

# Package ‘R2jags’

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**Title** Using R to Run 'JAGS'

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**BugReports** <https://github.com/suyusung/R2jags/issues/>

**Depends** R (>= 2.14.0), rjags (>= 3-3)

**Suggests** testthat (>= 3.0.0)

**Imports** abind, coda (>= 0.13), graphics, grDevices, methods,  
R2WinBUGS, parallel, stats, stringr, utils

**SystemRequirements** JAGS (<http://mcmc-jags.sourceforge.net>)

**Description** Providing wrapper functions to implement Bayesian analysis in JAGS. Some major features include monitoring convergence of a MCMC model using Rubin and Gelman Rhat statistics, automatically running a MCMC model till it converges, and implementing parallel processing of a MCMC model for multiple chains.

**License** GPL (> 2)

**NeedsCompilation** no

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attach.jags	<i>Attach/detach elements of 'JAGS' objects to search path</i>
-------------	----------------------------------------------------------------

---

### Description

These are wrapper functions for [attach.bugs](#) and [detach.bugs](#), which attach or detach three-way-simulation array of bugs object to the search path. See [attach.all](#) for details.

### Usage

```
attach.jags(x, overwrite = NA)
detach.jags()
```

### Arguments

x	An rjags object.
overwrite	If TRUE, objects with identical names in the Workspace (.GlobalEnv) that are masking objects in the database to be attached will be deleted. If NA (the default) and an interactive session is running, a dialog box asks the user whether masking objects should be deleted. In non-interactive mode, behaviour is identical to <code>overwrite=FALSE</code> , i.e. nothing will be deleted.

### Details

See [attach.bugs](#) for details

### Author(s)

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### References

Sibylle Sturtz and Uwe Ligges and Andrew Gelman. (2005). "R2WinBUGS: A Package for Running WinBUGS from R." *Journal of Statistical Software* 3 (12): 1–6.

### Examples

```
# See the example in ?jags for the usage.
```

---

`autojags`*Function for auto-updating 'JAGS' until the model converges*

---

**Description**

The `autojags` takes a `rjags` object as input. `autojags` will update the model until it converges.

**Usage**

```
## S3 method for class 'rjags'
update(object, n.iter=1000, n.thin=1,
       refresh=n.iter/50, progress.bar = "text", ...)
autojags(object, n.iter=1000, n.thin=1, Rhat=1.1, n.update=2,
        refresh=n.iter/50, progress.bar = "text", ...)
```

**Arguments**

<code>object</code>	an object of <code>rjags</code> class.
<code>n.iter</code>	number of total iterations per chain, default=1000
<code>n.thin</code>	thinning rate. Must be a positive integer, default=1
<code>...</code>	further arguments pass to or from other methods.
<code>Rhat</code>	convergence criterion, default=1.1.
<code>n.update</code>	the max number of updates, default=2.
<code>refresh</code>	refresh frequency for progress bar, default is <code>n.iter/50</code>
<code>progress.bar</code>	type of progress bar. Possible values are "text", "gui", and "none". 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 <code>progress.bar</code> is "none"

**Author(s)**

Yu-Sung Su <suyusung@tsinghua.edu.cn>

**References**

Gelman, A., Carlin, J.B., Stern, H.S., Rubin, D.B. (2003): *Bayesian Data Analysis*, 2nd edition, CRC Press.

**Examples**

```
# see ?jags for an example.
```

---

jags

*Run 'JAGS' from R*


---

## Description

The `jags` function takes data and starting values as input. It automatically writes a `jags` script, calls the model, and saves the simulations for easy access in R.

## Usage

```
jags(data, inits, parameters.to.save, model.file="model.bug",
      n.chains=3, n.iter=2000, n.burnin=floor(n.iter/2),
      n.thin=max(1, floor((n.iter - n.burnin) / 1000)),
      DIC=TRUE, pD = FALSE, n.iter.pd = NULL, n.adapt = 100,
      working.directory=NULL, jags.seed = 123,
      refresh = n.iter/50, progress.bar = "text", digits=5,
      RNGname = c("Wichmann-Hill", "Marsaglia-Multicarry",
                  "Super-Duper", "Mersenne-Twister"),
      jags.module = c("glm","dic"), quiet = FALSE,
      checkMissing = FALSE
    )
```

```
jags.parallel(data, inits, parameters.to.save, model.file = "model.bug",
              n.chains = 2, n.iter = 2000, n.burnin = floor(n.iter/2),
              n.thin = max(1, floor((n.iter - n.burnin)/1000)),
              n.cluster= n.chains, DIC = TRUE,
              working.directory = NULL, jags.seed = 123, digits=5,
              RNGname = c("Wichmann-Hill", "Marsaglia-Multicarry",
                          "Super-Duper", "Mersenne-Twister"),
              jags.module = c("glm","dic"),
              export_obj_names=NULL,
              envir = .GlobalEnv
            )
```

```
jags2(data, inits, parameters.to.save, model.file="model.bug",
       n.chains=3, n.iter=2000, n.burnin=floor(n.iter/2),
       n.thin=max(1, floor((n.iter - n.burnin) / 1000)),
       DIC=TRUE, jags.path="",
       working.directory=NULL, clearWD=TRUE,
       refresh = n.iter/50)
```

## Arguments

`data` (1) a vector or list of the names of the data objects used by the model, (2) a (named) list of the data objects themselves, or (3) the name of a "dump" format file containing the data objects, which must end in ".txt", see example below for details.

<code>inits</code>	a list with <code>n.chains</code> elements; each element of the list is itself a list of starting values for the BUGS model, <i>or</i> a function creating (possibly random) initial values. If <code>inits</code> is NULL, JAGS will generate initial values for parameters.
<code>parameters.to.save</code>	character vector of the names of the parameters to save which should be monitored.
<code>model.file</code>	file containing the model written in BUGS code. Alternatively, as in <b>R2WinBUGS</b> , <code>model.file</code> can be an R function that contains a BUGS model that is written to a temporary model file (see <code>tempfile</code> ) using <code>write.model</code>
<code>n.chains</code>	number of Markov chains (default: 3)
<code>n.iter</code>	number of total iterations per chain (including burn in; default: 2000)
<code>n.burnin</code>	length of burn in, i.e. number of iterations to discard at the beginning. Default is <code>n.iter/2</code> , that is, discarding the first half of the simulations. If <code>n.burnin</code> is 0, <code>jags()</code> will run 100 iterations for adaption.
<code>n.cluster</code>	number of clusters to use to run parallel chains. Default equals <code>n.chains</code> .
<code>n.thin</code>	thinning rate. Must be a positive integer. Set <code>n.thin &gt; 1</code> to save memory and computation time if <code>n.iter</code> is large. Default is <code>max(1, floor(n.chains * (n.iter - n.burnin) / 1000))</code> which will only thin if there are at least 2000 simulations.
DIC	logical; if TRUE (default), compute deviance, pD, and DIC. The rule <code>pD=var(deviance) / 2</code> is used.
pD	logical; if TRUE and DIC is also TRUE, then adds the computation of 'pD', using <code>'rjags::dic.samples()'</code> . Defaults to FALSE.
<code>n.iter.pd</code>	number of iterations to feed <code>'rjags::dic.samples()'</code> to compute 'pD'. Defaults at 1000.
<code>n.adapt</code>	number of iterations for which to run the adaptation, when creating the model object. Defaults at 100.
<code>working.directory</code>	sets working directory during execution of this function; This should be the directory where model file is.
<code>jags.seed</code>	random seed for JAGS, default is 123. This function is used for <code>jags.parallell()</code> and does not work for <code>jags()</code> . Use <code>set.seed()</code> instead if you want to produce identical result with <code>jags()</code>
.	
<code>jags.path</code>	directory that contains the JAGS executable. The default is "".
<code>clearWD</code>	indicating whether the files <code>'data.txt'</code> , <code>'inits[1:n.chains].txt'</code> , <code>'codaIndex.txt'</code> , <code>'jagsscript.txt'</code> , and <code>'CODAchain[1:nchains].txt'</code> should be removed after <code>jags</code> has finished, default=TRUE.
<code>refresh</code>	refresh frequency for progress bar, default is <code>n.iter/50</code>
<code>progress.bar</code>	type of progress bar. Possible values are "text", "gui", and "none". 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 <code>progress.bar</code> is "none"

digits	as in <code>write.model</code> in the <b>R2WinBUGS</b> package: number of significant digits used for BUGS input, see <code>formatC</code> . Only used if specifying a BUGS model as an R function.
RNGname	the name for random number generator used in JAGS. There are four RNGS supplied by the base module in JAGS: Wichmann-Hill, Marsaglia-Multicarry, Super-Duper, Mersenne-Twister
jags.module	the vector of jags modules to be loaded. Default are “glm” and “dic”. Input NULL if you don’t want to load any jags module.
export_obj_names	character vector of objects to export to the clusters.
envir	default is <code>.GlobalEnv</code>
quiet	Logical, whether to suppress stdout in <code>jags.model()</code> .
checkMissing	Default: FALSE. When TRUE, checks for missing data in categorical parameters and returns a <code>sim.list</code> with NA values if detected. It’s recommended to supply <code>jags()</code> with complete data.

## Details

To run:

1. Write a JAGS model in an ASCII file.
2. Go into R.
3. Prepare the inputs for the `jags` function and run it (see Example section).
4. The model will now run in JAGS. It might take awhile. You will see things happening in the R console.

## Author(s)

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## References

Plummer, Martyn (2003) “JAGS: A program for analysis of Bayesian graphical models using Gibbs sampling.” <https://www.r-project.org/conferences/DSC-2003/Proceedings/Plummer.pdf>.

Gelman, A., Carlin, J. B., Stern, H.S., Rubin, D.B. (2003) *Bayesian Data Analysis*, 2nd edition, CRC Press.

Sibylle Sturtz and Uwe Ligges and Andrew Gelman. (2005). “R2WinBUGS: A Package for Running WinBUGS from R.” *Journal of Statistical Software* 3 (12): 1–6.

## Examples

```
# An example model file is given in:
model.file <- system.file(package="R2jags", "model", "schools.txt")
# Let's take a look:
file.show(model.file)
# you can also write BUGS model as a R function, see below:
```

```

#####
# initialization #
#####

# data
J <- 8.0
y <- c(28.4,7.9,-2.8,6.8,-0.6,0.6,18.0,12.2)
sd <- c(14.9,10.2,16.3,11.0,9.4,11.4,10.4,17.6)

jags.data <- list("y","sd","J")
jags.params <- c("mu","sigma","theta")
jags.inits <- function(){
  list("mu"=rnorm(1),"sigma"=runif(1),"theta"=rnorm(J))
}

## You can input data in 4 ways
## 1) data as list of character
jagsfit <- jags(data=list("y","sd","J"), inits=jags.inits, jags.params,
               n.iter=10, model.file=model.file)

## 2) data as character vector of names
jagsfit <- jags(data=c("y","sd","J"), inits=jags.inits, jags.params,
               n.iter=10, model.file=model.file)

## 3) data as named list
jagsfit <- jags(data=list(y=y,sd=sd,J=J), inits=jags.inits, jags.params,
               n.iter=10, model.file=model.file)

## 4) data as a file
fn <- "tmpbugsdata.txt"
dump(c("y","sd","J"), file=fn)
jagsfit <- jags(data=fn, inits=jags.inits, jags.params,
               n.iter=10, model.file=model.file)
unlink("tmpbugsdata.txt")

## You can write bugs model in R as a function

schoolsmodel <- function() {
  for (j in 1:J){
    # J=8, the number of schools
    y[j] ~ dnorm (theta[j], tau.y[j]) # data model: the likelihood
    tau.y[j] <- pow(sd[j], -2)      # tau = 1/sigma^2
  }
  for (j in 1:J){
    theta[j] ~ dnorm (mu, tau)      # hierarchical model for theta
  }
  tau <- pow(sigma, -2)             # tau = 1/sigma^2
  mu ~ dnorm (0.0, 1.0E-6)         # noninformative prior on mu
  sigma ~ dunif (0, 1000)          # noninformative prior on sigma
}

jagsfit <- jags(data=jags.data, inits=jags.inits, jags.params,

```

```

n.iter=10, model.file=schoolsmodel)

#####
# RUN jags and postprocessing #
#####
jagsfit <- jags(data=jags.data, inits=jags.inits, jags.params,
  n.iter=5000, model.file=model.file)

# Can also compute the DIC using pD (=Dbar-Dhat), via dic.samples(), which
# is a closer approximation to the original formulation of Spiegelhalter et
# al (2002), instead of pV (=var(deviance)/2), which is the default in JAGS
jagsfit.pD <- jags(data=jags.data, inits=jags.inits, jags.params,
  n.iter=5000, model.file=model.file, pD=TRUE)

# Run jags parallely, no progress bar. R may be frozen for a while,
# Be patient. Currentlty update afterward does not run parallelly
#
jagsfit.p <- jags.parallel(data=jags.data, inits=jags.inits, jags.params,
  n.iter=5000, model.file=model.file)

# display the output
print(jagsfit)
plot(jagsfit)

# traceplot
traceplot(jagsfit.p)
traceplot(jagsfit)

# or to use some plots in coda
# use as.mcmc to convert rjags object into mcmc.list
jagsfit.mcmc <- as.mcmc(jagsfit.p)
jagsfit.mcmc <- as.mcmc(jagsfit)
## now we can use the plotting methods from coda
#require(lattice)
#xyplot(jagsfit.mcmc)
#densityplot(jagsfit.mcmc)

# if the model does not converge, update it!
jagsfit.upd <- update(jagsfit, n.iter=100)
print(jagsfit.upd)
print(jagsfit.upd, intervals=c(0.025, 0.5, 0.975))
plot(jagsfit.upd)

# before update parallel jags object, do recompile it
recompile(jagsfit.p)
jagsfit.upd <- update(jagsfit.p, n.iter=100)

# or auto update it until it converges! see ?autojags for details
# recompile(jagsfit.p)
jagsfit.upd <- autojags(jagsfit.p)

```



```

jagsfit.upd <- autojags(jagsfit)

# to get DIC or specify DIC=TRUE in jags() or do the following#
dic.samples(jagsfit.upd$model, n.iter=1000, type="pD")

# attach jags object into search path see "attach.bugs" for details
attach.jags(jagsfit.upd)

# this will show a 3-way array of the bugs.sim object, for example:
mu

# detach jags object into search path see "attach.bugs" for details
detach.jags()

# to pick up the last save session
# for example, load("RWorkspace.Rdata")
recompile(jagsfit)
jagsfit.upd <- update(jagsfit, n.iter=100)

recompile(jagsfit.p)
jagsfit.upd <- update(jagsfit, n.iter=100)

#=====#
# using jags2 #
#=====#
## jags can be run and produces coda files, but cannot be updated once it's done
## You may need to edit "jags.path" to make this work,
## also you need a write access in the working directory:
## e.g. setwd("d:/")

## NOT RUN HERE
## Not run:
jagsfit <- jags2(data=jags.data, inits=jags.inits, jags.params,
  n.iter=5000, model.file=model.file)
print(jagsfit)
plot(jagsfit)
# or to use some plots in coda
# use as.mcmc to convert rjags object into mcmc.list
jagsfit.mcmc <- as.mcmc.list(jagsfit)
traceplot(jagsfit.mcmc)
#require(lattice)
#xyplot(jagsfit.mcmc)
#densityplot(jagsfit.mcmc)

## End(Not run)

```

**Description**

This function reads Markov Chain Monte Carlo output in the CODA format produced by **jags** and returns an object of class `mcmc.list` for further output analysis using the **coda** package.

**Usage**

```
jags2bugs(path=getwd(), parameters.to.save,
          n.chains=3, n.iter=2000, n.burnin=1000, n.thin=2,
          DIC=TRUE)
```

**Arguments**

<code>path</code>	sets working directory during execution of this function; This should be the directory where CODA files are.
<code>parameters.to.save</code>	character vector of the names of the parameters to save which should be monitored.
<code>n.chains</code>	number of Markov chains (default: 3)
<code>n.iter</code>	number of total iterations per chain (including burn in; default: 2000)
<code>n.burnin</code>	length of burn in, i.e. number of iterations to discard at the beginning. Default is <code>n.iter/2</code> , that is, discarding the first half of the simulations.
<code>n.thin</code>	thinning rate, default is 2
<code>DIC</code>	logical; if TRUE (default), compute deviance, pD, and DIC. The rule $pD = \text{var}(\text{deviance}) / 2$ is used.

**Author(s)**

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---

recompile

*Function for recompiling rjags object*

---

**Description**

The `recompile` takes a `rjags` object as input. `recompile` will re-compile the previous saved `rjags` object.

**Usage**

```
recompile(object, n.iter, refresh, progress.bar)
## S3 method for class 'rjags'
recompile(object, n.iter=100, refresh=n.iter/50,
          progress.bar = "text")
```

**Arguments**

object	an object of <code>rjags</code> class.
<code>n.iter</code>	number of iteration for adapting, default is 100
<code>refresh</code>	refresh frequency for progress bar, default is <code>n.iter/50</code>
<code>progress.bar</code>	type of progress bar. Possible values are “text”, “gui”, and “none”. 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 <code>progress.bar</code> is “none”

**Author(s)**

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**Examples**

```
# see ?jags for an example.
```

---

traceplot	<i>Trace plot of bugs object</i>
-----------	----------------------------------

---

**Description**

Displays a plot of iterations *vs.* sampled values for each variable in the chain, with a separate plot per variable.

**Usage**

```
traceplot(x, ...)
## S4 method for signature 'rjags'
traceplot(x, mfrow = c(1, 1), varname = NULL,
  match.head = TRUE, ask = TRUE,
  col = rainbow( x$n.chains ),
  lty = 1, lwd = 1, ...)
```

**Arguments**

<code>x</code>	A bugs object
<code>mfrow</code>	graphical parameter (see <code>par</code> )
<code>varname</code>	vector of variable names to plot
<code>match.head</code>	matches the variable names by the beginning of the variable names in bugs object
<code>ask</code>	logical; if TRUE, the user is <i>asked</i> before each plot, see <code>par(ask=.)</code> .
<code>col</code>	graphical parameter (see <code>par</code> )
<code>lty</code>	graphical parameter (see <code>par</code> )
<code>lwd</code>	graphical parameter (see <code>par</code> )
<code>...</code>	further graphical parameters

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**See Also**

[densplot](#), [plot.mcmc](#), [traceplot](#)

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