

MCMCglmm Significance Testing - Brown Treesnakes (*Boiga irregularis*)

Overview

This R notebook details significance testing of heritability and repeatability 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.

Based off of sensitivity analysis of priors, the priors used for all models assumes phenotypic variation is split evenly between additive genetic, individual permanent environment, and residual variance components with a low degree of belief ($\nu = 0.2$).

The prior 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))`.

`p.var` = phenotypic variance of the trait as estimated from the data.

Significance of heritability for each trait was tested by comparing the deviance information criteria for models containing the “animal” term versus those of models without the “animal” term. A lower DIC is indicative of the preferred model, while $\text{DIC} < 10$ are strong evidence of a preferred model (Martin and Festa-Bianchet 2012).

Differently, significance of repeatability for each trait was testing by comparing the deviance information criteria for models containing the “individual” term (but not the “animal” term; note: additive genetic variation is a part of individual variation) versus models without the “individual” term.

For reduced models, the prior is adjusted to split phenotypic variation evenly among the remaining variance components.

1. Significance Testing – Heritability

Body Condition (BCI) Heritability

```
#Load 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 model with "animal" term for BCI
load("BCI_1_dummy_SVLfilt.RData")

#view model to confirm it's correct
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 to confirm their correct
prior_BCI1

## $G
## $G$G1
## $G$G1$V
##      [,1]
## [1,] 0.01367784
##
## $G$G1$nu
## [1] 0.2

```

```

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

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

#HPD intervals for heritability
x <- HPDinterval(herit)

#cat heritability estimate with 95% HPD
cat("The heritability estimate for BCI is: ", round(posterior.mode(herit),
digits = 3), "(", round(x[,1], digits = 3), "-", round(x[,2], digits = 3),
")", "\n")

## The heritability estimate for BCI is: 0.149 ( 0.059 - 0.22 )

#extract DIC from model with "animal" term
DIC_full <- model_BCI1$DIC

#Load model without "animal" term for BCI
load("BCI_1_SVLfilt_noVa.RData") #note: over-writing earlier BCI model

#view model to confirm it's correct
summary(model_BCI1)

##
## Iterations = 50001:4998501
## Thinning interval = 1500
## Sample size = 3300
##
## DIC: -292.4278
##

```

```

## G-structure: ~ID
##
##      post.mean l-95% CI u-95% CI eff.samp
## ID  0.009093  0.00464  0.01334      3504
##
## R-structure: ~units
##
##      post.mean l-95% CI u-95% CI eff.samp
## units  0.0325  0.02817  0.037      2900
##
## Location effects: BCI_RESID ~ SEX
##
##      post.mean  l-95% CI  u-95% CI eff.samp  pMCMC
## (Intercept)  0.041536  0.017211  0.066038    3300 0.00242 **
## SEXM         -0.003557 -0.039283  0.034657    3300 0.86909
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#view priors to confirm they're correct
prior_BCI1

## $G
## $G$G1
## $G$G1$V
##      [,1]
## [1,] 0.02051676
##
## $G$G1$nu
## [1] 0.2
##
##
##
## $R
## $R$V
##      [,1]
## [1,] 0.02051676
##
## $R$nu
## [1] 0.2

#extract DIC for model without "animal" term for BCI
DIC_reduced <- model_BCI1$DIC

#cat statement about the DICs of the models
cat("The DIC of the model with the animal term is: ", round(DIC_full, digits
= 3), "\n", "The DIC of the model without the animal term is: ",
round(DIC_reduced, digits = 3), "\n\n")

## The DIC of the model with the animal term is: -304.145
## The DIC of the model without the animal term is: -292.428

```

```

#calculate difference between DICs
diff <- DIC_reduced - DIC_full

#test whether heritability is significant
if(diff >= 10) {
  cat("BCI model with animal term has significantly smaller DIC:", diff >=
10, "\n", "BCI has significant heritability.\n")
} else {
  cat("BCI model with animal term has significantly smaller DIC:", diff >=
10, "\n", "BCI does not have significant heritability.")
}

## BCI model with animal term has significantly smaller DIC: TRUE
## BCI has significant heritability.

```

Snout-Vent Length (SVL) Heritability

```

#clear memory
rm(list=ls())

#load model with "animal" term for SVL
load("SVL_1_dummy_SVLfilt.RData")

#view model to confirm it's correct
summary(model_SVL1)

##
## Iterations = 50001:4998501
## Thinning interval = 1500
## Sample size = 3300
##
## DIC: 8069.45
##
## G-structure: ~animal
##
##      post.mean 1-95% CI u-95% CI eff.samp
## animal      341.9    65.44    711.4      3300
##
##      ~ID
##
##      post.mean 1-95% CI u-95% CI eff.samp
## ID      612.4    101.4    1235      3300
##
## R-structure: ~units
##
##      post.mean 1-95% CI u-95% CI eff.samp
## units      7754     6753     8681      3300
##
## Location effects: SVL ~ SEX
##
##      post.mean 1-95% 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 to confirm they're correct
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

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

#HPD intervals for heritability
x <- HPDinterval(herit)

#cat heritability estimate with 95% HPD
cat("The heritability estimate for SVL is: ", round(posterior.mode(herit),
digits = 3), "(", round(x[,1], digits = 3), "-", round(x[,2], digits = 3),
")", "\n")

## The heritability estimate for SVL is: 0.025 ( 0.007 - 0.08 )

```

```

#extract DIC from model with "animal" term
DIC_full <- model_SVL1$DIC

#load model without "animal" term for SVL
load("SVL_1_SVLfilt_noVa.RData") #note: over-writing earlier SVL model

#view model to confirm it's correct
summary(model_SVL1)

##
## Iterations = 50001:4998501
## Thinning interval = 1500
## Sample size = 3300
##
## DIC: 8067.09
##
## G-structure: ~ID
##
##      post.mean 1-95% CI u-95% CI eff.samp
## ID      861.5    201.8    1523    3300
##
## R-structure: ~units
##
##      post.mean 1-95% CI u-95% CI eff.samp
## units      7760    6764    8810    3300
##
## Location effects: SVL ~ SEX
##
##      post.mean 1-95% CI u-95% CI eff.samp pMCMC
## (Intercept)  1033.20  1023.31  1044.22    3300 <3e-04 ***
## SEXM          88.81    73.66   104.30    3300 <3e-04 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#view priors to confirm they're correct
prior_SVL1

## $G
## $G$G1
## $G$G1$V
##      [,1]
## [1,] 5309.986
##
## $G$G1$nu
## [1] 0.2
##
##
##
## $R
## $R$V

```

```
##           [,1]
## [1,] 5309.986
##
## $R$nu
## [1] 0.2

#extract DIC for model without "animal" term for BCI
DIC_reduced <- model_SVL1$DIC

#cat statement about the DICs of the models
cat("The DIC of the model with the animal term is: ", round(DIC_full, digits
= 3), "\n", "The DIC of the model without the animal term is: ",
round(DIC_reduced, digits = 3), "\n\n\n")

## The DIC of the model with the animal term is: 8069.45
## The DIC of the model without the animal term is: 8067.09

#calculate difference between DICs
diff <- DIC_reduced - DIC_full

#test whether heritability is significant
if(diff >= 10) {
  cat("SVL model with animal term has significantly smaller DIC:", diff >=
10, "\n", "SVL has significant heritability.\n")
} else {
  cat("SVL model with animal term has significantly smaller DIC:", diff >=
10, "\n", "SVL does not have significant heritability.")
}

## SVL model with animal term has significantly smaller DIC: FALSE
## SVL does not have significant heritability.
```

Trappability (TRAP) Heritability

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

#Load model with "animal" term for Trappability
load("TRAP_1_dummy_SVLfilt.RData")

#view model to confirm it's correct
summary(model_TRAP1)

##
## Iterations = 50001:4998501
## Thinning interval = 1500
## Sample size = 3300
##
## DIC: 2159.104
##
## G-structure: ~animal
```



```

##
##      post.mean 1-95% CI u-95% CI eff.samp
## animal      0.193  0.07385  0.3309      3300
##
##              ~ID
##
##      post.mean 1-95% CI u-95% CI eff.samp
## ID      0.1769  0.0724  0.3031      3300
##
## R-structure: ~units
##
##      post.mean 1-95% CI u-95% CI eff.samp
## units      2.457   1.987   2.977      3300
##
## Location effects: CAP_TRAP ~ SEX
##
##      post.mean 1-95% 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 to confirm they're correct
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

```

```

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

#HPD intervals for heritability
x <- HPDinterval(herit)

#cat heritability estimate with 95% HPD
cat("The heritability estimate for trappability is: ",
round(posterior.mode(herit), digits = 3), "(", round(x[,1], digits = 3), "-",
round(x[,2], digits = 3), ")", "\n")

## The heritability estimate for trappability is: 0.066 ( 0.027 - 0.116 )

#extract DIC from model with "animal" term
DIC_full <- model_TRAP1$DIC

#Load model without "animal" term for trappability
load("TRAP_1_SVLfilt_noVa.RData") #note: over-writing earlier trappability
model

#view model to confirm it's correct
summary(model_TRAP1)

##
## Iterations = 50001:4998501
## Thinning interval = 1500
## Sample size = 3300
##
## DIC: 2160.261
##
## G-structure: ~ID
##
##      post.mean 1-95% CI u-95% CI eff.samp
## ID      0.2284   0.1012   0.3859     3300
##
## R-structure: ~units
##
##      post.mean 1-95% CI u-95% CI eff.samp
## units      2.501    2.003    3.034     3300
##
## Location effects: CAP_TRAP ~ SEX
##
##      post.mean 1-95% CI u-95% CI eff.samp pMCMC
## (Intercept) -0.25626 -0.48815 -0.02445     3300 0.0285 *
## SEXM         0.12828 -0.18729  0.45216     3568 0.4327
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

#view priors to confirm they're correct
prior_TRAP1

## $G
## $G$G1
## $G$G1$V
##           [,1]
## [1,] 8.880674
##
## $G$G1$nu
## [1] 0.2
##
##
##
## $R
## $R$V
##           [,1]
## [1,] 8.880674
##
## $R$nu
## [1] 0.2

#extract DIC for model without "animal" term for trappability
DIC_reduced <- model_TRAP1$DIC

#cat statement about the DICs of the models
cat("The DIC of the model with the animal term is: ", round(DIC_full, digits
= 3), "\n", "The DIC of the model without the animal term is: ",
round(DIC_reduced, digits = 3), "\n\n\n")

## The DIC of the model with the animal term is: 2159.104
## The DIC of the model without the animal term is: 2160.261

#calculate difference between DICs
diff <- DIC_reduced - DIC_full

#test whether heritability is significant
if(diff >= 10) {
  cat("Trappability model with animal term has significantly smaller DIC:",
diff >= 10, "\n", "Trappability has significant heritability.\n")
} else {
  cat("Trappability model with animal term has significantly smaller DIC:",
diff >= 10, "\n", "Trappability does not have significant heritability.")
}

## Trappability model with animal term has significantly smaller DIC: FALSE
## Trappability does not have significant heritability.

```

2. Significance Testing - Repeatability

Body Condition (BCI) Repeatability

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

#load model with only "individual" term
load("BCI_1_SVLfilt_noVa.RData")

#view model to confirm it's correct
summary(model_BCI1)

##
## Iterations = 50001:4998501
## Thinning interval = 1500
## Sample size = 3300
##
## DIC: -292.4278
##
## G-structure: ~ID
##
##      post.mean 1-95% CI u-95% CI eff.samp
## ID  0.009093  0.00464  0.01334      3504
##
## R-structure: ~units
##
##      post.mean 1-95% CI u-95% CI eff.samp
## units  0.0325  0.02817  0.037      2900
##
## Location effects: BCI_RESID ~ SEX
##
##      post.mean 1-95% CI u-95% CI eff.samp pMCMC
## (Intercept)  0.041536  0.017211  0.066038      3300 0.00242 **
## SEXM        -0.003557 -0.039283  0.034657      3300 0.86909
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#view priors to confirm their correct
prior_BCI1

## $G
## $G$G1
## $G$G1$V
##      [,1]
## [1,] 0.02051676
##
## $G$G1$nu
## [1] 0.2
##
```

```
##
##
## $R
## $R$V
##           [,1]
## [1,] 0.02051676
##
## $R$nu
## [1] 0.2

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

#HPD intervals for repeatability
x <- HPDinterval(repeatability)

#cat statement about repeatability with 95% HPD
cat("The repeatability estimate for BCI is: ",
round(posterior.mode(repeatability), digits = 3), "(", round(x[,1], digits =
3), "-", round(x[,2], digits = 3), ")", "\n")

## The repeatability estimate for BCI is: 0.219 ( 0.122 - 0.312 )

#extract DIC from model with "ID" term
DIC_full <- model_BCI1$DIC

#Load model without "ID" term for BCI
load("BCI_1_SVLfilt_noVa_noI.RData") #note: over-writing earlier BCI model

#view model to confirm it's correct
summary(model_BCI1)

##
## Iterations = 50001:4998501
## Thinning interval = 1500
## Sample size = 3300
##
## DIC: -236.3787
##
## R-structure: ~units
##
##      post.mean 1-95% CI u-95% CI eff.samp
## units 0.04122 0.03702 0.04576 3300
##
## Location effects: BCI_RESID ~ SEX
##
##      post.mean 1-95% CI u-95% CI eff.samp pMCMC
## (Intercept) 3.783e-02 1.700e-02 5.799e-02 3134 0.00121 **
## SEXM 3.002e-05 -3.023e-02 3.094e-02 3477 0.99515
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#view priors to confirm they're correct
prior_BCI1

## $R
## $R$V
##           [,1]
## [1,] 0.04103353
##
## $R$nu
## [1] 0.2

#extract DIC for model without "ID" term for BCI
DIC_reduced <- model_BCI1$DIC

#cat statement about the DICs of the models
cat("The DIC of the model with the ID term is: ", round(DIC_full, digits =
3), "\n", "The DIC of the model without the ID term is: ", round(DIC_reduced,
digits = 3), "\n\n\n")

## The DIC of the model with the ID term is: -292.428
## The DIC of the model without the ID term is: -236.379

#calculate difference between DICs
diff <- DIC_reduced - DIC_full

#test whether repeatability is significant
if(diff >= 10) {
  cat("BCI model with ID term has significantly smaller DIC:", diff >= 10,
"\n", "BCI has significant repeatability.\n")
} else {
  cat("BCI model with ID term has significantly smaller DIC:", diff >= 10,
"\n", "BCI does not have significant repeatability.")
}

## BCI model with ID term has significantly smaller DIC: TRUE
## BCI has significant repeatability.
```

Snout-Vent Length (SVL) Repeatability

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

#load model with only "individual" term
load("SVL_1_SVLfilt_noVa.RData")

#view model to confirm it's correct
summary(model_SVL1)
```

```

##
## Iterations = 50001:4998501
## Thinning interval = 1500
## Sample size = 3300
##
## DIC: 8067.09
##
## G-structure: ~ID
##
##      post.mean l-95% CI u-95% CI eff.samp
## ID      861.5    201.8    1523      3300
##
## R-structure: ~units
##
##      post.mean l-95% CI u-95% CI eff.samp
## units      7760     6764     8810     3300
##
## Location effects: SVL ~ SEX
##
##      post.mean l-95% CI u-95% CI eff.samp pMCMC
## (Intercept)  1033.20  1023.31  1044.22     3300 <3e-04 ***
## SEXM          88.81    73.66   104.30     3300 <3e-04 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#view priors to confirm their correct
prior_SVL1

## $G
## $G$G1
## $G$G1$V
##      [,1]
## [1,] 5309.986
##
## $G$G1$nu
## [1] 0.2
##
##
##
## $R
## $R$V
##      [,1]
## [1,] 5309.986
##
## $R$nu
## [1] 0.2

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

```

```

#HPD intervals for repeatability
x <- HPDinterval(repeatability)

#cat statement about SVL repeatability with 95% HPD
cat("The repeatability estimate for SVL is: ",
round(posterior.mode(repeatability), digits = 3), "(", round(x[,1], digits =
3), "-", round(x[,2], digits = 3), ")", "\n")

## The repeatability estimate for SVL is: 0.089 ( 0.028 - 0.177 )

#extract DIC from model with "ID" term
DIC_full <- model_SVL1$DIC

#load model without "ID" term for SVL
load("SVL_1_SVLfilt_noVa_noI.RData") #note: over-writing earlier SVL model

#view model to confirm it's correct
summary(model_SVL1)

##
## Iterations = 50001:4998501
## Thinning interval = 1500
## Sample size = 3300
##
## DIC: 8078.792
##
## R-structure: ~units
##
##      post.mean l-95% CI u-95% CI eff.samp
## units      8576      7715      9558      3300
##
## Location effects: SVL ~ SEX
##
##      post.mean l-95% CI u-95% CI eff.samp pMCMC
## (Intercept) 1034.64 1025.89 1044.51    2744 <3e-04 ***
## SEXM        91.40   77.57  104.83    3733 <3e-04 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#view priors to confirm they're correct
prior_SVL1

## $R
## $R$V
##      [,1]
## [1,] 10619.97
##
## $R$nu
## [1] 0.2

```



```

#extract DIC for model without "ID" term for SVL
DIC_reduced <- model_SVL1$DIC

#cat statement about the DICs of the models
cat("The DIC of the model with the ID term is: ", round(DIC_full, digits =
3), "\n", "The DIC of the model without the ID term is: ", round(DIC_reduced,
digits = 3), "\n\n")

## The DIC of the model with the ID term is: 8067.09
## The DIC of the model without the ID term is: 8078.792

#calculate difference between DICs
diff <- DIC_reduced - DIC_full

#test whether trappability is significant
if(diff >= 10) {
  cat("SVL model with ID term has significantly smaller DIC:", diff >= 10,
"\n", "SVL has significant repeatability.\n")
} else {
  cat("SVL model with ID term has significantly smaller DIC:", diff >= 10,
"\n", "SVL does not have significant repeatability.")
}

## SVL model with ID term has significantly smaller DIC: TRUE
## SVL has significant repeatability.

```

Trappability (TRAP) Repeatability

```

#clear memory
rm(list=ls())

#Load model with only "individual" term
load("TRAP_1_SVLfilt_noVa.RData")

#view model to confirm it's correct
summary(model_TRAP1)

##
## Iterations = 50001:4998501
## Thinning interval = 1500
## Sample size = 3300
##
## DIC: 2160.261
##
## G-structure: ~ID
##
## post.mean l-95% CI u-95% CI eff.samp
## ID 0.2284 0.1012 0.3859 3300
##
## R-structure: ~units
##

```

```

##          post.mean l-95% CI u-95% CI eff.samp
## units          2.501    2.003    3.034      3300
##
## Location effects: CAP_TRAP ~ SEX
##
##          post.mean l-95% CI u-95% CI eff.samp pMCMC
## (Intercept)  -0.25626 -0.48815 -0.02445      3300 0.0285 *
## SEXM          0.12828 -0.18729  0.45216      3568 0.4327
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#view priors to confirm their correct
prior_TRAP1

## $G
## $G$G1
## $G$G1$V
##          [,1]
## [1,] 8.880674
##
## $G$G1$nu
## [1] 0.2
##
##
##
## $R
## $R$V
##          [,1]
## [1,] 8.880674
##
## $R$nu
## [1] 0.2

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

#HPD intervals for repeatability
x <- HPDinterval(repeatability)

#cat statement about repeatability with 95% HPD
cat("The repeatability estimate for Trappability is: ",
round(posterior.mode(repeatability), digits = 3), "(", round(x[,1], digits =
3), "-", round(x[,2], digits = 3), ")", "\n")

## The repeatability estimate for Trappability is: 0.071 ( 0.035 - 0.136 )

#extract DIC from model with "ID" term
DIC_full <- model_TRAP1$DIC

#Load model without "ID" term for Trappability

```

```

load("TRAP_1_SVLfilt_noVa_noI.RData") #note: over-writing earlier
Trappability model

#view model to confirm it's correct
summary(model_TRAP1)

##
## Iterations = 50001:4998501
## Thinning interval = 1500
## Sample size = 3300
##
## DIC: 2159.192
##
## R-structure: ~units
##
##      post.mean 1-95% CI u-95% CI eff.samp
## units      2.599    2.123    3.139    3300
##
## Location effects: CAP_TRAP ~ SEX
##
##      post.mean 1-95% CI u-95% CI eff.samp pMCMC
## (Intercept) -0.23748 -0.46352 -0.01784    3130 0.0321 *
## SEXM         0.12893 -0.15775  0.43818    3300 0.3915
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#view priors to confirm they're correct
prior_TRAP1

## $R
## $R$V
##      [,1]
## [1,] 17.76135
##
## $R$nu
## [1] 0.2

#extract DIC for model without "animal" term for trappabilitt
DIC_reduced <- model_TRAP1$DIC

#cat statement about the DICs of the models
cat("The DIC of the model with the ID term is: ", round(DIC_full, digits =
3), "\n", "The DIC of the model without the ID term is: ", round(DIC_reduced,
digits = 3), "\n\n\n")

## The DIC of the model with the ID term is: 2160.261
## The DIC of the model without the ID term is: 2159.192

#calculate difference between DICs
diff <- DIC_reduced - DIC_full

```

```
#test whether repeatability is significant
if(diff >= 10) {
  cat("Trappability model with ID term has significantly smaller DIC:", diff
  >= 10, "\n", "BCI has significant repeatability.\n")
} else {
  cat("Trappability model with ID term has significantly smaller DIC:", diff
  >= 10, "\n", "Trappability does not have significant repeatability.")
}

## Trappability model with ID term has significantly smaller DIC: FALSE
## Trappability does not have significant repeatability.
```