Rcode_Wichetal_Usingdronesto.R

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```r
# Wich et al. Using drones to determine chimpanzee absence at the edge
of their 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 Bonnin et al. 2018 to
estimate nest detection probability during a flight in a 50x500m plot
depending on GSD

# Load detection matrix (from Bonnin et al. 2018, cells indicate
numbers of nests 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
probability, 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:
##        GSD
##  Min.   : 1.377
##  1st Qu.: 2.505
##  Median : 3.455
##  Mean   : 4.280
##  3rd Qu.: 6.244
##  Max.   :10.007
```

```r
# 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.
```

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

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

```r
# 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.
```

```r
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.
```

```r
# 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)) # p = 0.161, model
fits

## t0 = -46.01168

## Running parametric bootstrap in parallel on 7 cores.

## Bootstrapped statistics not reported during parallel processing.

##
## 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)) # p = 0.579, model
fits

## 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)
```

```r
# check whether Poisson or NB mode provides a more realistic abundance
estimate (compared with ground data in Bonnin et al. 2018)
backTransform(fm1, type="state") # average nest abundance is 24.5 per
site which is less than reported in Bonnin et al. 2018
```

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

```r
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
```

```r
# check AICc
AICc(fm1) # AICc = 173.98
```

```
## [1] 173.984
```

```r
AICc(fm1NB) # AICc = 162.98 -> NB model better suitable than Poisson
model
```

```
## [1] 162.9758
```

```r
AICc(fm0)# AICc = 198.25 -> 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
```

```r
# 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 is
0.196 at average GSD (SE = 0.0454)
```

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

```r
backTransform(fm0, type='det') # back-transforemd nest detection
probability is 0.03 for null model at average GSD

## Backtransformed linear combination(s) of Detection estimate(s)
##
##  Estimate      SE LinComb (Intercept)
##    0.0307 0.00866   -3.45                1
##
## Transformation: logistic

# Predicting nest detection probability depending on GSD:
newdata <- data.frame(GSD=seq(1.46,5.86, length=480)) #predicting
different values from minimum GSD and maximum GSD used during Wich et
al. 2022 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).
```
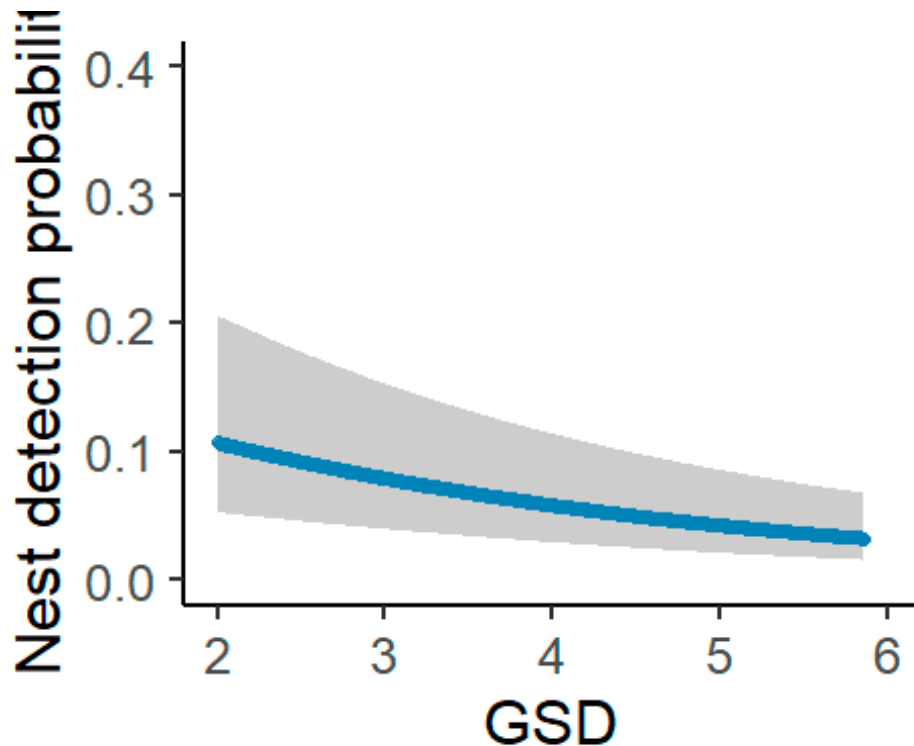
```
write.csv(Ep,'Predictions.csv')




# 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 variny plot
numbers for three different GSDs

# 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,
           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).
```