

Nest Provisioning in a Fire Disturbed Landscape

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Initialization

All relative paths begin at the final-project repository root directory.

Required Packages

```
# LaTeX
#install.packages("tinytex")

# Data manipulation and visualization
install.packages("tidyverse", repos='http://cran.us.r-project.org')

## Installing package into '/home/eliza/R/x86_64-pc-linux-gnu-library/4.0'
## (as 'lib' is unspecified)

install.packages("gridExtra", repos='http://cran.us.r-project.org')

## Installing package into '/home/eliza/R/x86_64-pc-linux-gnu-library/4.0'
## (as 'lib' is unspecified)

# LaTeX
#library(tinytex)
#tinytex::install_tinytex()

# Data manipulation and visualization
library(tidyverse)

## -- Attaching packages ----- tidyverse 1.3.0 --

## v ggplot2 3.3.2      v purrr  0.3.4
## v tibble  3.0.4      v dplyr  1.0.2
## v tidyr   1.1.2      v stringr 1.4.0
## v readr   1.4.0      v forcats 0.5.0

## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
library(gridExtra)
```

```
##  
## Attaching package: 'gridExtra'  
  
## The following object is masked from 'package:dplyr':  
##  
##      combine
```

Custom functions:

```
## getCI  
##  
## @param vec a vector  
## @param n_samp number of times to sample data  
##  
## @return upper and lower bootstrap confidence intervals  
##  
##  
## @examples  
##      getCI(1:20, 2000)  
## @export  
  
getCI <- function(vec, n_samp=1000) {  
  smp <- replicate(n_samp, mean(sample(vec, replace = TRUE), na.rm = TRUE))  
  CIs <- quantile(smp, c(0.025, 0.975), na.rm = T)  
  return(CIs)  
}
```

Prey Delivery Rates by Sex

Load prey delivery data.

```
pdOriginal <- read.csv("../data/pd_main.csv")  
  
#rename the first column, which imported with a special character  
names(pdOriginal)[1] <- "nest"
```

Filter to only include M and F (remove unknown and total), separate “nest” column into “study_site” and territory.

```
pdMF <- pdOriginal %>%  
  separate(col = nest, into = c("study_site", "territory"), sep = 1, remove = TRUE) %>%  
  filter(sex == "M" | sex == "F")
```

Check structure of data.

```
pd_str <- str(pdMF)
```

```
## 'data.frame': 1299 obs. of 55 variables:
## $ study_site : chr "A" "A" "B" "C" ...
## $ territory : chr "29_2007" "29_2007" "7_2005" "S1_1_2005" ...
## $ year : int 2007 2007 2005 2005 2005 2005 2006 2006 2014 2004 ...
## $ obs_date : chr "6/4/2007" "6/4/2007" "6/15/2005" "6/9/2005" ...
## $ clutch_size : chr "2" "2" "" "" ...
## $ brood_size : chr "2" "2" "" "" ...
## $ num_fledged : chr "2" "2" "" "" ...
## $ incubation_start : chr "6/6/2007" "6/6/2007" "" "" ...
## $ julian_incubation: int 157 157 NA NA NA NA 157 157 155 151 ...
## $ nest_age : chr "1" "1" "1" "1" ...
## $ sunset : int 2021 2021 NA 2025 2023 2020 2023 2023 2026 2019 ...
## $ sex : chr "M" "F" "F" "F" ...
## $ t15 : int NA NA 0 NA NA NA NA NA 2 NA ...
## $ t30 : int NA NA 0 NA NA NA NA NA NA 0 ...
## $ t45 : int NA NA 0 NA 0 NA NA NA NA 2 ...
## $ t60 : int NA NA 0 NA 0 NA NA NA NA 1 ...
## $ t75 : int NA NA 0 NA 0 NA 1 0 NA 3 ...
## $ t90 : int NA NA NA 0 0 NA 0 0 NA 0 ...
## $ t105 : int NA NA NA 0 0 0 0 0 NA 0 ...
## $ t120 : int NA NA NA 0 NA 0 0 0 NA 0 ...
## $ t135 : int NA NA NA 0 NA 0 0 0 NA NA ...
## $ t150 : int NA NA NA 0 NA 0 1 0 NA NA ...
## $ t165 : int NA NA NA NA NA 0 0 0 NA NA ...
## $ t180 : chr "1" "0" "" "" ...
## $ t195 : int 3 0 NA NA NA NA NA NA NA NA ...
## $ t210 : int 2 0 NA NA NA NA NA NA NA NA ...
## $ t225 : chr "1" "0" "" "" ...
## $ t240 : int 3 0 NA NA NA NA NA NA NA NA ...
## $ t255 : int NA NA NA NA NA NA NA NA NA NA ...
## $ t270 : int NA NA NA NA NA NA NA NA NA NA ...
## $ t285 : int NA NA NA NA NA NA NA NA NA NA ...
## $ t300 : int NA NA NA NA NA NA NA NA NA NA ...
## $ t315 : int NA NA NA NA NA NA NA NA NA NA ...
## $ t330 : int NA NA NA NA NA NA NA NA NA NA ...
## $ t345 : int NA NA NA NA NA NA NA NA NA NA ...
## $ t360 : int NA NA NA NA NA NA NA NA NA NA ...
## $ t375 : int NA NA NA NA NA NA NA NA NA NA ...
## $ t390 : int NA NA NA NA NA NA NA NA NA NA ...
## $ t405 : int NA NA NA NA NA NA NA NA NA NA ...
## $ t420 : int NA NA NA NA NA NA NA NA NA NA ...
## $ t435 : int NA NA NA NA NA NA NA NA NA NA ...
## $ t450 : int NA NA NA NA NA NA NA NA NA NA ...
## $ t465 : int NA NA NA NA NA NA NA NA NA NA ...
## $ t480 : int NA NA NA NA NA NA NA NA NA NA ...
## $ t495 : int NA NA NA NA NA NA NA NA NA NA ...
## $ t510 : int NA NA NA NA NA NA NA NA NA NA ...
## $ t525 : int NA NA NA NA NA NA NA NA NA NA ...
## $ t540 : int NA NA NA NA NA NA NA NA NA NA ...
## $ Comments : chr "passive" "passive" "Captured on Last Pd" "Capture F, start time reflects
## $ obs_time : chr "2313-2418" "2313-2418" "2015-2128" "2150-2254" ...
```

```
## $ start_time      : chr  "23:13" "23:13" "20:15" "21:50" ...
## $ stop_time       : chr  "24:18:00" "24:18:00" "21:28" "22:54" ...
## $ weather         : chr  "sprinkles, light wind" "sprinkles, light wind" "storm entering around 21
## $ fledge_date      : chr  "" "" "" "" ...
## $ fledge_accuracy : chr  "w/in 1 day" "w/in 1 day" "Predated" "abandoned" ...
```

```
unique(pdMF$t180) #at least one cell has an asterisk after the value
```

```
## [1] "1" "0" "" "4" "4*" "2" "9" "10" "3" "5"
```

```
unique(pdMF$t225) #same here
```

```
## [1] "1" "0" "" "6*" "3" "2" "8" "11" "7"
```

```
unique(pdMF$nest_age) #"pred" and "" can be converted to NA
```

```
## [1] "1" "2" "3" "4" "5" "6" "7" "8" "9" "10"
## [11] "11" "12" "13" "14" "15" "16" "17" "18" "19" "20"
## [21] "21" "22" "23" "24" "25" "26" "27" "28" "29" "30"
## [31] "31" "32" "33" "34" "35" "36" "37" "38" "39" "40"
## [41] "41" "42" "43" "44" "45" "46" "47" "48" "49" "50"
## [51] "51" "53" "100" "0" "pred" ""
```

Fix structure.

```
#remove asterisks
pdClean <- pdMF %>%
  mutate(t180 = gsub("\\*", "", t180)) %>%
  mutate(t225 = gsub("\\*", "", t225))

#change these columns to numeric
pdClean$t180 <- as.integer(pdClean$t180)
pdClean$t225 <- as.integer(pdClean$t225)
pdClean$nest_age <- as.integer(pdClean$nest_age)
```

```
## Warning: NAs introduced by coercion
```

```
#warning here is ok--NAs are replacing "pred" and "" values
```

Prey Deliveries Throughout Night

Data was separated by sex (M vs. F) and by incubation vs. nestling stage. Nestling period is defined as nest_age >= 22 days. If nest age was not indicated in original dataset, field notes were used to determine whether nest was in incubation (all eggs) or nestling (at least one nestling) stage. For these records, the following values were manually input: nest_age = 0 for incubation or nest_age = 100 for nestling, so that this data could be easily separated from known nest age. If it was later determined that nest had been predated before observation, “pred” was entered. If the nest stage could not be determined, it was left blank. “pred” and “” values were converted to NA earlier when this column was converted to numeric.

```

# Create independent dfs for M (nestling and incubation stage) and F (nestling and incubation state).

#select relevant columns, add column for stage, rename study sites, drop NAs
pdStage1 <- pdClean %>%
  dplyr::select(sex, nest_age, t15:t240) %>%
  mutate(
    stage =
      ifelse(nest_age < 22, "incubation", "nestling")) %>%
  drop_na(stage)

#change column names to remove "t" in front of time interval
colnames(pdStage1) <- c("sex", "nest_age", "15", "30", "45", "60", "75", "90", "105", "120", "135", "150")

#create independent dfs for each study site and stage
pdM_inc <- pdStage1 %>%
  filter(sex == "M", stage == "incubation") %>%
  dplyr::select('15':'240')

pdM_nest <- pdStage1 %>%
  filter(sex == "M", stage == "nestling") %>%
  dplyr::select('15':'240')

pdF_inc <- pdStage1 %>%
  filter(sex == "F", stage == "incubation") %>%
  dplyr::select('15':'240')

pdF_nest <- pdStage1 %>%
  filter(sex == "F", stage == "nestling") %>%
  dplyr::select('15':'240')

```

Mean PD tables

Four stand-alone data.frames, one for M (incubation), one for M (nestling), one for F (incubation), and one for F (nestling):

```

meanM_inc <- data.frame(
  time = as.numeric(colnames(pdM_inc)),
  M_incubation = colMeans(pdM_inc, na.rm = TRUE))

meanM_nest <- data.frame(
  time = as.numeric(colnames(pdM_nest)),
  M_nestling = colMeans(pdM_nest, na.rm = TRUE))

meanF_inc <- data.frame(
  time = as.numeric(colnames(pdF_inc)),
  F_incubation = colMeans(pdF_inc, na.rm = TRUE))

meanF_nest <- data.frame(
  time = as.numeric(colnames(pdF_nest)),
  F_nestling = colMeans(pdF_nest, na.rm = TRUE))

```

One table showing mean PDs for all study sites and stages:

```
meanMF <- data.frame(
  time = as.numeric(colnames(pdM_inc)),
  M_incubation = colMeans(pdM_inc, na.rm = TRUE),
  M_nestling = colMeans(pdM_nest, na.rm = TRUE),
  F_incubation = colMeans(pdF_inc, na.rm = TRUE),
  F_nestling = colMeans(pdF_nest, na.rm = TRUE)
)
```

Calculate confidence intervals

Write and apply function to obtain CIs.

```
#now apply it across the columns of PD data
ciM_inc <- apply(pdM_inc, 2, FUN = getCI)
ciM_nest <- apply(pdM_nest, 2, FUN = getCI)
ciF_inc <- apply(pdF_inc, 2, FUN = getCI)
ciF_nest <- apply(pdF_nest, 2, FUN = getCI)
```

Add CIs to a data frame. Remove rows where time > 180 for ciInc because no data is available for MGSA after this time.

```
ciInc_sex <- data.frame(
  sex = c(rep("M", nrow(meanM_inc)), rep("F", nrow(meanF_inc))),
  mean = c(colMeans(pdM_inc, na.rm = TRUE), colMeans(pdF_inc, na.rm = TRUE)),
  ci_l = c(ciM_inc[1,], ciF_inc[1,]),
  ci_h = c(ciM_inc[2,], ciF_inc[2,]),
  time = c(as.numeric(rownames(meanM_inc)), as.numeric(rownames(meanF_inc))),
  stage = "Incubation")

ciNest_sex <- data.frame(
  sex = c(rep("M", nrow(meanM_nest)), rep("F", nrow(meanF_nest))),
  mean = c(colMeans(pdM_nest, na.rm = TRUE), colMeans(pdF_nest, na.rm = TRUE)),
  ci_l = c(ciM_nest[1,], ciF_nest[1,]),
  ci_h = c(ciM_nest[2,], ciF_nest[2,]),
  time = c(as.numeric(rownames(meanM_nest)), as.numeric(rownames(meanF_nest))),
  stage = "Nestling")

ciAll_sex <- rbind(ciInc_sex, ciNest_sex)
```

Plot

Incubation:

```
plotInc_sex <- ggplot(data = ciInc_sex) +
  geom_point(aes(x = time, y = mean, color = sex, group = sex),
    position = position_dodge(width=0.75)) +
  geom_errorbar(aes(x=time, ymax = ci_h, ymin=ci_l, color = sex,
    group = sex),
    position = position_dodge(width=0.75)) +
  labs(x = "Time After Sunset (minutes)", y = "Mean Prey Deliveries",
```

```

    title = "Incubation", color = "Sex") +
  theme_minimal() +
  theme(plot.title = element_text(hjust = 0.5))

```

Nestling:

```

plotNest_sex <- ggplot(data = ciNest_sex) +
  geom_point(aes(x = time, y = mean, color = sex, group = sex),
             position = position_dodge(width=0.75)) +
  geom_errorbar(aes(x=time, ymax = ci_h, ymin=ci_l, color = sex,
                    group = sex),
               position = position_dodge(width=0.75)) +
  labs(x = "Time After Sunset (minutes)", y = "Mean Prey Deliveries",
       title = "Nestling", color = "Sex") +
  theme_minimal() +
  theme(plot.title = element_text(hjust = 0.5))

```

Plot both as separate plots, side by side:

```

pdf("../analysis/figures/figure1")    # creates new pd file
grid.arrange(plotInc_sex, plotNest_sex) # makes the actual plot
dev.off()                             # closes the PDF file

```

```

## pdf
## 2

```

Test for Difference

Independent t-test for incubation stage. $p = 5.163e-09$

```
t.test(meanF_inc$F_incubation, meanM_inc$M_incubation)
```

```

##
##  Welch Two Sample t-test
##
## data:  meanF_inc$F_incubation and meanM_inc$M_incubation
## t = -11.795, df = 15.078, p-value = 5.163e-09
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -1.1125110 -0.7720969
## sample estimates:
##  mean of x   mean of y
## 0.004058442 0.946362390

```

Independent t-test for nestling stage. $p = 1.355e-08$

```
t.test(meanF_nest$F_nestling, meanM_nest$M_nestling)
```

```

##
##  Welch Two Sample t-test

```

```
##
## data: meanF_nest$F_nestling and meanM_nest$M_nestling
## t = -8.0503, df = 26.534, p-value = 1.355e-08
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -1.2074419 -0.7166369
## sample estimates:
## mean of x mean of y
## 0.3543829 1.3164223
```

Prey Delivery Rates by Site

Filter pdMF to only include males in B (MGSA) and C (HFSA).

```
pdHM <- pdClean %>%
  filter(study_site == "B" | study_site == "C", sex == "M")
```

Visualize prey deliveries throughout night

Data was separated by study site (HFSA vs. MGSA) and by incubation vs. nestling stage.

since the last observation for HFSA is at time = 240, we'll end both datasets there.

First, create data frame with PDs for whole dataset, then broken down by each study site and stage.

```
#create independent dfs for HFSA (nestling and incubation stage) and MGSA (nestling and incubation stage)

#select relevant columns, add column for stage, rename study sites, drop NAs
pdStage <- pdClean %>%
  dplyr::select(study_site, nest_age, t15:t240) %>%
  mutate(
    stage =
      ifelse(nest_age < 22, "incubation", "nestling"),
    study_site =
      ifelse(study_site == "B", "MGSA", "HFSA")) %>%
  drop_na(stage)

#change column names to remove "t" in front of time interval
colnames(pdStage) <- c("study_site", "nest_age", "15", "30", "45", "60", "75", "90", "105", "120", "135", "150", "165", "180", "195", "210", "225", "240")

#create independent dfs for each study site and stage
pdHFSA_inc <- pdStage %>%
  filter(study_site == "HFSA", stage == "incubation") %>%
  dplyr::select('15':'240')

pdHFSA_nest <- pdStage %>%
  filter(study_site == "HFSA", stage == "nestling") %>%
  dplyr::select('15':'240')

pdMGSA_inc <- pdStage %>%
  filter(study_site == "MGSA", stage == "incubation") %>%
  dplyr::select('15':'240')
```



```
pdMGSA_nest <- pdStage %>%
  filter(study_site == "MGSA", stage == "nestling") %>%
  dplyr::select('15':'240')
```

Mean PD tables

Four stand-alone data.frames, one for (incubation), one for HFSA (nestling), one for MGSA(incubation), and one for MGSA (nestling):

```
meanHFSA_inc <- data.frame(
  time = as.numeric(colnames(pdHFSA_inc)),
  HFSA_incubation = colMeans(pdHFSA_inc, na.rm = TRUE))

meanHFSA_nest <- data.frame(
  time = as.numeric(colnames(pdHFSA_nest)),
  HFSA_nestling = colMeans(pdHFSA_nest, na.rm = TRUE))

meanMGSA_inc <- data.frame(
  time = as.numeric(colnames(pdMGSA_inc)),
  MGSA_incubation = colMeans(pdMGSA_inc, na.rm = TRUE))

meanMGSA_nest <- data.frame(
  time = as.numeric(colnames(pdMGSA_nest)),
  MGSA_nestling = colMeans(pdMGSA_nest, na.rm = TRUE))
```

Two tables, one for nestling stage and one for incubation stage. This is just for visualization, not used in further analysis.

One table showing mean PDs for all study sites and stages:

```
meanAll <- data.frame(
  time = as.numeric(colnames(pdHFSA_inc)),
  HFSA_incubation = colMeans(pdHFSA_inc, na.rm = TRUE),
  HFSA_nestling = colMeans(pdHFSA_nest, na.rm = TRUE),
  MGSA_incubation = colMeans(pdMGSA_inc, na.rm = TRUE),
  MGSA_nestling = colMeans(pdMGSA_nest, na.rm = TRUE)
)
```

Calculate confidence intervals

Write and apply function to obtain CIs.

```
#now apply it across the columns of PD data
ciHFSA_inc <- apply(pdHFSA_inc, 2, FUN = getCI)
ciHFSA_nest <- apply(pdHFSA_nest, 2, FUN = getCI)
ciMGSA_inc <- apply(pdMGSA_inc, 2, FUN = getCI)
ciMGSA_nest <- apply(pdMGSA_nest, 2, FUN = getCI)
```

Add CIs to a data frame. Remove rows where time > 180 for ciInc because no data is available for MGSA after this time.

```

ciInc <- filter(
  data.frame(
    study_area = c(rep("HFSA", nrow(meanHFSA_inc)), rep("MGSA", nrow(meanMGSA_inc))),
    mean = c(colMeans(pdHFSA_inc, na.rm = TRUE), colMeans(pdMGSA_inc, na.rm = TRUE)),
    ci_l = c(ciHFSA_inc[1,], ciMGSA_inc[1,]),
    ci_h = c(ciHFSA_inc[2,], ciMGSA_inc[2,]),
    time = c(as.numeric(rownames(meanHFSA_inc)), as.numeric(rownames(meanMGSA_inc))),
    stage = "Incubation"),
  time <= 180)

ciNest <- data.frame(
  study_area = c(rep("HFSA", nrow(meanHFSA_nest)), rep("MGSA", nrow(meanMGSA_nest))),
  mean = c(colMeans(pdHFSA_nest, na.rm = TRUE), colMeans(pdMGSA_nest, na.rm = TRUE)),
  ci_l = c(ciHFSA_nest[1,], ciMGSA_nest[1,]),
  ci_h = c(ciHFSA_nest[2,], ciMGSA_nest[2,]),
  time = c(as.numeric(rownames(meanHFSA_nest)), as.numeric(rownames(meanMGSA_nest))),
  stage = "Nestling")

ciAll <- rbind(ciInc, ciNest)

```

Plot

Incubation:

```

plotInc <- ggplot(data = ciInc) +
  geom_point(aes(x = time, y = mean, color = study_area, group = study_area),
    position = position_dodge(width=0.75)) +
  geom_errorbar(aes(x=time, ymax = ci_h, ymin=ci_l, color = study_area,
    group = study_area),
    position = position_dodge(width=0.75)) +
  labs(x = "Time After Sunset (minutes)", y = "Mean Prey Deliveries",
    title = "Incubation", color = "Study Area") +
  theme_minimal() +
  theme(plot.title = element_text(hjust = 0.5))

```

Nestling:

```

plotNest <- ggplot(data = ciNest) +
  geom_point(aes(x = time, y = mean, color = study_area, group = study_area),
    position = position_dodge(width=0.75)) +
  geom_errorbar(aes(x=time, ymax = ci_h, ymin=ci_l, color = study_area,
    group = study_area),
    position = position_dodge(width=0.75)) +
  labs(x = "Time After Sunset (minutes)", y = "Mean Prey Deliveries",
    title = "Nestling", color = "Study Area") +
  theme_minimal() +
  theme(plot.title = element_text(hjust = 0.5))

```

Both:

```
plotAll <- ggplot(data = ciAll) +
  geom_point(aes(x = time, y = mean, color = study_area, group = study_area),
    position = position_dodge(width=0.75)) +
  geom_errorbar(aes(x=time, ymax = ci_h, ymin=ci_l, color = study_area,
    group = study_area),
    position = position_dodge(width=0.75)) +
  labs(x = "Time After Sunset (minutes)", y = "Mean Prey Deliveries",
    title = "Average Prey Deliveries Throughout Night", color = "Study Area") +
  theme_minimal() +
  theme(plot.title = element_text(hjust = 0.5)) +
  facet_grid(~ stage)
```

Plot both as separate plots, side by side:

```
pdf("../analysis/figures/figure2")    # creates new pd file
grid.arrange(plotInc, plotNest) # makes the actual plot
dev.off()    # closes the PDF file
```

```
## pdf
## 2
```

Test for Difference

Independent t-tests for incubation stage. $p = 0.8786$

```
t.test(meanHFSA_inc$HFSA_incubation, meanMGSA_inc$MGSA_incubation)
```

```
##
## Welch Two Sample t-test
##
## data: meanHFSA_inc$HFSA_incubation and meanMGSA_inc$MGSA_incubation
## t = 0.4698, df = 21.664, p-value = 0.6432
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.1252531 0.1985364
## sample estimates:
## mean of x mean of y
## 0.4873974 0.4507558
```

Independent t-tests for nestling stage. $p = 0.377$

```
t.test(meanHFSA_nest$HFSA_nestling, meanMGSA_nest$MGSA_nestling)
```

```
##
## Welch Two Sample t-test
##
## data: meanHFSA_nest$HFSA_nestling and meanMGSA_nest$MGSA_nestling
## t = 0.89919, df = 25.484, p-value = 0.377
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
```

```
## -0.1472872 0.3759510
## sample estimates:
## mean of x mean of y
## 0.9076640 0.7933321
```