

Estimation of the Number of Male Capercaillie on Leks of the French Pyrenees Mountains from 2010 to 2019

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Introduction

This vignette is the supplementary material of the paper of Calenge et al. (in prep.). The aim of this paper is to estimate the number of male capercaillie in the 5 geographic regions of the French Pyrenees mountains, for each period of two years between 2010 and 2019. A companion package named `caperpyogm` contains the data and functions used for this paper, and is required to reproduce the calculations in this document. To install this package, first install the package `devtools` and use the function `install_github` to install `caperpyogm`:

```
## If devtools is not yet installed, type
install.packages("devtools")

## Install the package caperpyogm
devtools::install_github("ClementCalenge/caperpyogm", ref="main", build_vignettes=TRUE)
```

It is supposed throughout this vignette that the reader is familiar with the model developed in this paper. Nevertheless, we will present a brief reminder on this model in this vignette. This model combines three datasets:

1. the results of counts of singing males carried out every period of two years on capercaillie leks, which allow to model the time changes in the mean abundance of on the various types of leks (KAL = known active leks; KIL = known leks with indeterminate activity status; UL = leks unknown at the time of the definition of the sampling design), and in the different geographic regions;
2. the results of the search for new, unknown leks in grid cells randomly selected in the whole area. This dataset was required to estimate the number of leks on our study area, which were unknown at the time of the definition of the sampling design.
3. the results of an experiment carried out to estimate the probability to detect an active lek unknown to the observer in a grid cell during a grid cell search. This experiment involved both experienced or inexperienced observers searching for leks unknown to them (but known to us).

We developed two sub-models for (i) the mean number of males actually present on a lek of a given type (KAL, KIL, UL), during a given period and within a given geographic region, and (ii) the number of leks unknown to us at the time of the definition of the sampling design in a given geographic region.

In this document, we give a detailed information on this study, which completes the information given in the paper:

- In section 1, we present all the mathematical notations used in the paper and in the appendix in a table.
- In section 2, we give a brief reminder on the structure of the model used to estimate the number of males, and we show how to use the datasets and functions given in the package to reproduce the calculations given in the paper. Note that all the functions included in this paper have a very detailed help page explaining how they should be used. This section contains additional elements not presented in the paper (residual analysis, analysis of the convergence and the mixing of MCMC chains, sensitivity to outliers, etc.).
- In section 3, we demonstrate how a cross-validation approach was used to select the best model for the detection process during lek counts.

- In section 4, we study more in detail the case of the lek # 281. This lek is characterized by a strong residual in our model. We examined more precisely whether this lek had a strong influence on our inference.
- In section 5, we considered in detail the criticisms of the N-mixture models by [BAR17] and [LIN18]. In particular, we used simulations to assess the effect of unaccounted heterogeneity in detection probability as well as the effect of accidental double counting on the estimated number of males.
- In section 6, we give some additional elements describing the history of the monitoring program. In particular, we describe how the discovery that unknown leks were characterized by large number of males affected our program.

1 Notations

We present, in the table below, the notations used in this paper. We distinguish several types of notations:

- D: data used to fit the model
- P: stochastic parameter estimated with MCMC
- N: other notations

In the table below, we give:

- the notation
- the type of notation
- a description of the variable or parameter

Notation	Type	Description
$y_{i,t,k}$	D	Number of detected males during count occasions k of the year t on lek i
$b(t)$	N	Index of the two-year period containing the year t
$N_{i,b(t)}$	P	Number of males actually present on lek i during the two year-period $b(t)$
$p_{i,t,k}$	P	Probability of detection of a male present on lek i during count occasion k of year t
α_d	P	Intercept of the model for the process of detection of males during counts
β_d	P	Slope of the number of observers in the model for the detection process of males during counts
$o_{i,t,k}$	D	Number of observers participating to the count occasion k of the year t on lek i
$e_{g(i),t}$	P	Random effect of the year t on the detectability of males in geographic region g
σ_e	P	Standard deviation of the year random effect on the detectability of males during counts
$\lambda_{i,b(t)}$	P	Expectation of the Poisson distribution of the number of males on lek i during period $b(t)$
$\kappa_{g(i),\ell(i),b(t)}$	P	Parameter describing the average number of males during period $b(t)$ on a lek of type $\ell(i)$ in region $g(i)$
$\nu_{u(i)}$	P	Random effect of the natural unit $u(i)$
η_i	P	Random effect of the lek i
$\epsilon_{i,b(t)}$	P	Overdispersion residual
$\mu_{g(i),\ell(i)}$	P	Mean of the average numbers of males during period $b(t)$ on leks of type $\ell(i)$ in region $g(i)$
σ_κ	P	Standard deviation of the average numbers of males during period $b(t)$ on leks of type $\ell(i)$ in region $g(i)$
σ_ν	P	Standard deviation of the natural units random effects
σ_η	P	Standard deviation of the lek random effects
σ_ϵ	P	Standard deviation of the overdispersion residuals
z_q	D	Whether the cell q contains an unknown lek detected during a search of our program
f_q	D	Whether the cell q was sampled in 2018–2019
s_q	D	Whether the cell q contains an unknown lek detected before the search of our program
b_q	P	Whether the cell q actually contains an unknown lek
r_q	D	Proportion of the cell q covered by the presence area of the capercaillie
h_q	D	Whether the cell q already contains a known lek
π_q	P	Probability that the cell q contains an unknown lek
$a_{g(q)}$	P	Intercept of the model predicting π_q
$b_{g(q)}$	P	Slope of r_q in the model predicting π_q
d	P	Slope of h_q in the model predicting π_q
β	P	Probability of detection of an unknown lek during the search of a grid cell
α	P	Probability that an unknown lek present in the cell was discovered prior to its sampling
S_c	D	Number of the known leks present in grid cell c included in the search sector
D_c	D	Number of the known leks present in grid cell c detected by the observer
N_c	D	Number of the known leks present in grid cell c
δ	P	Probability to detect a lek during a search when the lek is in the search sector
$e(c)$	N	Level of experience of the observers searching the cell c
$\zeta_{e(c)}$	P	Probability that the search sector defines by the observer with experience $e(c)$ includes a lek present in a cell
$S_{g\ell}$	D/P	Number of leks of type ℓ in the region g (to be estimated for UL)
Q	D	Number of grid cells in the frame
$n_{g\ell b}$	P	Number of males on leks of type ℓ during the period b in region g
n_b	P	Number of males on all leks of the mountain range during period b

2 Model description and model fit

We describe in this section the two sub-models required for the estimation of the numbers of males present in the geographical regions of the Pyrenees, for each two-years period between 2010 and 2019.

2.1 Count model

2.1.1 Model description

We first describe the sub-model of the mean number of males detected during the lek counts carried out in the French Pyrenees mountains between 2010 and 2019.

Let $y_{i,t,k}$ be the number of males counted during the count occasion k of the year t on the lek i . We model these counts with a N-mixture model. We suppose that the number of detected animals is the realization of a binomial distribution:

$$y_{i,t,k} \sim \mathcal{B}(N_{i,b(t)}, p_{i,t,k}) \quad (1)$$

where $N_{i,b(t)}$ is the number of males actually present on lek i during the two-years period $b(t)$ including year t , and $p_{i,t,k}$ is the probability of detection characterizing this count occasion on this lek, this year. We suppose the following detection model:

$$\text{logit } p_{i,t,k} = \alpha_d + \beta_d \times o_{i,t,k} + e_{g(i),t} \quad (2)$$

where $o_{i,t,k}$ is the number of observers present on lek i during count occasion k of year t , α_d is the intercept of the model, β_d is the slope, and $e_{g(i),t}$ is a Gaussian random effect characterizing year t in the geographic region $g(i)$ where the lek i is located. More formally, we suppose:

$$e_{g(i),t} \sim \mathcal{N}(0, \sigma_e)$$

We discuss alternative detection models in section 3.

Moreover, we suppose that the actual number of males $N_{i,b(t)}$ on lek i during the two-years period $b(t)$ containing the year t is the realization of a Poisson distribution:

$$N_{i,b(t)} \sim \mathcal{P}(\lambda_{i,b(t)}) \quad (3)$$

And we suppose the following log-linear model for the expectation of this distribution:

$$\log \lambda_{i,b(t)} = \kappa_{g(i),\ell(i),b(t)} + \nu_{u(i)} \times I(\ell(i) = 2) + \eta_i + \epsilon_{i,b(t)} \quad (4)$$

Where $\kappa_{g(i),\ell(i),b(t)}$ is a random intercept characterizing the type $\ell(i)$ of the lek i (1 for KAL, 2 for KIL, and 3 for UL) in the geographic region $g(i)$ containing lek i during two-years period $b(t)$ including year t ; $\nu_{u(i)}$ is a random effect characterizing the effect of the natural unit $u(i)$ which contains the lek i (note that a random effect characterizing the natural unit is only included for KILs, see paper for an explanation); η_i is a random effect characterizing lek i , and $\epsilon_{i,b(t)}$ is a Gaussian overdispersion residual.

We furthermore suppose the following distributions for these parameters:

$$\begin{aligned} \kappa_{g(i),\ell(i),b(t)} &\sim \mathcal{N}(\mu_{g(i),\ell(i)}, \sigma_\kappa) \\ \nu_{u(i)} &\sim \mathcal{N}(0, \sigma_\nu) \\ \eta_i &\sim \mathcal{N}(0, \sigma_\eta^{\ell(i)}) \\ \epsilon_{i,b(t)} &\sim \mathcal{N}(0, \sigma_\epsilon) \end{aligned}$$

2.1.2 Fit of the count model

We load the library `caperpyogm`, which contains the data and the functions that we used to fit the model:

```
library(caperpyogm)

## Loading required package: dplyr
##
## Attaching package: 'dplyr'
## The following objects are masked from 'package:stats':
##
##   filter, lag
## The following objects are masked from 'package:base':
##
##   intersect, setdiff, setequal, union
## Loading required package: rjags
## Loading required package: coda
## Linked to JAGS 4.2.0
## Loaded modules: basemod,bugs
```

All the datasets of the package are “lazy-loaded”, i.e. they are immediately available:

```
head(lekcounts)

##   lek period nbobs nbmales gr type natun year
## 1  81      1    -1      2  3   1    1    1
## 2 238      1     0      0  4   1    1    1
## 3 324      1     0      7  5   1    1    1
## 4 324      1     3     11  5   1    1    2
## 5   1      1     0      2  1   1    1    1
## 6   1      1     0      1  1   1    1    1
```

This data.frame contains the results of the counts carried out on all leks in the Pyrenees mountains from 2010 to 2019. For each count occasion, this data.frame contains:

- The lek label, numbered from 1 to 330
- The two-years period during which the count occurred
- The number of observers. We have subtracted 2 to the number of observers, to improve the mixing of the MCMC chains.
- The number of males counted on the lek
- The number of geographic region containing the lek
- The type of the lek (1 = KAL, 2 = KIL, 3 = UL)
- The label of the natural unit containing the lek
- The year during which the count occurred.

We have programmed the model in JAGS:

```

cat(modelCountDetectBinREY)

## model {
##
##   ## Priors for top parameters of the state model
##   sigmanu~dgamma(0.01,0.01)
##   sigmaepsilon~dgamma(0.01,0.01)
##   sigmakappa~dgamma(0.01,0.01)
##   sigmaREY~dgamma(0.01,0.01)
##
##   ## Priors for top parameters of the detection model
##   interceptpd~dnorm(0,0.1)
##   pentelpd~dnorm(0,0.1)
##
##   ## Priors for other parameters
##   for (i in 1:Ntypes) {
##
##     sigmaeta[i]~dgamma(0.01,0.01)
##
##     for (j in 1:Ngr) {
##       mukappa[j,i]~dnorm(0,0.1)
##       for (k in 1:Nperiods) {
##         kappa[j,i,k]~dnorm(mukappa[j,i], sigmakappa)
##       }
##     }
##
##   }
##
##   ## Random effect period
##   for (i in 1:Ngr) {
##     for (j in 1:Nyears) {
##       REY[i,j]~dnorm(0, sigmaREY)
##     }
##   }
##
##   ## Random effects natural units
##   for (i in 1:Nnatun) {
##     nu[i]~dnorm(0,sigmanu)
##   }
##
##   ## Expectation of the number of males
##   for (i in 1:Nleks) {
##     eta[i]~dnorm(0,sigmaeta[ellp[i]])
##     for (j in 1:Nperiods) {
##       epsilon[i,j]~dnorm(0,sigmaepsilon)
##       loglambda[i,j] <- kappa[gr[i],ellp[i],j]+nu[natun[i]]*ell2[i]+eta[i]+epsilon[i,j]
##       log(lambda[i,j]) <- loglambda[i,j]
##     }
##   }
##
##
##
##   ## Likelihood
##   for (i in 1:Nlekperiods) {
##     N[i]~dpois(lambda[lek[i], period[i]] )
##     for (k in 1:repetition[i]) {

```



```
##      logit(pd[i,k]) <- interceptpd + pente1pd*observers[i,k] + REY[gr[lek[i]],year[i,k]]
##      y[i,k]~dbin(pd[i,k], N[i])
##    }
##  }
## }
```

We now use the function `dataCount2jags` to prepare the data to fit the JAGS model:

```
dataList <- dataCount2jags(lekcounts$lek, lekcounts$period,
                           lekcounts$nbobs, lekcounts$nbmales,
                           lekcounts$gr, as.numeric(factor(lekcounts$type)),
                           lekcounts$natun, lekcounts$year)
```

We can now use the function `fitModelCount` to fit this model. WARNING: THIS CALCULATION TAKES A VERY LONG TIME (several hours) !!!! Note that we have included the results of this calculation as a dataset of the package, so that the reader does not need to launch this function to reproduce the other calculations:

```
coefModelCountDetectBinREY <- fitModelCount(dataList, "modelCountDetectBinREY")
```

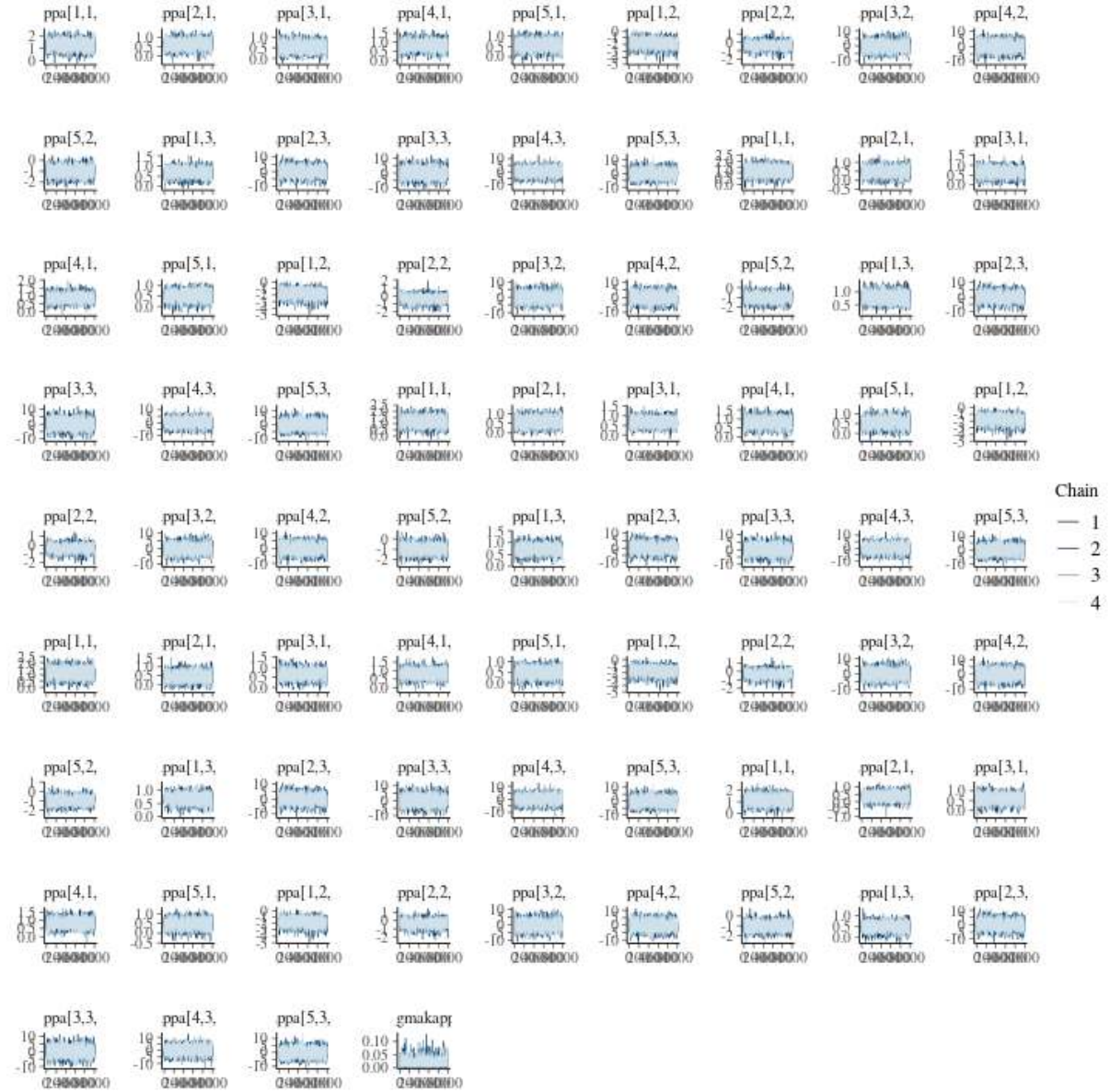
2.1.3 MCMC chains mixing

Once the MCMC samples have been obtained, we can plot the chain for a visual examination of the mixing. We present the traceplot for the parameters κ below:

```
library(bayesplot)

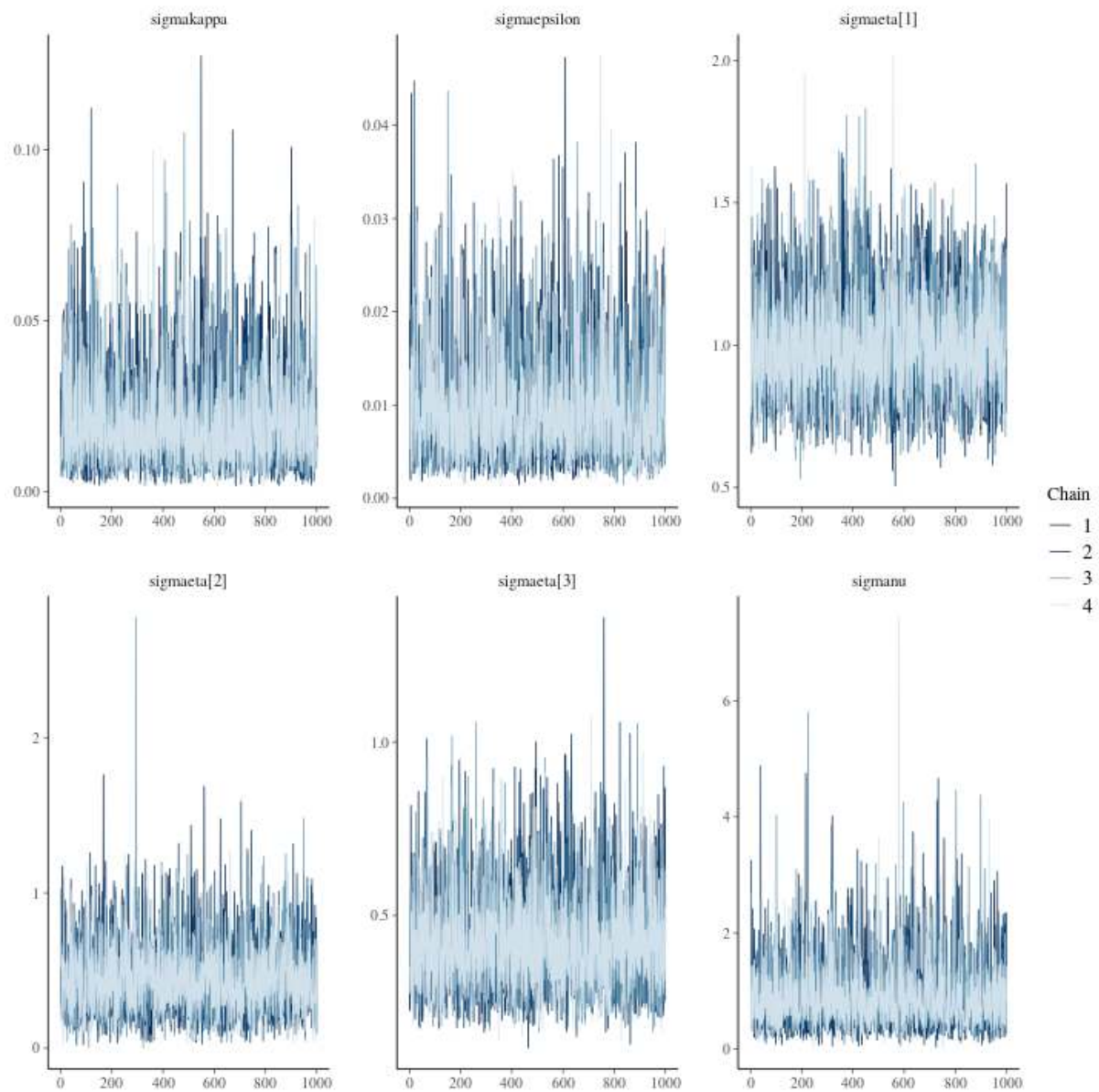
## Registered S3 methods overwritten by 'adehabitatMA':
## method      from
## print.SpatialPixelsDataFrame sp
## print.SpatialPixels      sp
## This is bayesplot version 1.8.0
## - Online documentation and vignettes at mc-stan.org/bayesplot
## - bayesplot theme set to bayesplot::theme_default()
## * Does _not_ affect other ggplot2 plots
## * See ?bayesplot_theme_set for details on theme setting

library(MCMCvis)
cm <- MCMCchains(coefModelCountDetectBinREY,
                 params=c("kappa","sigmakappa","sigmaepsilon","sigmaeta",
                           "sigmanu", "interceptpd","pente1pd","sigmaREY"),
                 mcmc.list=TRUE)
for (i in 1:length(cm)) {
  for (j in c("sigmakappa","sigmaepsilon","sigmaeta[1]",
              "sigmaeta[2]","sigmaeta[3]","sigmanu","sigmaREY"))
    cm[[i]][,j] <- 1/cm[[i]][,j]
}
mcmc_trace(cm, regex_pars="kappa")
```



We also present the traceplot for the variances of the state model:

```
mcmc_trace(cm, regex_pars=c("sigma_kappa", "sigma_epsilon", "sigma_eta",
                             "sigma_nu"))
```



Finally, we present the parameters for the detection model:

```
mcmc_trace(coefModelCountDetectBinREY,
  regex_pars=c("REY", "interceptpd", "pentelpd", "sigmaREY"))
```



We also calculate the Gelman diagnostic for the parameters. To save some space, we do not show the results of this diagnostic in this vignette and leave it to the reader to check the correct mixing based on this diagnostic:

```
gelman.diag(cm)
```

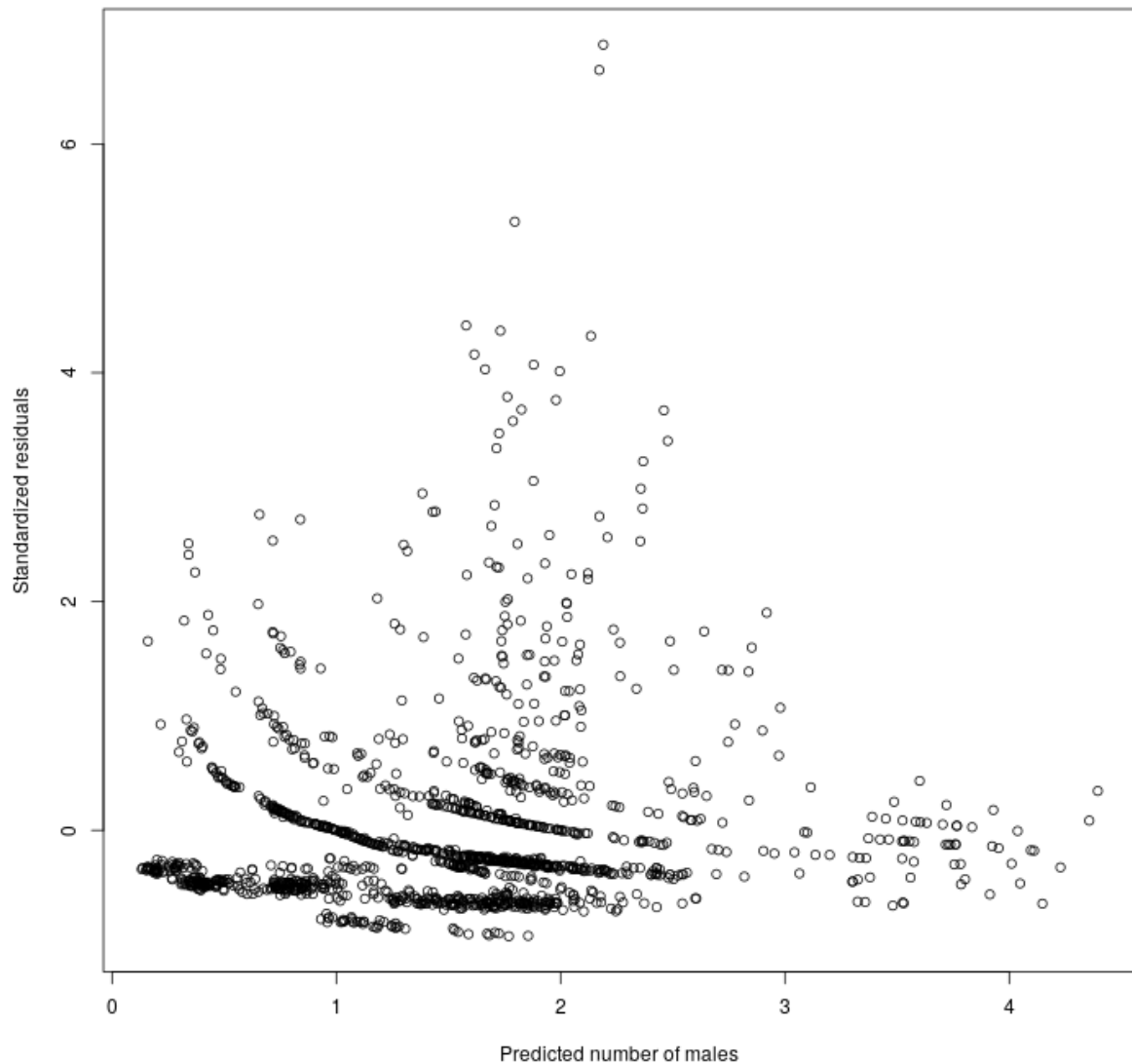
2.1.4 Goodness of fit

We then check the goodness of fit of the model. We simulate M virtual datasets (one per MCMC sample) and consider several summary statistics (see below). For each one, we compare the observed statistics (calculated on the actual dataset) with the distribution calculated on the simulated datasets. We first use the function `simulateModelCount` to simulate the datasets. WARNING!!! THIS CALCULATION CAN BE VERY LONG (about half an hour). Note that we have included the results of this calculation as a dataset of the package, so that the reader does not need to launch this function to reproduce further calculations:

```
simBinREY <- simulateModelCount(coefModelCountDetectBinREY, dataList)
```

We can then examine the distribution of the residuals of the model:

```
plot(predict(simBinREY), residuals(simBinREY),
      xlab="Predicted number of males",
      ylab="Standardized residuals")
```



Here, each point corresponds to a count occasion. These residuals do not present any problematic pattern, except a very small number standardized residuals greater than 6. This indicates a very minor overdispersion in the data.

Note that a group of count occasions with a residual greater than 6 correspond to the same lek. Indeed, this appears clearly if we calculate the residuals at the lek level:

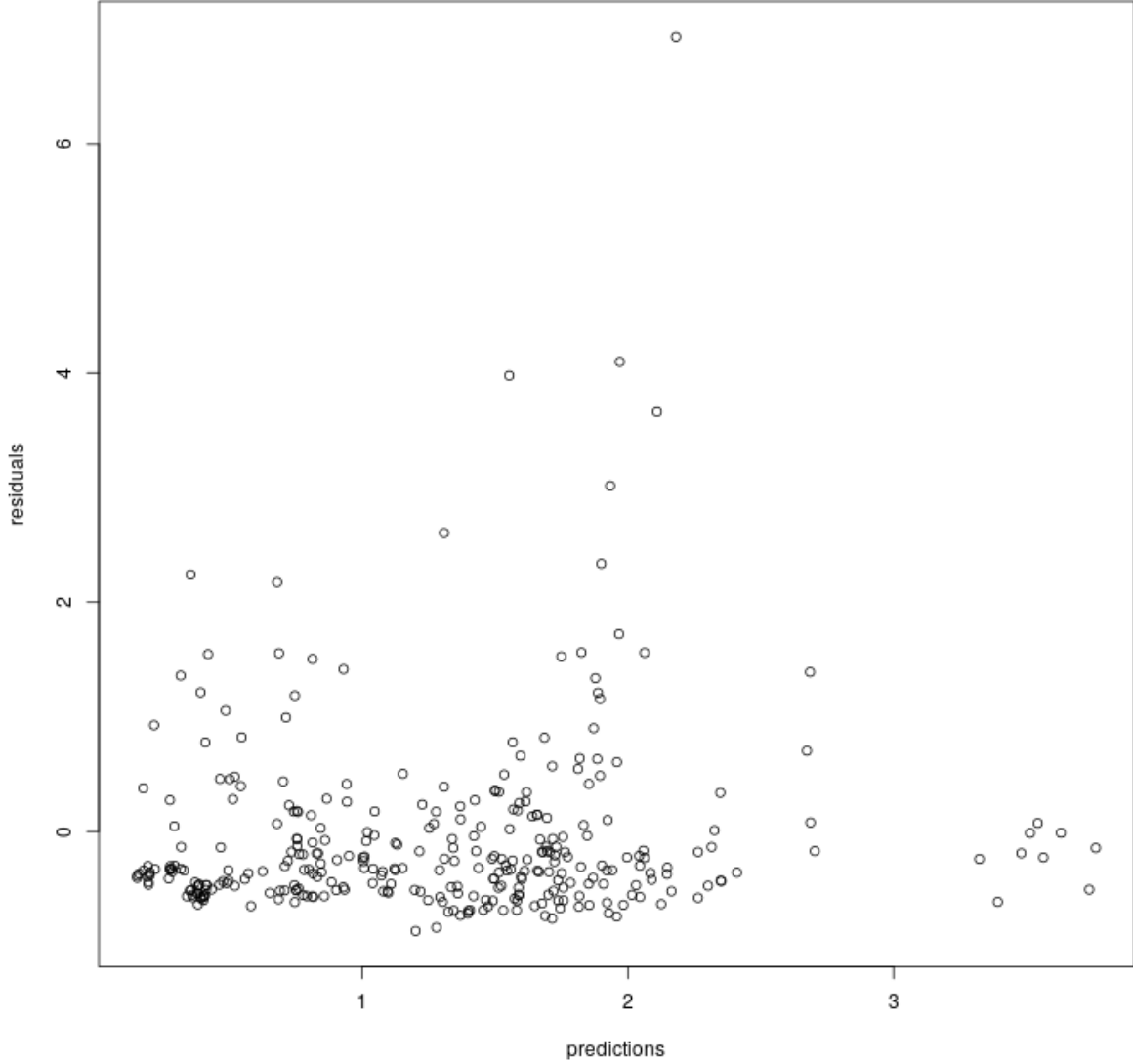
```
plot(predict(simBinREY, groupingFactor="lek"),
      residuals(simBinREY, groupingFactor="lek"),
```



```

xlab="predictions",
ylab="residuals")

```



Here, each point correspond to one lek. The largest residual correspond to the lek 281, an unknown lek that was discovered in 2013 and counted only this year. We study more in details in [section 4](#) the influence of this lek on our prediction.

2.1.5 Test of goodness of fit

We calculate various statistics to test the goodness of fit of our model. One possibility is to calculate, for each count occasion, the mean number of males \hat{y}_{itk} across all our simulated datasets. We can then calculate the chi-square statistics for the observed dataset:

$$\chi^2 = \sum_{i,t,k} \frac{(y_{itk} - \hat{y}_{itk})^2}{\hat{y}_{itk}}$$

We can then compare the observed χ^2 to the distribution of this statistics under the simulated datasets. We calculate below the proportion of simulated χ^2 lower than the observed value:

```

od <- simBinREY$origData
sim <- simBinREY$sim
ry <- od$nbmales

## Chi2 obs
chi2obs <- (sum(((ry-apply(sim,1,mean))^2)/apply(sim,1,mean)))

## distribution of simulated Chi2
chisq <- ((sim-apply(sim,1,mean))^2)/apply(sim,1,mean)
ch <- (colSums(chisq))

## proportion of chi-square
mean(ch>=chi2obs)

## [1] 0.67125

```

The observed chi-square is in the middle of the simulated distribution. We can also compare other statistics, e.g. compare the observed total number of detected males over the 10 years of the study with the distribution of simulated values:

```

mean(colSums(sim)>=sum(ry))

## [1] 0.317

```

We can also, for each count occasion, calculate a 80% credible interval on the expected detected number of males (using the simulated datasets), and calculate the proportion of count occasions falling in the credible interval:

```

q1 <- apply(sim,1,quantile,0.1)
q2 <- apply(sim,1,quantile,0.9)
mean((ry>=q1)&(ry<=q2))

## [1] 0.9150103

```

We define below a function named `comparef`, which calculates the proportion of simulated numbers greater than or equal to the observed number, for each level of a variable of the observed dataset `od`:

```

comparef <- function(na)
{
  ta <- tapply(ry,na,sum)
  app <- apply(sim,2,function(x) tapply(x,na,sum))
  sapply(1:nrow(app), function(i) mean(ta[i]>app[i,]))
}

```

We can for example calculate this proportion for each geographic region (and use as statistic for each one the total number of animals detected in a region over the 10 years of the study):

```

comparef(od$gr)

## [1] 0.56175 0.55800 0.79800 0.55175 0.77400

```

We can also use combination of variables, for example calculate this proportion for each combination of geographic region, type of lek, and period:

```
comparef(paste0(od$gr, "-", od$type, "-", od$period))

## [1] 0.50350 0.44475 0.35600 0.32625 0.00000 0.00000 0.39450
## [8] 0.22300 0.69625 0.00000 0.92525 0.98875 0.67100 0.74275
## [15] 0.31200 0.55750 0.56125 0.85525 0.17600 0.15650 0.54650
## [22] 0.57025 0.52075 0.66850 0.60300 0.85175 0.50225 0.89850
## [29] 0.65275 0.57175 0.63475 0.55300 0.29725 0.59800 0.74025
## [36] 0.84125 0.81200 0.88525 0.75675 0.35425 0.33600 0.45000
## [43] 0.31900 0.60200 0.23375
```

We have checked the goodness of fit of our model on other variables and combination of variables (leks, gr-years, etc.). We leave it to the reader to play with this function to check other variables if they want.

2.2 Grid cells search model

2.2.1 Model description

Consider a grid cell q sampled by our protocol. If this cell was sampled before 2018, our protocol implied that observers should search unknown leks in the sampled cell according to the protocol described in Calenge et al. (in prep). An update of our grid cells sampling frame in 2018-2019 resulted in the inclusion of additional information: indeed, several unknown leks have been discovered between 2010 and 2017 by the network of observers outside the framework of our monitoring (e.g. resulting either from accidental discovery, from compilation of local knowledge, or from local initiatives leading to the search for new leks). See a more detailed explanation of this update of our sampling frame in section 6. Therefore, some of the grid cells sampled in 2018-2019 may already contain an unknown lek discovered previously by the network. In such cases, no search was organized in the sampled grid cell, since the occurrence of an unknown lek was already known.

Let z_q be a binary variable taking the value 1 if this cell contains an unknown lek detected during a search organized within the framework of our program and 0 otherwise (thus, if a cell q contains an unknown lek discovered prior to its sampling, $z_q = 0$). Let f_q be a binary variable taking the value 1 if the cell was randomly sampled in 2018 or 2019, and 0 otherwise. Finally, let s_q be a binary variable taking the value 1 if cell q included an unknown lek discovered prior to its sampling and 0 otherwise.

We defined the following model to describe the probability of presence π_q of an unknown lek in a grid cell q :

$$\begin{aligned} z_q &\sim \mathcal{B}(b_q \times (1 - s_q) \times \beta) \\ s_q &\sim \mathcal{B}(b_q \times f_q \times \alpha) \\ b_q &\sim \mathcal{B}(\pi_q) \end{aligned}$$

where β is the probability of detection of an unknown lek during the search of a grid cell, and α is the probability that an unknown lek present in the cell was discovered prior to its sampling. The parameters α, β, π_q are unknown and must be estimated.

We modelled the probability of presence of an unknown lek in a grid cell with the following model:

$$\text{logit } \pi_q = a_{g(q)} + b_{g(q)} \times r_q + d \times h_q \quad (5)$$

where r_q measures the proportion of the grid cell q covered by area of presence of the species (defined by experts in 2009, before the onset of the program), and h_q is a binary variable taking the value 1 if the

grid cell q contains a known lek and 0 otherwise. The intercept $a_{g(q)}$ and slope of the area of presence $b_{g(q)}$ is supposed to vary between geographical regions.

We estimate the parameter β with the data collected during the experiment carried out to estimate the probability to detect a lek unknown to the observer in a grid. A sample of grid cells containing a known number of known leks (but unknown to the observers) was drawn and each cell was assigned to one observer. Two observers participated to this experiment: one experienced observer and one inexperienced one. Let N_c be the number of known leks included in the grid cell c . The observer searching this cell defines a search sector. Let S_c be the number of these known leks included in the search sector. Finally, let D_c be the number of known leks detected by the observer in this sector. We define the binary variable $e(c)$ taking the value 1 if the observer searching the cell c is experienced and 0 if the observer is inexperienced. We use the following model:

$$\begin{aligned} D_c &\sim \mathcal{B}(S_c, \delta) \\ S_c &\sim \mathcal{B}(N_c, \zeta_{e(c)}) \end{aligned}$$

where δ is the probability to detect a lek during the search, given that the lek is present in the search sector, and $\zeta_{e(c)}$ is the probability that the search sector defined by the observer includes the lek. Note that this latter probability depends on the experience of the observer. We supposed that the detection probability β was uniformly distributed between the minimum detection probability $\delta \times \zeta_0$ (characterizing inexperienced observers) and $\delta \times \zeta_1$ (characterizing highly experienced observers):

$$\beta \sim \mathcal{U}(\delta \times \zeta_0, \delta \times \zeta_1)$$

Thus, the unknown parameters of our model are $\{a_{g(q)}\}_{g=1}^3, \{b_{g(q)}\}_{g=1}^3, d, \delta, \zeta_0, \zeta_1$.

2.2.2 Model fit

We need two datasets to fit this model. First, the dataset `gridSearch` contains the data collected during grid cells search:

```
head(gridSearch)

##   presenceArea newUL previousSearch hasPreviousUL gr
## 1    0.9172760     0              0              0  1
## 2    0.4677633     1              0              0  1
## 3    0.4480399     0              0              0  1
## 4    0.9542109     0              0              0  1
## 5    0.5240671     0              0              0  2
## 6    0.6726517     0              0              0  1
##   presenceKL
## 1           1
## 2           1
## 3           0
## 4           0
## 5           1
## 6           1
```

For each grid cell search, this data.frame contains:

- The proportion of the grid cell covered by the area of presence of the capercaillie (as defined by a group of experts in 2009, before the onset of the program).
- Whether (1) or not (0) a new, unknown lek was discovered during the cell search.
- Whether (1) or not (0) the cell was sampled in 2018-2019 (i.e. could possibly contain an unknown lek discovered outside the framework of our program, prior to its sampling)

- Whether (1) or not (0) the cell contained an unknown lek discovered prior to its sampling.
- The label of the geographic region containing the grid cell (1= Piemont, 2=High area, 3 = Pyrenees national parc).
- Whether (1) or not (0) the grid cell contained a known lek.

We also need the data.frame **DetectionExpe**, containing the data collected during the experiment designed to assess the detectability of new leks during grid cells searches:

DetectionExpe

```
##      observer Nquad Nsect Ndete
## 1  Inexperienced     5     2     2
## 2  Inexperienced     2     1     0
## 3  Inexperienced     2     1     0
## 4  Inexperienced     1     1     1
## 5  Inexperienced     2     1     1
## 6  Inexperienced     4     1     1
## 7  Inexperienced     2     0     0
## 8  Inexperienced     1     1     1
## 9  Inexperienced     3     2     1
## 10 Experienced     1     1     1
## 11 Experienced     0     0     0
## 12 Experienced     1     0     0
## 13 Experienced     3     2     1
## 14 Experienced     2     2     2
## 15 Experienced     1     1     1
## 16 Experienced     1     1     0
```

For each grid cell sampled for this experiment, this data.frame contains:

- Whether the observer was experienced or inexperienced.
- The number of known leks in the cell.
- The number of known leks present in the search sector defined by the observer.
- The number of known leks detected by the observer.

We have programmed the model in JAGS:

```
cat(modelULPresence)

## model {
##
## P_inclusion_inex~dunif(0.0000001, 0.9999999)
## P_inclusion_expe~dunif(0.0000001, 0.9999999)
## P_detection~dunif(0.0000001, 0.9999999)
##
## for (i in 1:Ninex) {
##     inex_Nsect[i]~dbin(P_inclusion_inex, inex_Nquad[i])
##     inex_Ndete[i]~dbin(P_detection, inex_Nsect[i])
## }
```

```
##
##
## for (i in 1:Nexpe) {
##   expe_Nsect[i]~dbin(P_inclusion_expe, expe_Nquad[i])
##   expe_Ndete[i]~dbin(P_detection, expe_Nsect[i])
## }
##
## pmin <- P_detection*P_inclusion_inex
## pmax <- P_detection*P_inclusion_expe
## pd ~ dunif(pmin, pmax)
##
##
## pdprev~dunif(0,1)
## for (i in 1:Ngr) {
##   a[i]~dnorm(0,0.1)
##   b[i]~dnorm(0,0.1)
## }
## d~dnorm(0,0.1)
##
## for (i in 1:Nq) {
##   logit(pp[i]) <- a[gr[i]]+b[gr[i]]*presenceArea[i]+d*presenceKL[i]
##   pres[i]~dbern(pp[i])
##   hasPreviousUL[i]~dbern(pres[i]*previousSearch[i]*pdprev)
##   newUL[i]~dbern(pres[i]*(1-hasPreviousUL[i])*pd)
## }
##
## }
```

We prepare the datasets for the fit:

```
dataListQ <- datagrid2jags(gridSearch, DetectionExpe)
```

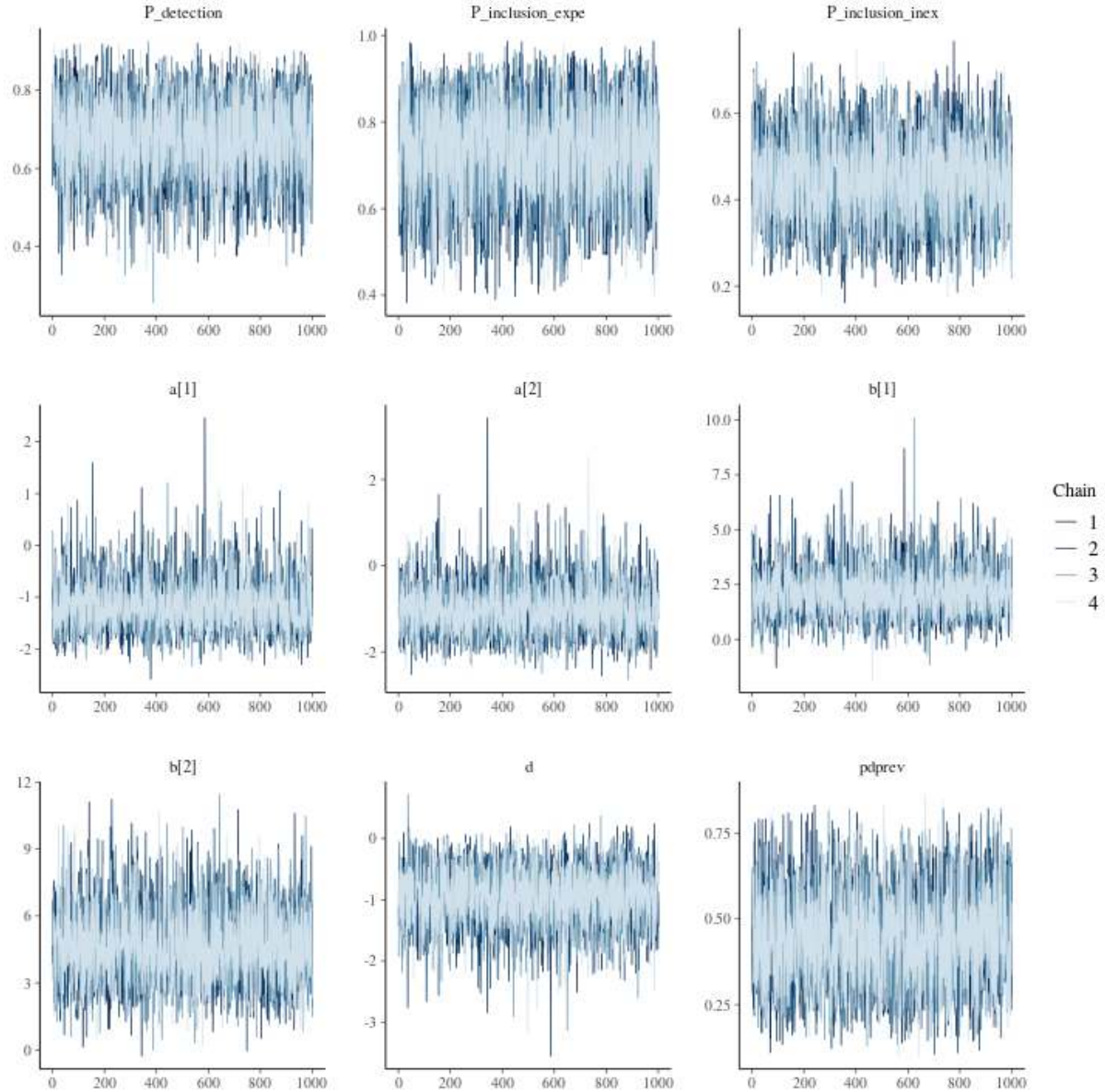
We can now use the function `fitModelGrid` to fit this model. WARNING: THIS CALCULATION TAKES A VERY LONG TIME (several hours) !!!! Note that we have included the results of this calculation as a dataset of the package, so that the reader does not need to launch this function to reproduce the other calculations:

```
coefModelULPresence <- fitModelGrid(dataListQ, "modelULPresence")
```

2.2.3 MCMC chains mixing

Once the MCMC samples have been obtained, we can plot the chain for a visual examination of the mixing:

```
mcmc_trace(coefModelULPresence)
```



We also calculate the Gelman diagnostic for the parameters:

```
gelman.diag(coefModelULPresence)
```

Mixing properties are excellent here.

2.2.4 Goodness of fit

We then check the goodness of fit of the model. As for the count model, we simulate M virtual datasets (one per MCMC sample) and consider several summary statistics (see below). For each one, we compare the observed statistics (calculated on the actual dataset) with the distribution calculated on the simulated datasets. We first use the function `simulateModelGrid` to simulate the datasets. Fortunately, this function is faster than the one used for the count model, so that it can readily be executed by the user:

```
sg <- simulateModelGrid(coefModelULPresence, dataListQ)
```

We can then calculate the proportion of the simulated values lower than the observed value of the total number of unknown leks discovered in our study:

```
obs <- sum(dataListQ$newUL)
sim <- colSums(sg$sim)
mean(sim<obs)

## [1] 0.4855
```

The observed value is in the middle of the distribution expected under our model. We can calculate the same proportion for each geographical region (piemont or high mountains):

```
obs <- tapply(dataListQ$newUL, dataListQ$gr, sum)
sim <- apply(sg$sim, 2, function(x) tapply(x, dataListQ$gr, sum))

## Region 1
mean(sim[,1]<obs[1])

## [1] 0.56475

## Region 2
mean(sim[,2]<obs[2])

## [1] 0.34575
```

The simulated values are well within the distribution.

2.3 Estimation of the number of males in each region

Let $S_{g\ell}$ be the number of leks of type ℓ in the region g . Note that this number needs to be estimated for unknown leks (i.e. for $\ell = 3$). The grid cell search model can be used to estimate S_{g3} . We estimate this number:

$$\widehat{S_{g3}} = \sum_{q=1}^Q \pi_q \quad (6)$$

where the probability π_q is calculated for each grid cell q with the equation 5, and the sum is calculated over all the grid cells of the frame where the searched cells have been sampled. Then, the number of males $n_{g\ell b}$ in the geographic region g for the type of lek ℓ during the period b can be estimated with:

$$\widehat{n_{g\ell b}} = \sum_{\ell=1}^3 S_{g\ell} \exp \{ \kappa_{g,\ell,b} + I(\ell = 2) \times \sigma_\nu^2/2 + \sigma_\eta^2/2 + \sigma_\epsilon^2/2 \}$$

Of course, we can calculate one estimate $\widehat{n_{g\ell b}}$ per MCMC iteration, so that the posterior distribution of the number of males in a given region during a given period can be readily obtained. Finally, the number of males over the whole mountain range during a given period b is calculated by:

$$\widehat{n_b} = \sum_{g=1}^5 \sum_{\ell=1}^2 \widehat{n_{g\ell b}}$$

We show how we estimated We store the number of KAL and KIL in each one of the five regions:

```
NKAL <- c(14L, 64L, 76L, 48L, 46L)
NKIL <- c(6L, 80L, 102L, 32L, 96L)
```

We use the function `estimateNmales` to combine the two models and estimate the number of males in the different geographical regions. The frame of grid cells as an argument is required for the estimation of the number of unknown leks in each region. This frame is stored in the dataset `gridFrame`:

```
head(gridFrame)

##   presenceArea presenceKL gr grqf
## 1  -0.40143980          0  2    2
## 2  -0.33081494          0  2    2
## 3  -0.40143980          0  2    2
## 4  -0.33839617          0  2    2
## 5  -0.35121600          0  2    2
## 6   0.03079977          0  2    2
```

This data.frame contains the following variables for each grid cell:

- proportion of the cell covered by the presence area of the capercaillie
- whether the cell contains (1) or not (0) a lek already known
- the geographic region (original partitioning in 5 regions)
- the geographic region code used in the grid cell search model (1 = piemont, 2 = high range)

```
nm <- estimateNmales(coefModelCountDetectBinREY, coefModelULPresence,
                    gridFrame, NKAL, NKIL)
```

The function `summary` allows to show the estimation of the number of males for each one of the five period:

```
summary(nm)

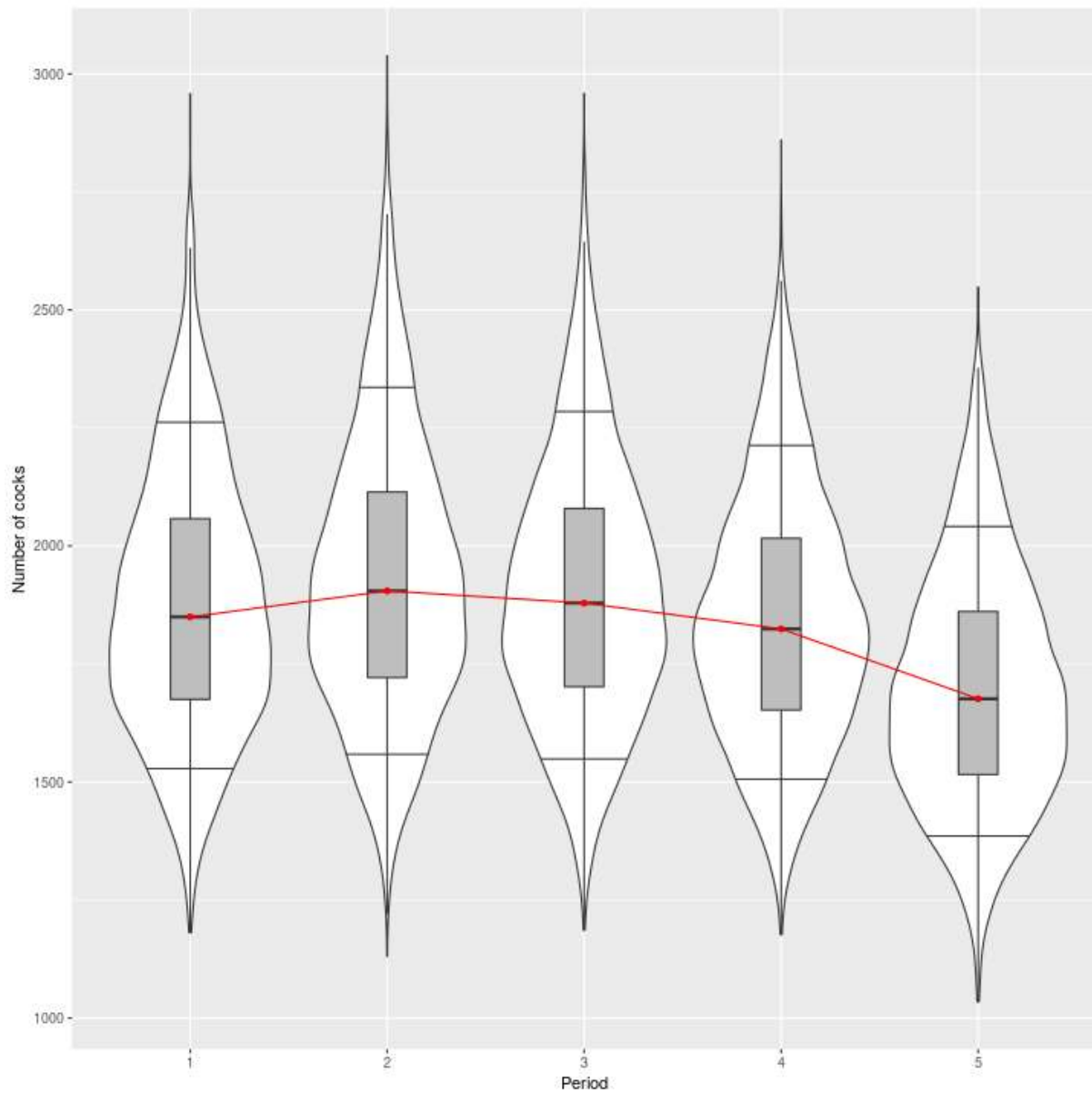
## Estimates of the number of males during the 5 periods
## in the whole Pyrenees Mountains (median and 80% CI):
##
##   Point.est   CIlow   CIup
## 1  1871.789 1542.350 2350.656
## 2  1922.285 1570.448 2440.920
## 3  1901.102 1562.484 2387.119
## 4  1841.119 1516.075 2308.645
## 5  1694.132 1398.089 2129.504
##
## Change rate between period 1 and period 5 is: -8.49% (80% CI: -20.24% -- 0.13%)
##
## Probability of scenari (decrease:< -10%; stability:-10--10%; increase:>10%):
##
##   scenario probability
## 1  decrease      0.43100
## 2  stability      0.56575
## 3  increase       0.00325
```

This function returns the point estimate of the population size each period (with a 80% credible interval), the point estimate of the rate of change of this size between the first and last period, and the probability of the three scenarios: increase (actual change rate > 10%), decrease (actual change rate < -10%), stability

(otherwise).

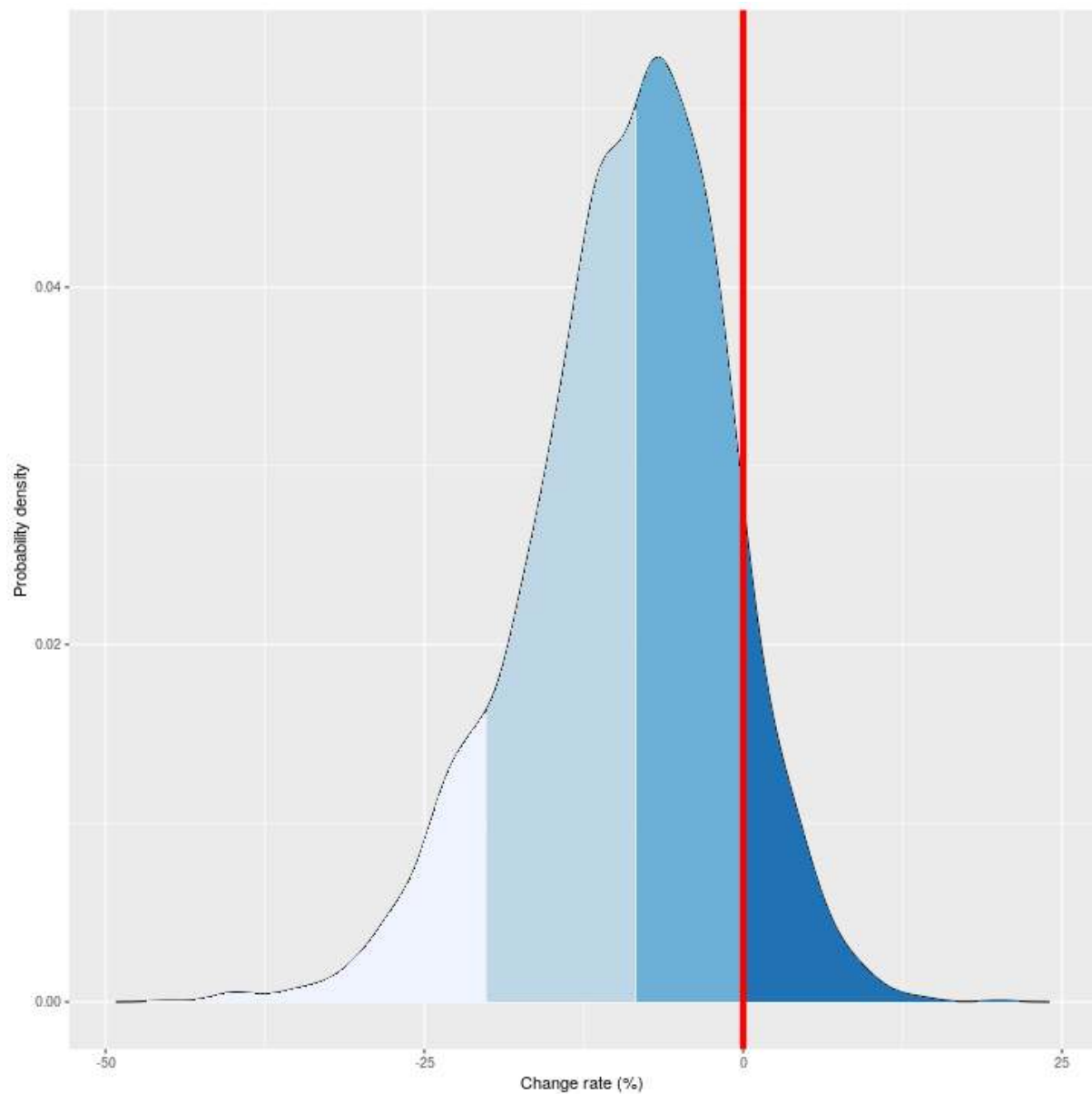
The function `distritime` shows the posterior distribution of the estimated population size during the 5 periods:

```
distritime(getTotal(nm))
```



The function `showChangeRate` can be used to estimate the rate of change of the population size between the first and last period:

```
showChangeRate(nm)
```



Note that we can estimate the number of males in a given region with the function `summary`. For example, for the region 1:

```
summary(nm,1)

## Estimates of the number of males during the 5 periods
## in the geographic region 1 (median and 80% CI):
##
##   Point.est    CIlow    CIup
## 1  155.9515  111.19115  227.6323
## 2  154.9948  109.65762  219.2993
## 3  149.0112  106.98677  213.7739
## 4  145.4841  104.07529  209.1013
## 5  135.4594   95.31548  198.5411
##
## Change rate between period 1 and period 5 is: -12.1% (80% CI: -28.59% -- 2.13%)
##
## Probability of scenari (decrease:< -10%; stability:-10--10%; increase:>10%):
##
```


##	scenario	probability
## 1	decrease	0.57125
## 2	stability	0.40050
## 3	increase	0.02825

3 Assumptions on the detection process and on constant number of males within two-years periods

3.1 List of alternative models

The population size estimation by a N-mixture model can be very sensitive to the misspecification of the detection process [LIN18]. We considered several alternative models for this process before choosing the approach detailed in our paper. We also tried to check our assumption of a constant number of males within the two-year periods. We describe these models in this section, and show in the next sections how we compared the different models with cross validation.

We recall the detection model used in the paper:

$$\text{logit } p_{i,t,k} = \alpha_d + \beta_d \times o_{i,t,k} + e_{g(i),t}$$

where $o_{i,t,k}$ is the number of observers partipating to the k-th count occasion on lek i during year t , and $e_{g(i),t}$ is a Gaussian random effect describing the variation in detectability during a given year in a given region. As already described, this model is programmed for the JAGS software in the dataset `modelCountDetectBinREY` of the package.

We first tested whether the year random effect was required in the model, by fitting the simpler model:

$$\text{logit } p_{i,t,k} = \alpha_d + \beta_d \times o_{i,t,k}$$

i.e., the same model as before, but without the year random effect. This model is programmed for the JAGS software in the dataset `modelCountDetectBin`.

We also tested the model `modelCountDetectBin` by considering one-year periods. Indeed, in our paper, we have supposed that the number of males present in a given region did not vary within two-years periods. Within a given period, the between year variation in the number of detected males was supposed to be caused by between year variability in the probability of detection. We therefore tried to check this assumption by setting $b(t) = t$ in equations 1, 3, and 4, and by fitting the binomial detection model without year random effects.

Then, we tested whether an extra-binomial variation was required for the detection process by modelling the number of detected animals as a beta-binomial distribution (see [MAR11]). That is, we suppose the following model:

$$\begin{aligned} \text{logit } d_{i,t,k} &= \alpha_d + \beta_d \times o_{i,t,k} + e_{g(i),t} \\ p_{i,t,k} &\sim \text{Beta} \left(d_{i,t,k} \times \frac{1 - \delta^2}{\delta^2}, (1 - d_{i,t,k}) \times \frac{1 - \delta^2}{\delta^2} \right) \end{aligned}$$

This model is programmed for the JAGS software in the dataset `modelCountDetectBetaBinREY`.

Finally, we tested whether the relationship between the probability of detection and the number of observer was linear by including a quadratic effect of this variable in our model:

$$\text{logit } p_{i,t,k} = \alpha_d + \beta_d \times o_{i,t,k} + \omega_d \times o_{i,t,k}^2$$

This model is programmed for the JAGS software in the dataset `modelCountDetectBinREY0bs2`.

3.2 On the use of cross-validation to compare several models. Theory

We have used the approach described by [VEH17] to compare various models for the detection process. This approach relies on cross-validation and allows to identify, in a set of alternative models, the one that will allow the best prediction of the values of the variables of interest. We describe this approach in this section, and show how we applied it in our case in the next section.

Consider two models \mathcal{M}_0 and \mathcal{M}_1 fit on the same dataset. We can use the *expected log pointwise predictive density for a new dataset*, or **elpd** as a criterion to compare the two models.

We have a dataset with n units, each unit i being characterized by the measure of a response variable y_i . The elpd, calculated on the dataset for a given model measures the ability of the model to predict the same variable y on a new independent dataset of the same size (i.e. with n units).

Consider a virtual example (we will consider our study in the next section). Imagine that we are studying a unique lek, and that we carry out n counts of the male capercaillie on this lek. We suppose, in our example, that the number of detected males y_i during count occasion i is drawn from a binomial distribution with parameters N (the actual number of males) and d (the detection probability). We measure the quality of our prediction by our model by calculating the elpd on four model, i.e. by trying to predict the number of detected males in n new count occasions in the same conditions.

In theory, for a given model \mathcal{M}_0 , this criterion should be calculated by:

$$\text{elpd} = \sum_{i=1}^n \int p_t(\tilde{y}_i) \log p(\tilde{y}_i|y, \mathcal{M}_0) d\tilde{y}_i$$

where \tilde{y}_i is the value of the variable y for the unit i in the new dataset (in our virtual exemple, the number of detected males during the count occasion i on the lek in our new dataset). The value of $p_t(\tilde{y}_i)$ is the *true* probability to have \tilde{y}_i (under the true process), and $p(\tilde{y}_i|y, \mathcal{M}_0)$ the probability to obtain \tilde{y}_i under the model \mathcal{M}_0 fit on the observed dataset y . When this criterion is high, the model is similar to the reality (as $p_t(\tilde{y}_i)$ is important when $p(\tilde{y}_i|y, \mathcal{M}_0)$ is important).

In practice, we cannot calculate the value of the elpd since we do not know the true model $p_t(\tilde{y}_i)$. [VEH17] propose several approaches relying on cross-validation to estimate the elpd with the available dataset. We will not describe all these approaches; instead, we describe the *K-fold cross validation* approach that we implemented in our study.

We randomly partition the dataset in K subsamples. Then, one subsample is retained as validation set and the remaining $K - 1$ subsamples are used as a calibration dataset: the model \mathcal{M}_0 is fit to this dataset. The fit of the model by MCMC allows to obtain S vectors $\theta^{s,k}$ randomly drawn from the posterior distribution $p(\theta|y_{-k}, \mathcal{M}_0)$, with y_{-k} the calibration dataset obtained after the removal of the subsample k . More simply, $\theta^{s,k}$ is the θ simulated at the iteration s of the MCMC used to fit the model after removal of the subsample k . Then, for each observation i belonging to the tests set k , we calculate the contribution of the observation i to the estimated elpd by:

$$\widehat{\text{elpd}}_i(\mathcal{M}_0) = \log \left(\frac{1}{S} \sum_{s=1}^S p(y_i|\theta^{k,s}, \mathcal{M}_0) \right)$$

with $p(y_i|\theta^{k,s}, \mathcal{M}_0)$ the probability to obtain the observed value y_i , for the parameter vector $\theta^{s,k}$ generated by the s -th MCMC iteration. This probability can be calculated thanks to the model \mathcal{M}_0 .

This operation is repeated on all subsamples k , which allows to obtain an estimate of the contribution $\widehat{\text{elpd}}_i$ to the elpd for all observations i of the dataset. We can estimate the total elpd by:

$$\widehat{\text{elpd}}_{\text{xval}}(\mathcal{M}_0) = \sum_i \widehat{\text{elpd}}_i(\mathcal{M}_0)$$

More simply, this estimate of the elpd is obtained by summing on all statistical units the mean log posterior probability to obtain the response variable for this unit thanks to the model that would have been fit without this unit. We predict the data thanks to a model fit without these data.

3.3 K-fold cross-validation in our study

Now consider our study, and in particular the N-mixture model used to predict the mean number of males on leks. This is a hierarchical model, which raises the question of the level at which we wish to assess the predictive ability of our model. Considering the aim of the model is essential to choose this level [MER19]. Actually, our aim is to be able to predict the time changes of the actual number of males on leks not included in the sample.

We partition our dataset in $K = 10$ subsamples ([VEH17] indeed recommend to define at least 10 subsamples in *K-fold cross validation* approaches). As our aim is to predict the number of males that would have been detected on leks not included in the sample, we include *all* the counts carried out on a leks (all count occasions and all years) to the same subsample. This approach is the *grouped K-fold for leave-one-group out* defined in https://avehtari.github.io/modelselection/rats_kcv.html. In other words, we have N leks (each one being counted one or several years, with one or several count occasions every year), and these N leks are partitionned in K subsamples of N/k leks.

As described in the previous section, we fit a model on a calibration dataset excluding a subsample for each subsample k in turn. For each calibration dataset excluding a subsample k , we then have a sample of S MCMC generated vectors of parameters $\theta^{k,s}$ containing the parameters at the top of the model $(\kappa_{g(i),\ell(i),b(t)}, \sigma_\kappa, \sigma_\epsilon, \sigma_\eta, \sigma_\nu, \alpha_d, \beta_d, \sigma_e)$.

We assess for each lek of the group k , the contribution to the elpd of the set of counts carried out on lek i . Thus, if \mathbf{y}_i is the vector containing the set of counts carried out on lek i between 2010 and 2019, we need to calculate the probability $p(\mathbf{y}_i|\theta^{k,s}, \mathcal{M}_0)$ to get this set of count for each vector $\theta^{k,s}$. The contribution of the lek i to the elpd is calculated by:

$$\widehat{\text{elpd}}_i(\mathcal{M}_0) = \log \left(\frac{1}{S} \sum_{s=1}^S p(\mathbf{y}_i|\theta^{k,s}, \mathcal{M}_0) \right)$$

And the total elpd is calculated by summing these contributions over all leks.

The calculation of $p(\mathbf{y}_i|\theta^{k,s}, \mathcal{M}_0)$, required for the calculation of elpd, is a bit tricky. Indeed, it can be calculated by:

$$p(\mathbf{y}_i|\theta^{k,s}, \mathcal{M}_0) = \int p(\mathbf{r}_i|\mathbf{N}_i) \times p(\mathbf{N}_i|\theta^{k,s}, \mathcal{M}_0) d\mathbf{N}_i$$

with \mathbf{N}_i the vector containing the numbers of detected males for each two-years periods. We approximate this integral by a Montecarlo approach [ROB10]. For each vector $\theta^{k,s}$ generated by MCMC, we simulated $R = 1000$ vectors $\mathbf{N}_i^{(r)}$ using our model. For each simulated vector: (i) we simulated for each a lek effect η_i , an overdispersion residual ϵ_{ij} , and possibly a natural unit effect $\nu_{u(i)}$; (ii) we summed these effects and added the simulated value of $\kappa_{g(i),\ell(i),b}$ to calculate the value of $\log \lambda_{it}^{(r)}$; (iii) we randomly sampled R actual number of males $N_{it}^{(r)}$ in a Poisson distribution with parameter $\lambda_{it}^{(r)}$, and we derived from each vector $\mathbf{N}_i^{(r)} = \{N_{it}^{(r)}\}_{p=1}^5$ the probability $p(\mathbf{y}_i|\mathbf{N}_i^{(r)}, \theta^{k,s})$ under our detection model. The probability $p(\mathbf{y}_i|\theta^{k,s}, \mathcal{M}_0)$ is then equal to the mean over all R simulations of these probabilities $p(\mathbf{y}_i|\mathbf{N}_i^{(r)}, \theta^{k,s})$:

$$\hat{p}(\mathbf{y}_i|\theta^{k,s}, \mathcal{M}_0) = \frac{1}{R} p(\mathbf{y}_i|\mathbf{N}_i^{(r)}, \theta^{k,s})$$

The probability $p(\mathbf{y}_i|\mathbf{N}_i^{(r)}, \theta^{k,s})$ is calculated by the product of the probabilities $p(y_{itk}|N_{it}, \theta^{k,s})$ over all count occasions carried out during our study period.

To sum up, *in theory*, for a given model \mathcal{M}_0 , the elpd is calculated by summing the individual contributions $\widehat{\text{elpd}}_i(\mathcal{M}_0)$ over all leks i . However, the number of count occasions differs a lot between leks (between 1 to 19 count occasions in 10 years). But the probability to observe a given set of counts will decrease when the number of count occasions increase: for example, if p is the probability to detect n males during a count occasion, then the probability to detect n males during each one of two count occasions is p^2 if these two counts are independent. In other words, the probability to observe a given set of counts will decrease with the size of the set. In other words, the logarithm of the mean of $p(\mathbf{y}_i|\theta^{k,s}, \mathcal{M}_0)$ over all simulations s will be much smaller for leks with many count occasions: these leks will have a much larger weight in the calculation the elpd.

This problem was not considered in [VEH17] (who focus their paper on leave-one-out cross-validation, where this difference in sample size among units is not considered). We propose to complete this analysis with an approach attempting to correct these unequal weights. As noted before, the order of magnitude of the probability to observe n events will be p^n if the probability to observe one event is p and if these events are independent. Therefore, the log-probability will be equal to $n \log p$.

Therefore, *if the c_i counts carried out on a given lek i were independent*, we would expect $\widehat{\text{elpd}}_i(\mathcal{M}_0)$ to decrease linearly with c_i . In such a case, replacing $\widehat{\text{elpd}}_i(\mathcal{M}_0)$ in the calculation of the elpd with $\widehat{\text{elpd}}_i(\mathcal{M}_0)/c_i$ would allow to give the same weight to all leks in the calculation of the elpd. Let elpd^c be the elpd “corrected” by this approach.

However, note that in our study, the c_i counts carried out on a given lek *are not* independent: some counts are carried out during the same year and some during different years; some are carried out during the same period and some during different periods, etc. Therefore, c_i is an overestimation of the “effective” sample size for lek i , and dividing the $\widehat{\text{elpd}}_i(\mathcal{M}_0)$ by c_i will “over-correct” the places with the largest number of count occasions.

Thus, elpd gives too much weight to the big leks in the model comparison, and elpd^c does not give enough weight to these leks. However, if these two criteria return the same conclusions, we will be confident that the selected model is the best one in the set of compared models.

We calculated the contributions to elpd and elpd^c for each model. We also calculated the standard deviation of the difference between the elpd/ elpd^c of a model \mathcal{M}_r and the elpd/ elpd^c of the best model \mathcal{M}_b in the set. This standard deviation is calculated by:

$$\sqrt{\frac{n}{n-1} \sum_{i=1}^n (\Delta_i - \bar{\Delta})^2}$$

Where $\Delta_i = \widehat{\text{elpd}}_i(\mathcal{M}_s) - \widehat{\text{elpd}}_i(\mathcal{M}_b)$, and $\bar{\Delta}$ is the mean of the Δ_i . The standard deviation for the elpd^c is obtained similarly by replacing elpd by elpd^c in the above formula.

Finally, we carried out a randomization test to determine if the elpd of a model was significantly different from the elpd of the best model. We used the following test criterion:

$$T = \sum_i \Delta_i$$

which is the difference between the elpd of the model and the elpd of the best model. We then carried out a randomization test, changing randomly the sign of the Δ_i ’s and calculating again the criterion. We repeated this randomization 1000 times, and calculated the proportion of simulated values for T greater than the observed value.

3.4 Implementation in R

The K-fold cross validation approach is implemented in the function `kfoldCVModelCount`. Our dataset contains 330 leks, so that we define a partition of 10 groups of 33 leks:

```
set.seed(980)
ooo <- sample(c(rep(1:10, each=33)))
```

Then, we can use the function `kfoldCVModelCount` to implement cross-validation. We illustrate the process below for the model `modelCountDetectBinREY` used in our paper. WARNING!!! THIS CALCULATION CAN TAKE SEVERAL HOURS. Note that we have included the results of this calculation as a dataset of the package, so that the reader does not need to launch this function to reproduce further calculations:

```
listCoefsCVBinREY <- kfoldCVModelCount(ooo, dataList, "modelCountDetectBinREY")
```

The resulting object `listCoefsCVBinREY` is a list containing the value of the coefficients sampled by MCMC by excluding each group of leks in turn (the first element of the list contains the coefficients sampled by MCMC when fitting the model on a dataset excluding the group 1 of lek, etc.). We can then use the function `LLCount` to calculate the matrix containing the probabilities $p(\mathbf{y}_i | \mathbf{N}_i^{(r)}, \theta^{k,s})$ to observe the set of detected males during all count occasions for a given lek (rows) under the model with a given sampled vector of parameters (columns). WARNING, this calculation can also be very long. The result of this calculation is also available as a dataset in the package:

```
llcBinREY <- LLCount(dataList, listCoefsCVBinREY, ooo)
```

Finally, we can calculate the contribution of each lek to the elpd:

```
elpdBInREY <- elpdLeks(llcBinREY)
```

The same approach is used for other models. Note that because the lists of coefficients sampled by MCMC returned by the function `kfoldCVModelCount` are very large objects (> 40 MB), we do not include such objects for other models. However, the result of the function `LLCount` is presented for all of them. For the record, the code used to obtain such object, WHICH TAKES SEVERAL DAYS OF COMPUTING, is presented below. The resulting objects (with names starting by `llc`) are stored as datasets of the package:

```
## K-fold CV for different models
listCoefsCVBin <- kfoldCVModelCount(ooo, dataList, "modelCountDetectBin")
listCoefsCVBinREYObs2 <- kfoldCVModelCount(ooo, dataList, "modelCountDetectBinREYObs2")
listCoefsCVBetaBinREY <- kfoldCVModelCount(ooo, dataList, "modelCountDetectBetaBinREY")

## The list
llcBin <- LLCount(dataList, listCoefsCVBinREY, ooo)
llcBinREYObs2 <- LLCount(dataList, listCoefsCVBinREY, ooo)
llcBetaBinREY <- LLCount(dataList, listCoefsCVBinREY, ooo)
```

We then carry out the same approach with the model `modelCountDetectBin`, considering yearly periods instead of two-years periods. We need to prepare the data again to test this model:

```
dataList2 <- dataCount2jags(lekcounts$lek, lekcounts$year,
                           lekcounts$nbobs, lekcounts$nbmales,
                           lekcounts$gr, as.numeric(factor(lekcounts$type)),
                           lekcounts$natun, lekcounts$year)
```

And we carry out the same approach for this model:

```
listCoefsCVBinPerYear <- kfoldCVMModelCount(ooo, dataList2, "modelCountDetectBin")
llcBinPerYear <- LLCCount(dataList2, listCoefsCVBinPerYear, ooo)
```

We derive the contribution of each lek to the elpd of each model:

```
elpdBin <- elpdLeks(llcBin)
elpdBinREYObs2 <- elpdLeks(llcBinREYObs2)
elpdBetaBinREY <- elpdLeks(llcBetaBinREY)
elpdBinPerYear <- elpdLeks(llcBinPerYear)
```

And we also calculate the contributions to the “corrected” elpd for each model:

```
## Number of occasions for each lek
cid1 <- tapply(dataList$repetition, dataList$lek, sum)
cid2 <- tapply(dataList2$repetition, dataList2$lek, sum)

## corrected contribution
elpdcBinREY <- elpdBinREY/cid1
elpdcBin <- elpdBin/cid1
elpdcBinREYObs2 <- elpdBinREYObs2/cid1
elpdcBetaBinREY <- elpdBetaBinREY/cid1
elpdcBinPerYear <- elpdBinPerYear/cid1
```

Finally, we calculated the elpd/elpdc, the standard deviation for each model of their difference with the best model, and we performed the randomization test for each criterion:

```
## ELPD
## Randomization test
library(ade4)
pv <- sapply(list(elpdBin, elpdBinREY, elpdBinREYObs2, elpdBetaBinREY,
  elpdBinPerYear), function(x) {

  sim <- sapply(1:1000, function(i)
    sum(sample(c(-1,1), length(elpdBinREY),
      replace=TRUE)*(elpdBinREY-x)))
  obs <- sum(elpdBinREY-x)
  as.randtest(sim,obs)$pvalue
})

## criterion elpd
elpds <- c(sum(elpdBin),sum(elpdBinREY),
  sum(elpdBinREYObs2),sum(elpdBetaBinREY),
  sum(elpdBinPerYear))

## SD difference with the best model
elpdDiffsd <- sqrt(length(elpdBin))*c(sd(elpdBin-elpdBinREY),
  0, sd(elpdBinREYObs2-elpdBinREY),
  sd(elpdBetaBinREY-elpdBinREY),
  sd(elpdBinPerYear-elpdBinREY))

## "Corrected" ELPD
## Randomization test
pvc <- sapply(list(elpdcBin, elpdBinREY, elpdBinREYObs2, elpdBetaBinREY,
  elpdBinPerYear), function(x) {
```

```

sim <- sapply(1:1000, function(i)
  sum(sample(c(-1,1), length(elpdcBinREY),
            replace=TRUE)*(elpdcBinREY-x)))
obs <- sum(elpdcBinREY-x)
as.randtest(sim,obs)$pvalue
})

## criterion
elpdcs <- c(sum(elpdcBin),sum(elpdcBinREY),
            sum(elpdcBinREYObs2),sum(elpdcBetaBinREY),
            sum(elpdcBinPerYear))

## SD Difference with the best model
elpdcDiffsd <- sqrt(length(elpdcBin))*c(sd(elpdcBin-elpdcBinREY),
                                       0, sd(elpdcBinREYObs2-elpdcBinREY),
                                       sd(elpdcBetaBinREY-elpdcBinREY),
                                       sd(elpdcBinPerYear-elpdcBinREY))

## Data.frame containing the result for elpd
dfelpd <- data.frame(Model=c("modelCountDetectBin","modelCountDetectBinREY",
                             "modelCountDetectBinREYObs2",
                             "modelCountDetectBetaBinREY",
                             "modelCountDetectBin per year"),
                    elpd=elpds,
                    SDDiff=elpdDiffsd,
                    Pvalue=round(pv,3))

## for elpdc
dfelpdc <- data.frame(Model=c("modelCountDetectBin","modelCountDetectBinREY",
                              "modelCountDetectBinREYObs2",
                              "modelCountDetectBetaBinREY",
                              "modelCountDetectBin per year"),
                    elpdc=elpdcs,
                    SDDiffc=elpdcDiffsd,
                    Pvalue=round(pvc,3))

```

3.5 Discussion

We now interpret the results of the model comparison. We first interpret the “classical” elpd:

```

dfelpd

##           Model      elpd   SDDiff Pvalue
## 1 modelCountDetectBin -2305.641 2.8502815 0.003
## 2 modelCountDetectBinREY -2297.861 0.0000000 1.000
## 3 modelCountDetectBinREYObs2 -2299.556 2.4552215 0.267
## 4 modelCountDetectBetaBinREY -2299.329 0.9985594 0.065
## 5 modelCountDetectBin per year -2315.347 3.7525104 0.001

```

Here, for each model, we present the estimated elpd (the closer to 0 = the better), the standard deviation of the difference between the elpd of each model and the elpd of the best model (therefore equal to 0 for the best model), and the proportion of simulated differences greater than or equal to the observed

difference between the elpd of a model and the elpd of the best model.

The model used in the paper (binomial distribution with the logit of the detection probability modelled as a linear effect of the number of observers + a year random effect) is the best model in the set according to the elpd. Note that adding a quadratic effect of the number of observers or supposing an extra-binomial variation in the detection probability did not lead to a significant improvement of the prediction. However, removing the year random effect from the detection model led to a decrease of the elpd. Moreover, estimating one number of males in each region using one year-period led to a strong decrease of the elpd. Clearly, our choice to consider two year periods is a better one.

The same conclusions are reached when working on the “corrected” elpd:

```
dfelpdc

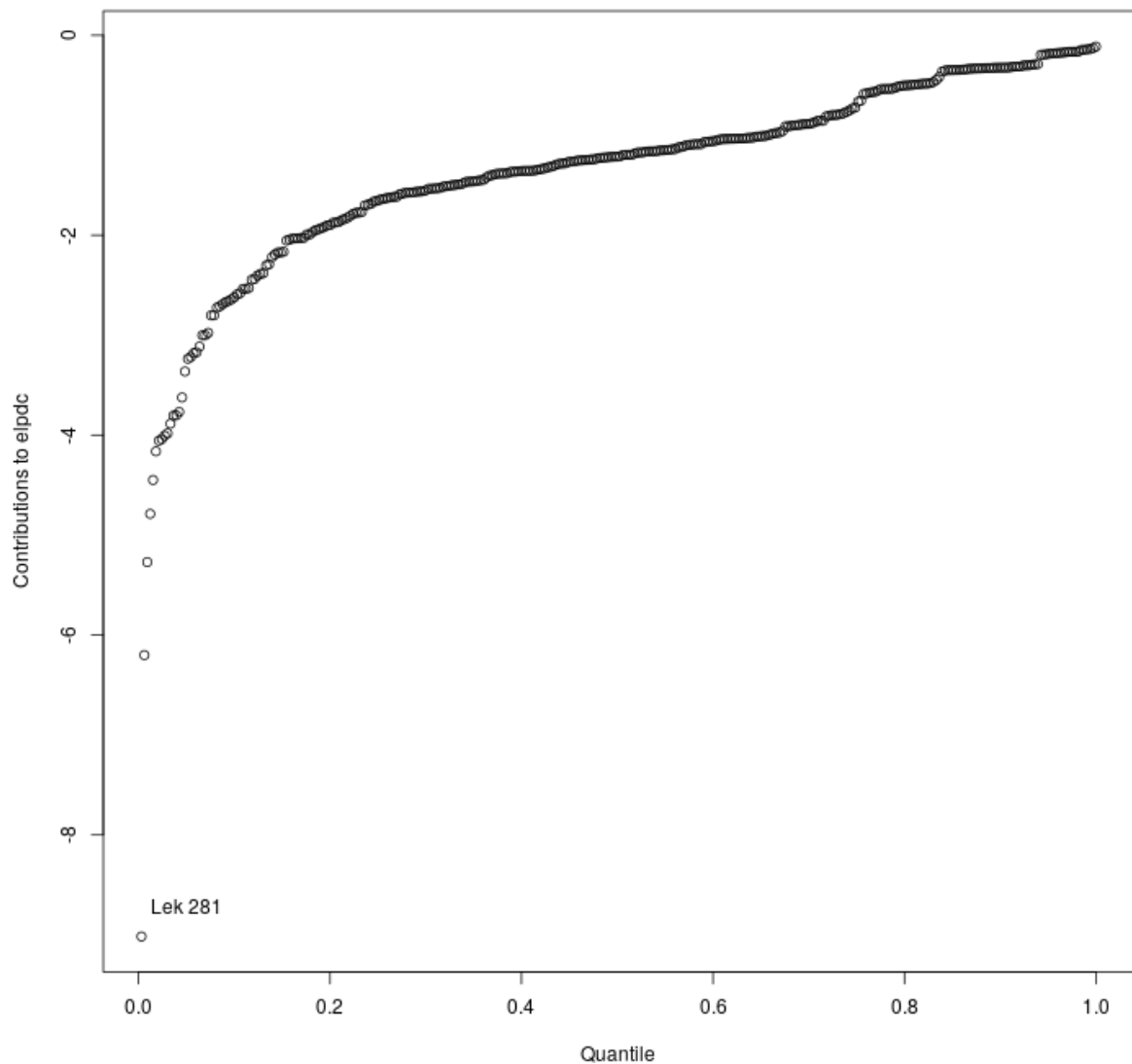
##           Model      elpd  SDDiffc Pvalue
## 1 modelCountDetectBin -453.1691 0.6705215 0.011
## 2 modelCountDetectBinREY -451.5471 0.0000000 1.000
## 3 modelCountDetectBinREYObs2 -451.8273 0.5481937 0.295
## 4 modelCountDetectBetaBinREY -451.6960 0.2046681 0.276
## 5 modelCountDetectBin per year -455.4702 1.0848683 0.001
```

4 The lek # 281

We have seen in the section 2.1.4 that the lek # 281 was characterized by a very large residual in our model. This lek is an unknown lek discovered by the grid cell searches carried out in 2013, which is characterized by a very large number of detected animals (the two counts carried out on this lek resulted in 18 and 17 males respectively).

The examination of the quantile plot of the contributions of each lek to the corrected elpd shows that the lek 281 contributes significantly to the elpd:

```
plot(c(1:length(elpdcBinREY))/length(elpdcBinREY),
     sort(elpdcBinREY), xlab="Quantile",
     ylab="Contributions to elpd")
text(0.05, -8.71, "Lek 281")
```

Other state models that we have tried during previous years on this dataset identify the same problem: this lek is an outlier characterized by a much larger number of detected males than other unknown leks. Since the number of detected unknown leks is low (32 leks), any outlier will have a strong effect on the inference.

We wanted to assess more precisely the effect of this lek on our inference, by trying to fit the model again without this lek, and by estimating again the number of males in each region. WARNING: THIS CALCULATION TAKES A VERY LONG TIME (several hours)!!!! Fortunately, the package contains the result `coefModelm281` of the fit as a dataset in the package:

```
lcb <- lekcounts %>% filter(lek!=281)
lcb$lek <- as.numeric(factor(lcb$lek))
dataListwo281 <- dataCount2jags(lcb$lek, lcb$period,
                                lcb$nbobs, lcb$nbmales,
                                lcb$gr, as.numeric(factor(lcb$type)),
                                lcb$natun, lcb$year)

coefModelm281 <- fitModelCount(dataListwo281, "modelCountDetectBinREY")
```

We then estimate the number of males in each region with this new model:

```
nmwo281 <- estimateNmales(coefModelm281, coefModelULPresence,
                          gridFrame, NKAL, NKIL)
summary(nmwo281)

## Estimates of the number of males during the 5 periods
## in the whole Pyrenees Mountains (median and 80% CI):
##
##   Point.est   CIlow   CIup
## 1  1782.205  1488.828  2222.923
## 2  1795.783  1489.977  2243.659
## 3  1803.610  1505.648  2246.265
## 4  1769.254  1474.038  2189.760
## 5  1637.393  1367.850  2013.980
##
## Change rate between period 1 and period 5 is: -7.39% (80% CI: -17.59% -- 0.52%)
##
## Probability of scenarii (decrease:< -10%; stability:-10--10%; increase:>10%):
##
##   scenario probability
## 1  decrease      0.3620
## 2  stability     0.6355
## 3  increase      0.0025
```

We recall the estimates of our model:

```
summary(nm)

## Estimates of the number of males during the 5 periods
## in the whole Pyrenees Mountains (median and 80% CI):
##
##   Point.est   CIlow   CIup
## 1  1871.789  1542.350  2350.656
## 2  1922.285  1570.448  2440.920
## 3  1901.102  1562.484  2387.119
## 4  1841.119  1516.075  2308.645
## 5  1694.132  1398.089  2129.504
##
## Change rate between period 1 and period 5 is: -8.49% (80% CI: -20.24% -- 0.13%)
##
## Probability of scenarii (decrease:< -10%; stability:-10--10%; increase:>10%):
##
##   scenario probability
## 1  decrease      0.43100
## 2  stability     0.56575
## 3  increase      0.00325
```

Removing this lek from the dataset results in a decrease of the estimated population size of about 70 to 100 males, i.e. about a 5% decrease in the population size estimated for the whole mountain range. Note that the lek 281 was located in the geographical region 1 and discovered in period 2, so that we could expect a larger effect of this lek in this region during this period. We compare the estimates of region 1 with this lek...

```
summary(nm, 1)

## Estimates of the number of males during the 5 periods
```

```
## in the geographic region 1 (median and 80% CI):
##
##   Point.est      CIlow      CIup
## 1  155.9515  111.19115  227.6323
## 2  154.9948  109.65762  219.2993
## 3  149.0112  106.98677  213.7739
## 4  145.4841  104.07529  209.1013
## 5  135.4594   95.31548  198.5411
##
## Change rate between period 1 and period 5 is: -12.1% (80% CI: -28.59% -- 2.13%)
##
## Probability of scenarii (decrease:< -10%; stability:-10--10%; increase:>10%):
##
##   scenario probability
## 1  decrease      0.57125
## 2  stability      0.40050
## 3  increase      0.02825
```

...and without this lek:

```
summary(nmwo281,1)

## Estimates of the number of males during the 5 periods
## in the geographic region 1 (median and 80% CI):
##
##   Point.est      CIlow      CIup
## 1  149.1638  105.41717  211.2579
## 2  143.5529  102.32480  200.2430
## 3  142.5922  102.24431  198.9411
## 4  140.8573   99.66753  197.3924
## 5  131.0549   92.35818  188.5257
##
## Change rate between period 1 and period 5 is: -10.53% (80% CI: -26.86% -- 3.22%)
##
## Probability of scenarii (decrease:< -10%; stability:-10--10%; increase:>10%):
##
##   scenario probability
## 1  decrease      0.51825
## 2  stability      0.45150
## 3  increase      0.03025
```

The removal of this lek from the dataset results in a decrease of the estimated population size in this region of about 10 males, i.e. about a 6.5% decrease in the population size. Actually, this lek has a strong effect on the estimation of the number of males, has the same effect in all regions. Actually, the estimates of the random effects $\kappa_{g(i),\ell(i),b(t)}$, which represent how the median number of males on a lek varies across regions and periods, are very similar whether we remove lek 281 or not:

```
library(matrixStats)

##
## Attaching package: 'matrixStats'
## The following object is masked from 'package:dplyr':
##
##   count

kap <- MCMCchains(coefModelm281, "kappa")
```

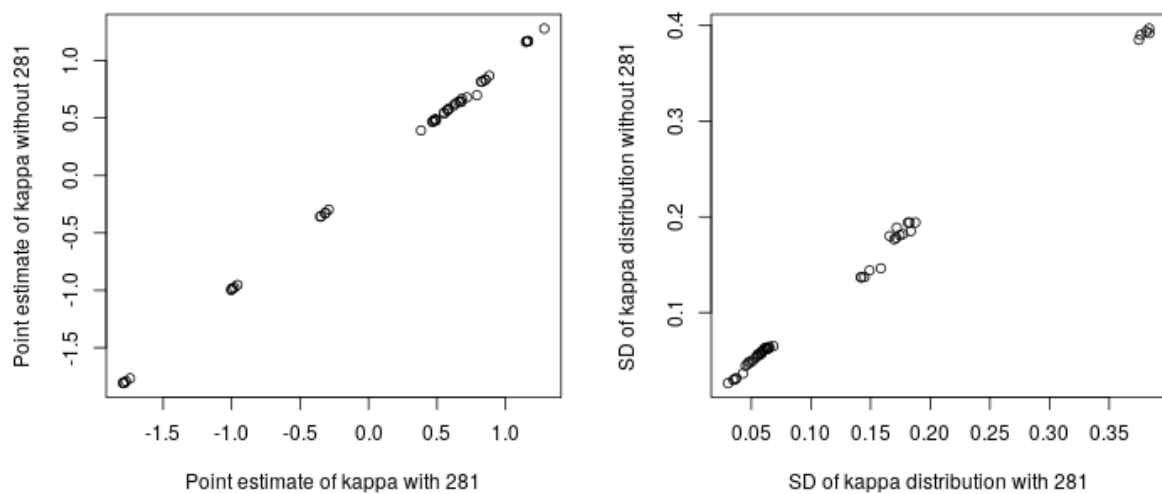
```

kapb <- MCMCchains(coefModelCountDetectBinREY, "kappa")
par(mfrow=c(1,2))
cmbk <- colMeans(kapb)
cmbv <- colVars(kapb)
cmk <- colMeans(kap)
cmv <- colVars(kap)

## Remove the "virtual levels" included in the model to have
## a square matrix region x period x types of leks
## (we included these levels because we do not have the
## same number of regions for all types of lek)
cmbk <- cmbk[cmv<8]
cmbv <- cmbv[cmv<8]
cmk <- cmk[cmv<8]
cmv <- cmv[cmv<8]

plot(cmbk, cmk, xlab="Point estimate of kappa with 281",
      ylab="Point estimate of kappa without 281")
plot(cmbv, cmv, xlab="SD of kappa distribution with 281",
      ylab="SD of kappa distribution without 281")

```

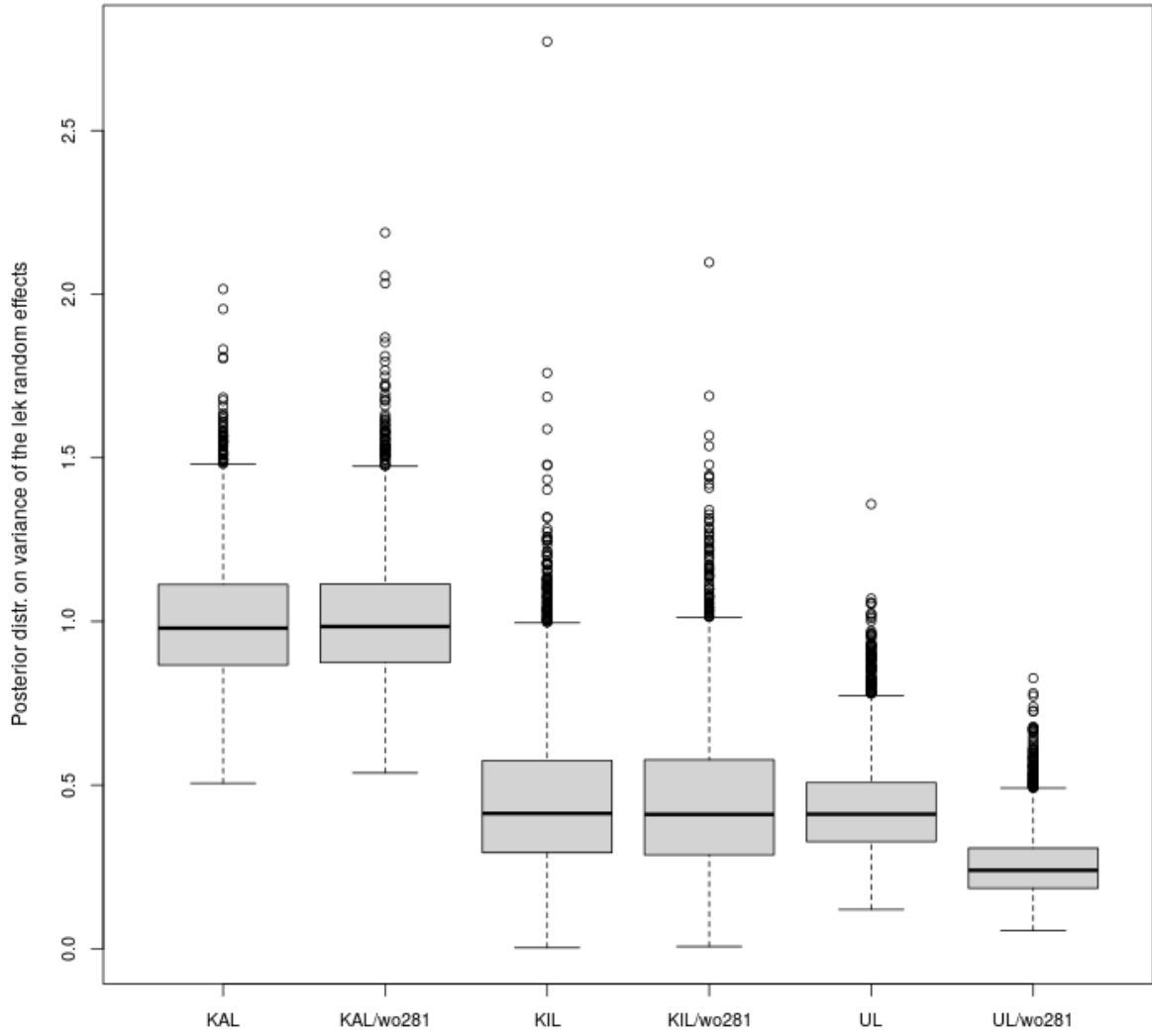


Actually, this lek increases the estimate of the variance of the lek random effects:

```

set <- 1/MCMCchains(coefModelm281, "sigmaeta")
setb <- 1/MCMCchains(coefModelCountDetectBinREY, "sigmaeta")
colnames(setb) <- c("KAL", "KIL", "UL")
colnames(set) <- paste0(c("KAL", "KIL", "UL"), "/wo281")
setg <- cbind(setb, set)[,c(1,4,2,5,3,6)]
boxplot(setg, cex.axis=0.9, ylab="Posterior distr. on variance of the lek random effects")

```



The estimated variance for unknown leks is much smaller when the lek 281 is removed. Examination of other parameters show that adding/removing count data of the lek # 281 does not change the posterior distribution.

Removing this lek from our dataset would lead to a decrease of about 5% of our population size estimate, which is probably an underestimation: we have no reason to exclude this lek, as it has been discovered by our protocol, and actually “represents” other unknown leks of similar size, which – although they are probably not very frequent in the mountain range – do exist but are not yet discovered. Today, as the number of unknown leks detected during grid cells searches is small, any big lek will have a strong effect on the inference, which is what we show here. Today, this lek is an outlier, and as such, has a significant effect on our inference, though not that strong (probably less than 5%). But as more and more data on unknown leks will be collected in the future, the weight of this lek on our estimate will decrease and we will have a finer understanding of the distribution of the number of males on unknown leks.

5 Sensitivity of our model to the violation of several hypotheses

5.1 Criticisms of [LIN18] and [BAR17]

Two recent papers by [LIN18] and [BAR17] identified many problems with N-mixture models that can strongly affect estimates by these models. In this section, we review the criticisms by these authors about N-mixture models to consider whether they apply to our model. These authors consider the inference of abundance N drawn from a Poisson distribution and a binomial detection process characterized by a detection probability p :

[BAR17] suggests that in some studies, the abundance N may not exist as a parameter. We understand that this situation may occur in some point count studies, where the definition of a “site” may not be very clear. An observer count the number of birds of a given species.

When the detection probability $p \rightarrow 0$, the binomial distribution describing the detection process converges towards a Poisson distribution with parameter $\lambda = Np$. In other words, the parameters N and p are not separable when p is small. Several simulations illustrate how

But the most serious criticisms by these authors concern the effect of unaccounted variation in detection probability. These two papers show, in the case of a state model corresponding to a simple Poisson distribution that even a small amount of unaccounted variation can lead to a considerable bias in the estimation of N . They show the same problem with accidental double counting. Thus, [LIN18] note: “2% rate of double counts or a standard deviation of 2% in detection rates might seem insubstantial, but each is large enough to produce a 20% bias in estimation of mean abundance”. This is a worrying result, as no model could ascertain that the amount of unaccounted variation in the detection process is so small. In the next two sections, we carry out some simulations to test the effect of unaccounted variation in detection probability and accidental double counting on the estimation of the number of males.

5.2 Unaccounted variation in detection probability

5.2.1 Simulation of both the state and detection process

We tested the effect of unaccounted variation in detection probability on the estimation of the number of males in the whole mountain range. We used the model fitted in section 2.1.2 to generate new datasets (i.e. simulating the state process, and then the detection process), adding a level of unaccounted variation in the detection probability. More precisely, we used the same state model as the one used in the paper to generate numbers of males on the sampled leks. We also used the same model to simulate the *average* probability of detection for each count occasion. For the count occasion k of year t on lek i , this average probability is $d_{i,t,k}$ and the actual probability is supposed to be drawn from a beta distribution:

$$p_{i,t,k} \sim \text{Beta} \left(d_{i,t,k} \times \frac{1 - \delta^2}{\delta^2}, (1 - d_{i,t,k}) \times \frac{1 - \delta^2}{\delta^2} \right)$$

The parameter δ^2 controls the amount of extra-binomial variation added to the detection process. We considered the following values for the parameter δ^2 :

```
delta2b <- c(0, 0.001, 0.005, 0.01, 0.05, 0.1, 0.3)
```

For each value of δ^2 , we simulated 10 datasets, and we estimated the posterior distribution of the number of males. We used the function `simulateDataList`, included in the package to simulate this data generating process. We then calculated the median of this distribution. **WARNING!!! THIS CALCULATION TAKES A VERY LONG TIME (several hours)!!!!** Fortunately, the package contains the result `medianNmalesBB` of this calculation (matrix with 10 columns – the 10 repetitions – and 7 rows – the 7 values of δ^2 – containing the median of the posterior distributions):

```

libtt <- list()

for (j in 1:10) {
  cat("#####",
      "\n#####",
      "\n#####",
      "\n#####",
      "\n### Iteration", j, "\n\n\n")
  liresuBeta <- list()
  for (i in 1:7) {
    cat("#####\n### Model", i, "\n\n\n")
    if (i!=1) {
      sdl <- simulateDataList(coefModelCountDetectBinREY,
                             dataList, betaBinDelta=delta2b[i])
    } else {
      sdl <- simulateDataList(coefModelCountDetectBinREY, dataList)
    }
    fm <- fitModelCount(sdl, "modelCountDetectBinREY", n.iter=30000, thin=30)
    liresuBeta[[i]] <- list(dataList=sdl, coefs=fm)
    saveRDS(liresuBeta, file="liresuBeta.Rds")
  }
  libtt[[j]] <- liresuBeta
  saveRDS(libtt, file="libtt.Rds")
}

listNmalesBB <- lapply(libtt, function(liresuBeta)
  lapply(liresuBeta, function(x)
    estimateNmales(x$coefs, coefModelULPresence, gridFrame, NKAL, NKIL)))

medianNmalesBB <- sapply(listNmalesBB, function(z)
  sapply(z, function(x) median(getTotal(x)[,1])))

```

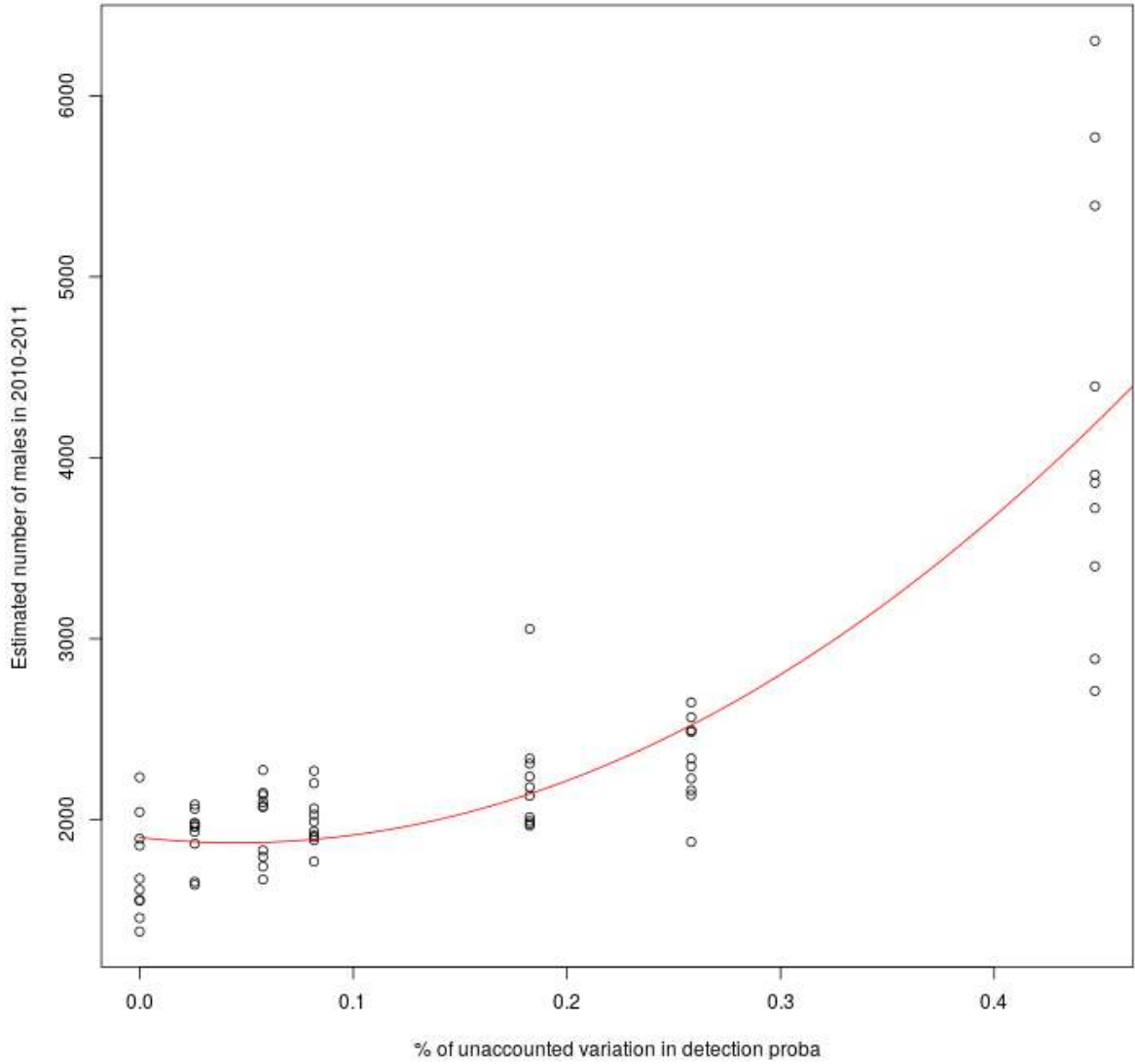
We present below how the median of the estimated posterior distribution on the number of males for the reference period 2010-2011 in the whole mountain range varies with the proportion of unaccounted variation. As the estimated detection probability in our study is about 0.6, we calculated the coefficient of variation of a beta distribution of the average detection probabilities was equal to 0.6, for each value of δ^2 . This allowed to display the relationship between the proportion of unaccounted variation and the estimated number of males:

```

## coefficient of variation
coefvar <- c(0,sapply(delta2b[-1], function(delta2) {
  alpha <- 0.6*(1-delta2)/delta2
  beta <- 0.4*(1-delta2)/delta2
  sqrt(alpha*beta/((alpha+beta)^2 * (alpha+beta+1)))/0.6
})))

plot(rep(coefvar, 10),as.vector(medianNmalesBB),
     xlab="% of unaccounted variation in detection proba",
     ylab="Estimated number of males in 2010-2011")
xy <- data.frame(x=rep(coefvar, 10), y=as.vector(medianNmalesBB))
xv <- seq(0,0.5,length=200)
lines(xv, predict(lm(y~x+I(x^2), data=xy), newdata=data.frame(x=xv)), col="red")

```



The case $\delta^2 = 0$ corresponds to zero unaccounted extra-binomial variation. Note that the overestimation in the number of males is not linearly related to the coefficient of variation of the detection probability.

Although increasing the amount of unaccounted variation in the detection probability indeed results in an increase in the estimated number of males, our model seems quite robust to this source of bias: even with $\sim 10\%$ of unexplained variability in the detection probability, the resulting bias is nearly unnoticeable in comparison to the imprecision of our estimation.

5.2.2 Simulating the detection process only

In the previous section, we have assessed the effect of unaccounted heterogeneity in the detection process on the estimation of the number of males by simulating the whole process (both the state process generating the true number of males on sampled leks, and the detection process), while adding a certain amount of unaccounted variability in the process. However, since we are working on unaccounted variation in detection probability, it would be interesting to keep the true number of males fixed in our simulations while varying the amount of unaccounted variation in detection probability.

We used the function `simulateN` to simulate the true number of males present on the sampled leks/periods.

```
set.seed(1)
simn <- simulateN(coefModelCountDetectBinREY,dataList)
```

Then, for this particular simulated true number of males, we simulated the detection process with various levels of unaccounted detection probability. WARNING!!! THIS CALCULATION TAKES A VERY LONG TIME (several hours)!!!! Fortunately, the package contains the result `medianNmalesBB2` of this calculation (matrix with 10 columns – the 10 repetitions – and 5 rows – the 5 values of h – containing the median of the posterior distributions):

```
delta2b <- c(0, 0.004, 0.015, 0.05, 0.1, 0.2)
libtt2 <- list()
for (j in 1:10) {
  cat("#####",
      "\n#####",
      "\n#####",
      "\n#####",
      "\n### Iteration", j, "\n\n")
  liresuBeta <- list()
  for (i in 1:6) {
    cat("#####\n### Model", i, "\n\n")
    if (i!=1) {
      sdl <- simulateDataList2(coefModelCountDetectBinREY,dataList,
                              simn, betaBinDelta=delta2b[i])
    } else {
      sdl <- simulateDataList2(coefModelCountDetectBinREY,
                              dataList, simn)
    }
    fm <- fitModelCount(sdl, "modelCountDetectBinREY", n.iter=10000, thin=10)
    liresuBeta[[i]] <- list(dataList=sdl, coefs=fm)
  }
  libtt2[[j]] <- liresuBeta
  saveRDS(libtt2, file="libtt2.Rds")
}

listNmalesBB2 <- lapply(libtt2, function(liresuBeta)
  lapply(liresuBeta, function(x)
    estimateNmales(x$coefs, coefModelULPresence,
                  gridFrame, NKAL, NKIL)))

medianNmalesBB2 <- sapply(listNmalesBB2, function(z)
  sapply(z, function(x) mean(getTotal(x)[,1])))
save(medianNmalesBB2, file="medianNmalesBB2.rda")
```

We show below how the median of the estimated posterior distribution on the number of males for the reference period 2010-2011 in the whole mountain range varies with the coefficient of variation of the detection probability when this probability is equal to 0.6:

```
delta2b <- c(0, 0.004, 0.015, 0.05, 0.1, 0.2)

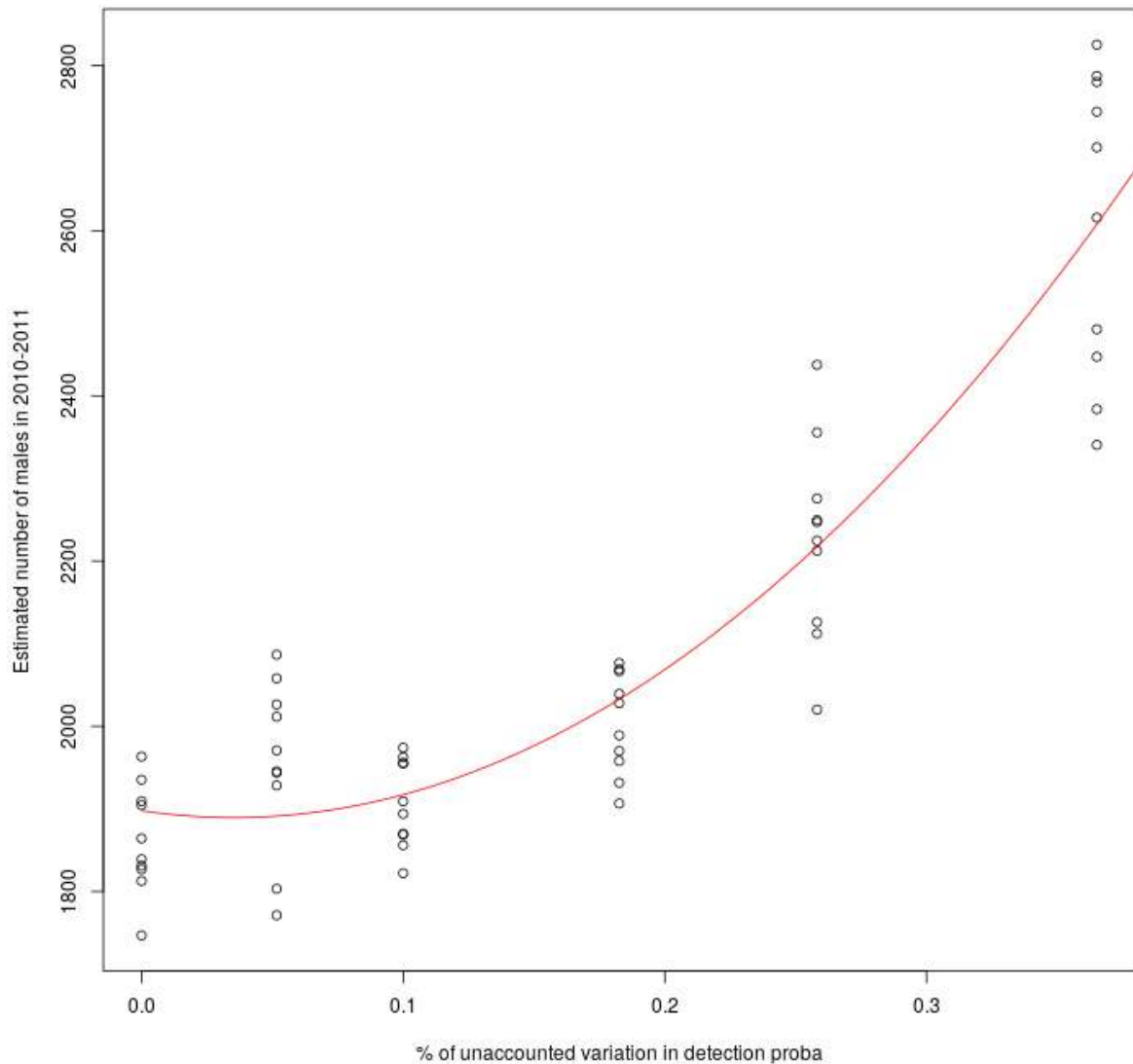
## coefficient of variation
coefvar <- c(0,sapply(delta2b[-1], function(delta2) {
  alpha <- 0.6*(1-delta2)/delta2
  beta <- 0.4*(1-delta2)/delta2
  sqrt(alpha*beta/((alpha+beta)^2 * (alpha+beta+1)))/0.6
```

```

)))

plot(rep(coefvar, 10), as.vector(medianNmalesBB2),
     xlab="% of unaccounted variation in detection proba",
     ylab="Estimated number of males in 2010-2011")
xy <- data.frame(x=rep(coefvar, 10), y=as.vector(medianNmalesBB2))
xv <- seq(0, 0.5, length=200)
lines(xv, predict(lm(y~x+I(x^2), data=xy), newdata=data.frame(x=xv)), col="red")

```



Keeping fixed the actual number of males while varying the unaccounted variation in detection probability does not change the results obtained in the previous section. Accidental double counting can generate a strong bias in the estimated number of males. is unnoticeable when the coefficient of variation of the detection probability is $< 15\%$. When this coefficient of variation reaches 25% , this results in a point estimate of ~ 2200 males instead of ~ 1900 , i.e. $(2200-1900)/1900 \approx 15\%$ overestimate.

This result is very different from the 20% bias in estimated number of males resulting from the 2% unaccounted variation in [LIN18]. Actually, these authors considered a very simple Poisson state model: with

their simple model, any unaccounted heterogeneity in detection probability will result in an increase of the estimated Poisson parameter. Our model is more complex, with many random effects accounting for the hierarchical structure of the state process: the unaccounted heterogeneity in detection probability is likely absorbed by the various random effects of the state model, which limits this effect.

In conclusion, the unaccounted heterogeneity in detection process is unlikely to strongly affect our inference.

5.3 Effect of accidental double counting

5.3.1 Simulation of both the state and detection process

We also tested the effect of accidental double counting on our estimation. As for the assessment of the effect of unaccounted heterogeneity, we first generated datasets by simulating the state process, and then the detection process. We also used the model fitted in section 2.1.2 to generate new datasets, but this time, we added a random proportion of animals counted twice to the simulated counts. More precisely, we used the same state model as the one used in the paper to generate numbers of males on the sampled leks. We also used the same model to simulate the probability of detection for each count occasion. If $y_{i,t,k}$ is the number of distinct males detected on lek i during count occasion k of year t , then we suppose that the number of animals counted twice during this occasion is randomly drawn from a Binomial distribution $\mathcal{B}(y_{i,t,k}, h)$, where h is the proportion of animals counted twice. We tested the following values of h :

```
doubleCountspb <- c(0.05, 0.1, 0.2, 0.3, 0.5)
```

For each value of h , we simulated 10 datasets, and we estimated the posterior distribution of the number of males. We again used the function `simulateDataList`, included in the package to simulate this data generating process. We then calculated the median of this distribution. WARNING!!! THIS CALCULATION TAKES A VERY LONG TIME (several hours)!!!! Fortunately, the package contains the result `medianNmalesBB` of this calculation (matrix with 10 columns – the 10 repetitions – and 5 rows – the 5 values of h – containing the median of the posterior distributions):

```
lidtt <- list()
for (j in 1:10) {
  cat("#####",
      "\n#####",
      "\n#####",
      "\n#####",
      "\n### Iteration", j, "\n\n")
  liresudc <- list()
  for (i in 1:5) {
    cat("#####\n### Model", i, "\n\n")
    sdl <- simulateDataList(coefModelCountDetectBinREY, dataList,
                          doubleCountspb=doubleCountspb[i])
    fm <- fitModelCount(sdl, "modelCountDetectBinREY", n.iter=30000, thin=30)
    liresudc[[i]] <- list(dataList=sdl, coefs=fm)
    saveRDS(liresudc, file="liresudc.Rds")
  }
  lidtt[[j]] <- liresudc
  saveRDS(lidtt, file="lidtt.Rds")
}

listNmalesDC <- lapply(lidtt, function(liresudc)
  lapply(liresudc, function(x)
    estimateNmales(x$coefs, coefModelULPresence, gridFrame, NKAL, NKIL)))

medianNmalesDC <- sapply(listNmalesDC,
```

```

function(z)
  apply(z, function(x) median(getTotal(x)[,1]))

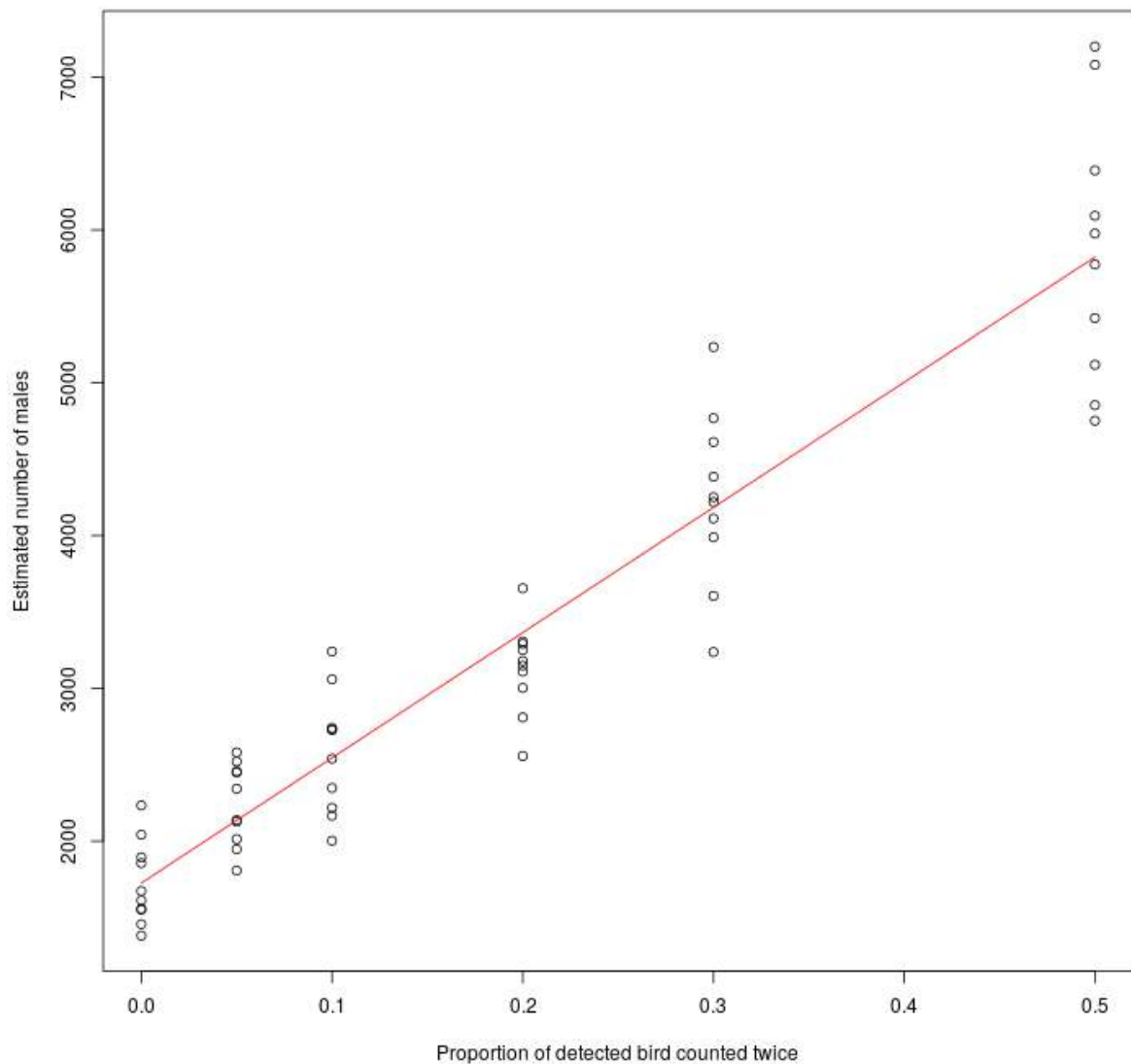
```

We present below how the median of the estimated posterior distribution on the number of males for the reference period 2010-2011 in the whole mountain range varies with the proportion of accidental double counting:

```

## Add the case where h=0 (simulated in the previous section)
plot(rep(c(0,doubleCountsPB), 10),
     as.vector(rbind(medianNmalesBB[1,], medianNmalesDC)),
     xlab="Proportion of detected bird counted twice",
     ylab="Estimated number of males")
xy <- data.frame(x=rep(c(0,doubleCountsPB), 10),
                 y=as.vector(rbind(medianNmalesBB[1,], medianNmalesDC)))
xv <- seq(0,0.5,length=200)
lines(xv, predict(lm(y~x, data=xy), newdata=data.frame(x=xv)), col="red")

```



Accidental double counting has a much stronger effect on the estimation than unaccounted variation in

detection probability. Indeed, even a moderate average proportion of 10% of detected animals counted twice results in an estimate of about 2550 animals in 2010 (instead of the average 1730 obtained in this set of simulations). This corresponds to an overestimation of $\sim 50\%$. We therefore confirm the results of [LIN18] here.

5.3.2 Simulating the detection process only

In the previous section, we have assessed the effect of accidental double counting on the estimation of the number of males by simulating the whole process (both the state process generating the true number of males on sampled leks, and the detection process), while adding a certain number of males counted twice. However, again, we are working on the detection process so that it would be interesting to keep the true number of males fixed in our simulations while varying the proportion of detected males counted twice.

We used the same vector `simn` of true number of males simulated in section 5.2.2 as the “true” state of the system, and for this particular simulated true number of males, we simulated the detection process with various levels of accidental double counting. WARNING!!! THIS CALCULATION TAKES A VERY LONG TIME (several hours)!!!! Fortunately, the package contains the result `medianNmalesDC2` of this calculation (matrix with 10 columns – the 10 repetitions – and 5 rows – the 5 values of h – containing the median of the posterior distributions):

```
doubleCountspb <- c(0.05, 0.1, 0.2, 0.3, 0.5)

lidtt2 <- list()
for (j in 1:10) {
  cat("#####",
      "\n#####",
      "\n#####",
      "\n#####",
      "\n### Iteration", j, "\n\n\n")
  liresudc <- list()
  for (i in 1:5) {
    cat("#####\n### Model", i, "\n\n\n")
    sdl <- simulateDataList2(coefModelCountDetectBinREY, dataList, simn,
                           doubleCountspb=doubleCountspb[i])
    fm <- fitModelCount(sdl, "modelCountDetectBinREY", n.iter=10000, thin=10)
    liresudc[[i]] <- list(dataList=sdl, coefs=fm)
    saveRDS(liresudc, file="liresudc.Rds")
  }
  lidtt2[[j]] <- liresudc
  saveRDS(lidtt2, file="lidtt2.Rds")
}

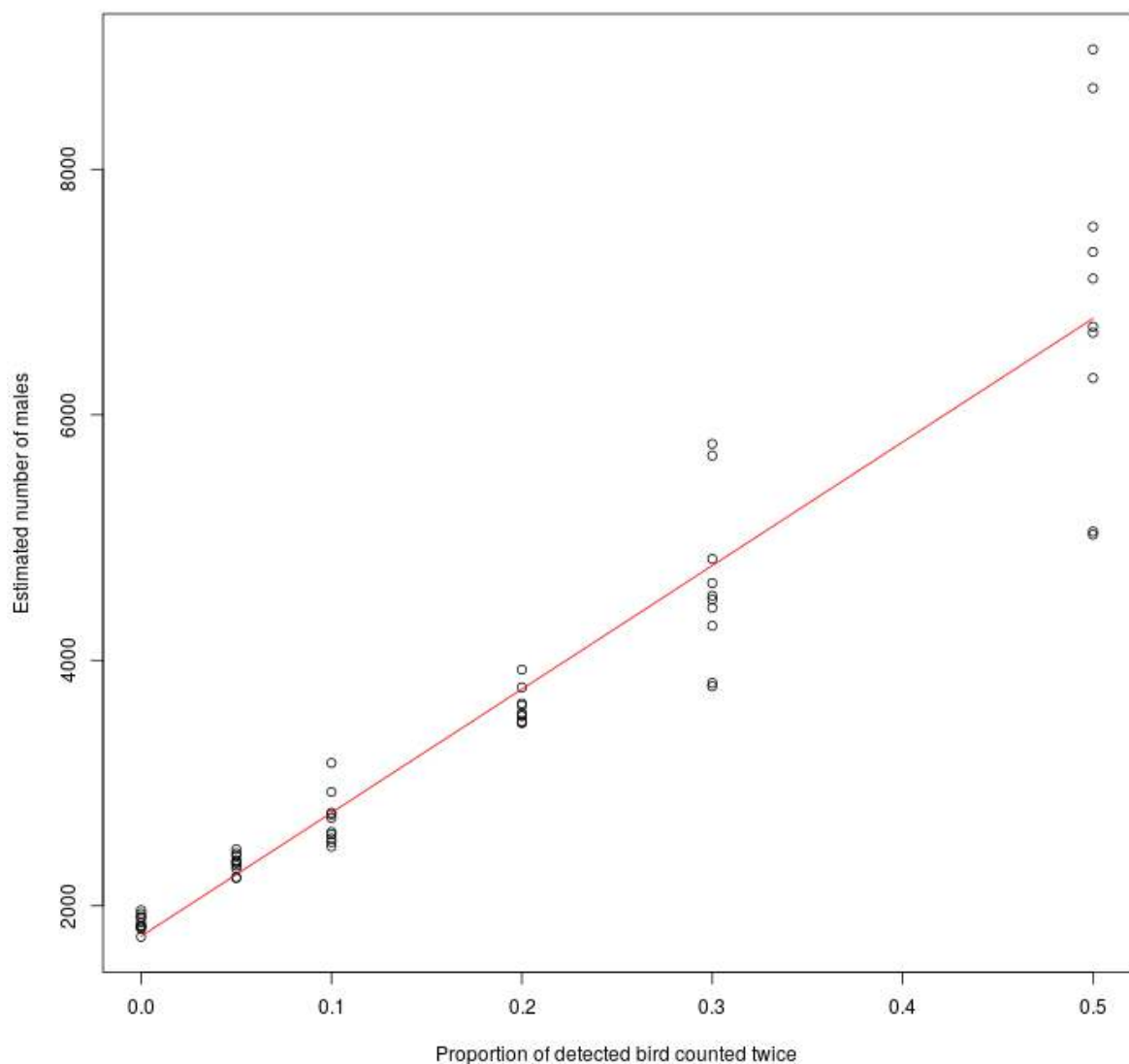
listNmalesDC2 <- lapply(lidtt2, function(liresuBeta)
  lapply(liresuBeta, function(x)
    estimateNmales(x$coefs, coefModelULPresence, gridFrame, NKAL, NKIL)))

medianNmalesDC2 <- sapply(listNmalesDC2, function(z)
  sapply(z, function(x) mean(getTotal(x)[,1])))
```

We show below how the median of the estimated posterior distribution on the number of males for the reference period 2010-2011 in the whole mountain range varies with the proportion of accidental double counting:

```
doubleCountspb <- c(0.05, 0.1, 0.2, 0.3, 0.5)

## Note that we add the case where h=0 (simulated in the previous section)
plot(rep(c(0,doubleCountspb), 10),
     as.vector(rbind(medianNmalesBB2[1,], medianNmalesDC2)),
     xlab="Proportion of detected bird counted twice",
     ylab="Estimated number of males")
xy <- data.frame(x=rep(c(0,doubleCountspb), 10),
                 y=as.vector(rbind(medianNmalesBB2[1,], medianNmalesDC2)))
xv <- seq(0,0.5,length=200)
lines(xv, predict(lm(y~x, data=xy), newdata=data.frame(x=xv)), col="red")
```



Keeping fixed the actual number of males while varying the probability that a detected male was counted twice does not change the results obtained in the previous section. Even a moderate average proportion of 10% of detected animals counted twice results in an estimate of about 2750 animals in 2010 (instead of the average 1750 obtained in this set of simulations). This corresponds to an overestimation of $\sim 55\%$.

In conclusion, the unaccounted double counting during count occasions can have a very strong effect on

our estimation.

6 History of the program

The original sampling design was developed in 2009, and its first use during the period 2010–2011. Our aim was to estimate the true number of males at different spatial scales over the mountain range, the smaller scale being the natural unit. For this reason, we initially decided to stratify the sampling of both grid cells for cell searches and known leks for counts by natural unit. First, a sample of natural units was drawn. The sample of KILs/KALs and grid cells were sampled in those NUs. The same sample of NUs were monitored for the first three periods, so that at the end of the third period, all the grid cells of those units had been searched for new ULs. For the fourth period, a new sample of natural units (partially matching the previously sampled NUs, to allow a longitudinal monitoring at least for some leks).

After the first application in 2010–2011, only 6 new unknown leks were discovered following the searches carried out in 77 grid cells carried out this year. Thus, despite a substantial field work, the number of discovered UL was too small to allow the fit of a statistical distribution describing the true number of males present on a lek in average in the whole range, let alone for each region. We therefore made the assumption that the number of males on UL had a statistical distribution similar to the number of males on KILs. Indeed:

- We thought at that time that most large leks on the mountain range had already been discovered and were already registered as KALs in our sampling frame. Thus, we expected that unknown leks were “appearing” small sized leks, probably characterized by a tendency to increase, just as KILs.
- The discovered leks were indeed characterized by a small number of detected males (four leks with one detected male and one lek with three detected males), which seemed to confirm this assumption.
- One of the “discovered” lek was actually already known by the observer before the sampling. It was a small lek that was known but which had never been counted. However the observer had forgotten to report it to the program managers prior to the definition of the sampling design in 2009. In other words, this UL shared all characteristics of a KIL.
- None of the goodness of fit tests carried out at that time seemed to indicate that we were wrong in making this assumption.

However, with time, the number of ULs discovered after grid cell searches increased, and after the period 4 (in 2017), we realized that this assumption did not hold. In particular, the true number of males was much larger on ULs than on KILs. This matched the impression of some partners of the program that this number was probably underestimated.

This had the unfortunate consequence to increase the uncertainty of our estimation. Indeed, by essence, this category of lek is not well known, and only a small number of them is counted every year (though it is increasing). The uncertainty on the estimated number of males on all unknown leks results from the fact that we need to estimate both the number of ULs and the distribution of the true number of males on ULs. As by definition none of these components were known at the onset of the program, the total number of males present on ULs is the most uncertain quantity in our model. However, when we supposed that the number of males on ULs had the same distribution as the number of males on KILs, we could benefit from a larger dataset.

The discovery that the number of males on ULs was higher than previously thought led to a much higher imprecision of the estimates of the total number of males. Indeed, it implied that the proportion of the

population present in a badly known compartment of the population is larger than previously imagined, resulting in more uncertain estimates.

As a result, we changed our sampling approach for the selection of grid cells to be searched. The only way to decrease uncertainty was to put a maximum effort in the discovery of new ULs. We then increased the effort put in grid cell searches for the period 2018–2019. Moreover, we modified the sampling design to increase the probability that a grid cell search result into the discovery of new ULs. We did not restrain our sampling to a set of sampled natural units.

We used a map of the area of presence of the species defined by a group of experts in 2009, before the onset of the program as a guide to select grid cells. We sampled the grid cells to be searched with a probability proportional to the proportion of the cells covered by the area of presence. Moreover, we decided to no longer stratify the grid cells by natural units: it appeared that there were no clear differences of the probability of presence of UL between the natural units. To suppress this stratification allowed to sample grid cells over the whole range and thereby maximize the probability to find new ULs in sampled grid cells.

However, between 2010 and 2017, many ULs discovered by the network of observers outside the framework of our monitoring (e.g. resulting either from accidental discovery, from compilation of local knowledge, or from local initiatives leading to the search for new leks) were reported to the program managers. When a sampled grid cell contained such an UL, no search was organised for this cell, and the presence of an UL was reported. Our model differentiate these ULs from the ULs discovered following grid cells.

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