

MCMCglmm Diagnostics – Brown Treesnake (*Boiga irregularis*) Heritability

Overview

This R notebook details the testing of two different priors in variance component estimation for 3 traits important to Brown Treesnake control and reproduction: **body condition (BCI)**, **snout-vent length (SVL)**, and **trappability**. Refer to Levine *et al.* (2019) for details regarding this data set. The pedigree includes 73 dummy individuals.

The two different sets of priors tested are:

Prior 1: Phenotypic variation split evenly between additive genetic, individual permanent environment, and residual variance components with a low degree of belief ($n = 0.2$).

Prior 1 was specified with the code: `list(G = list(G1 = list(V = matrix(p.var/3), nu = 0.2), G2 = list(V = matrix(p.var/3), nu = 0.2)), R = list(V = matrix(p.var/3, nu = 0.2))`

Prior 2: 95% of phenotypic variance is due to the additive genetic effect, with the remaining 5% of phenotypic variance due evenly to individual permanent environment (2.5%) and residual (2.5%) effects, with a low degree of belief ($n = 0.2$).

Prior 2 was specified with the code: `list(G = list(G1 = list(V = matrix(p.var x 0.95), nu = 0.2), G2 = list(V = matrix(p.var x 0.025), nu = 0.2), R = list(V = matrix(p.var x 0.025), nu = 0.2))`

For both priors, `p.var` = phenotypic variance of the trait as estimated from the data.

Note: The priors were tested for each trait, denoted by 1 or 2. For example, BCI1 is the model for BCI tested with prior 1, BCI2 is the model for BCI tested with prior 2.

1. MCMCglmm Diagnostics for Body Condition–

BCI1

```
#Load the MCMCglmm package
library(MCMCglmm)
```

```
## Warning: package 'MCMCglmm' was built under R version 3.5.3
```

```
## Loading required package: Matrix
```

```
## Loading required package: coda
```

```
## Warning: package 'coda' was built under R version 3.5.3
```

```
## Loading required package: ape
```

```

## Warning: package 'ape' was built under R version 3.5.3

#Load R output
load("BCI_1_dummy_SVLfilt.RData")

#set the dimensions for the graphics
par(mar=c(1,1,1,1))

#view model
summary(model_BCI1)

##
## Iterations = 50001:4998501
## Thinning interval = 1500
## Sample size = 3300
##
## DIC: -304.1445
##
## G-structure: ~animal
##
##      post.mean 1-95% CI u-95% CI eff.samp
## animal  0.005672 0.002244 0.009338      3300
##
##      ~ID
##
##      post.mean 1-95% CI u-95% CI eff.samp
## ID  0.002982 0.0003669 0.006497      3300
##
## R-structure: ~units
##
##      post.mean 1-95% CI u-95% CI eff.samp
## units  0.03236 0.02829 0.03684      3300
##
## Location effects: BCI_RESID ~ SEX
##
##      post.mean 1-95% CI u-95% CI eff.samp pMCMC
## (Intercept)  0.053537 0.025489 0.083280      3297 0.000606 ***
## SEXM        -0.006297 -0.038441 0.029803      3300 0.719394
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#view priors for model
prior_BCI1

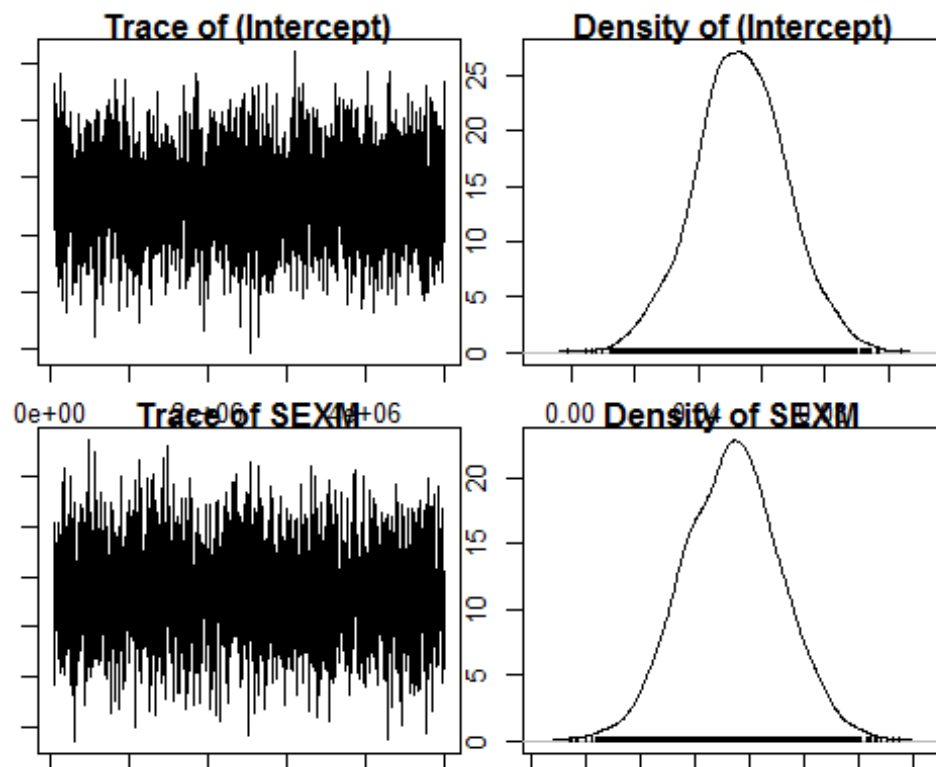
## $G
## $G$G1
## $G$G1$V
##      [,1]
## [1,] 0.01367784
##
## $G$G1$nu

```

```
## [1] 0.2
##
##
## $$G2
## $$G2$V
##           [,1]
## [1,] 0.01367784
##
## $$G2$nu
## [1] 0.2
##
##
##
## $R
## $R$V
##           [,1]
## [1,] 0.01367784
##
## $R$nu
## [1] 0.2
```

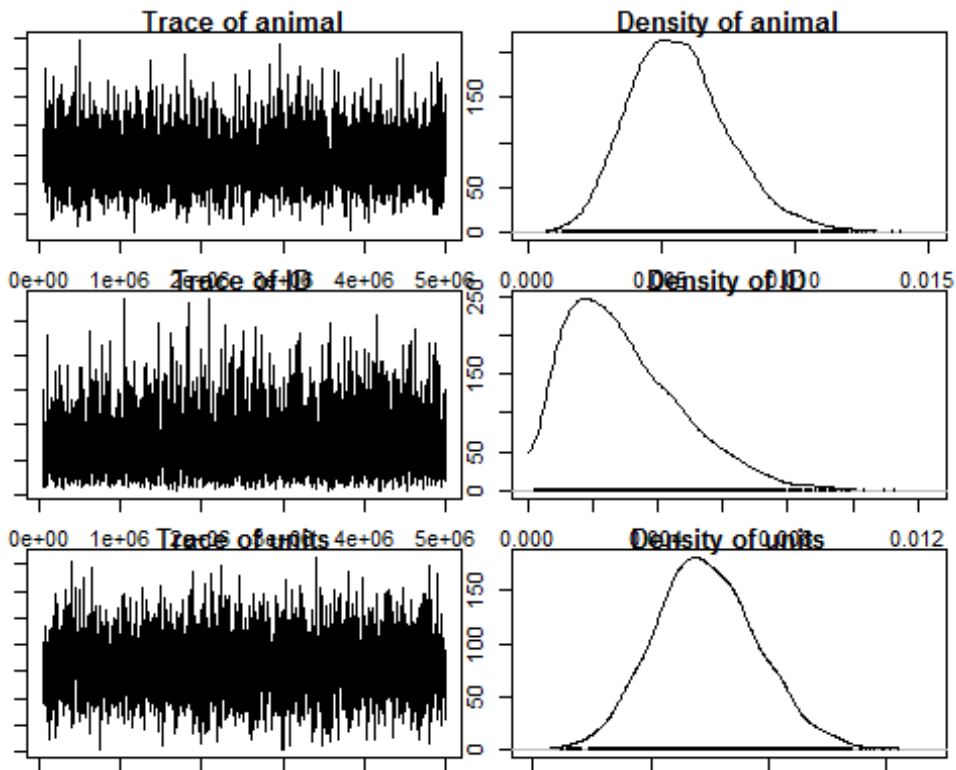
#view trace plots for fixed effects

```
plot(model_BCI1$Sol)
```



#view trace plots for random effects

```
plot(model_BCI1$VCV)
```



```
#view autocorrelation for fixed effects
```

```
autocorr.diag(model_BCI1$Sol)
```

```
##           (Intercept)           SEXM
## Lag 0      1.00000000    1.0000000000
## Lag 1500   -0.03290082    0.0003651446
## Lag 7500   -0.03194334    0.0091542745
## Lag 15000  -0.01925928   -0.0226177758
## Lag 75000   0.02213516   -0.0269244137
```

```
#view autocorrelation for random effects
```

```
autocorr.diag(model_BCI1$VCV)
```

```
##           animal           ID           units
## Lag 0      1.00000000    1.000000000    1.000000000
## Lag 1500    0.002039804    0.006102521   -0.001639099
## Lag 7500   -0.001173542    0.007721046   -0.030410453
## Lag 15000   0.020028539   -0.019526628   -0.007073601
## Lag 75000  -0.020191332    0.008865378   -0.001047085
```

```
#view effective size for fixed effects
```

```
effectiveSize(model_BCI1$Sol)
```

```
## (Intercept)           SEXM
##    3296.749      3300.000
```

```
#view effective size for random effects
```

```
effectiveSize(model_BCI1$VCV)
```

```

## animal      ID  units
##    3300    3300    3300

#test for convergence of fixed effect
heidel.diag(model_BCI1$Sol)

##
##           Stationarity start      p-value
##           test      iteration
## (Intercept) passed          1      0.259
## SEXM        passed          1      0.333
##
##           Halfwidth Mean      Halfwidth
##           test
## (Intercept) passed      0.0535 0.000493
## SEXM        passed      -0.0063 0.000601

#test for convergence of random effect
heidel.diag(model_BCI1$VCV)

##
##           Stationarity start      p-value
##           test      iteration
## animal passed          1      0.7665
## ID    passed          1      0.0939
## units passed          1      0.8480
##
##           Halfwidth Mean      Halfwidth
##           test
## animal passed      0.00567 6.35e-05
## ID    passed      0.00298 6.09e-05
## units passed      0.03236 7.48e-05

#view posterior mode of additive genetic variance
cat("Posterior Mode of Additive Genetic Variance for BCI1: ",
round(posterior.mode(model_BCI1$VCV[, "animal"]), digits = 3))

## Posterior Mode of Additive Genetic Variance for BCI1:  0.005

#view posterior mode of individual
cat("Posterior Mode of Individual Variance for BCI1: ",
round(posterior.mode(model_BCI1$VCV[, "ID"]), digits = 3))

## Posterior Mode of Individual Variance for BCI1:  0.002

#calculate heritability
herit <- model_BCI1$VCV[, "animal"]/(model_BCI1$VCV[, "animal"] +
model_BCI1$VCV[, "ID"] + model_BCI1$VCV[, "units"] )

#view posterior mode of heritability
cat("Posterior Mode of Heritability for BCI1: ",round(posterior.mode(herit),
digits = 3) )

```

```
## Posterior Mode of Heritability for BCI1: 0.149

#calculate repeatability
repeatability <- (model_BCI1$VCV[, "animal"] + model_BCI1$VCV[,
"ID"])/(model_BCI1$VCV[, "animal"] + model_BCI1$VCV[, "ID"] +
model_BCI1$VCV[, "units"])

#view posterior mode of repeatability
cat("Posterior Mode of Repeatability for BCI1:
",round(posterior.mode(repeatability), digits = 3) )

## Posterior Mode of Repeatability for BCI1: 0.199
```

BCI2

```
#clear memory
rm(list=ls())

#Load R output
load("BCI_2_dummy_SVLfilt.RData")

#set the dimensions for the graphics
par(mar=c(1,1,1,1))

#view model
summary(model_BCI2)

##
## Iterations = 50001:4998501
## Thinning interval = 1500
## Sample size = 3300
##
## DIC: -301.4652
##
## G-structure: ~animal
##
##          post.mean 1-95% CI u-95% CI eff.samp
## animal  0.006519 0.002956 0.01019      3300
##
##          ~ID
##
##          post.mean 1-95% CI u-95% CI eff.samp
## ID  0.001595 2.448e-05 0.004984      3300
##
## R-structure: ~units
##
##          post.mean 1-95% CI u-95% CI eff.samp
## units  0.03295 0.02857 0.03716      3300
##
## Location effects: BCI_RESID ~ SEX
##
```

```
##               post.mean l-95% CI u-95% CI eff.samp  pMCMC
## (Intercept)    0.05398  0.02199  0.08106      3300 <3e-04 ***
## SEXM          -0.00605 -0.04041  0.02821      3300  0.731
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

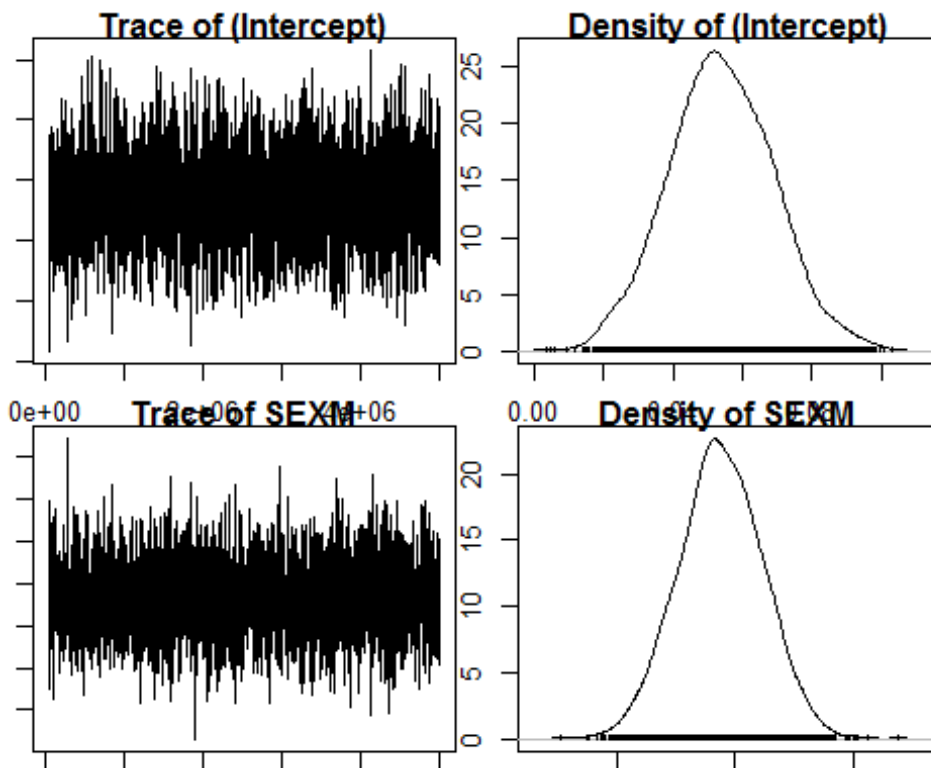
#view priors for model

prior_BCI2

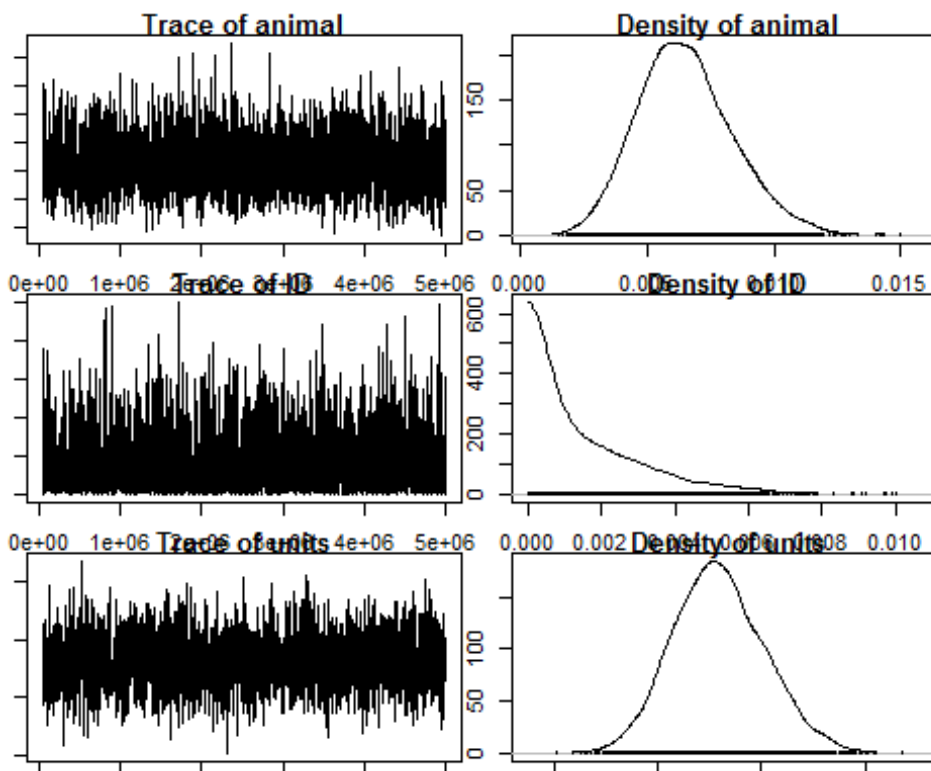
```
## $G
## $G$G1
## $G$G1$V
##               [,1]
## [1,] 0.03898185
##
## $G$G1$nu
## [1] 0.2
##
##
## $G$G2
## $G$G2$V
##               [,1]
## [1,] 0.001025838
##
## $G$G2$nu
## [1] 0.2
##
##
## $R
## $R$V
##               [,1]
## [1,] 0.001025838
##
## $R$nu
## [1] 0.2
```

#view trace plots for fixed effects

`plot(model_BCI2$Sol)`



```
#view trace plots for random effects  
plot(model_BCI2$VCV)
```



#view autocorrelation for fixed effects

autocorr.diag(model_BCI2\$Sol)

```
##           (Intercept)          SEXM
## Lag 0      1.000000000  1.000000000
## Lag 1500  -0.004308741 -0.012108522
## Lag 7500   0.008944336  0.001401384
## Lag 15000  0.019388076 -0.010357421
## Lag 75000 -0.016585553 -0.014811226
```

#view autocorrelation for random effects

autocorr.diag(model_BCI2\$VCV)

```
##           animal          ID          units
## Lag 0      1.000000000  1.000000000  1.000000000
## Lag 1500  -0.006349962 -0.016394251 -0.006436313
## Lag 7500  -0.026043594  0.030647520 -0.012713372
## Lag 15000 -0.001848260 -0.001574878  0.039654520
## Lag 75000 -0.008658645 -0.018375578 -0.021456516
```

#view effective size for fixed effects

effectiveSize(model_BCI2\$Sol)

```
## (Intercept)          SEXM
##          3300          3300
```

#view effective size for random effects

effectiveSize(model_BCI2\$VCV)

```
## animal    ID    units
##   3300    3300    3300
```

#test for convergence of fixed effect

heidel.diag(model_BCI2\$Sol)

```
##
##           Stationarity start      p-value
##           test      iteration
## (Intercept) passed          1      0.624
## SEXM        passed          1      0.872
##
##           Halfwidth Mean      Halfwidth
##           test
## (Intercept) passed    0.05399 0.000512
## SEXM        passed    -0.00605 0.000603
```

#test for convergence of random effect

heidel.diag(model_BCI2\$VCV)

```
##
##           Stationarity start      p-value
##           test      iteration
```

```

## animal passed      1      0.800
## ID      passed      1      0.870
## units   passed      1      0.788
##
##      Halfwidth Mean      Halfwidth
##      test
## animal passed      0.00652 6.44e-05
## ID      passed      0.00160 5.47e-05
## units   passed      0.03295 7.52e-05

#view posterior mode of additive genetic variance
cat("Posterior Mode of Additive Genetic Variance for BCI2: ",
round(posterior.mode(model_BCI2$VCV[, "animal"]), digits = 3))

## Posterior Mode of Additive Genetic Variance for BCI2:  0.006

#view posterior mode of individual
cat("Posterior Mode of Individual Variance for BCI2: ",
round(posterior.mode(model_BCI2$VCV[, "ID"]), digits = 3))

## Posterior Mode of Individual Variance for BCI2:  0

#calculate heritability
herit <- model_BCI2$VCV[, "animal"]/(model_BCI2$VCV[, "animal"] +
model_BCI2$VCV[, "ID"] + model_BCI2$VCV[, "units"] )

#view posterior mode of heritability
cat("Posterior Mode of Heritability for BCI2: ",round(posterior.mode(herit),
digits = 3) )

## Posterior Mode of Heritability for BCI2:  0.148

#calculate repeatability
repeatability <- (model_BCI2$VCV[, "animal"] + model_BCI2$VCV[,
"ID"])/(model_BCI2$VCV[, "animal"] + model_BCI2$VCV[, "ID"] +
model_BCI2$VCV[, "units"])

#view posterior mode of repeatability
cat("Posterior Mode of Repeatability for BCI2:
",round(posterior.mode(repeatability), digits = 3) )

## Posterior Mode of Repeatability for BCI2:  0.196

```

2. MCMCglmm Diagnostics for Snout-Vent Length–

SVL1

```

#clear memory
rm(list=ls())

#Load R output

```

```

load("SVL_1_dummy_SVLfilt.RData")

#set the dimensions for the graphics
par(mar=c(1,1,1,1))

#view model
summary(model_SVL1)

##
## Iterations = 50001:4998501
## Thinning interval = 1500
## Sample size = 3300
##
## DIC: 8069.45
##
## G-structure: ~animal
##
##      post.mean l-95% CI u-95% CI eff.samp
## animal      341.9    65.44    711.4      3300
##
##      ~ID
##
##      post.mean l-95% CI u-95% CI eff.samp
## ID          612.4    101.4    1235      3300
##
## R-structure: ~units
##
##      post.mean l-95% CI u-95% CI eff.samp
## units        7754     6753     8681      3300
##
## Location effects: SVL ~ SEX
##
##      post.mean l-95% CI u-95% CI eff.samp pMCMC
## (Intercept)  1035.04  1023.22  1045.43     3300 <3e-04 ***
## SEXM          87.72    72.00   102.13     3300 <3e-04 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

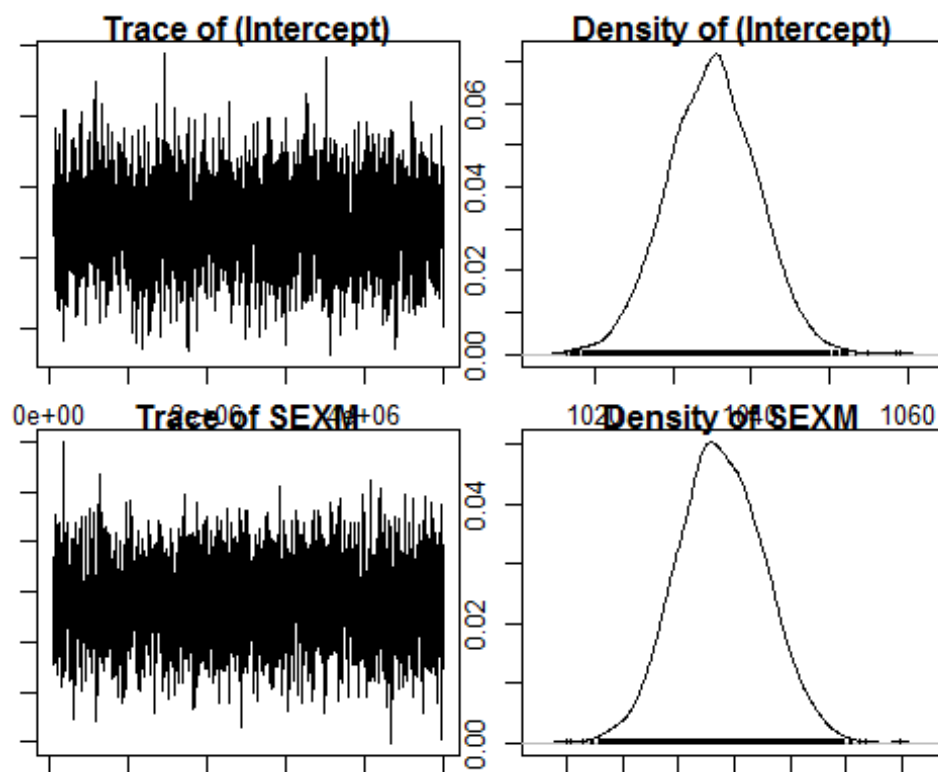
#view priors for model
prior_SVL1

## $G
## $G$G1
## $G$G1$V
##      [,1]
## [1,] 3539.991
##
## $G$G1$nu
## [1] 0.2
##

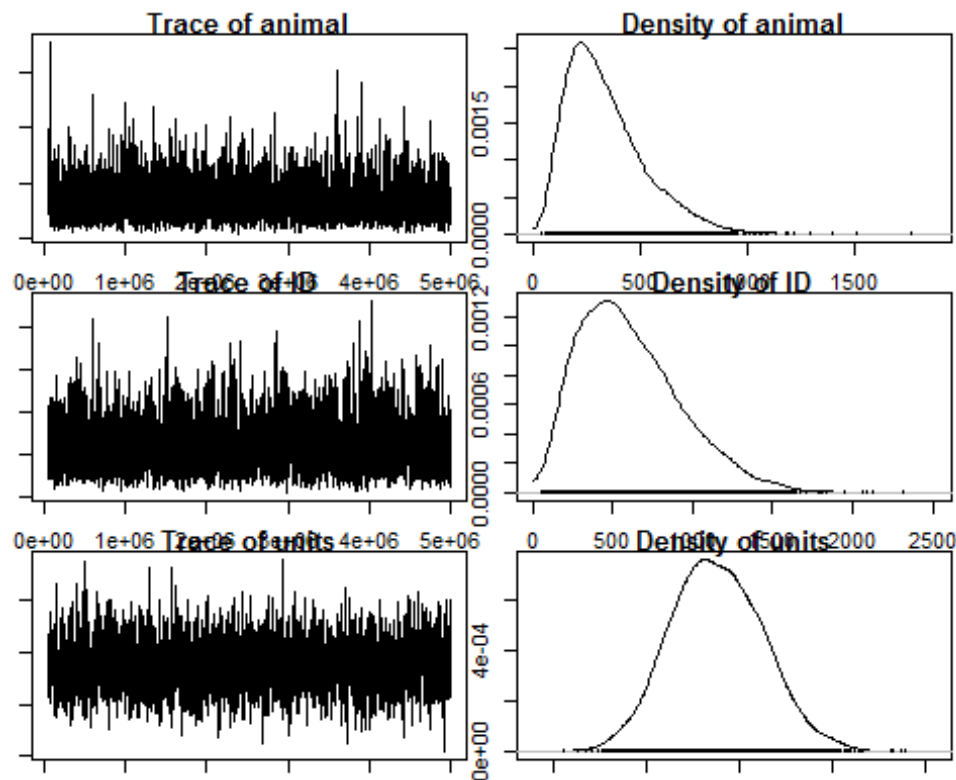
```

```
##
## $G$G2
## $G$G2$V
##           [,1]
## [1,] 3539.991
##
## $G$G2$nu
## [1] 0.2
##
##
##
## $R
## $R$V
##           [,1]
## [1,] 3539.991
##
## $R$nu
## [1] 0.2
```

```
#view trace plots for fixed effects
plot(model_SVL1$Sol)
```



```
#view trace plots for random effects
plot(model_SVL1$VCV)
```



```
#view autocorrelation for fixed effects
```

```
autocorr.diag(model_SVL1$Sol)
```

```
##           (Intercept)           SEXM
## Lag 0      1.000000000  1.000000000
## Lag 1500   -0.016310082 -0.019815426
## Lag 7500    0.004795029 -0.016456874
## Lag 15000  -0.016647473 -0.016732502
## Lag 75000  -0.045005561 -0.007054787
```

```
#view autocorrelation for random effects
```

```
autocorr.diag(model_SVL1$VCV)
```

```
##           animal           ID           units
## Lag 0      1.000000000  1.000000000  1.000000000
## Lag 1500   -0.004951634 -0.008411056 -0.014937623
## Lag 7500    0.014279997  0.011693135 -0.005422837
## Lag 15000  -0.020267796  0.021555351 -0.008038002
## Lag 75000  0.008240858 -0.014221616 -0.024686799
```

```
#view effective size for fixed effects
```

```
effectiveSize(model_SVL1$Sol)
```

```
## (Intercept)           SEXM
##           3300           3300
```

```
#view effective size for random effects
```

```
effectiveSize(model_SVL1$VCV)
```

```

## animal      ID  units
##   3300    3300   3300

#test for convergence of fixed effect
heidel.diag(model_SVL1$Sol)

##
##           Stationarity start      p-value
##           test      iteration
## (Intercept) passed          1      0.980
## SEXM        passed          1      0.877
##
##           Halfwidth Mean  Halfwidth
##           test
## (Intercept) passed    1035.0 0.194
## SEXM        passed      87.7 0.265

#test for convergence of random effect
heidel.diag(model_SVL1$VCV)

##
##           Stationarity start      p-value
##           test      iteration
## animal passed          991      0.1010
## ID      passed           1      0.0779
## units   passed           1      0.7196
##
##           Halfwidth Mean Halfwidth
##           test
## animal passed          338  7.49
## ID      passed          612 10.92
## units   passed       7754 17.02

#view posterior mode of additive genetic variance
cat("Posterior Mode of Additive Genetic Variance for SVL1: ",
round(posterior.mode(model_SVL1$VCV[, "animal"]), digits = 3))

## Posterior Mode of Additive Genetic Variance for SVL1:  205.318

#view posterior mode of individual
cat("Posterior Mode of Individual Variance for SVL1: ",
round(posterior.mode(model_SVL1$VCV[, "ID"]), digits = 3))

## Posterior Mode of Individual Variance for SVL1:  482.074

#calculate heritability
herit <- model_SVL1$VCV[, "animal"]/(model_SVL1$VCV[, "animal"] +
model_SVL1$VCV[, "ID"] + model_SVL1$VCV[, "units"] )

#view posterior mode of heritability
cat("Posterior Mode of Heritability for SVL1: ",round(posterior.mode(herit),
digits = 3) )

```

```
## Posterior Mode of Heritability for SVL1: 0.025

#calculate repeatability
repeatability <- (model_SVL1$VCV[, "animal"] + model_SVL1$VCV[,
"ID"])/(model_SVL1$VCV[, "animal"] + model_SVL1$VCV[, "ID"] +
model_SVL1$VCV[, "units"])

#view posterior mode of repeatability
cat("Posterior Mode of Repeatability for SVL1:
",round(posterior.mode(repeatability), digits = 3) )

## Posterior Mode of Repeatability for SVL1: 0.111
```

SVL2

```
#clear memory
rm(list=ls())

#Load R output
load("SVL_2_dummy_SVLfilt.RData")

#set the dimensions for the graphics
par(mar=c(1,1,1,1))

#view model
summary(model_SVL2)

##
## Iterations = 50001:4998501
## Thinning interval = 1500
## Sample size = 3300
##
## DIC: 8073.027
##
## G-structure: ~animal
##
##      post.mean 1-95% CI u-95% CI eff.samp
## animal      537.6   180.2   977.9     3641
##
##      ~ID
##
##      post.mean 1-95% CI u-95% CI eff.samp
## ID          312.9    3.941    892.9     3300
##
## R-structure: ~units
##
##      post.mean 1-95% CI u-95% CI eff.samp
## units        7893    6891    8881     3300
##
## Location effects: SVL ~ SEX
##
```

```
##               post.mean l-95% CI u-95% CI eff.samp  pMCMC
## (Intercept)   1036.12  1024.08  1047.24     3300 <3e-04 ***
## SEXM          87.77   72.85   102.42     3300 <3e-04 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

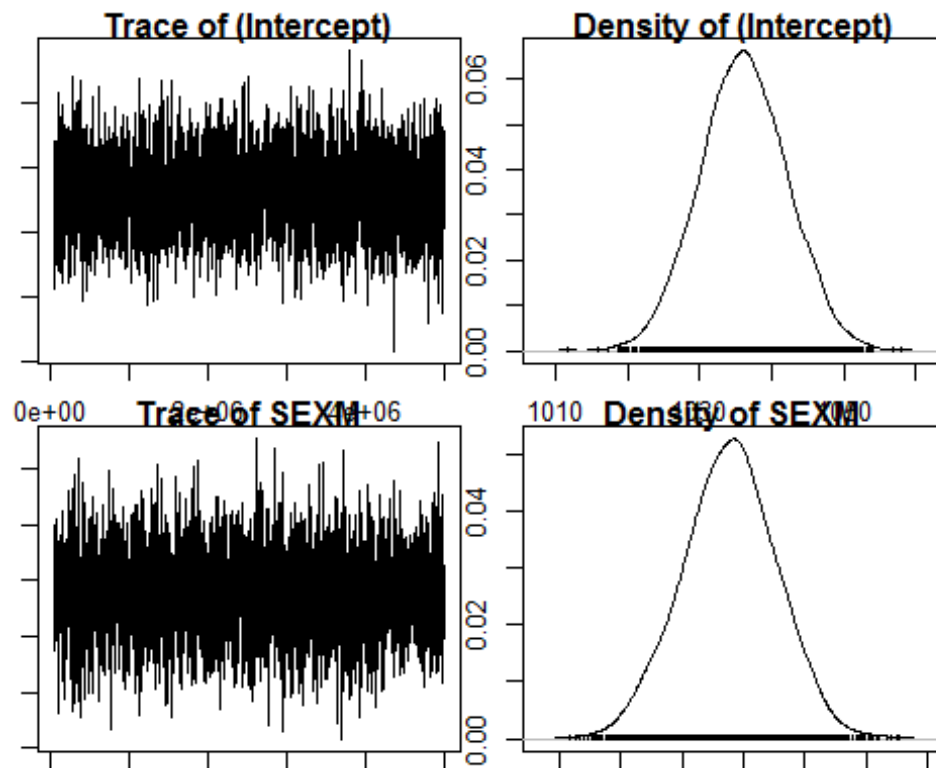
#view priors for model

prior_SVL2

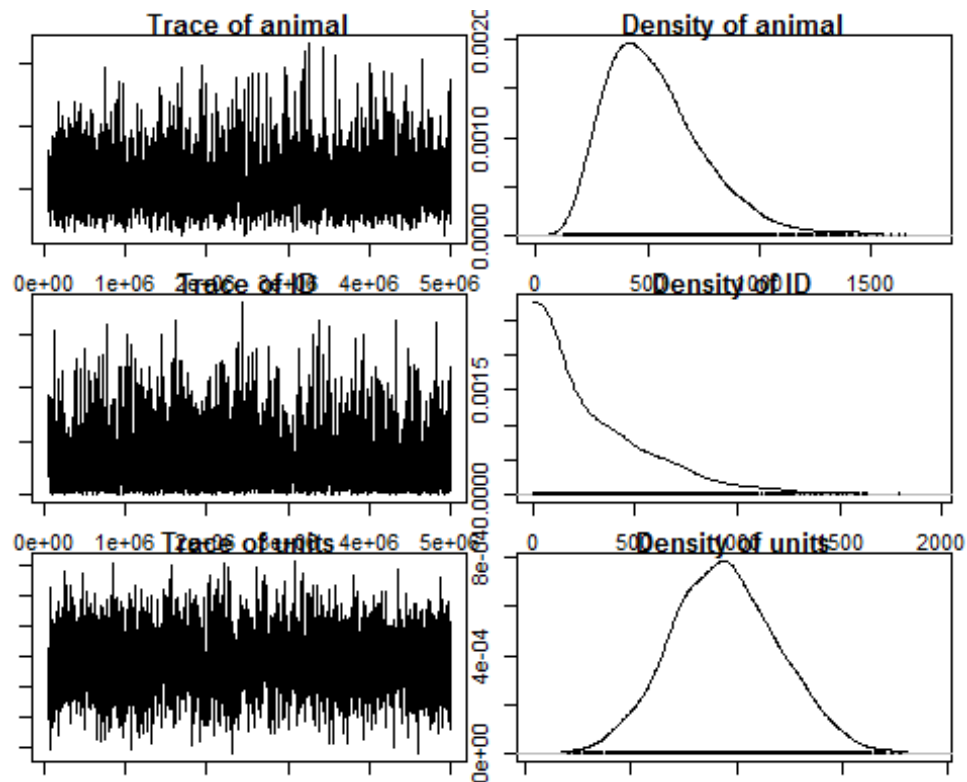
```
## $G
## $G$G1
## $G$G1$V
##           [,1]
## [1,] 10088.97
##
## $G$G1$nu
## [1] 0.2
##
##
## $G$G2
## $G$G2$V
##           [,1]
## [1,] 265.4993
##
## $G$G2$nu
## [1] 0.2
##
##
## $R
## $R$V
##           [,1]
## [1,] 265.4993
##
## $R$nu
## [1] 0.2
```

#view trace plots for fixed effects

`plot(model_SVL2$Sol)`



```
#view trace plots for random effects
plot(model_SVL2$VCV)
```



```
#view autocorrelation for fixed effects
```

```
autocorr.diag(model_SVL2$Sol)
```

```
##           (Intercept)           SEXM
## Lag 0      1.00000000  1.000000000
## Lag 1500   -0.01181699  0.002645437
## Lag 7500   -0.03289124 -0.024830585
## Lag 15000  0.00170318 -0.028144786
## Lag 75000  0.01415656  0.017411129
```

```
#view autocorrelation for random effects
```

```
autocorr.diag(model_SVL2$VCV)
```

```
##           animal           ID           units
## Lag 0      1.000000000  1.000000000  1.000000000
## Lag 1500   -0.0142236976 -0.004284348  0.0175379601
## Lag 7500   -0.0002975608 -0.016866471  0.0001140294
## Lag 15000  0.0040908111  0.002287870  0.0111063677
## Lag 75000  0.0111461571  0.015645928  0.0036216598
```

```
#view effective size for fixed effects
```

```
effectiveSize(model_SVL2$Sol)
```

```
## (Intercept)           SEXM
##           3300           3300
```

```
#view effective size for random effects
```

```
effectiveSize(model_SVL2$VCV)
```

```
## animal           ID           units
## 3640.553 3300.000 3300.000
```

```
#test for convergence of fixed effect
```

```
heidel.diag(model_SVL2$Sol)
```

```
##
##           Stationarity start      p-value
##           test      iteration
## (Intercept) passed          1      0.0986
## SEXM         passed          1      0.2515
##
##           Halfwidth Mean      Halfwidth
##           test
## (Intercept) passed    1036.1 0.205
## SEXM         passed      87.8 0.262
```

```
#test for convergence of random effect
```

```
heidel.diag(model_SVL2$VCV)
```

```
##
##           Stationarity start      p-value
##           test      iteration
```

```

## animal passed      1      0.203
## ID      passed      1      0.213
## units   passed      1      0.131
##
##      Halfwidth Mean Halfwidth
##      test
## animal passed      538  7.36
## ID      passed      313  9.91
## units   passed     7893 17.33

#view posterior mode of additive genetic variance
cat("Posterior Mode of Additive Genetic Variance for SVL2: ",
round(posterior.mode(model_SVL2$VCV[, "animal"]), digits = 3))

## Posterior Mode of Additive Genetic Variance for SVL2:  400.947

#view posterior mode of individual
cat("Posterior Mode of Individual Variance for SVL2: ",
round(posterior.mode(model_SVL2$VCV[, "ID"]), digits = 3))

## Posterior Mode of Individual Variance for SVL2:  31.753

#calculate heritability
herit <- model_SVL2$VCV[, "animal"]/(model_SVL2$VCV[, "animal"] +
model_SVL2$VCV[, "ID"] + model_SVL2$VCV[, "units"] )

#view posterior mode of heritability
cat("Posterior Mode of Heritability for SVL2: ",round(posterior.mode(herit),
digits = 3) )

## Posterior Mode of Heritability for SVL2:  0.051

#calculate repeatability
repeatability <- (model_SVL2$VCV[, "animal"] + model_SVL2$VCV[,
"ID"])/(model_SVL2$VCV[, "animal"] + model_SVL2$VCV[, "ID"] +
model_SVL2$VCV[, "units"])

#view posterior mode of repeatability
cat("Posterior Mode of Repeatability for SVL2:
",round(posterior.mode(repeatability), digits = 3) )

## Posterior Mode of Repeatability for SVL2:  0.082

```

MCMCglimm Diagnostics for Trappability–

TRAP1

```

#clear memory
rm(list=ls())

#Load R output

```

```

load("TRAP_1_dummy_SVLfilt.RData")

#set the dimensions for the graphics
par(mar=c(1,1,1,1))

#view model
summary(model_TRAP1)

##
## Iterations = 50001:4998501
## Thinning interval = 1500
## Sample size = 3300
##
## DIC: 2159.104
##
## G-structure: ~animal
##
##      post.mean l-95% CI u-95% CI eff.samp
## animal      0.193  0.07385   0.3309     3300
##
##      ~ID
##
##      post.mean l-95% CI u-95% CI eff.samp
## ID      0.1769   0.0724   0.3031     3300
##
## R-structure: ~units
##
##      post.mean l-95% CI u-95% CI eff.samp
## units      2.457    1.987    2.977     3300
##
## Location effects: CAP_TRAP ~ SEX
##
##      post.mean l-95% CI u-95% CI eff.samp pMCMC
## (Intercept) -0.21619 -0.48208  0.05838     3300 0.117
## SEXM        0.11723 -0.21052  0.43140     3300 0.499

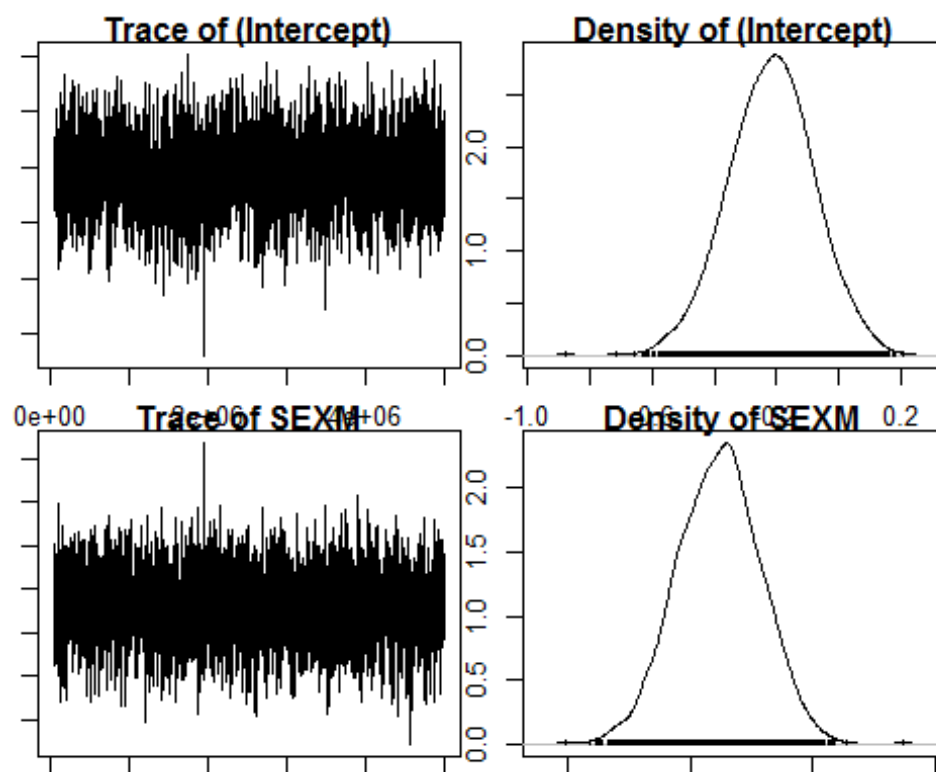
#view priors for model
prior_TRAP1

## $G
## $G$G1
## $G$G1$V
##      [,1]
## [1,] 5.92045
##
## $G$G1$nu
## [1] 0.2
##
##
## $G$G2

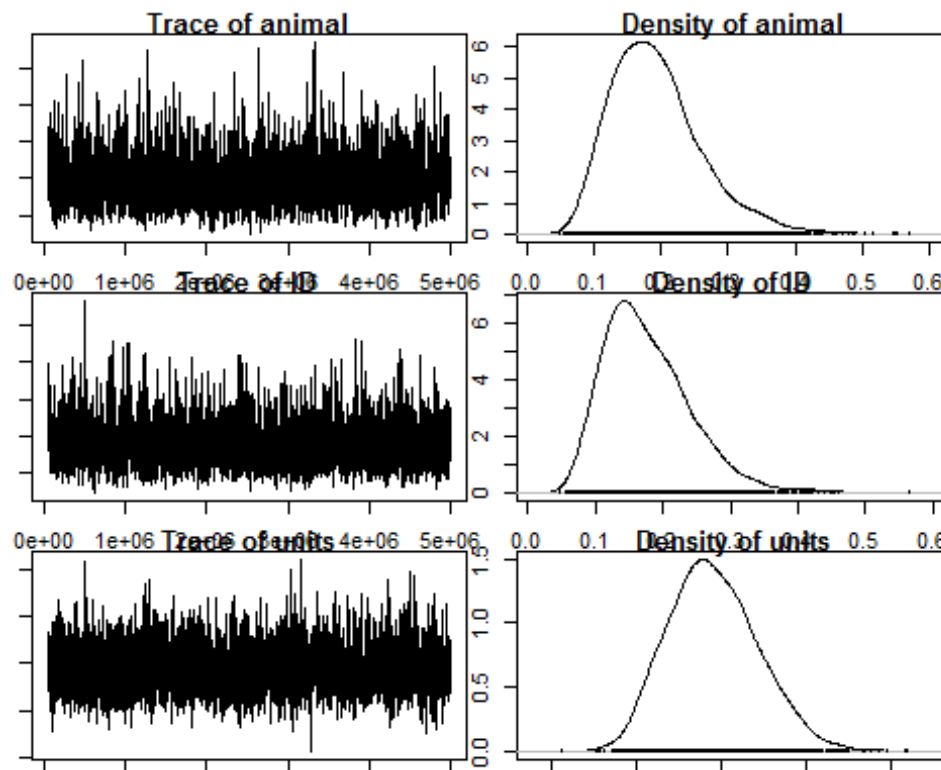
```

```
## $G$G2$V
##      [,1]
## [1,] 5.92045
##
## $G$G2$nu
## [1] 0.2
##
##
##
## $R
## $R$V
##      [,1]
## [1,] 5.92045
##
## $R$nu
## [1] 0.2
```

```
#view trace plots for fixed effects
plot(model_TRAP1$Sol)
```



```
#view trace plots for random effects
plot(model_TRAP1$VCV)
```



```
#view autocorrelation for fixed effects
```

```
autocorr.diag(model_TRAP1$Sol)
```

```
##           (Intercept)           SEXM
## Lag 0      1.00000000    1.00000000
## Lag 1500   0.01112254    0.005532726
## Lag 7500  -0.02847046   -0.043540528
## Lag 15000 -0.04377388    0.003187301
## Lag 75000 -0.06104991   -0.047947949
```

```
#view autocorrelation for random effects
```

```
autocorr.diag(model_TRAP1$VCV)
```

```
##           animal           ID           units
## Lag 0      1.00000000    1.00000000    1.00000000
## Lag 1500   -0.003488810  -0.018248547  0.017829918
## Lag 7500   -0.006346560  0.027665238  0.015389604
## Lag 15000  0.019178360  -0.008617812  -0.007518905
## Lag 75000  -0.006153974  0.007226693  0.029046824
```

```
#view effective size for fixed effects
```

```
effectiveSize(model_TRAP1$Sol)
```

```
## (Intercept)           SEXM
##           3300           3300
```

```
#view effective size for random effects
```

```
effectiveSize(model_TRAP1$VCV)
```

```

## animal      ID  units
##   3300    3300   3300

#test for convergence of fixed effect
heidel.diag(model_TRAP1$Sol)

##
##           Stationarity start      p-value
##           test      iteration
## (Intercept) passed          1      0.203
## SEXM        passed          1      0.905
##
##           Halfwidth Mean   Halfwidth
##           test
## (Intercept) passed    -0.216 0.00468
## SEXM        passed     0.117 0.00574

#test for convergence of random effect
heidel.diag(model_TRAP1$VCV)

##
##           Stationarity start      p-value
##           test      iteration
## animal passed          1      0.223
## ID      passed          1      0.437
## units   passed          1      0.768
##
##           Halfwidth Mean   Halfwidth
##           test
## animal passed     0.193 0.00237
## ID      passed     0.177 0.00221
## units   passed     2.457 0.00901

#view posterior mode of additive genetic variance
cat("Posterior Mode of Additive Genetic Variance for TRAP1: ",
round(posterior.mode(model_TRAP1$VCV[, "animal"]), digits = 3))

## Posterior Mode of Additive Genetic Variance for TRAP1:  0.16

#view posterior mode of individual
cat("Posterior Mode of Individual Variance for TRAP1: ",
round(posterior.mode(model_TRAP1$VCV[, "ID"]), digits = 3))

## Posterior Mode of Individual Variance for TRAP1:  0.125

#calculate heritability
herit <- model_TRAP1$VCV[, "animal"]/(model_TRAP1$VCV[, "animal"] +
model_TRAP1$VCV[, "ID"] + model_TRAP1$VCV[, "units"] )

#view posterior mode of heritability
cat("Posterior Mode of Heritability for TRAP1: ",round(posterior.mode(herit),
digits = 3) )

```

```
## Posterior Mode of Heritability for TRAP1: 0.066

#calculate repeatability
repeatability <- (model_TRAP1$VCV[, "animal"] + model_TRAP1$VCV[,
"ID"])/(model_TRAP1$VCV[, "animal"] + model_TRAP1$VCV[, "ID"] +
model_TRAP1$VCV[, "units"])

#view posterior mode of repeatability
cat("Posterior Mode of Repeatability for TRAP1:
",round(posterior.mode(repeatability), digits = 3) )

## Posterior Mode of Repeatability for TRAP1: 0.134
```

TRAP2

```
#clear memory
rm(list=ls())

#Load R output
load("TRAP_2_dummy_SVLfilt.RData")

#set the dimensions for the graphics
par(mar=c(1,1,1,1))

#view model
summary(model_TRAP2)

##
## Iterations = 50001:4998501
## Thinning interval = 1500
## Sample size = 3300
##
## DIC: 2159.362
##
## G-structure: ~animal
##
##      post.mean 1-95% CI u-95% CI eff.samp
## animal    0.3055  0.1597  0.4694    3507
##
##      ~ID
##
##      post.mean 1-95% CI u-95% CI eff.samp
## ID    0.05532 0.008215  0.1339    3300
##
## R-structure: ~units
##
##      post.mean 1-95% CI u-95% CI eff.samp
## units    2.464   1.926   3.004    3300
##
## Location effects: CAP_TRAP ~ SEX
##
```



```
##               post.mean l-95% CI u-95% CI eff.samp pMCMC
## (Intercept)  -0.19584 -0.47698  0.06197    3300 0.158
## SEXM          0.11218 -0.23046  0.41713    3300 0.504
```

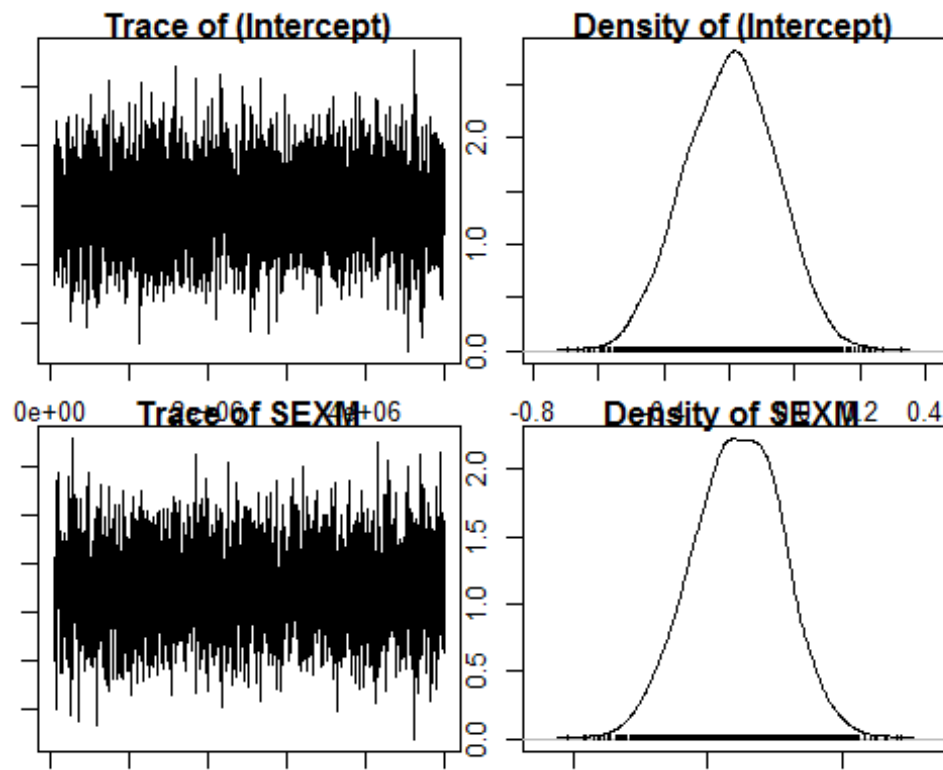
#view priors for model

prior_TRAP2

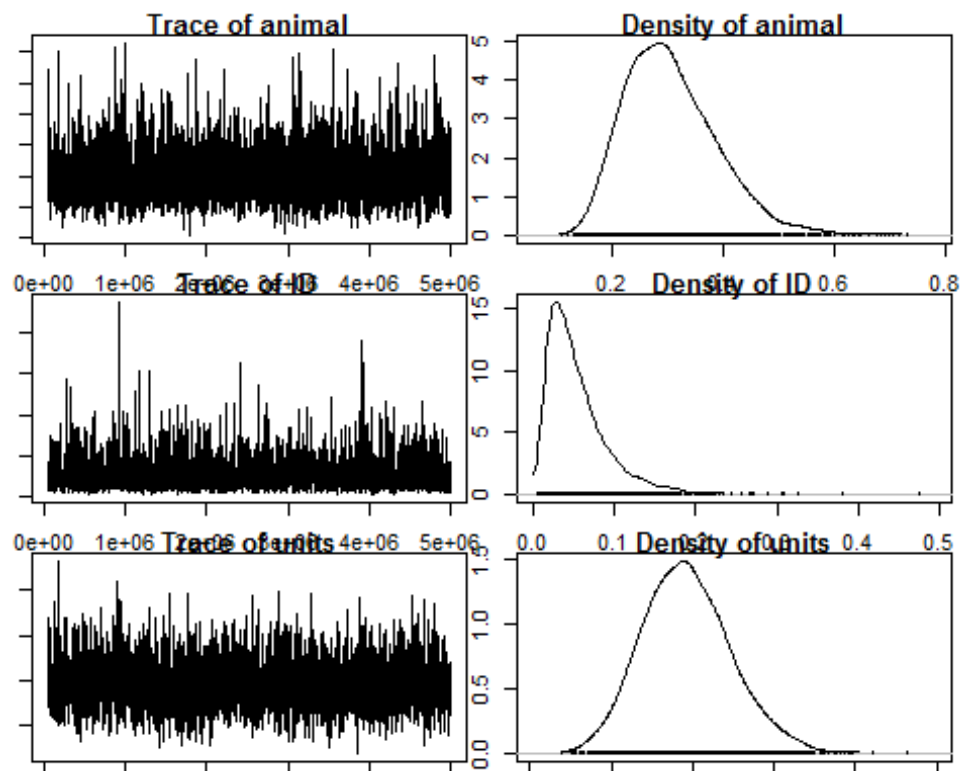
```
## $G
## $G$G1
## $G$G1$V
##           [,1]
## [1,] 16.87328
##
## $G$G1$nu
## [1] 0.2
##
##
## $G$G2
## $G$G2$V
##           [,1]
## [1,] 0.4440337
##
## $G$G2$nu
## [1] 0.2
##
##
## $R
## $R$V
##           [,1]
## [1,] 0.4440337
##
## $R$nu
## [1] 0.2
```

#view trace plots for fixed effects

`plot(model_TRAP2$Sol)`



```
#view trace plots for random effects
plot(model_TRAP2$VCV)
```



```
#view autocorrelation for fixed effects  
autocorr.diag(model_TRAP2$Sol)
```

```
##           (Intercept)          SEXM  
## Lag 0      1.000000000  1.000000000  
## Lag 1500   0.010068480  0.004165354  
## Lag 7500  -0.038097024 -0.017190653  
## Lag 15000  0.014256603  0.005750643  
## Lag 75000  0.003492932  0.021863447
```

```
#view autocorrelation for random effects  
autocorr.diag(model_TRAP2$VCV)
```

```
##           animal          ID          units  
## Lag 0      1.000000000  1.000000000  1.000000000  
## Lag 1500  -0.030526700  0.008646778 -0.013070738  
## Lag 7500   0.006574773  0.039892683  0.002146123  
## Lag 15000 -0.004578583 -0.012785392 -0.032798759  
## Lag 75000 -0.011976996  0.010705617  0.018600812
```

```
#view effective size for fixed effects  
effectiveSize(model_TRAP2$Sol)
```

```
## (Intercept)          SEXM  
##          3300          3300
```

```
#view effective size for random effects  
effectiveSize(model_TRAP2$VCV)
```

```
## animal          ID          units  
## 3506.757 3300.000 3300.000
```

```
#test for convergence of fixed effect  
heidel.diag(model_TRAP2$Sol)
```

```
##  
##           Stationarity start      p-value  
##           test      iteration  
## (Intercept) passed          1      0.114  
## SEXM        passed          1      0.884  
##  
##           Halfwidth Mean  Halfwidth  
##           test  
## (Intercept) passed    -0.196 0.00476  
## SEXM        passed     0.112 0.00572
```

```
#test for convergence of random effect  
heidel.diag(model_TRAP2$VCV)
```

```
##  
##           Stationarity start      p-value  
##           test      iteration
```

```

## animal passed      1      0.318
## ID      passed      1      0.981
## units   passed      1      0.101
##
##      Halfwidth Mean   Halfwidth
##      test
## animal passed    0.3055 0.00283
## ID      passed    0.0553 0.00136
## units   passed    2.4640 0.00937

#view posterior mode of additive genetic variance
cat("Posterior Mode of Additive Genetic Variance for TRAP2: ",
round(posterior.mode(model_TRAP2$VCV[, "animal"]), digits = 3))

## Posterior Mode of Additive Genetic Variance for TRAP2:  0.284

#view posterior mode of individual
cat("Posterior Mode of Individual Variance for TRAP2: ",
round(posterior.mode(model_TRAP2$VCV[, "ID"]), digits = 3))

## Posterior Mode of Individual Variance for TRAP2:  0.026

#calculate heritability
herit <- model_TRAP2$VCV[, "animal"]/(model_TRAP2$VCV[, "animal"] +
model_TRAP2$VCV[, "ID"] + model_TRAP2$VCV[, "units" ])

#view posterior mode of heritability
cat("Posterior Mode of Heritability for TRAP2: ",round(posterior.mode(herit),
digits = 3) )

## Posterior Mode of Heritability for TRAP2:  0.119

#calculate repeatability
repeatability <- (model_TRAP2$VCV[, "animal"] + model_TRAP2$VCV[,
"ID"])/(model_TRAP2$VCV[, "animal"] + model_TRAP2$VCV[, "ID"] +
model_TRAP2$VCV[, "units"])

#view posterior mode of repeatability
cat("Posterior Mode of Repeatability for TRAP2:
",round(posterior.mode(repeatability), digits = 3) )

## Posterior Mode of Repeatability for TRAP2:  0.121

```

,