```r
# Example of initializing parameters
# Load the lars package and the diabetes dataset
library(reshape2)
library(lars)
```

Loaded lars 1.3

```r
data(diabetes)
library(GGally)
```

Loading required package: ggplot2

Registered S3 method overwritten by 'GGally':
method from
+.gg   ggplot2

```r
library(ggplot2)
library(gridExtra)

library("rstan") # observe startup messages
```

Loading required package: StanHeaders

##
rstan version 2.32.3 (Stan version 2.26.1)

For execution on a local, multicore CPU with excess RAM we recommend calling
options(mc.cores = parallel::detectCores()).
To avoid recompilation of unchanged Stan programs, we recommend calling
rstan_options(auto_write = TRUE)
For within-chain threading using `reduce_sum()` or `map_rect()` Stan functions,
change `threads_per_chain` option:
rstan_options(threads_per_chain = 1)

```r
options(mc.cores = parallel::detectCores())
rstan_options(auto_write = TRUE)

library(rjags)
```

Loading required package: coda

##
Attaching package: 'coda'

The following object is masked from 'package:rstan':
##
traceplot

Linked to JAGS 4.3.2

Loaded modules: basemod,bugs

```r
#data
X_matrix <- diabetes$x
class(X_matrix) <- "matrix"
y_vector <- diabetes$y

X_design <- cbind(1, X_matrix)
set.seed(123)
split_ind <- sample(1:length(y_vector), size=round(length(y_vector)*0.8))
```

```r
y_train <- y_vector[split_ind]
y_test <- y_vector[-split_ind]

X_train <- X_design[split_ind,]
X_test <- X_design[-split_ind]



K <- ncol(X_train)
inits <- list(z = rep(0, K-1),
              beta = rep(0, K),
              sigma2temp = 1,
              mu_beta = rep(0, K),
              v0 = 1,
              s0 = 1)

data_list <- list(
  N = dim(X_train)[1],
  K = dim(X_train)[2],
  x = X_train,
  y = y_train,
  Ik = diag(K),
  C0 = diag(K)
)

data_ols <- data.frame(cbind(y_vector, X_matrix))

ttt <- lm(y_vector~., data=data_ols)
summary(step(ttt))
```

```
## Start:  AIC=3539.64
## y_vector ~ age + sex + bmi + map + tc + ldl + hdl + tch + ltg +
##     glu
##
##         Df Sum of Sq      RSS    AIC
## - age    1        82 1264066 3537.7
## - hdl    1       663 1264646 3537.9
## - glu    1      3080 1267064 3538.7
## - tch    1      3526 1267509 3538.9
## <none>               1263983 3539.6
## - ldl    1      5799 1269782 3539.7
## - tc     1     10600 1274583 3541.3
## - sex    1     45000 1308983 3553.1
## - ltg    1     56015 1319998 3556.8
## - map    1     72103 1336086 3562.2
## - bmi    1    179028 1443011 3596.2
##
## Step:  AIC=3537.67
## y_vector ~ sex + bmi + map + tc + ldl + hdl + tch + ltg + glu
##
##         Df Sum of Sq      RSS    AIC
## - hdl    1       646 1264712 3535.9
## - glu    1      3001 1267067 3536.7
## - tch    1      3543 1267608 3536.9
```

```
## <none>                 1264066 3537.7
## - ldl    1       5751 1269817 3537.7
## - tc     1      10569 1274635 3539.4
## - sex    1      45831 1309896 3551.4
## - ltg    1      55963 1320029 3554.8
## - map    1      73850 1337915 3560.8
## - bmi    1     179079 1443144 3594.2
##
## Step:  AIC=3535.9
## y_vector ~ sex + bmi + map + tc + ldl + tch + ltg + glu
##
##         Df Sum of Sq     RSS    AIC
## - glu    1       3093 1267805 3535.0
## - tch    1       3247 1267959 3535.0
## <none>                 1264712 3535.9
## - ldl    1       7505 1272217 3536.5
## - tc     1      26840 1291552 3543.2
## - sex    1      46382 1311094 3549.8
## - map    1      73536 1338248 3558.9
## - ltg    1      97509 1362221 3566.7
## - bmi    1     178537 1443249 3592.3
##
## Step:  AIC=3534.98
## y_vector ~ sex + bmi + map + tc + ldl + tch + ltg
##
##         Df Sum of Sq     RSS    AIC
## - tch    1       3686 1271491 3534.3
## <none>                 1267805 3535.0
## - ldl    1       7472 1275277 3535.6
## - tc     1      26378 1294183 3542.1
## - sex    1      44686 1312491 3548.3
## - map    1      82154 1349959 3560.7
## - ltg    1     102520 1370325 3567.3
## - bmi    1     189970 1457775 3594.7
##
## Step:  AIC=3534.26
## y_vector ~ sex + bmi + map + tc + ldl + ltg
##
##         Df Sum of Sq     RSS    AIC
## <none>                 1271491 3534.3
## - ldl    1      39378 1310869 3545.7
## - sex    1      41858 1313349 3546.6
## - tc     1      65237 1336728 3554.4
## - map    1      79627 1351119 3559.1
## - bmi    1     190586 1462077 3594.0
## - ltg    1     294094 1565585 3624.2
##
## Call:
## lm(formula = y_vector ~ sex + bmi + map + tc + ldl + ltg, data = data_ols)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -158.277  -39.476   -2.068   37.221  148.693
```

```
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  152.133      2.572  59.159  < 2e-16 ***
## sex         -226.511     59.857  -3.784 0.000176 ***
## bmi          529.873     65.620   8.075 6.69e-15 ***
## map          327.220     62.693   5.219 2.79e-07 ***
## tc          -757.938    160.435  -4.724 3.12e-06 ***
## ldl          538.586    146.738   3.670 0.000272 ***
## ltg          804.192     80.173  10.031  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 54.06 on 435 degrees of freedom
## Multiple R-squared:  0.5149, Adjusted R-squared:  0.5082
## F-statistic: 76.95 on 6 and 435 DF,  p-value: < 2.2e-16

```
```