Package ‘rjags’

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Description

The rjags package provides an interface from R to the JAGS library for Bayesian data analysis. JAGS uses Markov Chain Monte Carlo (MCMC) to generate a sequence of dependent samples from the posterior distribution of the parameters.

Details

JAGS is a clone of BUGS (Bayesian analysis Using Gibbs Sampling). See Lunn et al (2009) for a history of the BUGS project. Note that the rjags package does not include a copy of the JAGS library: you must install this separately. For instructions on downloading JAGS, see the home page at https://mcmc-jags.sourceforge.io.

To fully understand how JAGS works, you need to read the JAGS User Manual. The manual explains the basics of modelling with JAGS and shows the functions and distributions available in the dialect of the BUGS language used by JAGS. It also describes the command line interface. The rjags package does not use the command line interface but provides equivalent functionality using R functions.

Analysis using the rjags package proceeds in steps:

1. Define the model using the BUGS language in a separate file.
2. Read in the model file using the jags.model function. This creates an object of class “jags”.
3. Update the model using the update method for “jags” objects. This constitutes a ‘burn-in’ period.
4. Extract samples from the model object using the coda.samples function. This creates an object of class “mcmc.list” which can be used to summarize the posterior distribution. The coda package also provides convergence diagnostics to check that the output is valid for analysis (see Plummer et al 2006).

Author(s)

Martyn Plummer
adapt

Adaptive phase for JAGS models

Description

Update the model in adaptive mode.

Usage

adapt(object, n.iter, end.adaptation=FALSE, ...)

Arguments

object a jags model object
n.iter length of the adaptive phase
end.adaptation logical flag. If TRUE then adaptive mode will be turned off on exit.
... additional arguments to the update method

Details

This function is not normally called by the user. It is called by the jags.model function when the model object is created.

When a JAGS model is compiled, it may require an initial sampling phase during which the samplers adapt their behaviour to maximize their efficiency (e.g. a Metropolis-Hastings random walk algorithm may change its step size). The sequence of samples generated during this adaptive phase is not a Markov chain, and therefore may not be used for posterior inference on the model.

The adapt function updates the model for n.iter iterations in adaptive mode. Then each sampler reports whether it has achieved optimal performance (e.g. whether the rejection rate of a Metropolis-Hasting sampler is close to the theoretical optimum). If any sampler reports failure of this test then adapt returns FALSE.

If end.adaptation = TRUE, then adaptive mode is turned off on exit, and further calls to adapt() do nothing. The model may be maintained in adaptive mode with the default option end.adaptation = FALSE so that successive calls to adapt() may be made until adaptation is satisfactory.

Value

Returns TRUE if all the samplers in the model have successfully adapted their behaviour to optimum performance and FALSE otherwise.
Description

This is a wrapper function for jags.samples which sets a trace monitor for all requested nodes, updates the model, and coerces the output to a single mcmc.list object.

Usage

coda.samples(model, variable.names, n.iter, thin = 1, na.rm=TRUE, ...)

Arguments

- model: a jags model object
- variable.names: a character vector giving the names of variables to be monitored
- n.iter: number of iterations to monitor
- thin: thinning interval for monitors
- na.rm: logical flag that indicates whether variables containing missing values should be omitted. See details.
- ...: optional arguments that are passed to the update method for jags model objects

Details

If na.rm=TRUE (the default) then elements of a variable that are missing (NA) for any iteration in at least one chain will be dropped.

This argument was added to handle incompletely defined variables. From JAGS version 4.0.0, users may monitor variables that are not completely defined in the BUGS language description of the model, e.g. if y[i] is defined in a for loop starting from i=3 then y[1], y[2] are not defined. The user may still monitor variable y and the monitored values corresponding to y[1], y[2] will have value NA for all iterations in all chains. Most of the functions in the coda package cannot handle missing values so these variables are dropped by default.

Value

An mcmc.list object.

Author(s)

Martyn Plummer
Control

See Also

jags.samples

Examples

data(LINE)
LINE$recompile()
LINE.out <- coda.samples(LINE, c("alpha","beta","sigma"), n.iter=1000)
summary(LINE.out)

Description

JAGS modules contain factory objects for samplers, monitors, and random number generators for a JAGS model. These functions allow fine-grained control over which factories are active.

Usage

list.factories(type)
set.factory(name, type, state)

Arguments

name name of the factory to set
type type of factory to query or set. Possible values are "sampler", "monitor", or "rng"
state a logical. If TRUE then the factory will be active, otherwise the factory will become inactive.

Value

list.factories returns a data frame with two columns, the first column shows the names of the factory objects in the currently loaded modules, and the second column is a logical vector indicating whether the corresponding factory is active or not.

set.factory is called to change the future behaviour of factory objects. If a factory is set to inactive then it will be skipped.

Note

When a module is loaded, all of its factory objects are active. This is also true if a module is unloaded and then reloaded.

Author(s)

Martyn Plummer
Examples

```r
list.factories("sampler")
list.factories("monitor")
list.factories("rng")
set.factory("base::Slice", "sampler", FALSE)
list.factories("sampler")
set.factory("base::Slice", "sampler", TRUE)
```

dic.samples | Generate penalized deviance samples

Description

Function to extract random samples of the penalized deviance from a jags model.

Usage

```r
dic.samples(model, n.iter, thin = 1, type, ...)
```

Arguments

- `model`: a jags model object
- `n.iter`: number of iterations to monitor
- `thin`: thinning interval for monitors
- `type`: type of penalty to use
- `...`: optional arguments passed to the update method for jags model objects

Details

The `dic.samples` function generates penalized deviance statistics for use in model comparison. The two alternative penalized deviance statistics generated by `dic.samples` are the deviance information criterion (DIC) and the penalized expected deviance. These are chosen by giving the values "pD" and "popt" respectively as the type argument.

DIC (Spiegelhalter et al 2002) is calculated by adding the “effective number of parameters” (pD) to the expected deviance. The definition of pD used by `dic.samples` is the one proposed by Plummer (2002) and requires two or more parallel chains in the model.

DIC is an approximation to the penalized plug-in deviance, which is used when only a point estimate of the parameters is of interest. The DIC approximation only holds asymptotically when the effective number of parameters is much smaller than the sample size, and the model parameters have a normal posterior distribution.

The penalized expected deviance (Plummer 2008) is calculated by adding the optimism (popt) to the expected deviance. The popt penalty is at least twice the size of the pD penalty, and penalizes complex models more severely.
**Value**

An object of class “dic”. This is a list containing the following elements:

- **deviance**: A numeric vector, with one element for each observed stochastic node, containing the mean deviance for that node.
- **penalty**: A numeric vector, with one element for each observed stochastic node, containing an estimate of the contribution towards the penalty.
- **type**: A string identifying the type of penalty: “pD” or “popt”.

**Note**

The popt penalty is estimated by importance weighting, and may be numerically unstable.

**Author(s)**

Martyn Plummer

**References**


**See Also**

diffdic

diffdic

Differences in penalized deviance

**Description**

Compare two models by the difference of two dic objects.

**Usage**

dic1 - dic2
diffdic(dic1, dic2)

**Arguments**

dic1, dic2 Objects inheriting from class “dic”
Details

A `diffdic` object represents the difference in penalized deviance between two models. A negative value indicates that `dic1` is preferred and vice versa.

Value

An object of class “diffdic”. This is a numeric vector with an element for each observed stochastic node in the model.

The `diffdic` class has its own print method, which will display the sum of the differences, and its sample standard deviation.

Note

The problem of determining what is a noteworthy difference in DIC (or other penalized deviance) between two models is currently unsolved. Following the results of Ripley (1996) on the Akaike Information Criterion, Plummer (2008) argues that there is no absolute scale for comparison of two penalized deviance statistics, and proposes that the difference should be calibrated with respect to the sample standard deviation of the individual contributions from each observed stochastic node.

Author(s)

Martyn Plummer

References


See Also

dic

diffdic

dic

diffdic

jags.model

Create a JAGS model object

Description

`jags.model` is used to create an object representing a Bayesian graphical model, specified with a BUGS-language description of the prior distribution, and a set of data.

Usage

```r
jags.model(file, data, inits, 
    n.chains = 1, n.adapt=1000, quiet=FALSE)
```
Arguments

file  the name of the file containing a description of the model in the JAGS dialect of
      the BUGS language.
      Alternatively, file can be a readable text-mode connection, or a complete URL.

data  a list or environment containing the data. Any numeric objects in data cor-
      responding to node arrays used in file are taken to represent the values of
      observed nodes in the model.

inits optional specification of initial values in the form of a list or a function (see
      Initialization below). If omitted, initial values will be generated automatic-
      ally. It is an error to supply an initial value for an observed node.

n.chains the number of parallel chains for the model

n.adapt the number of iterations for adaptation. See adapt for details. If n.adapt = 0
      then no adaptation takes place.

quiet if TRUE then messages generated during compilation will be suppressed, as well
      as the progress bar during adaptation.

Value

jags.model returns an object inheriting from class jags which can be used to generate dependent
samples from the posterior distribution of the parameters

An object of class jags is a list of functions that share a common environment. This environment
encapsulates the state of the model, and the functions can be used to query or modify the model
state.

ptr() Returns an external pointer to an object created by the JAGS library

data() Returns a list containing the data that define the observed nodes in the model

model() Returns a character vector containing the BUGS-language representation of the
      model

state(internal=FALSE) Returns a list of length equal to the number of parallel chains in the model. Each
      element of the list is itself a list containing the current parameter values in that
      chain. If internal=TRUE then the returned lists also include the RNG names
      (.RNG.name) and states (.RNG.state). This is not the user-level interface: use
      the coef.jags method instead.

update(n.iter) Updates the model by n.iter iterations. This is not the user-level interface: use
      the update.jags method instead.

Initialization

There are various ways to specify initial values for a JAGS model. If no initial values are sup-
plied, then they will be generated automatically by JAGS. See the JAGS User Manual for details.
Otherwise, the options are as follows:

1. A list of numeric values. Initial values for a single chain may supplied as a named list of
   numeric values. If there are multiple parallel chains then the same list is re-used for each
   chain.
2. A list of lists. Distinct initial values for each chain may be given as a list of lists. In this case, the list should have the same length as the number of chains in the model.

3. A function. A function may be supplied that returns a list of initial values. The function is called repeatedly to generate initial values for each chain. Normally this function should call some random number generating functions so that it returns different values every time it is called. The function should either have no arguments, or have a single argument named chain. In the latter case, the supplied function is called with the chain number as argument. In this way, initial values may be generated that depend systematically on the chain number.

Random number generators

Each chain in a model has its own random number generator (RNG). RNGs and their initial seed values are assigned automatically when the model is created. The automatic seeds are calculated from the current time.

If you wish to make the output from the model reproducible, you may specify the RNGs to be used for each chain, and their starting seeds as part of the inits argument (see Initialization above). This is done by supplementing the list of initial parameter values for a given chain with two additional elements named ".RNG.name", and ".RNG.seed":

-.RNG.name  a character vector of length 1. The names of the RNGs supplied in the base module are:
  • “base::Wichmann-Hill”
  • “base::Marsaglia-Multicarry”
  • “base::Super-Duper”
  • “base::Mersenne-Twister”

If the lecuyer module is loaded, it provides “lecuyer::RngStream”

-.RNG.seed  a numeric vector of length 1 containing an integer value.

Note that it is also possible to specify ".RNG.state” rather than ".RNG.seed” - see for example the output of parallel.seeds

Author(s)

Martyn Plummer

Description

A JAGS module is a dynamically loaded library that extends the functionality of JAGS. These functions load and unload JAGS modules and show the names of the currently loaded modules.

Usage

load.module(name, path, quiet=FALSE)
unload.module(name, quiet=FALSE)
list.modules()
Arguments

name  name of the load module to be loaded
path  file path to the location of the DLL. If omitted, the option jags.moddir is used to locate the modules
quiet  a logical. If TRUE, no message will be printed about loading the package

Author(s)

Martyn Plummer

Examples

list.modules()
load.module(“glm”)
list.modules()
unload.module(“glm”)
list.modules()

Description

A jags object represents a Bayesian graphical model described using the BUGS language.

Usage

## S3 method for class ’jags’
coef(object, chain=1, ...)
## S3 method for class ’jags’
variable.names(object, ...)
list.samplers(object)

Arguments

object  a jags model object
chain  chain number to query
...  additional arguments to the call (ignored)

Value

The coef function returns a list with an entry for each Node array that contains an unobserved Node. Elements corresponding to observed Nodes or deterministic Nodes are given missing values.

The variable.names function returns a character vector of names of node arrays used in the model.

The list.samplers function returns a named list with an entry for each Sampler used by the model. Each list element is a character vector containing the names of stochastic Nodes that are updated.
together in a block. The names of the list elements indicate the sampling methods that are used to update each block. Stochastic nodes that are updated by forward sampling from the prior are not listed.

Author(s)

Martyn Plummer

Examples

data(LINE)
LINE$recompile()
coef(LINE)
variable.names(LINE)
list.samplers(LINE)

jags.samples

Generate posterior samples

Description

Function to extract random samples from the posterior distribution of the parameters of a jags model.

Usage

jags.samples(model, variable.names, n.iter, thin = 1,
             type="trace", force.list=FALSE, ...)

Arguments

model a jags model object
variable.names a character vector giving the names of variables to be monitored
n.iter number of iterations to monitor
thin thinning interval for monitors
type type of monitor (can be vectorised)
force.list option to consistently return a named list of monitor types even if a single monitor type is requested
... optional arguments passed to the update method for jags model objects

Details

The jags.samples function creates monitors for the given variables, runs the model for n.iter iterations and returns the monitored samples.
Value

A list of mcarray objects, with one element for each element of the variable.names argument. If more than one type of monitor is requested (or if force.list is TRUE) then the return value will be a (named) list of lists of mcarray objects, with one element for each monitor type.

Author(s)

Martyn Plummer

See Also

jags.model, coda.samples

Examples

data(LINE)
LINE$recompile()
LINE.samples <- jags.samples(LINE, c("alpha","beta","sigma"),
n.iter=1000)
LINE.samples
LINE.samples <- jags.samples(LINE, c("alpha","beta","sigma"),
force.list=TRUE, n.iter=1000)
LINE.samples
LINE.samples <- jags.samples(LINE, c("alpha","alpha"),
n.iter=1000, type=c("trace","mean"))
LINE.samples$trace
LINE.samples$mean

---

jags.version  JAGS version

Description

Get the version of the JAGS library which is currently linked to this R session

Usage

jags.version()

Value

The version of JAGS formatted as a package version string (see package_version)
Description

The LINE model is a trivial linear regression model with only 5 observations. It’s main use is to allow automated checks of the \texttt{rjags} package.

Format

A \texttt{jags.model} object, which must be recompiled before use.

\textbf{mcarray.object} 

Objects for representing MCMC output

Description

An \texttt{mcarray} object is used by the \texttt{jags.samples} function to represent MCMC output from a JAGS model. It is an array with named dimensions, for which the dimensions "iteration" and "chain" have a special status.

Usage

\begin{verbatim}
## S3 method for class 'mcarray'
summary(object, FUN, ...)
## S3 method for class 'mcarray'
print(x, ...)
## S3 method for class 'mcarray'
as.mcmc.list(x, ...)
\end{verbatim}

Arguments

- \texttt{object,x} an \texttt{mcarray} object
- \texttt{FUN} a function to be used to generate summary statistics
- \texttt{...} additional arguments to the call

Details

The \texttt{coda} package defines \texttt{mcmc} objects for representing output from an MCMC sampler, and \texttt{mcmc.list} for representing output from multiple parallel chains. These objects emphasize the time-series aspect of the MCMC output, but lose the original array structure of the variables they represent. The \texttt{mcarray} class attempts to rectify this by preserving the dimensions of the original node array defined in the JAGS model.
parallel

Value

The summary method for mcarray objects applies the given function to the array, marginalizing the "chain" and "iteration" dimensions.

The print method applies the summary function with FUN=mean.

The as.mcmc.list method coerces an mcarray to an mcmc.list object so that the diagnostics provided by the coda package can be applied to the MCMC output it represents.

Author(s)

Martyn Plummer

parallel

Get initial values for parallel RNGs

Description

On a multi-processor system, you may wish to run parallel chains using multiple jags.model objects, each running a single chain on a separate processor. This function returns a list of values that may be used to initialize the random number generator of each chain.

Usage

parallel.seeds(factory, nchain)

Arguments

factory Name of the RNG factory to use.
nchain Number of chains for which to initialize RNGs.

Value

parallel.seeds returns a list of RNG states. Each element is a list of length 2 with the following elements:

.RNG.name The name of the RNG
.RNG.state An integer vector giving the state of the RNG.

Note

It is not yet possible to make the results of parallel.seeds reproducible. This will be fixed in a future version of JAGS.

Author(s)

Martyn Plummer
See Also

`jags.model`, section “Random number generators”, for further details on RNG initialization; `list.factories` to find the names of available RNG factories.

Examples

```r
## The BaseRNG factory generates up to four distinct types of RNG. If
## more than 4 chains are requested, it will recycle the RNG types, but
## use different initial values
parallel.seeds("base::BaseRNG", 3)

## The lecuyer module provides the RngStream factory, which allows large
## numbers of independent parallel RNGs to be generated.
load.module("lecuyer")
list.factories(type="rng")
parallel.seeds("lecuyer::RngStream", 5);
```

Description

Read data for a JAGS model from a file.

Usage

```r
read.jagsdata(file)
read.bugsdata(file)
```

Arguments

- `file` name of a file containing a text representation of the data for a jags model

Details

The command line interface for JAGS reads data and initial values from a text file. The data format used for jags data files is the same as the R `dump` function. Thus the data values can be read into an R session using the `source` function, but this will create objects in the global environment. The `read.jagsdata` function is a simple wrapper that reads the data into a list instead.

OpenBUGS also reads data and initial values from a text file. The format of these files is described as "S-PLUS" format by the OpenBUGS authors. It superficially resembles the format used by the `dput` function (and in fact can be parsed by the `dget` function). However, in BUGS "S-PLUS" format, arrays are stored in row-major order instead of the column-major order used by R. The `read.bugsdata` function reads OpenBUGS "S-PLUS" format files and permutes the elements of arrays so that they appear in the correct order.

Either function returns a list which can be used as the `data` or `inits` argument of `jags.model`. 

---

**read.jagsdata**

Read data files for jags models

--

Description

Read data for a JAGS model from a file.

Usage

```r
read.jagsdata(file)
read.bugsdata(file)
```

Arguments

- `file` name of a file containing a text representation of the data for a jags model

Details

The command line interface for JAGS reads data and initial values from a text file. The data format used for jags data files is the same as the R `dump` function. Thus the data values can be read into an R session using the `source` function, but this will create objects in the global environment. The `read.jagsdata` function is a simple wrapper that reads the data into a list instead.

OpenBUGS also reads data and initial values from a text file. The format of these files is described as "S-PLUS" format by the OpenBUGS authors. It superficially resembles the format used by the `dput` function (and in fact can be parsed by the `dget` function). However, in BUGS "S-PLUS" format, arrays are stored in row-major order instead of the column-major order used by R. The `read.bugsdata` function reads OpenBUGS "S-PLUS" format files and permutes the elements of arrays so that they appear in the correct order.

Either function returns a list which can be used as the `data` or `inits` argument of `jags.model`. 

---

**read.jagsdata**

Read data files for jags models
Value

A named list of numeric vectors or arrays.

Note

Earlier versions of the rjags package had a read.data function which read data in either format, but the function name was ambiguous (There are many data file format in R) so this is now deprecated.

Author(s)

Martyn Plummer

Description

These functions are provided for compatibility with older versions of the rjags package and will soon be defunct.

Usage

read.data(file, format=c("jags","bugs"))

Arguments

file name of a file containing a text representation of the data for a jags model
format format of the data

Details

read.data with format="jags" is a deprecated synonym for read.jagsdata and with format="bugs" is a deprecated synonym for read.bugsdata.
update

Update jags models

Description
Update the Markov chain associated with the model.

Usage
## S3 method for class 'jags'
update(object, n.iter=1, by, progress.bar, ...)

Arguments
- object: a jags model object
- n.iter: number of iterations of the Markov chain to run
- by: refresh frequency for progress bar. See Details
- progress.bar: type of progress bar. Possible values are "text", "gui", and "none". See Details.
- ...: additional arguments to the update method (ignored)

Details
Since MCMC calculations are typically long, a progress bar is displayed during the call to update. The type of progress bar is determined by the progress.bar argument. Type "text" is displayed on the R console. Type "gui" is a graphical progress bar in a new window. The progress bar is suppressed if progress.bar is "none" or NULL, if the update is less than 100 iterations, or if R is not running interactively.

The default progress bar type is taken from the option jags.pb.

The progress bar is refreshed every by iterations. The update can only be interrupted when the progress bar is refreshed. Therefore it is advisable not to set by to a very large value. By default by is either n.iter/50 or 100, whichever is smaller.

Value
The update method for jags model objects modifies the original object and returns NULL.

Author(s)
Martyn Plummer
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