

Jags example

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```
> library('glmmBUGS')
> haveR2jags = require('R2jags', quietly=TRUE)
> print(haveR2jags)
```

```
[1] TRUE
```

```
> requireNamespace('rjags', quietly=TRUE)
> haveRjags = try(
+     loadNamespace('rjags'),
+     silent=TRUE)
> if(class(haveRjags) == 'try-error') {
+     haveR2jags = FALSE
+ }
```

If Jags isn't available, the `rjags` namespace will give an error when loaded.

1 Muscle data

```
> data('Muscle', package='nlme')

> muscleRagged = glmmBUGS(conc ~ length, data=Muscle,
+     effects="Strip", family="gaussian",
+     modelFile='model.bug', reparam='Strip')
> startingValues = muscleRagged$startingValues

> source("getInits.R")
> if(haveR2jags) {
+     muscleResult = jags(
+     muscleRagged$ragged, getInits,
+     parameters.to.save = names(getInits()),
+     model.file="model.bug", n.chain=3, n.iter=1000,
+     n.burnin=100, n.thin=10, refresh=200,
+     working.directory=getwd())
+ }
```

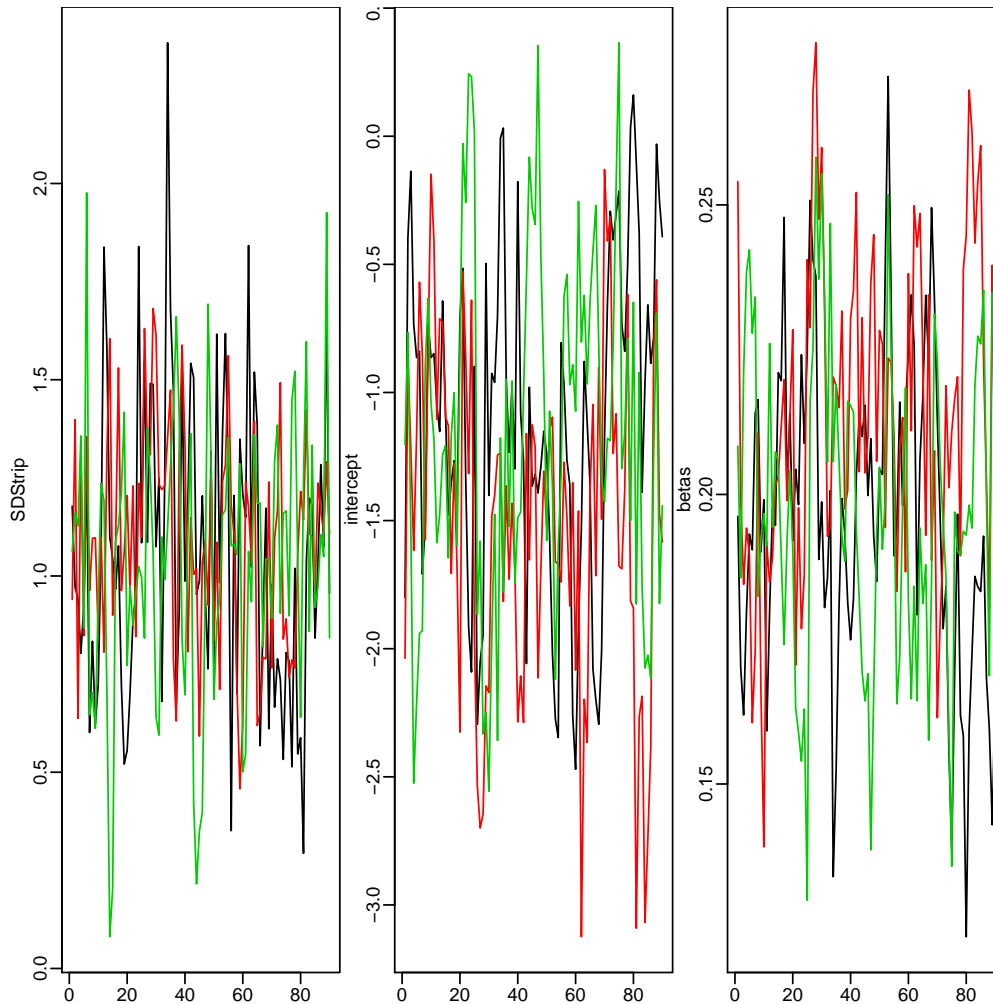
```
Compiling model graph
  Resolving undeclared variables
  Allocating nodes
Graph information:
  Observed stochastic nodes: 60
  Unobserved stochastic nodes: 25
  Total graph size: 291
```

```
Initializing model
```

```
> if(haveR2jags) {
+   muscleParams = restoreParams(
+     muscleResult$BUGSoutput,
+     muscleRagged$ragged)
+ summaryChain(muscleParams)$scalars[,c('mean', '2.5pct', '97.5pct')]
+ }
```

	mean	2.5pct	97.5pct
SDStrip	1.0629735	0.4175768	1.68439547
intercept	-1.2536538	-2.5402147	0.02005051
betas	0.2029297	0.1419052	0.25870488

```
> if(haveR2jags) {
+   checkChain(muscleParams)
+ }
```



2 Bacteria

```

> data('bacteria', package='MASS')
> bacterianew <- bacteria
> bacterianew$yInt = as.integer(bacterianew$y == "y")
> levels(bacterianew$trt) <- c("placebo", "drug", "drugplus")

> bacrag <- glmmBUGS(formula = yInt ~ trt + week,
+   data = bacterianew,
+   effects = "ID", modelFile = "bacteria.txt",
+   family = "bernoulli",brugs=TRUE)
> source("getInits.R")
> startingValues = bacrag$startingValues

> if(haveR2jags) {
+   bacResult = R2jags::jags(bacrag$ragged,
+     inits=getInits,
+     model.file = "bacteria.txt", n.chain = 3,

```

```

+       n.iter = 600, n.burnin = 10, refresh=200,
+       parameters = names(getInits()),
+       n.thin = 4)
+ } else {
+       bacResult = list()
+ }

```

```

Compiling model graph
  Resolving undeclared variables
  Allocating nodes
Graph information:
  Observed stochastic nodes: 220
  Unobserved stochastic nodes: 55
  Total graph size: 1163

```

Initializing model

```

> if(haveR2jags) {
+   bacParams = restoreParams(bacResult$BUGSoutput,
+     bacrag$ragged)
+ }

```

```

> if(haveR2jags) {
+   bacsummary = summaryChain(bacParams)
+
+   bacsummary$betas[,c('mean', 'sd')]
+ }

```

	mean	sd
trtdrug	-1.5325610	0.82160037
trtdrugplus	-0.9403734	0.83543603
betaobservations	-0.1657366	0.05906621

```

> if(haveR2jags) {
+   checkChain(bacParams, c("intercept", "SDID"), oneFigure=TRUE)
+ }

```

