

Crested porcupine (*Hystrix cristata*) abundance estimation using Bayesian methods: first data from a highly agricultural environment in central Italy

Mammal Research

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Mathematical approach

```
rm(list=ls())
```

```
# Lambda:
```

```
(lambda <- 27*(1996.17/273.97))
```

```
[1] 196.7244
```

```
# Range of porcupines inhabiting A1:
```

```
library(wiqid)
```

```
(min <- 197 - 17)
```

```
[1] 180
```

```
(max <- 197 + 40)
```

```
[1] 237
```

```
hystrix <- c(180:237)
```

```
# Mean and standard deviation:
```

```
mean(hystrix)
```

```
[1] 208.5
```

```
sd(hystrix)
```

```
[1] 16.88688
```

```
# Prior distribution:
```

```
priorDens <- dgamma2(hystrix, 200.5, 16.88688)
```

```
(priorPars <- getGammaPar(208.5, 16.88688))
```

```
      shape      rate
```

```
[1,] 152.445 0.7311512
```

**# Data obtained from both the likelihood and prior distribution
were combined to obtain the posterior distribution:**

```
(postPars <- priorPars + c(27, 1/7.29))
```

```
      shape      rate
```

```
[1,] 179.445 0.8683255
```

```
postDens <- dgamma(hystrix, shape=postPars[1], rate=postPars[2])
```

```
plot(hystrix, postDens, main="", xlab="N", ylab="Probability",  
xlim=c(160,250), ylim=c(0,0.03), type='l', lwd=2, col='brown')
```

```
lines(hystrix, priorDens, lwd=2, col='blue')
```

```
(llh <- dpois(27, hystrix/7.29))
```

```
llh2plot <- llh/sum(llh)
```

```
lines(hystrix, llh2plot)
```

```
(mean <- postPars[1] / postPars[2])
```

```
[1] 206.6564
```

```
abline(v=mean, col='red')
```

```
(hdi <- hdi(qgamma, shape=postPars[1], rate=postPars[2]))
```

```
      lower      upper
```

```
176.7962 237.1647
```

```
attr("credMass")
```

```
[1] 0.95
```

```
abline(v=hdi, lty=2, col='red')
```

The plot showing the trend of the likelihood and both the prior and posterior distributions is showed in Fig. 3.

Computational approach

```
rm(list=ls())
```

```
# Creating a vector defining the interval input (i.e., the minimum  
and maximum number of crested porcupines estimated within the  
area):
```

```
hystrix <- c(180:237)
```

```
# Mean and standard deviation:
```

```
mean(hystrix)
```

```
[1] 208.5
```

```
sd(hystrix)
```

```
[1] 16.88688
```

```
# Libraries used:
```

```
library(jagsUI)
```

```
library(wiqid)
```

```
# Preparing the data:
```

```
( priorPars <- getGammaPar(208.5, 16.88688) )
```

```
      shape      rate
```

```
[1,] 152.445 0.7311512
```

```
jagsData <- list(shape=priorPars[1], rate=priorPars[2], a =  
1/7.29, C = 27)
```

1/7.29 tells us that within an area corresponding to approximately one seventh of the norther area falling within the provinces of Grosseto and Siena, the presence of 27 individuals (at the very least) is estimated (in this case, we used data on road-killed porcupine as a referring value). The value 7.29 was calculated from the ratio between the area defined by the 100% Minimum Convex Polygon (100% MCP) calculated using both independent opportunistic observations and camera-trapping independent positive detections in the northern area of the provinces of Grosseto and Siena, and the area obtained from the 100% MCP calculated using the recovery coordinates of each road-killed porcupine, and only considering the surface covered by suitable (i.e., canopy-covered and open areas) and moderately suitable (i.e., agricultural areas) habitats.

Model run with JAGS:

```
jagsout <- jags(jagsData, inits=NULL, parameters.to.save="N",  
model.file="hystrix.jags", n.chains=3, n.iter=20000, n.burnin=0,  
DIC=FALSE)
```

The JAGS model code saved in the file named "hystrix.jags" presents the following syntax:

```
model {
```

```
# Likelihood:
```

```
lambda <- N * a
```

```
C ~ dpois(lambda)
```

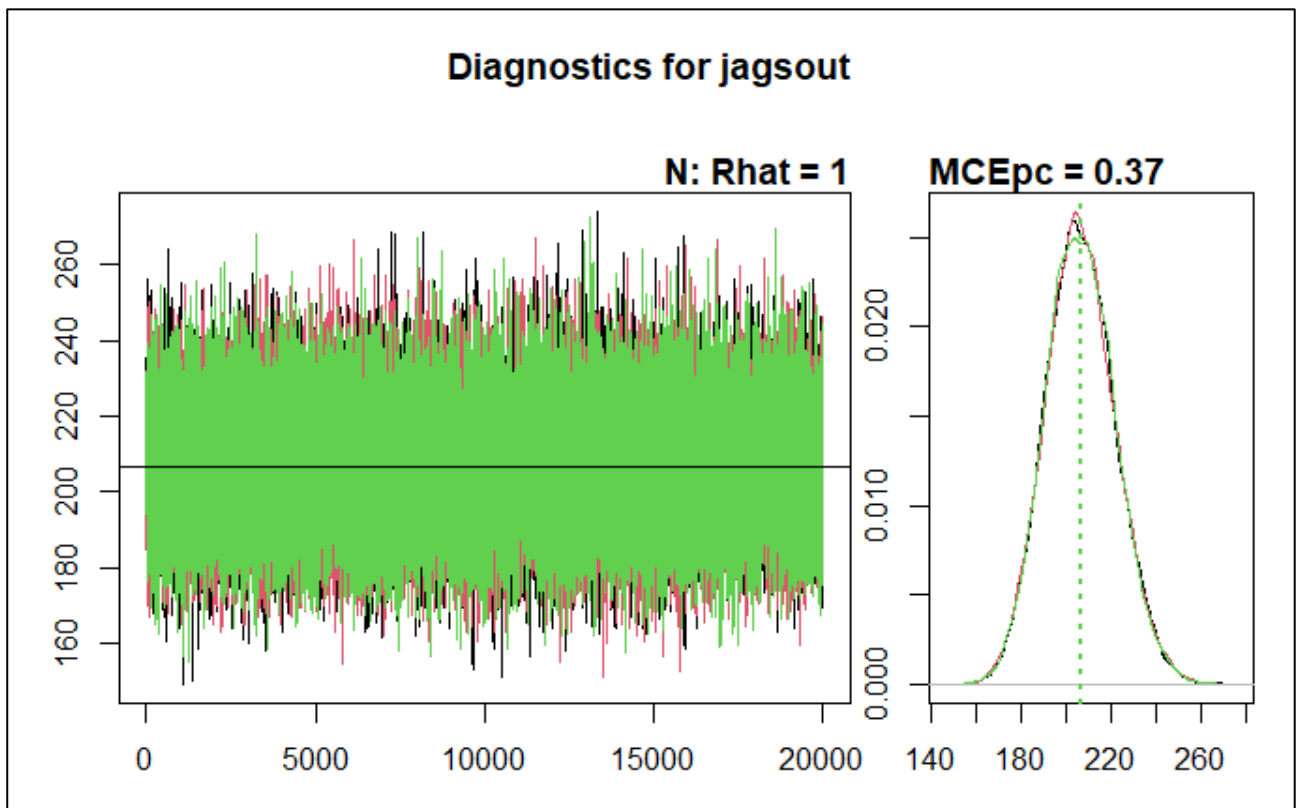
```
# Prior:
```

```
N ~ dgamma(shape, rate)
```

```
}
```

```
# Diagnostic plot:
```

```
diagPlot(jagsout)
```



The diagnostic plot is good. The chart on the left shows the Rhat index, which represents the scale reduction factor indicating convergence between chains. Perfect convergence is obtained when $Rhat = 1$ (Gelman et al. 2004; Gelman & Hill 2007; Kruschke 2014). The chart on the right shows the MCEpc value which expresses the error in the mean estimation (expressed as a percentage value) compared to the target distribution. Values below to 5% indicate good mean estimation. However, values below to 1.5% indicate

excellent mean estimation in relation to the chosen confidence interval (Lunn et al. 2013).

Model output:

jagsout

JAGS output for model 'hystrix.jags', generated by jagsUI.

Estimates based on 3 chains of 20000 iterations,

adaptation = 100 iterations (sufficient),

burn-in = 0 iterations and thin rate = 1,

yielding 60000 total samples from the joint posterior.

MCMC ran for 0.002 minutes at time 2022-01-05 19:47:22.

	mean	sd	2.5%	50%	97.5%	overlap0	f	Rhat	n.eff
N	206.559	15.41	177.396	206.093	237.794	FALSE	1	1	60000

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.

The model shows an average minimum number of approximately 207 porcupines estimated within the suitable and moderately suitable habitats falling in the northern territory of the provinces of Grosseto and Siena.

Literature cited in the present document was added within the *References* paragraph.