

Rcode_Wichetal_Usingdronesto.R

2023-03-02

```
# Wich et al. Using drones to determine chimpanzee absence at the edge of the  
# ir distribution in western Tanzania  
library(unmarked)  
  
## Warning: package 'unmarked' was built under R version 4.1.3  
  
library(MuMIn)  
library(AICcmodavg)  
  
##  
## Attaching package: 'AICcmodavg'  
  
## The following objects are masked from 'package:MuMIn':  
##  
##      AICc, DIC, importance  
  
# 1) Running N-mixture models using data from Bonnini et al. 2018 to estimate  
# nest detection probability during a flight in a 50x500m plot depending on GSD  
  
# Load detection matrix (from Bonnini et al. 2018, cells indicate numbers of n  
# ests detected during a drone survey)  
data_presence <- read.csv("nmix_observation_matrix.csv", sep=";", header=TRUE  
)  
data.y <- data_presence[, -1]  
  
# Load observation-level covariates (covariates affecting detection probabili  
# ty, in this case only GSD)  
cov.det<- read.csv("covariate_matrix_GSD.csv", sep=";", header=TRUE)  
obsCovs <- list(GSD=cov.det[,2:4])  
  
# Create data frame to be used for running N-mixture models  
data.umf <- unmarkedFramePCount (y=data.y, obsCovs = obsCovs)  
summary(data.umf)  
  
## unmarkedFrame Object  
##  
## 12 sites  
## Maximum number of observations per site: 3  
## Mean number of observations per site: 3  
## Sites with at least one detection: 11  
##  
## Tabulation of y observations:  
## 0 1 2 3 4 5 9 10  
## 11 9 2 5 3 2 1 3  
##  
## Observation-level covariates:
```

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##      GSD
## Min.   : 1.377
## 1st Qu.: 2.505
## Median : 3.455
## Mean    : 4.280
## 3rd Qu.: 6.244
## Max.    :10.007

# create null and full model using a poisson distribution (abundance is assumed constant at all sites)
fm0 <- pcount (~1 ~1, data=data.umf)

## Warning in pcount(~1 ~ 1, data = data.umf): K was not specified and was set to
## 110.

fm1 <- pcount(~GSD ~1, data=data.umf)

## Warning in pcount(~GSD ~ 1, data = data.umf): K was not specified and was set to
## 110.

# create null and full model using a negativ-binomial distribution (assumes nests to show a clumped distribution)
fm0NB <- pcount (~1 ~1, data=data.umf, mixture=c("NB"))

## Warning in pcount(~1 ~ 1, data = data.umf, mixture = c("NB")): K was not specified and was set to 110.

fm1NB <- pcount (~GSD ~1, data=data.umf, mixture=c("NB"))

## Warning in pcount(~GSD ~ 1, data = data.umf, mixture = c("NB")): K was not specified and was set to 110.

# run goodness of fit test for global detection models using either distribution:
chisq <- function(fm) {
  umf <- getData(fm)
  y <- getY(umf)
  y[y>1] <- 1
  sr <- fm@sitesRemoved
  if(length(sr)>0)
    y <- y[-sr,,drop=FALSE]
  fv <- fitted(fm, na.rm=TRUE)
  y[is.na(fv)] <- NA
  sum((y-fv)^2/(fv*(1-fv)), na.rm=TRUE)
}
(pb <- parboot(fm1, chisq, nsim=1000, report=1))

## t0 = -46.01168

## Running parametric bootstrap in parallel on 7 cores.

## Bootstrapped statistics not reported during parallel processing.

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##
## Call: parboot(object = fm1, statistic = chisq, nsim = 1000, report = 1)
##
## Parametric Bootstrap Statistics:
##      t0 mean(t0 - t_B) StdDev(t0 - t_B) Pr(t_B > t0)
## 1 -46          -39.1          172          0.139
##
## t_B quantiles:
##      0% 2.5% 25% 50% 75% 97.5% 100%
## t*1 -2302 -92 -24 -13 -2.5 102 2801
##
## t0 = Original statistic computed from data
## t_B = Vector of bootstrap samples

(pb <- parboot(fm1NB, chisq, nsim=1000, report=1))

## t0 = 16.98767

## Running parametric bootstrap in parallel on 7 cores.
## Bootstrapped statistics not reported during parallel processing.

##
## Call: parboot(object = fm1NB, statistic = chisq, nsim = 1000, report = 1)
##
## Parametric Bootstrap Statistics:
##      t0 mean(t0 - t_B) StdDev(t0 - t_B) Pr(t_B > t0)
## 1 17          23.7          182          0.565
##
## t_B quantiles:
##      0% 2.5% 25% 50% 75% 97.5% 100%
## t*1 -1007 -138 -27 -13 -3.5 128 3399
##
## t0 = Original statistic computed from data
## t_B = Vector of bootstrap samples

# both full poisson and NB distribution fit the data (p > 0.05 indicates that
modeled data are not different from observed data based on results from 1000
simulations)

# check whether Poisson or NB mode provides a more realistic abundance estima
te (compared with ground data in Bonnini et al. 2018)
backTransform(fm1, type="state") # average nest abundance is 24.5 per site wh
ich is less than reported in Bonnini et al. 2018

## Backtransformed linear combination(s) of Abundance estimate(s)
##
##      Estimate    SE LinComb (Intercept)
##      24.5 22.9      3.2              1
##
## Transformation: exp

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backTransform(fm1NB, type="state") # average nest abundance is 39.6 per site
which coincides with information reported in Bonnin et al. 2018

## Backtransformed linear combination(s) of Abundance estimate(s)
##
## Estimate SE LinComb (Intercept)
##      39.6 15.1    3.68          1
##
## Transformation: exp

# check AICc
AICc(fm1)

## [1] 173.984

AICc(fm1NB) # NB model better suitable than Poisson model

## [1] 162.9758

AICc(fm0) # delta AIC is larger than 7 (delta AIC = 35.27 compared to fm1NB),
indicating that GSD is a valid predictor for detection probability

## [1] 198.2533

# choose NB model for further calculation:
detback <- linearComb(fm1NB, c(0,4.280), type="det") # 4.280 is the average
GSD used in Bonnin et al. 2018
backTransform(detback) # back-transformed nest detection probability

## Backtransformed linear combination(s) of Detection estimate(s)
##
## Estimate SE LinComb (Intercept) GSD
##      0.196 0.0454    -1.41          0 4.28
##
## Transformation: logistic

# Predicting nest detection probability depending on GSD:
newdata <- data.frame(GSD=seq(1.46,5.86, length=480)) #predicting different v
alues from minimum GSD and maximum GSD used during Wich et al. flights
Ep <- predict(fm1NB, type="det", newdata=newdata, appendData=TRUE)

# Graph for Figure 3 based on predicted values
library(ggplot2)

## Warning: package 'ggplot2' was built under R version 4.1.3

ggplot(data = Ep,
       aes(x = GSD,
           y = Predicted)) +
  geom_ribbon(aes(x=GSD, ymin=lower, ymax=upper), fill="gray80")+

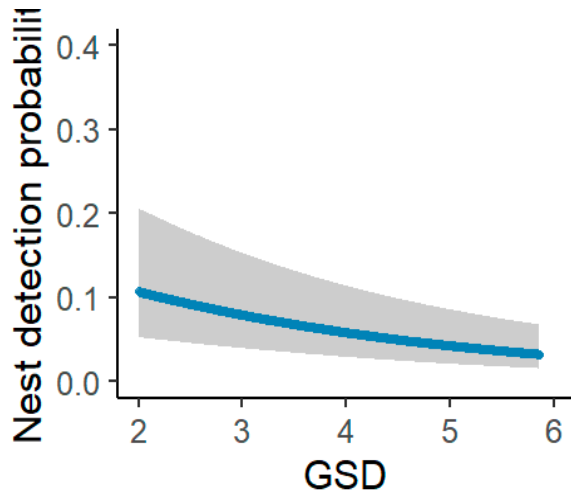
```

```

scale_y_continuous(limits = c(0, 0.4))+
geom_point(color="steelblue",
           size = 2,
           alpha=.8) +
xlim(2,6)+
labs(x = "GSD",
     y = "Nest detection probability") +
theme_classic(base_size=23)

```

Warning: Removed 59 rows containing missing values (geom_point).



```
write.csv(Ep, 'Predictions.csv')
```

2) Use predicted data from Predictions.csv to calculate nest detection probability during flights from Wich et al. (reported in Table 2)

3) Predicting false-absence probabilities depending on GSD and number of surveyed plots

```
Figure5 <- read.csv("Predictions_Figure5.csv", sep=";", header=TRUE) # based
on predictions from Predictions.csv, extrapolated for varying plot numbers for
minimum, median and maximum values of GSD
```

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# Graph for Figure 5 based on predicted values from Predictions_Figure5
ggplot(data = Figure5,
       aes(x = Plots,
           y = FN_prob)) +
  geom_ribbon(aes(x=Plots, ymin=FN_lower, ymax=FN_upper), fill="gray80")+
  scale_y_continuous(limits = c(0, 0.5))+
  geom_point(color="steelblue",
            size = 2,

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    alpha=.8) +
xlim(0,150)+
labs(x = "Number of surveyed plots",
     y = "False-absence probability") +
theme_classic(base_size=23)+
geom_hline(yintercept = 0.05, linetype = 2, color="red")+
facet_grid(cols=vars(GSD))

```

Warning: Removed 207 rows containing missing values (geom_point).

