.
- The [bayesGARCH](#) package provides a function which perform the Bayesian estimation of the GARCH(1,1) model with Student's t innovations.
- [BayesSummaryStatLM](#) provides two functions: one function that computes summary statistics of data and one function that carries out the MCMC posterior sampling for Bayesian linear regression models where summary statistics are used as input.
- [Bayesthresh](#) fits a linear mixed model for ordinal categorical responses using Bayesian inference via Monte Carlo Markov Chains. Default is Nandran and Chen algorithm using Gaussian link function and saving just the summaries of the chains.
- [BayesTree](#) implements BART (Bayesian Additive Regression Trees) by Chipman, George, and McCulloch (2006).
- [bayesQR](#) supports Bayesian quantile regression using the asymmetric Laplace distribution, both continuous as well as binary dependent variables.
- [BayHaz](#) contains a suite of R functions for Bayesian estimation of smooth hazard rates via Compound Poisson Process (CPP) priors.
- [BAYSTAR](#) provides functions for Bayesian estimation of threshold autoregressive models.
- [bbemkr](#) implements Bayesian bandwidth estimation for Nadaraya-Watson type multivariate kernel regression with Gaussian error.
- [BCE](#) contains function to estimates taxonomic compositions from biomarker data using a Bayesian approach.
- [BCBCSF](#) provides functions to predict the discrete response based on selected high dimensional features, such as gene expression data.
- [bclust](#) builds a dendrogram with log posterior as a natural distance defined by the model. It is also capable to computing Bayesian discrimination probabilities equivalent to the implemented Bayesian clustering. Spike-and-Slab models are adopted in a way to be able to produce an importance measure for clustering and discriminant variables.
- [bcp](#) implements a Bayesian analysis of changepoint problem using Barry and Hartigan product partition model.
- [bfp](#) implements the Bayesian paradigm for fractional polynomial models under the assumption of normally distributed error terms.
- [bisoreg](#) implements the Bayesian isotonic regression with Bernstein polynomials.
- [BLR](#) provides R functions to fit parametric regression models using different types of shrinkage methods.
- The [BMA](#) package has functions for Bayesian model averaging for linear models, generalized linear models, and survival models. The complementary package [ensembleBMA](#) uses the [BMA](#) package to create probabilistic forecasts of ensembles using a mixture of normal distributions.
- [BMS](#) is Bayesian Model Averaging library for linear models with a wide choice of (customizable) priors. Built-in priors include coefficient priors (fixed, flexible and hyper-g priors), and 5 kinds of model priors.
- [Bmix](#) is a bare-bones implementation of sampling algorithms for a variety of Bayesian stick-breaking (marginally DP) mixture models, including particle learning and Gibbs sampling for static DP mixtures, particle learning for dynamic BAR stick-breaking, and DP mixture regression.
- [bnlearn](#) is a package for Bayesian network structure learning (via constraint-based, score-based and hybrid algorithms), parameter learning (via ML and Bayesian estimators) and inference.
- [bqtl](#) can be used to fit quantitative trait loci (QTL) models. This package allows Bayesian estimation of multi-gene models via Laplace approximations and provides tools for interval mapping of genetic loci. The package also contains graphical tools for QTL analysis.

- [bspec](#) performs Bayesian inference on the (discrete) power spectrum of time series.
- [bspmma](#) is a package for Bayesian semiparametric models for meta-analysis.
- [BSquare](#) models the quantile process as a function of predictors.
- [BVS](#) is a package for Bayesian variant selection and Bayesian model uncertainty techniques for genetic association studies.
- [catnet](#) is a package that handles discrete Bayesian network models and provides inference using the frequentist approach.
- [coalescentMCMC](#) provides a flexible framework for coalescent analyses in R.
- [cslogistic](#) has a function that performs a Bayesian analysis of a conditionally specified logistic regression model.
- [dclone](#) provides low level functions for implementing maximum likelihood estimating procedures for complex models using data cloning and MCMC methods.
- [deal](#) provides R functions for Bayesian network analysis; the current version of covers discrete and continuous variables under Gaussian network structure.
- [dlm](#) is a package for Bayesian (and likelihood) analysis of dynamic linear models. It includes the calculations of the Kalman filter and smoother, and the forward filtering backward sampling algorithm.
- [EbayesThresh](#) implements Bayesian estimation for thresholding methods. Although the original model is developed in the context of wavelets, this package is useful when researchers need to take advantage of possible sparsity in a parameter set.
- [eco](#) fits Bayesian ecological inference models in two by two tables using MCMC methods.
- [ebdbNet](#) can be used to infer the adjacency matrix of a network from time course data using an empirical Bayes estimation procedure based on Dynamic Bayesian Networks.
- [eigenmodel](#) estimates the parameters of a model for symmetric relational data (e.g., the above-diagonal part of a square matrix), using a model-based eigenvalue decomposition and regression using MCMC methods.
- [evdbayes](#) provides tools for Bayesian analysis of extreme value models.
- [exactLoglinTest](#) provides functions for log-linear models that compute Monte Carlo estimates of conditional P-values for goodness of fit tests.
- [factorQR](#) is a package to fit Bayesian quantile regression models that assume a factor structure for at least part of the design matrix.
- [FME](#) provides functions to help in fitting models to data, to perform Monte Carlo, sensitivity and identifiability analysis. It is intended to work with models be written as a set of differential equations that are solved either by an integration routine from deSolve, or a steady-state solver from rootSolve.
- The `gbayes()` function in [Hmisc](#) derives the posterior (and optionally) the predictive distribution when both the prior and the likelihood are Gaussian, and when the statistic of interest comes from a two-sample problem.
- [ggmcmc](#) is a tool for assessing and diagnosing convergence of Markov Chain Monte Carlo simulations, as well as for graphically display results from full MCMC analysis.
- [growcurves](#) is a package for Bayesian semi and nonparametric growth curve models that additionally include multiple membership random effects.
- The [HI](#) package has functions to implement a geometric approach to transdimensional MCMC methods and random direction multivariate Adaptive Rejection Metropolis Sampling.
- The [hbsae](#) package provides functions to compute small area estimates based on a basic area or unit-level model. The model is fit using restricted maximum likelihood, or in a hierarchical Bayesian way.
- [iterLap](#) performs an iterative Laplace approximation to build a global approximation of the posterior (using mixture distributions) and then uses importance sampling for simulation based inference.

- The function `krige.bayes()` in the [geoR](#) package performs Bayesian analysis of geostatistical data allowing specification of different levels of uncertainty in the model parameters. The `binom.krige.bayes()` function in the [geoRglm](#) package implements Bayesian posterior simulation and spatial prediction for the binomial spatial model (see the [Spatial](#) view for more information).
- The [lmm](#) package contains R functions to fit linear mixed models using MCMC methods.
- [MasterBayes](#) is an R package that implements MCMC methods to integrate over uncertainty in pedigree configurations estimated from molecular markers and phenotypic data.
- [matchingMarkets](#) implements a structural model based on a Gibbs sampler to correct for the bias from endogenous matching (e.g. group formation or two-sided matching).
- [MCMCglmm](#) is package for fitting Generalised Linear Mixed Models using MCMC methods.
- The `mcmcsmpl()` function in [lme4](#) allows MCMC sampling for the linear mixed model and generalized linear mixed model.
- The [mlogitBMA](#) Provides a modified function `bic.glm()` of the [BMA](#) package that can be applied to multinomial logit (MNL) data.
- The [MNP](#) package fits multinomial probit models using MCMC methods.
- [mombf](#) performs model selection based on non-local priors, including MOM, eMOM and iMOM priors..
- [monomvn](#) is an R package for estimation of multivariate normal and Student-t data of arbitrary dimension where the pattern of missing data is monotone.
- [MSBVAR](#) is an R package for estimating Bayesian Vector Autoregression models and Bayesian structural Vector Autoregression models.
- [pacbpred](#) perform estimation and prediction in high-dimensional additive models, using a sparse PAC-Bayesian point of view and a MCMC algorithm.
- [PottsUtils](#) comprises several functions related to the Potts model defined on undirected graphs.
- [predmixcor](#) provides functions to predict the binary response based on high dimensional binary features modeled with Bayesian mixture models.
- [prevalence](#) provides functions for the estimation of true prevalence from apparent prevalence in a Bayesian framework. MCMC sampling is performed via JAGS/rjags.
- [profdpm](#) facilitates profile inference (inference at the posterior mode) for a class of product partition models.
- The [pscl](#) package provides R functions to fit item-response theory models using MCMC methods and to compute highest density regions for the Beta distribution and the inverse gamma distribution.
- The [PAWL](#) package implements parallel adaptive Metropolis-Hastings and sequential Monte Carlo samplers for sampling from multimodal target distributions.
- [PReMiuM](#) is a package for profile regression, which is a Dirichlet process Bayesian clustering where the response is linked non-parametrically to the covariate profile.
- [rcppbugs](#) is a package that attempts to provide an R alternative to using OpenBUGS/WinBUGS/JAGS using random walk Metropolis sampling.
- The [RJaCGH](#) package implements Bayesian analysis of CGH microarrays using hidden Markov chain models. The selection of the number of states is made via their posterior probability computed by reversible jump Markov chain Monte Carlo Methods.
- The `hitro.new()` function in [Runuran](#) provides an MCMC sampler based on the Hit-and-Run algorithm in combination with the Ratio-of-Uniforms method.
- [RSGHB](#) can be used to estimate models using a hierarchical Bayesian framework and provides flexibility in allowing the user to specify the likelihood function directly instead of assuming predetermined model structures.
- [rstiefel](#) simulates random orthonormal matrices from linear and quadratic exponential family distributions on the Stiefel manifold using the Gibbs sampling method. The most general type of distribution covered is the matrix-variate Bingham-von Mises-Fisher distribution.

- [RxCcolInf](#) fits the R x C inference model described in Greiner and Quinn (2009).
- [SamplerCompare](#) provides a framework for running sets of MCMC samplers on sets of distributions with a variety of tuning parameters, along with plotting functions to visualize the results of those simulations.
- [SampleSizeMeans](#) contains a set of R functions for calculating sample size requirements using three different Bayesian criteria in the context of designing an experiment to estimate a normal mean or the difference between two normal means.
- [SampleSizeProportions](#) contains a set of R functions for calculating sample size requirements using three different Bayesian criteria in the context of designing an experiment to estimate the difference between two binomial proportions.
- [sbgcop](#) estimates parameters of a Gaussian copula, treating the univariate marginal distributions as nuisance parameters as described in Hoff(2007). It also provides a semiparametric imputation procedure for missing multivariate data.
- [SimpleTable](#) provides a series of methods to conduct Bayesian inference and sensitivity analysis for causal effects from 2 x 2 and 2 x 2 x K tables.
- [sna](#), an R package for social network analysis, contains functions to generate posterior samples from Butt's Bayesian network accuracy model using Gibbs sampling.
- [spBayes](#) provides R functions that fit Gaussian spatial process models for univariate as well as multivariate point-referenced data using MCMC methods.
- [spikeslab](#) provides functions for prediction and variable selection using spike and slab regression.
- [spikeSlabGAM](#) implements Bayesian variable selection, model choice, and regularized estimation in (geo-)additive mixed models for Gaussian, binomial, and Poisson responses.
- [spTimer](#) fits, spatially predict and temporally forecast large amounts of space-time data using Bayesian Gaussian Process Models, Bayesian Auto-Regressive (AR) Models, and Bayesian Gaussian Predictive Processes based AR Models.
- [stochvol](#) provides efficient algorithms for fully Bayesian estimation of stochastic volatility (SV) models.
- The [tgp](#) package implements Bayesian treed Gaussian process models: a spatial modeling and regression package providing fully Bayesian MCMC posterior inference for models ranging from the simple linear model, to nonstationary treed Gaussian process, and others in between.
- [vbmp](#) is a package for variational Bayesian multinomial probate regression with Gaussian process priors. It estimates class membership posterior probability employing variational and sparse approximation to the full posterior. This software also incorporates feature weighting by means of Automatic Relevance Determination.
- The `vcov.gam()` function the [mgcv](#) package can extract a Bayesian posterior covariance matrix of the parameters from a fitted `gam` object.
- [zic](#) provides functions for an MCMC analysis of zero-inflated count models including stochastic search variable selection.

Post-estimation tools

- [BayesValidate](#) implements a software validation method for Bayesian softwares.
- The [boa](#) package provides functions for diagnostics, summarization, and visualization of MCMC sequences. It imports draws from BUGS format, or from plain matrices. [boa](#) provides the Gelman and Rubin, Geweke, Heidelberger and Welch, and Raftery and Lewis diagnostics, the Brooks and Gelman multivariate shrink factors.
- The [coda](#) (Convergence Diagnosis and Output Analysis) package is a suite of functions that can be used to summarize, plot, and and diagnose convergence from MCMC samples. [coda](#) also defines an `mcmc` object and related methods which are used by other packages. It can easily import MCMC output from WinBUGS, OpenBUGS, and JAGS, or from plain matrices. [coda](#) contains the Gelman and Rubin, Geweke, Heidelberger and Welch, and Raftery and Lewis diagnostics.

- [ramps](#) implements Bayesian geostatistical analysis of Gaussian processes using a reparameterized and marginalized posterior sampling algorithm.

Packages for learning Bayesian statistics

- [AtelieR](#) is a GTK interface for teaching basic concepts in statistical inference, and doing elementary bayesian statistics (inference on proportions, multinomial counts, means and variances).
- The [BaM](#) package is an R package associated with Jeff Gill's book, "Bayesian Methods: A Social and Behavioral Sciences Approach, Second Edition" (CRC Press, 2007).
- [BayesDA](#) provides R functions and datasets for "Bayesian Data Analysis, Second Edition" (CRC Press, 2003) by Andrew Gelman, John B. Carlin, Hal S. Stern, and Donald B. Rubin.
- The [Bolstad](#) package contains a set of R functions and data sets for the book Introduction to Bayesian Statistics, by Bolstad, W.M. (2007).
- The [LearnBayes](#) package contains a collection of functions helpful in learning the basic tenets of Bayesian statistical inference. It contains functions for summarizing basic one and two parameter posterior distributions and predictive distributions and MCMC algorithms for summarizing posterior distributions defined by the user. It also contains functions for regression models, hierarchical models, Bayesian tests, and illustrations of Gibbs sampling.

Packages that link R to other sampling engines

- [bayesmix](#) is an R package to fit Bayesian mixture models using [JAGS](#).
- [BayesX](#) provides functionality for exploring and visualizing estimation results obtained with the software package [BayesX](#).
- **BRugs** provides an R interface to [OpenBUGS](#). It works under Windows and Linux. **BRugs** used to be available from CRAN, now it is located at the [CRANextras](#) repository.
- [cudaBayesreg](#) provides a Compute Unified Device Architecture (CUDA) implementation of a Bayesian multilevel model for the analysis of brain fMRI data. CUDA is a software platform for massively parallel high-performance computing on NVIDIA GPUs.
- There are two packages that can be used to interface R with [WinBUGS](#). [R2WinBUGS](#) provides a set of functions to call WinBUGS on a Windows system and a Linux system; [rbugs](#) supports Linux systems through [OpenBUGS](#) on Linux (LinBUGS).
- [glmmBUGS](#) writes BUGS model files, formats data, and creates starting values for generalized linear mixed models.
- There are three packages that provide R interface with [Just Another Gibbs Sampler \(JAGS\)](#): [rjags](#), [R2jags](#), and [runjags](#).
- All of these BUGS engines use graphical models for model specification. As such, the [gR](#) task view may be of interest.
- Note that [rcppbugs](#) is a package that attempts to provide a pure R alternative to using OpenBUGS/WinBUGS/JAGS for MCMC.
- [rstan](#) provides R functions to parse, compile, test, estimate, and analyze Stan models by accessing the header-only Stan library provided by the `'StanHeaders'` package. The [Stan](#) project develops a probabilistic programming language that implements full Bayesian statistical inference via MCMC and (optionally penalized) maximum likelihood estimation via optimization.

The Bayesian Inference Task View is written by Jong Hee Park (Seoul National University, South Korea), Andrew D. Martin (University of Michigan, Ann Arbor, MI, USA), and Kevin M. Quinn (UC Berkeley, Berkeley, CA, USA). Please email the [task view maintainer](#) with suggestions.

CRAN packages:

- [abc](#)
- [AdMit](#)
- [arm](#) (core)
- [AtelieR](#)
- [BaBooN](#)
- [BACCO](#) (core)
- [BaM](#)
- [BayesDA](#)
- [bayesGARCH](#)
- [bayesm](#) (core)
- [bayesmix](#)
- [bayesQR](#)
- [BayesSummaryStatLM](#)
- [bayesSurv](#) (core)
- [Bayesthresh](#)
- [BayesTree](#)
- [BayesValidate](#)
- [BayesX](#)
- [BayHaz](#)
- [BAYSTAR](#)
- [bbemkr](#)
- [BCBCSF](#)
- [BCE](#)
- [bclust](#)
- [bcp](#)
- [bfp](#)
- [bisoreg](#)
- [BLR](#)
- [BMA](#)
- [Bmix](#)
- [BMS](#)
- [bnlearn](#)
- [boa](#) (core)
- [Bolstad](#)
- [bqtl](#)
- [bspec](#)
- [bspmma](#)
- [BSquare](#)
- [BVS](#)
- [catnet](#)
- [coalescentMCMC](#)
- [coda](#) (core)
- [cslogistic](#)
- [cudaBayesreg](#)
- [dclone](#)
- [deal](#)
- [dlm](#)
- [DPpackage](#) (core)
- [EbayesThresh](#)
- [ebdbNet](#)

- [eco](#)
- [eigenmodel](#)
- [ensembleBMA](#)
- [evdbayes](#)
- [exactLoglinTest](#)
- [factorQR](#)
- [FME](#)
- [geoR](#)
- [geoRglm](#)
- [ggmcmc](#)
- [glmmBUGS](#)
- [growcurves](#)
- [hbsae](#)
- [HI](#)
- [Hmisc](#)
- [iterLap](#)
- [LearnBayes](#)
- [lme4](#)
- [lmm](#)
- [MasterBayes](#)
- [matchingMarkets](#)
- [mcmc \(core\)](#)
- [MCMCglmm](#)
- [MCMCpack \(core\)](#)
- [mgcv](#)
- [mlogitBMA](#)
- [MNP](#)
- [mombf](#)
- [monomvn](#)
- [MSBVAR](#)
- [pacbpred](#)
- [PAWL](#)
- [PottsUtils](#)
- [predmixcor](#)
- [PReMiuM](#)
- [prevalence](#)
- [profdpm](#)
- [pscl](#)
- [R2jags](#)
- [R2WinBUGS](#)
- [ramps](#)
- [rbugs](#)
- [rcppbugs](#)
- [RJaCGH](#)
- [rjags](#)
- [RSGHB](#)
- [RSGHB](#)
- [rstan](#)
- [rstiefel](#)
- [runjags](#)

- [Runuran](#)
- [RxCEcolInf](#)
- [SamplerCompare](#)
- [SampleSizeMeans](#)
- [SampleSizeProportions](#)
- [sbgcop](#)
- [SimpleTable](#)
- [sna](#)
- [spBayes](#)
- [spikeslab](#)
- [spikeSlabGAM](#)
- [spTimer](#)
- [stochvol](#)
- [tgp](#)
- [zic](#)

Related links:

- [Bayesian Statistics and Marketing \(bayesm\)](#)
- [BayesX](#)
- [Just Another Gibbs Sampler \(JAGS\)](#)
- [MCMCpack](#)
- [The BUGS Project \(WinBUGS\)](#)
- [OpenBUGS](#)
- [BRugs in CRANextras](#)
- [Stan](#)
- CRAN Task View: [gR](#)
- Bioconductor Package: [vbmp](#)
- [BOA](#)