

# GLM - GLMM

2023-03-31

## GLM - efecto volumen vegetal sin especies

```
rm(list=ls())
library(jagsUI)
data <- read.csv("ejemplo_AF.csv", header=T)
attach(data)
str(data)

## 'data.frame':   92 obs. of  9 variables:
##  $ Id           : chr  "Cv36069" "Cv36136" "Cv36164" "Cv36179" ...
##  $ sp_nom        : chr  "cv" "cv" "cv" "cv" ...
##  $ sp            : int  0 0 0 0 0 0 0 0 0 ...
##  $ sp_fac        : int  1 1 1 1 1 1 1 1 1 ...
##  $ cv            : int  1 1 1 1 1 1 1 1 1 ...
##  $ cm            : int  0 0 0 0 0 0 0 0 0 ...
##  $ Mahalanobis.FA.score: num  2.68 3.44 3.78 3.79 3.34 ...
##  $ vv            : num  0.444 1.01 0.406 0.444 0.59 ...
##  $ centroide     : num  38.7 40.6 40.1 36.4 40.6 ...

win.data <- list(vv = data$vv, centroide = data$centroide, n= nrow(data))

# Define the model
sink("GLM_normal_general.jags")
cat("
model {

  # Priors
  beta0 ~ dnorm(0, 1e-6)
  beta1 ~ dnorm(0, 1e-6)
  sigma ~ dunif(0, 10)
  tau <- 1 / (sigma * sigma)

  # Likelihood
  for (i in 1:n) {
    centroide[i] ~ dnorm(mu[i], tau)
    mu[i] <- beta0 + beta1 * vv[i]
  }
}
",fill = TRUE)

##
## model {
##
##   # Priors
##   beta0 ~ dnorm(0, 1e-6)
```

```

##  beta1 ~ dnorm(0, 1e-6)
##  sigma ~ dunif(0, 10)
##  tau <- 1 / (sigma * sigma)
##
##  # Likelihood
##  for (i in 1:n) {
##    centroe[i] ~ dnorm(mu[i], tau)
##    mu[i] <- beta0 + beta1 * vv[i]
##  }
## }

sink()

#valores iniciales
inits <- function() list(beta0 = runif(1, -2, 2), beta1 = runif(1, -3, 3))

# Parametros monitoreados
params <- c("beta0", "beta1")

# MCMC settings
ni <- 10000
nt <- 2
nb <- 1000
nc <- 3

# Call JAGS from R (BRT < 1 min)
#out_general <- jags(data = win.data, inits = inits, parameters.to.save = params,
#  #
#    model.file = "GLM_normal_general.jags", n.chains = nc, n.thin = nt,
#    #
#    n.iter = ni, n.burnin = nb)
load("~/Documentos/TRABAJO/Curso Ocupacion Mendoza/out_general")

out_general

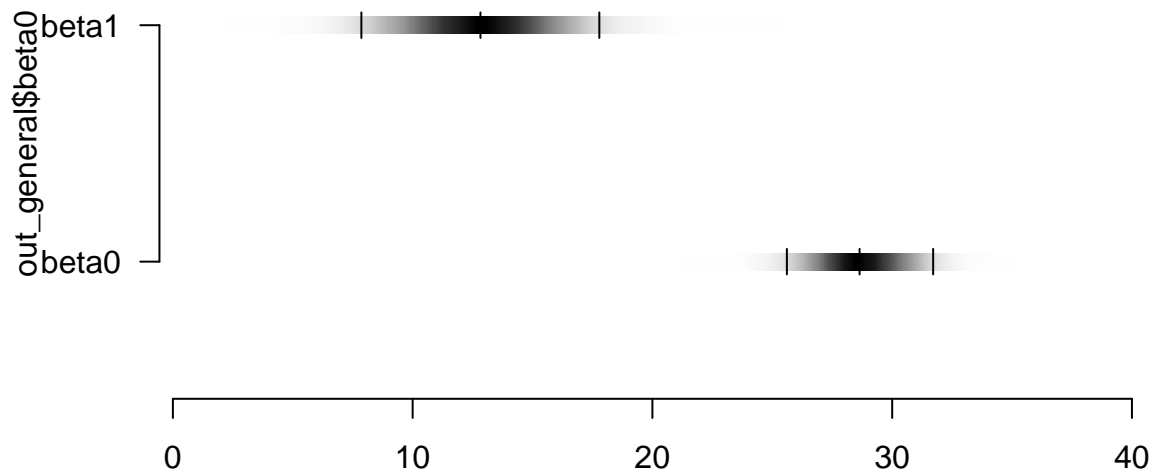
## JAGS output for model 'GLM_normal_general.jags', generated by jagsUI.
## Estimates based on 3 chains of 10000 iterations,
## adaptation = 100 iterations (sufficient),
## burn-in = 1000 iterations and thin rate = 2,
## yielding 13500 total samples from the joint posterior.
## MCMC ran for 0.009 minutes at time 2023-03-31 16:00:49.
##
##          mean    sd   2.5%   50%   97.5% overlap0 f Rhat n.eff
## beta0      28.662 1.552  25.608  28.640  31.708    FALSE 1    1 13500
## beta1      12.822 2.524   7.863  12.828  17.786    FALSE 1    1 13500
## deviance  515.459 2.497 512.612 514.811 521.923    FALSE 1    1 13500
##
## Successful convergence based on Rhat values (all < 1.1).
## Rhat is the potential scale reduction factor (at convergence, Rhat=1).
## For each parameter, n.eff is a crude measure of effective sample size.
##
## overlap0 checks if 0 falls in the parameter's 95% credible interval.
## f is the proportion of the posterior with the same sign as the mean;
## i.e., our confidence that the parameter is positive or negative.
##
## DIC info: (pD = var(deviance)/2)

```

```
## pD = 3.1 and DIC = 518.577
## DIC is an estimate of expected predictive error (lower is better).

library("denstrip")
plot(out_general$beta0, xlim = c(1,40), ylim = c(0.5,2.5), xlab="", type = "n",
     axes = F, main = "Efecto del vv sin especies")
axis(1)
axis(2, at=1:2, labels = c("beta0", "beta1"), las=1)
for(k in 1:2){
  denstrip(unlist(out_general$sims.list[k]), at = k,
           ticks = out_general$summary[k,c(3,5,7)])
}
```

## Efecto del vv sin especies



```
# Plot
b0 <- out_general$mean$beta0
out_general$sims.list$mean$beta0

## NULL
b1 <- out_general$mean$beta1

tmp <- out_general$sims.list
nsamp <- out_general$mcmc.info$n.samples
vv.pred <- seq(min(data$vv),max(data$vv),length.out = 500)

pred_general <- array(NA, 500)

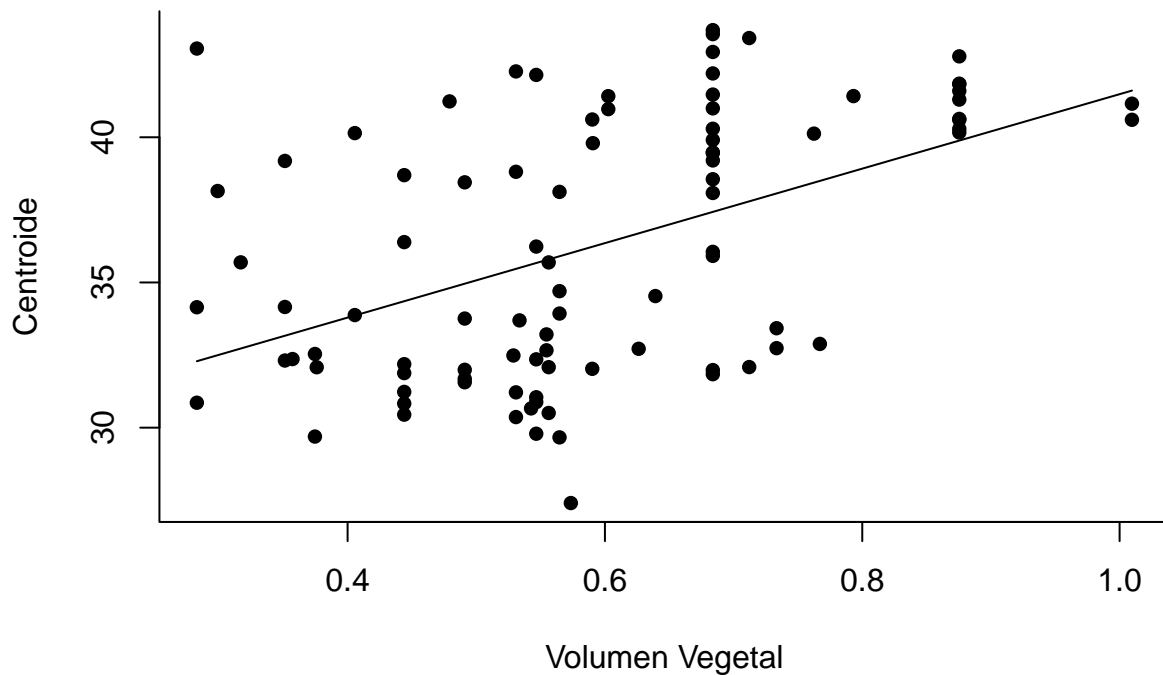
for(i in 1:500){
```

```

  pred_general[i] <- out_general$mean$beta0 + out_general$mean$beta1*vv.pred[i]
}
plot( data$vv,data$centroide,
      ylab= "Centroide",xlab = "Volumen Vegetal",
      pch=16, bty="l")

lines(vv.pred,pred_general)

```



```

##### GLM random odernada por especie #####
win.data <- list(vv = data$vv, centroide = centroide, n = nrow(data),
                sp = sp_fac)

str(win.data)

## List of 4
## $ vv      : num [1:92] 0.444 1.01 0.406 0.444 0.59 ...
## $ centroide: num [1:92] 38.7 40.6 40.1 36.4 40.6 ...
## $ n       : int 92
## $ sp      : int [1:92] 1 1 1 1 1 1 1 1 1 1 ...

# Define the model
sink("GLM_normal_random_ordenada.jags")
cat("
model {

  # Priors
  tau <- pow(sd, -2)

```

```

sd ~ dunif(0,1000)
beta1 ~ dnorm(0, 1e-6)

for (k in 1:2) {
  beta0[k]~ dnorm(0, 1e-6)
}

# Likelihood
for (i in 1:n) {
  centroide[i] ~ dnorm(mu[i], tau)
  mu[i] <- beta0[sp[i]] + beta1 * vv[i]

  #1 cv
  #2 cm

}
}
",fill = TRUE)

```

```

##
## model {
##
##   # Priors
##   tau <- pow(sd, -2)
##   sd ~ dunif(0,1000)
##   beta1 ~ dnorm(0, 1e-6)
##
##   for (k in 1:2) {
##     beta0[k]~ dnorm(0, 1e-6)
##   }
##
##   # Likelihood
##   for (i in 1:n) {
##     centroide[i] ~ dnorm(mu[i], tau)
##     mu[i] <- beta0[sp[i]] + beta1 * vv[i]
##
##     #1 cv
##     #2 cm
##
##   }
## }

```

```

sink()

```

```

#valores iniciales
inits <- function() list(beta0 = rnorm(2, 3), beta1 = rnorm(1,3))

# Parametros monitoreados
params <- c("beta0", "beta1")

# MCMC settings
ni <- 10000
nt <- 2

```

```

nb <- 1000
nc <- 3

# Call JAGS from R (BRT < 1 min)
# out_random_ord <- jags(data = win.data, inits = inits, parameters.to.save = params,
#                         model.file = "GLM_normal_random_ordenada.jags",
#                         n.chains = nc, n.thin = nt,
#                         n.iter = ni, n.burnin = nb)

#save(out_random_ord, file = "out_random_ordenada")
load("~/Documentos/TRABAJO/Curso Ocupacion Mendoza/out_random_ordenada")

out_random_ord

## JAGS output for model 'GLM_normal_random_ordenada.jags', generated by jagsUI.
## Estimates based on 3 chains of 10000 iterations,
## adaptation = 100 iterations (sufficient),
## burn-in = 1000 iterations and thin rate = 2,
## yielding 13500 total samples from the joint posterior.
## MCMC ran for 0.01 minutes at time 2023-04-02 10:59:37.
##
##          mean    sd   2.5%   50%   97.5% overlap0      f Rhat n.eff
## beta0[1] 38.128 0.957 36.240 38.124 40.019   FALSE 1.000    1 5511
## beta0[2] 30.601 0.772 29.068 30.596 32.119   FALSE 1.000    1 13500
## beta1     3.324 1.369  0.599  3.325  5.990   FALSE 0.991    1 9453
## deviance 385.452 2.913 381.849 384.752 392.833   FALSE 1.000    1 13500
##
## Successful convergence based on Rhat values (all < 1.1).
## Rhat is the potential scale reduction factor (at convergence, Rhat=1).
## For each parameter, n.eff is a crude measure of effective sample size.
##
## overlap0 checks if 0 falls in the parameter's 95% credible interval.
## f is the proportion of the posterior with the same sign as the mean;
## i.e., our confidence that the parameter is positive or negative.
##
## DIC info: (pD = var(deviance)/2)
## pD = 4.2 and DIC = 389.695
## DIC is an estimate of expected predictive error (lower is better).

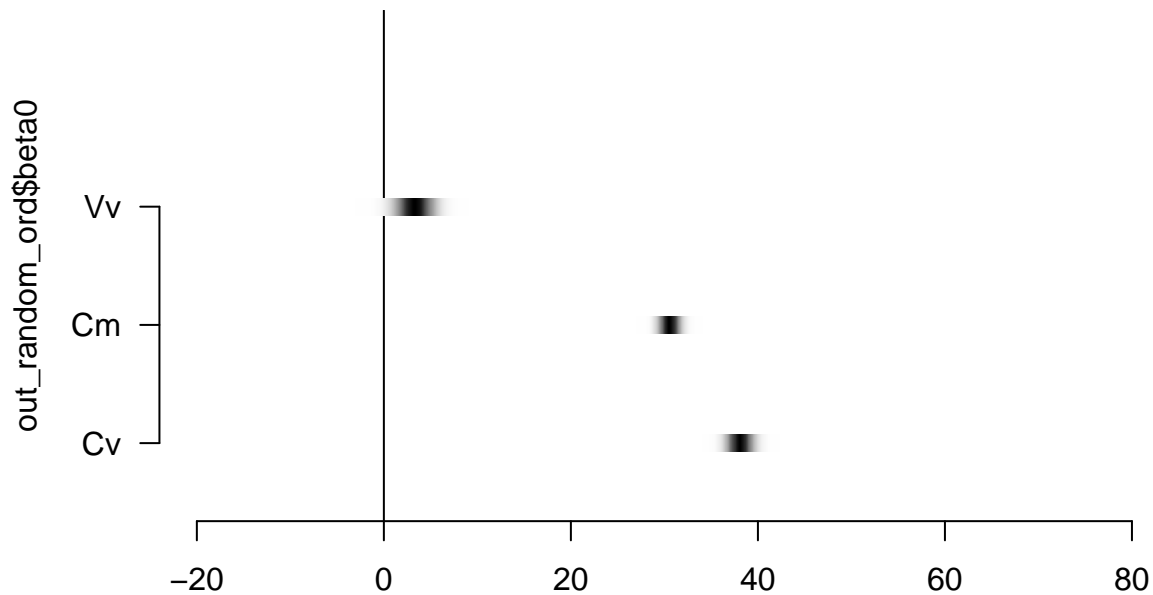
library("denstrip")

#1 cv
#2 cm

plot(out_random_ord$beta0, xlim = c(-20,80), ylim = c(0.5,4.5), xlab="", type = "n",
     axes = F, main = "Ordenada por especie - fijas")
axis(1)
axis(2, at=1:3, labels = c("Cv", "Cm", "Vv"),
     las=1)
abline(v=0)
denstrip(unlist(out_random_ord$sims.list[[1]][,1]), at =1)
denstrip(unlist(out_random_ord$sims.list[[1]][,2]), at =2)
denstrip(unlist(out_random_ord$sims.list[2]), at =3)

```

## Ordenada por especie – fijas



```
#Plot lineas
vv.pred <- seq(min(data$vv),max(data$vv),length.out = 500)

ordenada_cv <- array(NA, 500)
for(i in 1:500){
  ordenada_cv[i] <- out_random_ord$mean$beta0[1] + out_random_ord$mean$beta1*vv.pred[i]
}

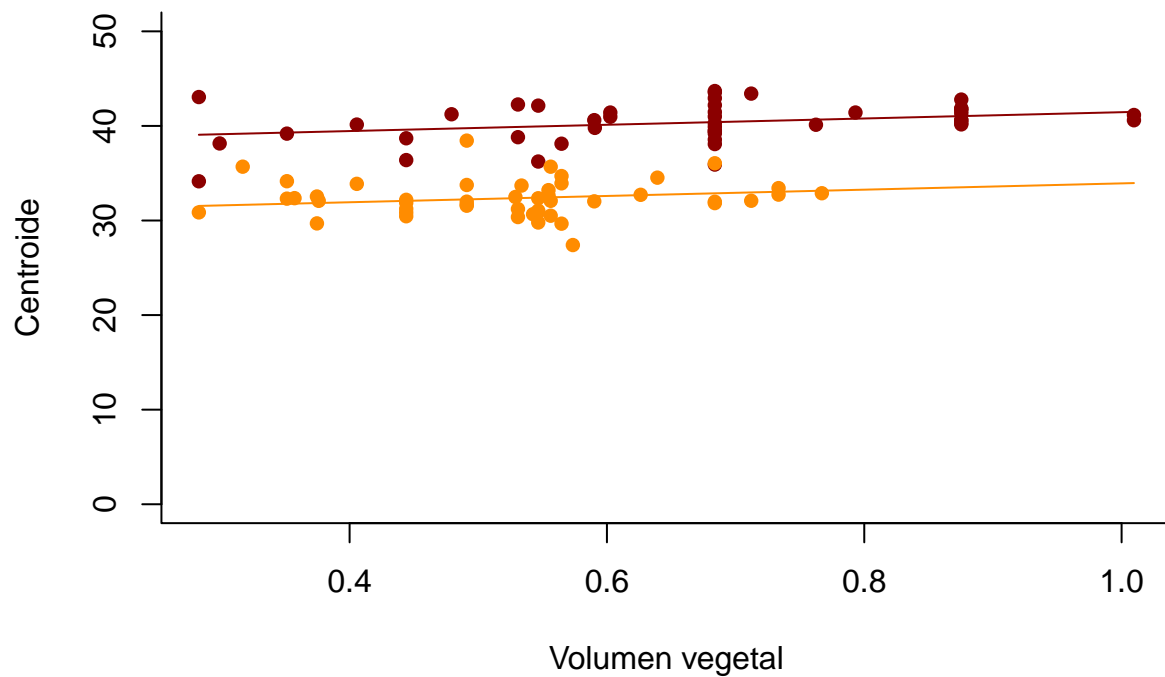
ordenada_cm <- array(NA, 500)
for(i in 1:500){
  ordenada_cm[i] <- out_random_ord$mean$beta0[2] + out_random_ord$mean$beta1*vv.pred[i]
}

#Grafico
plot(data$vv[data$sp_fac==1],data$centroide[data$sp_fac==1],      #grafico primero solo venustus
      ylab= "Centroide",xlab = "Volumen vegetal",
      pch=16, bty="l", col = "darkred", ylim = c(0,50))

points(data$vv[data$sp_fac==2],data$centroide[data$sp_fac==2],    #grafico cm
        pch=16, bty="l", col = "darkorange")

lines(vv.pred,ordenada_cv, col= "darkred")

lines(vv.pred,ordenada_cm, col = "darkorange")
```



```
##### GLM random odernada y pendiente por especie #####
win.data <- list(vv = data$vv, centroide = centroide, n= nrow(data),
                sp = sp_fac)

# Define the model
sink("GLM_dos_fijas.jags")
cat("
model {

  # Priors
  tau <- pow(sd, -2)
  sd ~ dunif(0,1000)

  for (k in 1:2) {
    beta0[k]~ dnorm(0, 1e-6)
    beta1[k] ~ dnorm(0, 1e-6)
  }

  # Likelihood
  for (i in 1:n) {
    centroide[i] ~ dnorm(mu[i], tau)
    mu[i] <- beta0[sp[i]] + beta1[sp[i]] * vv[i]

    #1 cv
    #2 cm
  }
}
```



```

    }
  }

  ",fill = TRUE)

##
## model {
##
##   # Priors
##   tau <- pow(sd, -2)
##   sd ~ dunif(0,1000)
##
##   for (k in 1:2) {
##     beta0[k] ~ dnorm(0, 1e-6)
##     beta1[k] ~ dnorm(0, 1e-6)
##   }
##
##   # Likelihood
##   for (i in 1:n) {
##     centroe[i] ~ dnorm(mu[i], tau)
##     mu[i] <- beta0[sp[i]] + beta1[sp[i]] * vv[i]
##
##     #1 cv
##     #2 cm
##   }
## }
##
##
sink()

#valores iniciales
inits <- function() list(beta0 = rnorm(2, 2), beta1 = rnorm(2,2))

# Parametros monitoreados
params <- c("beta0", "beta1")

# MCMC settings
ni <- 10000
nt <- 2
nb <- 1000
nc <- 3

# Call JAGS from R (BRT < 1 min)
#out_dos_fijas <- jags(data = win.data, inits = inits, parameters.to.save = params,
#                       model.file = "GLM_dos_fijas.jags", n.chains = nc, n.thin = nt,
#                       n.iter = ni, n.burnin = nb)

#save(out_dos_fijas, file = "out_dos_fijas")
load("~/Documentos/TRABAJO/Curso Ocupacion Mendoza/out_dos_fijas")

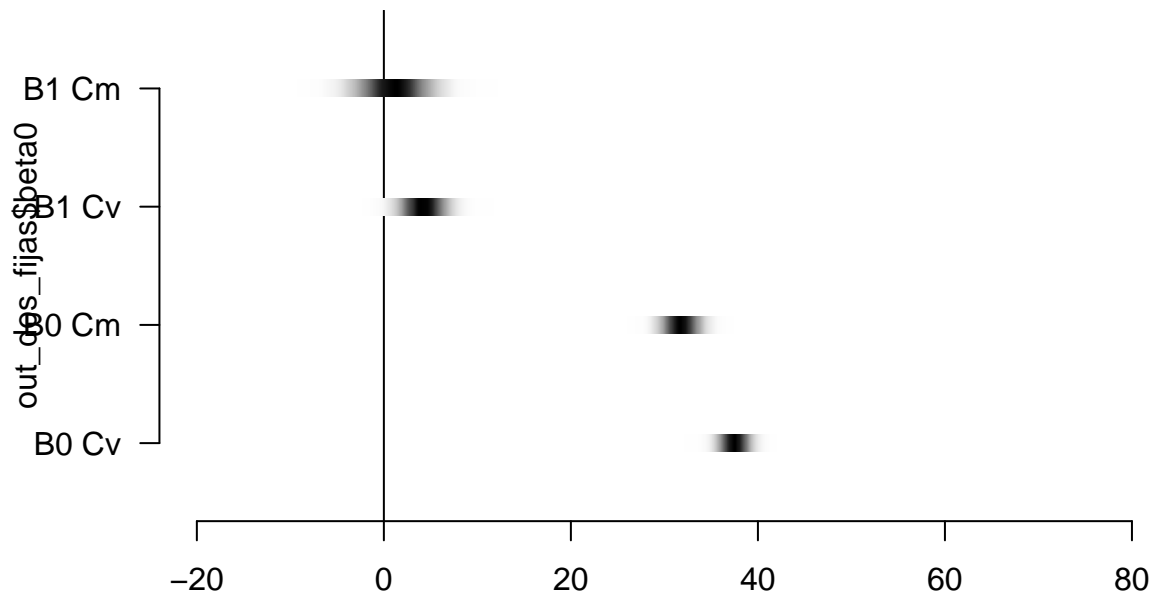
out_dos_fijas

```

```
## JAGS output for model 'GLM_dos_fijas.jags', generated by jagsUI.
## Estimates based on 3 chains of 10000 iterations,
## adaptation = 100 iterations (sufficient),
## burn-in = 1000 iterations and thin rate = 2,
## yielding 13500 total samples from the joint posterior.
## MCMC ran for 0.011 minutes at time 2023-04-02 11:39:18.
##
##          mean    sd   2.5%   50%   97.5% overlap0    f Rhat n.eff
## beta0[1] 37.522 1.126 35.321 37.526 39.742    FALSE 1.000    1 13500
## beta0[2] 31.797 1.371 29.087 31.784 34.509    FALSE 1.000    1 11506
## beta1[1]  4.233 1.643  1.012  4.230  7.468    FALSE 0.995    1 13500
## beta1[2]  1.048 2.555 -3.998  1.075  6.071     TRUE 0.660    1  8453
## deviance 385.381 3.298 380.980 384.705 393.499    FALSE 1.000    1 13500
##
## Successful convergence based on Rhat values (all < 1.1).
## Rhat is the potential scale reduction factor (at convergence, Rhat=1).
## For each parameter, n.eff is a crude measure of effective sample size.
##
## overlap0 checks if 0 falls in the parameter's 95% credible interval.
## f is the proportion of the posterior with the same sign as the mean;
## i.e., our confidence that the parameter is positive or negative.
##
## DIC info: (pD = var(deviance)/2)
## pD = 5.4 and DIC = 390.821
## DIC is an estimate of expected predictive error (lower is better).

library("denstrip")
plot(out_dos_fijas$beta0, xlim = c(-20,80), ylim = c(0.5,4.5), xlab="", type = "n",
     axes = F, main = "Especies Fijas ordenada y pendiente")
axis(1)
axis(2, at=1:4, labels = c("B0 Cv", "B0 Cm", "B1 Cv", "B1 Cm"),
     las=1)
abline(v=0)
denstrip(unlist(out_dos_fijas$sims.list[[1]][,1]), at =1)
denstrip(unlist(out_dos_fijas$sims.list[[1]][,2]), at =2)
denstrip(unlist(out_dos_fijas$sims.list[[2]][,1]), at =3)
denstrip(unlist(out_dos_fijas$sims.list[[2]][,2]), at =4)
```

## Especies Fijas ordenada y pendiente



```
#Plot lines
vv.pred <- seq(min(data$vv),max(data$vv),length.out = 500)

ord_pred_cv <- array(NA, 500)
for(i in 1:500){
  ord_pred_cv[i] <- out_dos_fijas$mean$beta0[1] + out_dos_fijas$mean$beta1[1]*vv.pred[i]
}

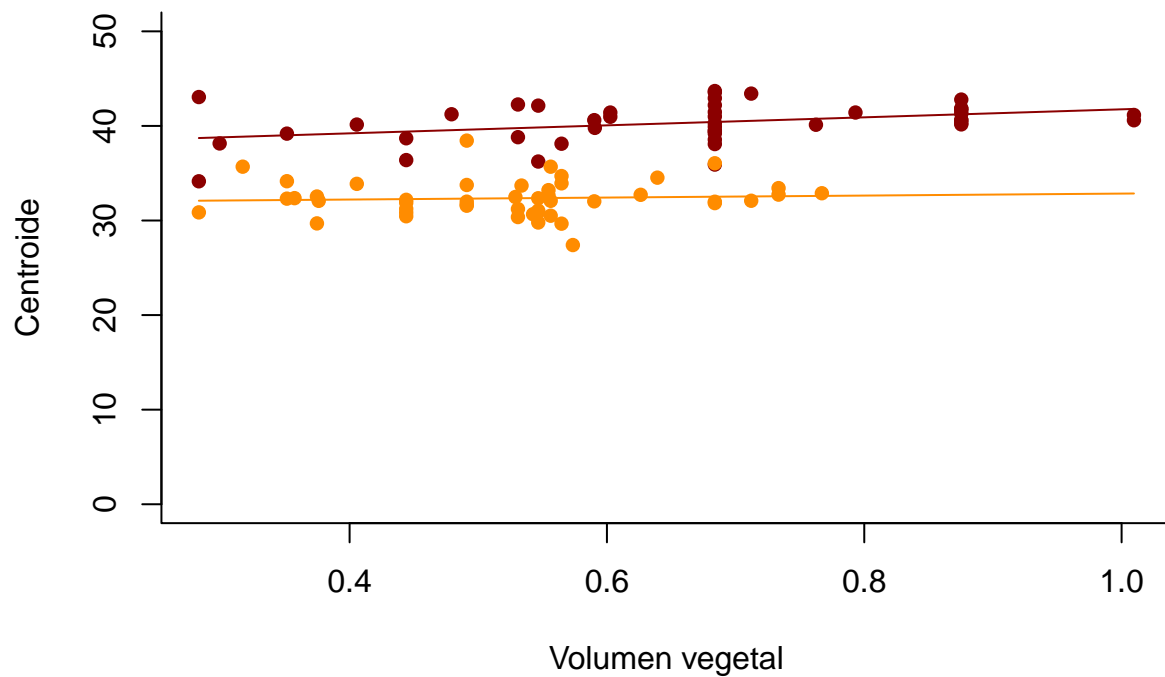
ord_pred_cm <- array(NA, 500)
for(i in 1:500){
  ord_pred_cm[i] <- out_dos_fijas$mean$beta0[2] + out_dos_fijas$mean$beta1[2]*vv.pred[i]
}

#Grafico
plot(data$vv[data$sp_fac==1],data$centroide[data$sp_fac==1],      #grafico primero solo venustus
      ylab= "Centroide",xlab = "Volumen vegetal",
      pch=16, bty="l", col = "darkred", ylim = c(0,50))

points(data$vv[data$sp_fac==2],data$centroide[data$sp_fac==2],    #grafico cm
        pch=16, bty="l", col = "darkorange")

lines(vv.pred,ord_pred_cv, col= "darkred")

lines(vv.pred,ord_pred_cm, col = "darkorange")
```



```
##### GLMM random especie #####
```

```
win.data <- list(vv = data$vv, centroide = centroide, n= nrow(data),
                 sp = sp_fac)
```

```
# Define the model
```

```
sink("GLMM_random.jags")
```

```
cat(" "
```

```
model {
```

```
  # Priors
```

```
  mu.beta0 ~ dnorm(0, 1e-6)
```

```
  tau.beta0 <- pow(sd.beta0, -2)
```

```
  sd.beta0 ~ dunif(0, 10)
```

```
  mu.beta1 ~ dnorm(0, 1e-6)
```

```
  tau.beta1 <- pow(sd.beta1, -2)
```

```
  sd.beta1 ~ dunif(0, 10)
```

```
  tau <- pow(sd, -2)
```

```
  sd ~ dunif(0,1000)
```

```
  for (k in 1:2) {
```

```
    beta0[k]~ dnorm(mu.beta0, tau.beta0 )
```

```
    beta1[k] ~ dnorm(mu.beta1, tau.beta1)
```

```
  }
```

```
# Likelihood
```

```

    for (i in 1:n) {
      centroe[i] ~ dnorm(mu[i], tau)
      mu[i] <- beta0[sp[i]] + beta1[sp[i]] * vv[i]
    }
  }
",fill = TRUE)

##
## model {
##
##   # Priors
##   mu.beta0 ~ dnorm(0, 1e-6)
##   tau.beta0 <- pow(sd.beta0, -2)
##   sd.beta0 ~ dunif(0, 10)
##   mu.beta1 ~ dnorm(0, 1e-6)
##   tau.beta1 <- pow(sd.beta1, -2)
##   sd.beta1 ~ dunif(0, 10)
##
##   tau <- pow(sd, -2)
##   sd ~ dunif(0,1000)
##
##   for (k in 1:2) {
##     beta0[k]~ dnorm(mu.beta0, tau.beta0 )
##     beta1[k] ~ dnorm(mu.beta1, tau.beta1)
##   }
##
##   # Likelihood
##   for (i in 1:n) {
##     centroe[i] ~ dnorm(mu[i], tau)
##     mu[i] <- beta0[sp[i]] + beta1[sp[i]] * vv[i]
##   }
## }

sink()

#valores iniciales
inits <- function() list(beta0 = rnorm(2, 2), beta1 = rnorm(2,2))

# Parametros monitoreados
params <- c("beta0", "beta1", "mu.beta0", "mu.beta1")

# MCMC settings
ni <- 10000
nt <- 2
nb <- 1000
nc <- 3

# Call JAGS from R (BRT < 1 min)
#out_random_hiper <- jags(data = win.data, inits = inits, parameters.to.save = params,
#                          model.file = "GLMM_random.jags", n.chains = nc, n.thin = nt,
#                          n.iter = ni, n.burnin = nb)

#save(out_random_hiper, file = "out_random_hiper")

```

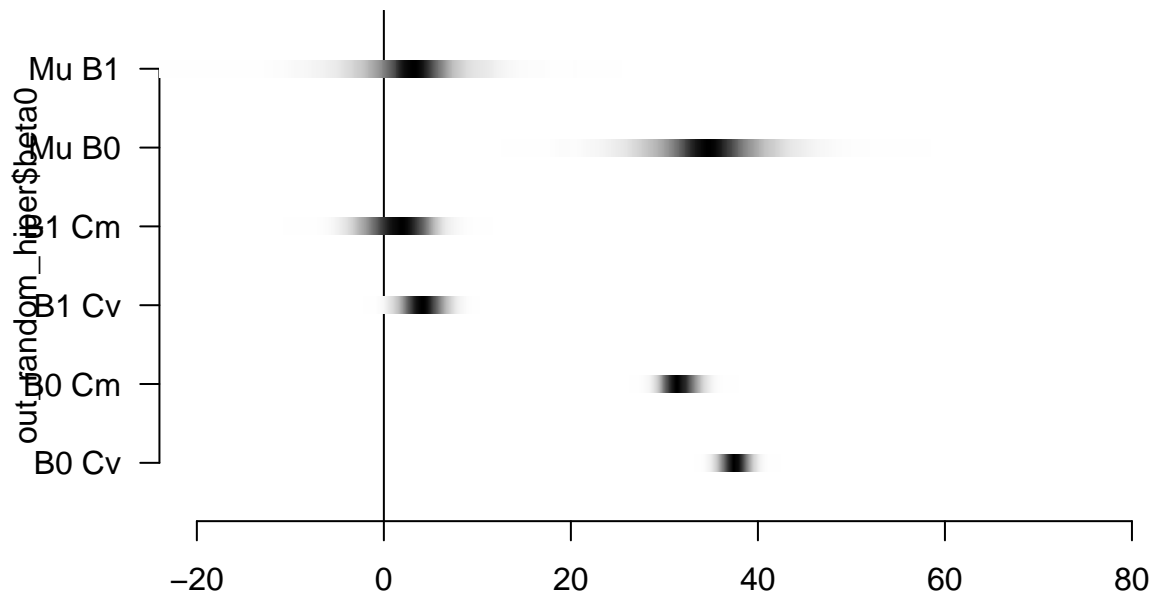
```
load("~/Documentos/TRABAJO/Curso Ocupacion Mendoza/out_random_hiper")
```

```
out_random_hiper
```

```
## JAGS output for model 'GLMM_random.jags', generated by jagsUI.
## Estimates based on 3 chains of 10000 iterations,
## adaptation = 100 iterations (sufficient),
## burn-in = 1000 iterations and thin rate = 2,
## yielding 13500 total samples from the joint posterior.
## MCMC ran for 0.009 minutes at time 2023-04-02 12:05:56.
##
##      mean    sd   2.5%   50%   97.5% overlap0    f  Rhat n.eff
## beta0[1] 37.566 1.095 35.388 37.568 39.741    FALSE 1.000 1.001 4033
## beta0[2] 31.619 1.335 29.140 31.562 34.349    FALSE 1.000 1.000 5519
## beta1[1]  4.146 1.585  0.981  4.136  7.299    FALSE 0.997 1.001 5150
## beta1[2]  1.413 2.483 -3.680  1.541  5.932     TRUE 0.722 1.000 4608
## mu.beta0 34.619 4.485 25.294 34.643 43.948    FALSE 1.000 1.000 6170
## mu.beta1  2.765 3.978 -5.944  2.889 11.031     TRUE 0.805 1.001 10611
## deviance 385.269 3.118 381.062 384.630 393.053    FALSE 1.000 1.001 13500
##
## Successful convergence based on Rhat values (all < 1.1).
## Rhat is the potential scale reduction factor (at convergence, Rhat=1).
## For each parameter, n.eff is a crude measure of effective sample size.
##
## overlap0 checks if 0 falls in the parameter's 95% credible interval.
## f is the proportion of the posterior with the same sign as the mean;
## i.e., our confidence that the parameter is positive or negative.
##
## DIC info: (pD = var(deviance)/2)
## pD = 4.9 and DIC = 390.128
## DIC is an estimate of expected predictive error (lower is better).
```

```
library("denstrip")
plot(out_random_hiper$beta0, xlim = c(-20,80), ylim = c(0.5,6.5), xlab="", type = "n",
     axes = F, main = "Especies Aleatorias")
axis(1)
axis(2, at=1:6, labels = c("B0 Cv", "B0 Cm", "B1 Cv", "B1 Cm", "Mu B0", "Mu B1"),
     las=1)
abline(v=0)
denstrip(unlist(out_random_hiper$sims.list[[1]][,1]), at =1)
denstrip(unlist(out_random_hiper$sims.list[[1]][,2]), at =2)
denstrip(unlist(out_random_hiper$sims.list[[2]][,1]), at =3)
denstrip(unlist(out_random_hiper$sims.list[[2]][,2]), at =4)
denstrip(unlist(out_random_hiper$sims.list[3]), at =5)
denstrip(unlist(out_random_hiper$sims.list[4]), at =6)
```

## Especies Aleatorias



```
#Plot lines
vv.pred <- seq(min(data$vv),max(data$vv),length.out = 500)

pred_cv_ran <- array(NA, 500)
for(i in 1:500){
  pred_cv_ran[i] <- out_random_hiper$mean$beta0[1] + out_random_hiper$mean$beta1[1]*vv.pred[i]
}

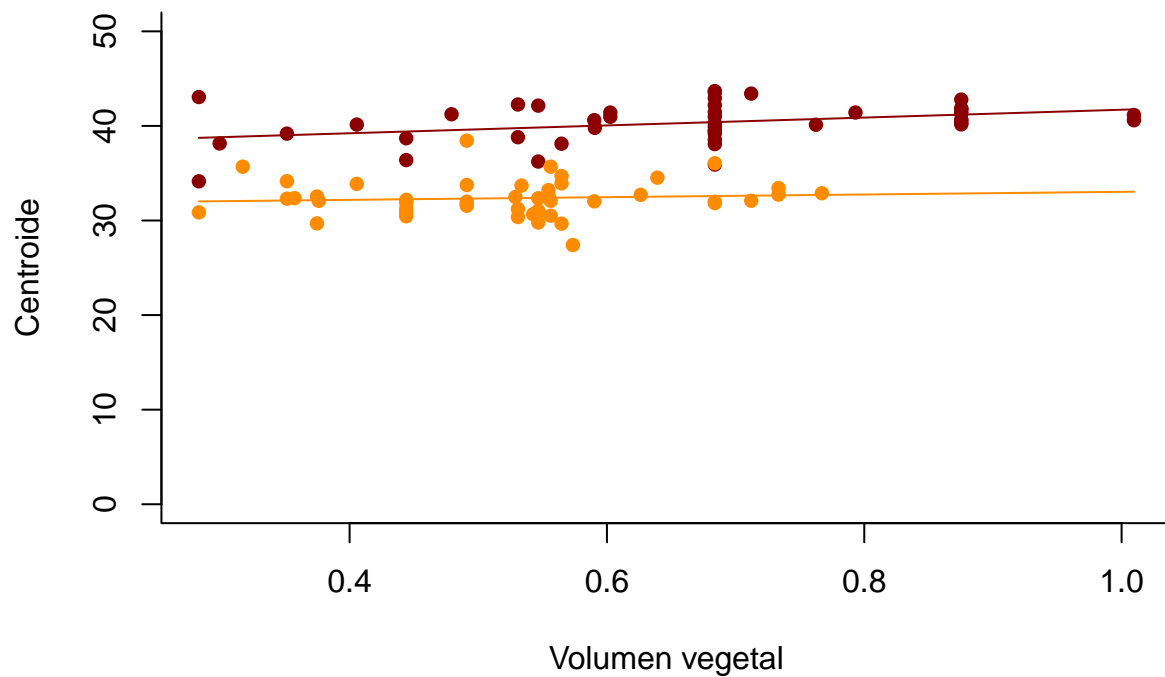
ord_cm_ran <- array(NA, 500)
for(i in 1:500){
  ord_cm_ran[i] <- out_random_hiper$mean$beta0[2] + out_random_hiper$mean$beta1[2]*vv.pred[i]
}

#Grafico
plot(data$vv[data$sp_fac==1],data$centroide[data$sp_fac==1],      #grafico primero solo venustus
      ylab= "Centroide",xlab = "Volumen vegetal",
      pch=16, bty="l", col = "darkred", ylim = c(0,50))

points(data$vv[data$sp_fac==2],data$centroide[data$sp_fac==2],    #grafico cm
        pch=16, bty="l", col = "darkorange")

lines(vv.pred,pred_cv_ran, col= "darkred")

lines(vv.pred,ord_cm_ran, col = "darkorange")
```



```
##### GLM todas INTERACCON SP fijas #####
win.data <- list(vv = data$vv, centroide = data$centroide, n= nrow(data),
                sp = sp)
#BETAS FIJOS

# Define the model
sink("GLM_FIJO.jags")
cat("
model {

  # Priors
  beta0 ~ dnorm(0, 1e-6)
  beta1 ~ dnorm(0, 1e-6)
  beta2 ~ dnorm(0, 1e-6)
  beta3 ~ dnorm(0, 1e-6)
  sigma ~ dunif(0, 10)
  tau <- 1 / (sigma * sigma)

  # Likelihood
  for (i in 1:n) {
    centroide[i] ~ dnorm(mu[i], tau)
    mu[i] <- beta0 + beta1 * vv[i] + beta2 * sp[i] +
              beta3 * sp[i] * vv[i]
  }
}
```



```

",fill = TRUE)

##
## model {
##
##   # Priors
##   beta0 ~ dnorm(0, 1e-6)
##   beta1 ~ dnorm(0, 1e-6)
##   beta2 ~ dnorm(0, 1e-6)
##   beta3 ~ dnorm(0, 1e-6)
##   sigma ~ dunif(0, 10)
##   tau <- 1 / (sigma * sigma)
##
##   # Likelihood
##   for (i in 1:n) {
##     centroide[i] ~ dnorm(mu[i], tau)
##     mu[i] <- beta0 + beta1 * vv[i] + beta2 * sp[i] +
##       beta3 * sp[i] * vv[i]
##   }
## }

sink()

#valores iniciales
inits <- function() list(beta0 = runif(1, -2, 2), beta1 = runif(1, -3, 3),
  beta2 = runif(1, -3, 3), beta3 = runif(1, -3, 3))

# Parametros monitoreados
params <- c("beta0", "beta1", "beta2", "beta3")

# MCMC settings
ni <- 10000
nt <- 2
nb <- 1000
nc <- 3

# Call JAGS from R (BRT < 1 min)
#out_FIJOS <- jags(data = win.data, inits = inits, parameters.to.save = params,
#  model.file = "GLM_normal_FIJO.jags", n.chains = nc, n.thin = nt,
#  n.iter = ni, n.burnin = nb)

load("~/Documentos/TRABAJO/Curso Ocupacion Mendoza/out_FIJOS")
out_FIJOS

## JAGS output for model 'GLM_normal_FIJO.jags', generated by jagsUI.
## Estimates based on 3 chains of 10000 iterations,
## adaptation = 100 iterations (sufficient),
## burn-in = 1000 iterations and thin rate = 2,
## yielding 13500 total samples from the joint posterior.
## MCMC ran for 0.012 minutes at time 2023-04-02 12:06:53.
##
##           mean      sd    2.5%    50%    97.5% overlap0      f Rhat n.eff

```

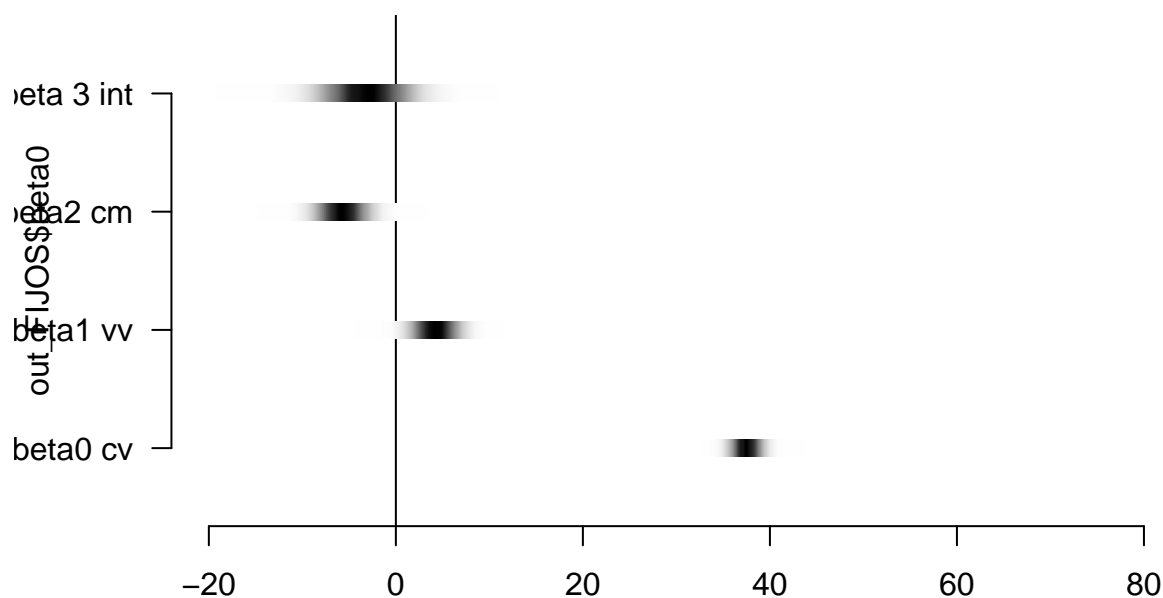
```

## beta0      37.524 1.131 35.304 37.514 39.734 FALSE 1.000 1 13500
## beta1      4.231 1.640 1.002 4.231 7.473 FALSE 0.995 1 13500
## beta2     -5.730 1.798 -9.278 -5.736 -2.162 FALSE 0.999 1 13500
## beta3     -3.176 3.066 -9.202 -3.168 2.788 TRUE 0.849 1 13500
## deviance 385.354 3.270 380.990 384.728 393.309 FALSE 1.000 1 13500
##
## Successful convergence based on Rhat values (all < 1.1).
## Rhat is the potential scale reduction factor (at convergence, Rhat=1).
## For each parameter, n.eff is a crude measure of effective sample size.
##
## overlap0 checks if 0 falls in the parameter's 95% credible interval.
## f is the proportion of the posterior with the same sign as the mean;
## i.e., our confidence that the parameter is positive or negative.
##
## DIC info: (pD = var(deviance)/2)
## pD = 5.3 and DIC = 390.702
## DIC is an estimate of expected predictive error (lower is better).

library("denstrip")
plot(out_FIJOS$beta0, xlim = c(-20,80), ylim = c(0.5,4.5), xlab="", type = "n",
     axes = F, main = " Fijos Especies")
axis(1)
axis(2, at=1:4, labels = c("beta0 cv", "beta1 vv", "beta2 cm", "beta 3 int"),
     las=1)
abline(v=0)
for(k in 1:5){
  denstrip(unlist(out_FIJOS$sims.list[k]), at = k)
}

```

## Fijos Especies



```
#Plot lineas
vv.pred <- seq(min(data$vv),max(data$vv),length.out = 500)

cv_FIJO <- array(NA, 500)
for(i in 1:500){
  cv_FIJO[i] <- out_FIJOS$mean$beta0 + out_FIJOS$mean$beta1 * vv.pred[i] +
    out_FIJOS$mean$beta2 * 0 + out_FIJOS$mean$beta3 * vv.pred[i] * 0
}

cm_FIJO <- array(NA, 500)
for(i in 1:500){
  cm_FIJO[i] <- out_FIJOS$mean$beta0 + out_FIJOS$mean$beta1 * vv.pred[i] +
    out_FIJOS$mean$beta2 * 1 + out_FIJOS$mean$beta3 * vv.pred[i] * 1
}

#Grafico
plot(data$vv[data$sp_fac==1],data$centroide[data$sp_fac==1],      #grafico primero solo venustus
      ylab= "Centroide",xlab = "Volumen vegetal",
      pch=16, bty="l", col = "darkred", ylim = c(0,50))

points(data$vv[data$sp_fac==2],data$centroide[data$sp_fac==2],    #grafico cm
        pch=16, bty="l", col = "darkorange")

lines(vv.pred,cv_FIJO, col= "darkred")
```

```
lines(vv.pred,cm_FIJ0, col = "darkorange")
```

