

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 <- 655*(17111.52/6236.37))
```

```
[1] 1797.207
```

```
# Range of porcupines inhabiting A3:
```

```
library(wiqid)
```

```
(min <- 1797 - 42)
```

```
[1] 1755
```

```
(max <- 1797 + 57)
```

```
[1] 1854
```

```
hystrix <- c(1755:1854)
```

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

```
mean(hystrix)
```

```
[1] 1804.5
```

```
sd(hystrix)
```

```
[1] 29.01149
```

```
# Prior distributions:
```

```
priorDens <- dgamma2(hystrix, 1804.5, 29.01149)
```

```
(priorPars <- getGammaPar(1804.5, 29.01149))
```

```
      shape      rate
```

```
[1,] 3868.777 2.143961
```

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

```
(postPars <- priorPars + c(655, 1/2.74))
```

```
      shape      rate
```

```
[1,] 4523.777 2.508924
```

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

```
plot(hystrix, postDens, main="", xlab="N", ylab="Probability",  
xlim=c(1700,1900), ylim=c(0,0.03), type='l', lwd=2, col='brown')
```

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

```
(llh <- dpois(655, hystrix/2.74))
```

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

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

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

```
[1] 1803.074
```

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

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

```
      lower      upper
```

```
1750.647 1855.725
```

```
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. 5.

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(1755:1854)
```

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

```
mean(hystrix)
```

```
[1] 1804.5
```

```
sd(hystrix)
```

```
[1] 29.01149
```

```
# Libraries used:
```

```
library(jagsUI)
```

```
library(wiqid)
```

```
# Preparing the data:
```

```
( priorPars <- getGammaPar(1804.5, 29.01149) )
```

```
      shape      rate
```

```
[1,] 3868.777 2.143961
```

```
jagsData <- list(shape=priorPars[1], rate=priorPars[2], a =  
1/(2.74), C = 655)
```

1/2.74 tells us that within an area corresponding to approximately one third of the whole monitoring area, the presence of 655 individuals (at the very least) is estimated. The value 2.74 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 collected in the whole monitoring area, and the area obtained from the 100% MCP calculated using both independent opportunistic observations and camera-trapping independent positive detections collected in the provinces of Grosseto and Siena, 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:
```

```

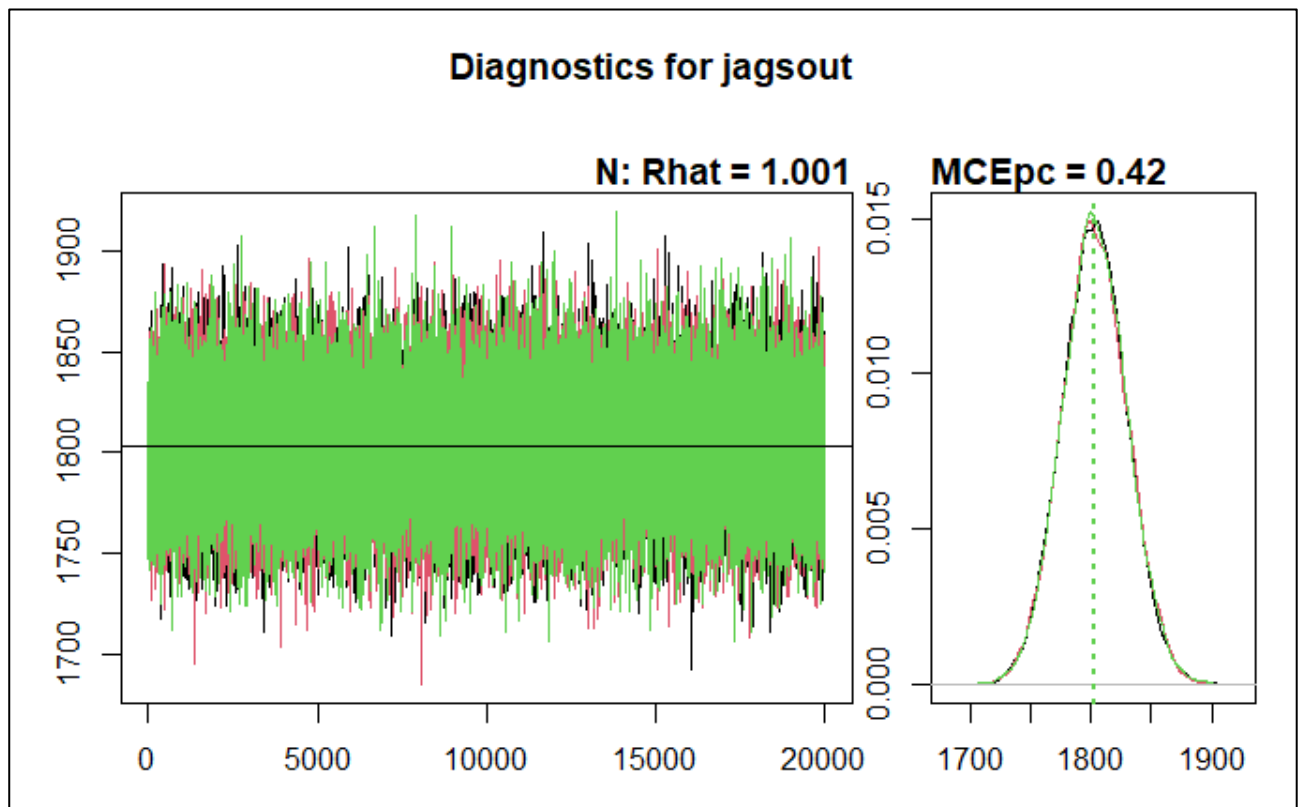
N ~ dgamma(shape, rate)

}

```

Diagnostic plot:

```
diagPlot(jagsout)
```



The diagnostic plot is good (see Electronic Online Resource 1 for details).

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 0.001 minutes at time 2022-01-05 22:44:29.

	mean	sd	2.5%	50%	97.5%	overlap0	f	Rhat	n.eff
N	1803.188	26.892	1751.087	1803.06	1856.316	FALSE	1	1	56607

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 1803 porcupines estimated within the suitable and moderately suitable habitats falling the whole monitoring area.