

Nest Provisioning in a Fire Disturbed Landscape

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Introduction

Fire plays an important role as a consistent disturbance in maintaining open stands of old-growth Ponderosa Pine (*Pinus ponderosa*) forests by helping to eliminate understory and limit fuel loads [Veblen et al., 2000]. Before human intervention, Ponderosa Pine forests naturally underwent forest fires in 5-50 year intervals [Veblen et al., 2000]. Over the past century, however, tree planting initiatives and increased implementation of fire suppression have led to increased density of stands [Griffis et al., 2001], making forest stands that are already drought stressed even more susceptible to high severity crown fires [Veblen et al., 2000]. In 2002, a human-caused wildfire, the Hayman Fire, burned 138,000 acres of old-growth Ponderosa pine forests in Colorado's Pike National Forest [Graham, 2003].

The Flammulated Owl (*Psiloscops flammeolus*) is a territorial, insectivorous, and nocturnal raptor native to montane forests in portions of the Rocky Mountains, Sierra Nevada Mountains, and the Occidental Mountains [Linkhart and McCallum, 2013]. The diet of the owl primarily consists of moths native to these regions [Linkhart and McCallum, 2013]. As a highly specialized secondary cavity nesting raptor, the Flammulated Owl is deemed an indicator species, meaning that the health of an ecosystem can be estimated based on the health of their population. Survival models have shown that Flammulated Owl survival in the HFSA is currently lower than survival in MGSA, suggesting that mortality, rather than emigration, explains most of the population declines following the Hayman Fire (Linkhart and Yanco, unpublished data).

Here, I examine one possible explanation for increased mortality in HFSA: prey availability. High severity burns dramatically alter vegetation structure, which in turn alters insect communities. Over time, insect communities within high intensity burn scars can crash, leaving avian predators without important food resources [Nappi et al., 2010]. If Flammulated Owls are adapting their behavior in response to changing prey availability, I would expect that the rate of prey deliveries to active nests would increase or decrease (increase if prey is lower quality, decrease if prey is more scarce or difficult to detect) [Zárybnická et al., 2009]. If Flammulated Owls are not adapting their behavior, this could mean that prey availability has either not changed or, more likely, that Flammulated Owls, which do not occupy landscapes prone to high severity burns, do not adapt their behavior in response to large-scale landscape changes. This would make them highly sensitive to large-scale disturbances that affect foraging at important times, such as during the breeding season.

The objectives for this analysis are to examine:

1. How do prey delivery rates change throughout the night?
2. How do male and female nest provisioning differ?
3. How is nest provisioning affected by high severity burns?

Methods

Data Collection

From summer 2002 to summer 2020, researchers monitored Flammulated Owl territories in the Hayman Fire Study Area (HFSA), located in the western portion of the Hayman Fire scar, and four other study areas within a 10 mile radius: Missouri Gulch Study Area (MGSA), Hotel Gulch Study Area (HGSA), and Trout Creek Study Area (TCSA). Researchers detected all Flammulated Owl nests at the beginning of each breeding season and monitored then until fledging or predation occurred. Each nest was observed for 1-2 hours per week, during which time researchers recorded the number of times the male or female breeder delivered prey to the nest. During incubation, the male exclusively delivers prey to the female, who stays on the nest. During the nestling stage, both parents delivery prey, although the female spends less time on each forage and sits on the nest between prey deliveries (observational data). While observing, researchers recorded which individual delivered prey, which was determined by vocal cues if both individuals were off the nest at the time. Data was recorded in fifteen minute intervals.

Analysis

First, average prey delivery rates for both males and females were compared at 15-minute intervals throughout the night. Any prey deliveries recorded at “Unknown” were discarded. Bootstrap confidence intervals were generated by sampling each time interval 1000 times, and means with CIs were visualized by plotting.

Then, the data was filtered to include only HFSA, our treatment area, and MGSA, an unburned study site ~5 miles from HFSA, with similar habitat. Means and bootstrap confidence intervals were plotted using the above technique.

Analysis

Initialization

All relative paths begin at the final-project/analysis subdirectory.

```
knitr::opts_chunk$set(message = FALSE)
```

Required Packages

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

# Data manipulation and visualization
library(tidyverse)
library(gridExtra)
```

Working directory:

Custom functions:

getCI is designed to generate bootstrap confidence intervals from a given vector.

```

#' 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)
}

```

testNormality runs a Shapiro-Wilk test on each time interval in a pd data frame and returns p values based on the null hypothesis that the data is normally distributed. If $p < 0.05$, data is not normally distributed.

```

#' testNormality
#'
#' @param dat a data.frame where columns = time intervals and rows = # prey deliveries
#' @param margin.a margin for apply statement running shapiro.test. default = 2.
#'
#' @return vector of p.values for each column of dat
#'
#'
#' @examples
#'   testNormality(pdM_inc, 2)
#' @export

testNormality <- function(dat, margin = 2) {
  norms <- apply(dat, margin, FUN = shapiro.test)
  return(sapply(norms, function(x){x[["p.value"]]}))
}

```

testWilcox runs a Wilcoxon test on the nth columns of two different data frames (i.e. df1[1] and df2[1], df1[2] and df2[2], etc.). We add the argument exact = FALSE to suppress the Warning message that exact p.values with ties can't be computed (warning comes from assumption that values are continuous). This is useful in testing for difference between prey delivery observations at time = 15 in one study site and at time = 15 in a second study site, when the data are not normally distributed.

```

#' testWilcox
#'
#' @param a a data.frame where columns = time intervals and rows = # prey deliveries
#' @param b a second data.frame where columns = time intervals and rows = # prey deliveries
#'
#' @return data.frame of p values (values) and corresponding time intervals (ind)
#'
#'
#' @examples

```

```
#'   testWilcox(pdMGSA_inc, pdHFSA_inc)
#' @export

testWilcox <- function(a, b){
  tmp <- mapply(wilcox.test, a, b, exact = FALSE)
  p.values <- stack(mapply(function(x, y) wilcox.test(x, y, exact = FALSE)$p.value, a, b))
  return(p.values)
}
```

Study Area

Hayman Fire Study Area (HFSA)

Load in fire scar polygon. Projected coordinate reference system: UTM Zone 13N.

Load in fire severity raster data:

Plot nest locations (n = 45) on Hayman Fire severity map:

Plot Hayman over CO basemap (maybe remove):

Prey Delivery Rates by Sex

First, we compared average prey delivery rates for males and females at all study sites at fifteen minute intervals throughout the night.

Read in Data

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 by removing asterisks and converting to integer class. NAs will be generated by coercion, eliminating any blank cells ("") and cells containing "pred" (indicating the nest was predated before the nest age could be confirmed).

```
#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
```

Organize Data

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).

pdStage_sex <- pdClean %>%
  dplyr::select(sex, nest_age, t15:t240) %>% #select relevant columns
  mutate(
```

```

    stage =
      ifelse(nest_age < 22, "incubation", "nestling")) %>% #add column for 'stage'
    drop_na(stage) #get rid of any rows blank values here, as they can't be used for analysis

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

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

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

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

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

```

Mean PD tables

Create four stand-alone data.frames, one for M (incubation), one for M (nestling), one for F (incubation), and one for F (nestling). These will be used for t-tests.

```

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))

```

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

Calculate confidence intervals

Apply getCI function across data.frames for each sex and stage.

```

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)

```

Create new data.frames (one for nestling stage and one for incubation stage) with means and CIs. 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)

```

Test for Difference

Test for normality for each time interval in M_inc, M_nest, and F_nest (excluded pdF_inc because all values = 0, as female did not deliver prey while incubating).

```

# Store results of testNormality in new df
normality_sex <- data.frame(
  M_inc = testNormality(pdM_inc, 2),
  M_nest = testNormality(pdM_nest, 2),
  F_nest = testNormality(pdF_nest, 2)
)

# Test if any values are not significant
any(normality_sex >= 0.05)

```

```
## [1] FALSE
```

All vectors in each list are significantly different from null hypothesis of Shapiro-Wilk normality test, meaning that no vector is normally distributed. Therefore, we use the unpaired two-sample Wilcoxon test to compare median values of M and F prey deliveries during each time interval, for incubation and nestling stages.

```

# Incubation Stage
wilcox_inc_sex <- testWilcox(pdM_inc, pdF_inc)

any(wilcox_inc_sex$values <= 0.05) #test if any p.values are significantly different: TRUE

```



```
## [1] TRUE
```

```
all(wilcox_inc_sex$values <= 0.05) #test if all p.values are significantly different: FALSE
```

```
## [1] FALSE
```

```
dplyr::filter(wilcox_inc_sex, values <= 0.05) #print which rows have p.value that is significantly diff
```

```
##           values ind
## 1  2.054022e-06   15
## 2  2.962959e-08   30
## 3  1.662023e-14   45
## 4  1.139046e-19   60
## 5  6.363476e-15   75
## 6  4.309115e-13   90
## 7  1.333988e-08  105
## 8  1.102312e-06  120
## 9  3.546280e-05  135
## 10 1.193741e-05  150
## 11 3.625618e-03  165
## 12 9.670479e-04  180
## 13 3.590980e-02  195
## 14 8.858782e-03  210
```

```
# Nestling Stage
```

```
wilcox_nest_sex <- testWilcox(pdM_nest, pdF_nest)
```

```
any(wilcox_nest_sex$values <= 0.05) #test if any p.values are significantly different: TRUE
```

```
## [1] TRUE
```

```
all(wilcox_nest_sex$values <= 0.05) #test if all p.values are significantly different: TRUE
```

```
## [1] TRUE
```

From the Wilcoxon tests, we see that all median time intervals during the nestling stage are significantly different between males and females. However, during the incubation stage, median prey delivery rates at time = 2255 and time = 240 are not significantly different between males and females.

Plot

Incubation (including star indicating non-significant Wilcoxon test at t = 225 and t = 240):

```
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)) +
geom_point(aes(x = 225, y = 4.5), shape = 8, stroke = 0.1) +
geom_point(aes(x = 240, y = 3.5), shape = 8, stroke = 0.1)
```

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))
```

The final plot compares both incubation and nestling stages.

```
grid.arrange(plotInc_sex, plotNest_sex)
```

Prey Delivery Rates by Site

The original spreadsheet contains prey delivery data from two other studies that were not considered in this analysis. Therefore, they were filtered out, and “B” (MGSA) and “C” (HFSA) were preserved for the analysis. Females were also excluded because there was not sufficient data for reliable analysis.

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

Organize Data

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. End incubation data frames at t = 180 and nesting data frames at t = 240 because this is the maximum time when there is data for both sites.

```
#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 =
```

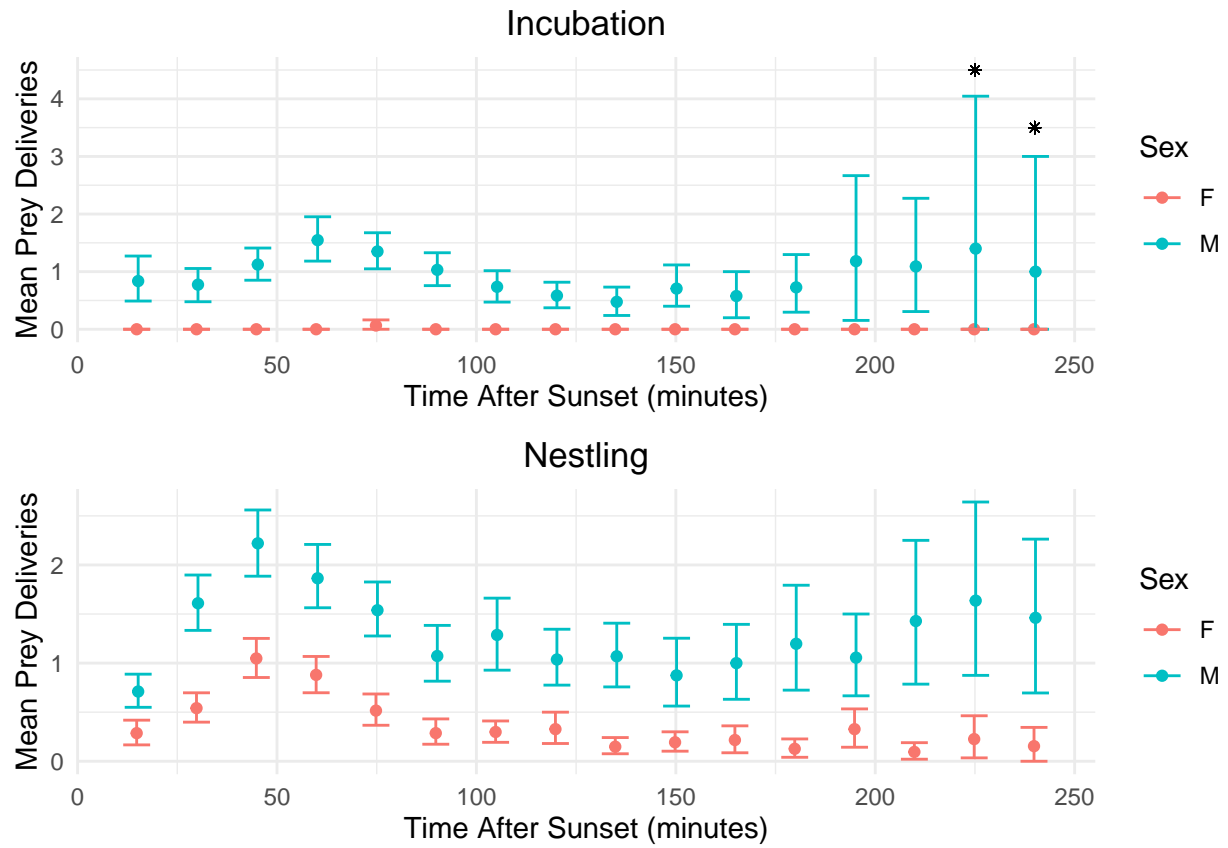


Figure 1: Mean prey deliveries during the incubation stage (top) and nestling stage (bottom). Males are shown in blue and females in red. Stars indicate non-significant differences in medians based on unpaired two-sample Wilcoxon tests.

```

      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")

#create independent dfs for each study site and stage
pdHFSA_inc <- pdStage %>%
  filter(study_site == "HFSA", stage == "incubation") %>%
  dplyr::select('15':'180')

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':'180')

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

```

Mean PD tables

Create four stand-alone data.frames, one for HFSA (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))

```

DELETE Create one table showing mean PDs for all study sites and stages.

Calculate confidence intervals

Apply getCI across each data.frame, taking each time interval as vector.

```

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.

```

ciInc <- 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")

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)

```

Test for Difference

Test for normality for each time interval in pdMGSA_inc, pdMGSA_nest, pdHFSA_inc, and pdHFSA_nest.

```

# Store results of testNormality in new df
normality_site <- list(
  MGSA_inc = testNormality(pdMGSA_inc, 2),
  MGSA_nest = testNormality(pdMGSA_nest, 2),
  HFSA_inc = testNormality(pdHFSA_inc, 2),
  HFSA_nest = testNormality(pdHFSA_nest, 2))

# Test if any values are not significant
sapply(normality_site, FUN = function(x){any(x >= 0.05)})

```

```

## MGSA_inc MGSA_nest HFSA_inc HFSA_nest
## FALSE FALSE FALSE FALSE

```

All vectors in each list are significantly different from null hypothesis of Shapiro-Wilk normality test, meaning that no vector is normally distributed. Therefore, we use the unpaired two-sample Wilcoxon test to compare median values for each time interval in MGSA and HFSA, for incubation and nestling stages.

```

# Incubation Stage
wilcox_inc <- testWilcox(pdMGSA_inc, pdHFSA_inc)
print(wilcox_inc)

```

```
##          values ind
## 1  0.8856867  15
## 2  0.5688739  30
## 3  0.3943537  45
## 4  0.9802463  60
## 5  0.2187071  75
## 6  0.3430303  90
## 7  0.4221215 105
## 8  0.9601425 120
## 9  0.1674084 135
## 10 0.1482079 150
## 11 0.5055388 165
## 12 0.6702783 180
```

```
any(wilcox_inc$values <= 0.05) #test if any p.values are significantly different: FALSE
```

```
## [1] FALSE
```

```
all(wilcox_inc$values > 0.05) #test if all p.values are not significant (double-checking first logical
```

```
## [1] TRUE
```

```
# Nestling Stage
```

```
wilcox_nest <- testWilcox(pdMGSA_nest, pdHFSA_nest)
print(wilcox_nest)
```

```
##          values ind
## 1  0.94970196  15
## 2  0.67158087  30
## 3  0.22037822  45
## 4  0.43641197  60
## 5  0.13753444  75
## 6  0.45695064  90
## 7  0.48124642 105
## 8  0.11508571 120
## 9  0.83764080 135
## 10 0.13535971 150
## 11 0.01047295 165
## 12 0.77862619 180
## 13 0.20597828 195
## 14 0.40201683 210
## 15 0.56634953 225
## 16 0.06390017 240
```

```
any(wilcox_nest$values <= 0.05) #test if any p.values are significantly different: TRUE
```

```
## [1] TRUE
```

```
dplyr::filter(wilcox_nest, values <= 0.05) #print which row has p.value that is significantly different
```

```
##          values ind
## 1 0.01047295 165
```

From the Wilcoxon tests, we see that no median time intervals during the incubation stage are different between MGSA and HFSA. However, during the nestling stage, median prey delivery rates at time = 165 are significantly different between MGSA and HFSA.

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))
```

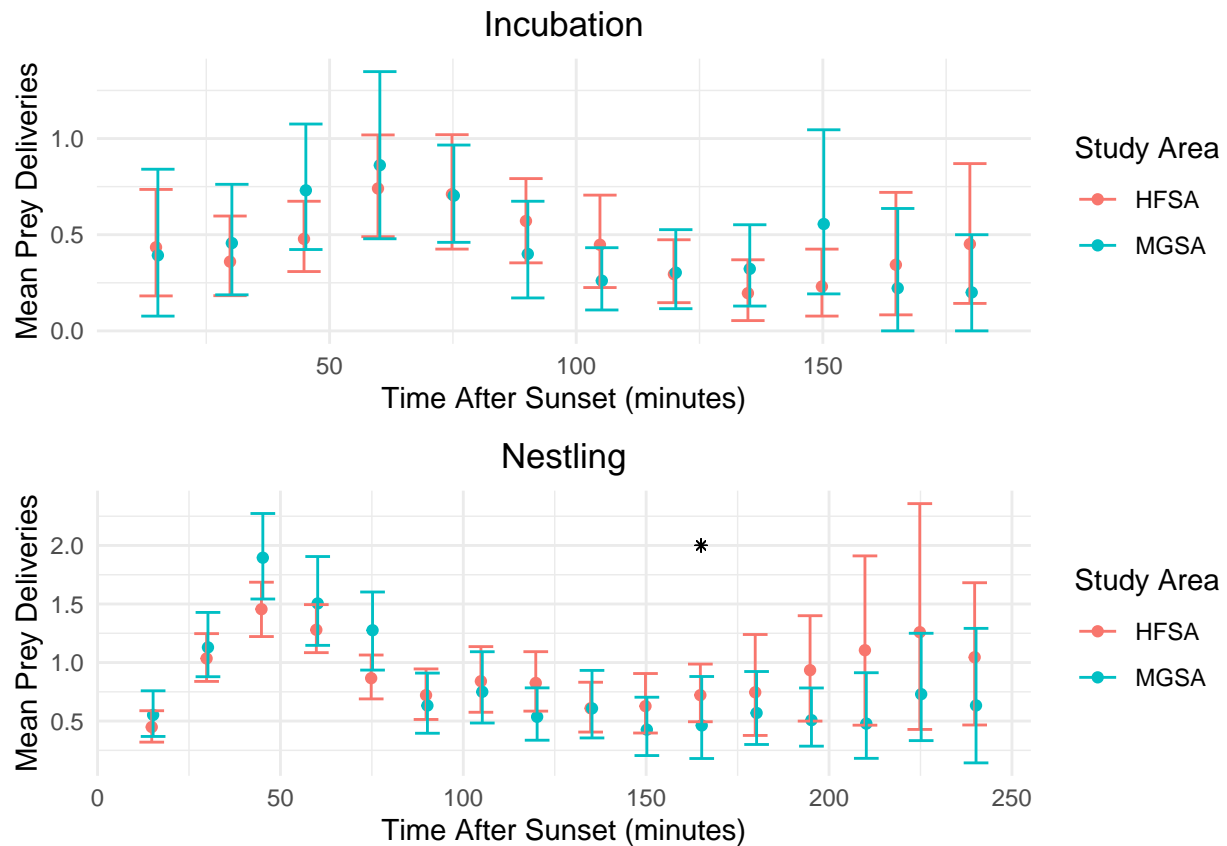
Nestling (including star indicating significant Wilcoxon test at t = 165):

```
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)) +
  geom_point(aes(x = 165, y = 2.0), shape = 8, stroke = 0.1)
```

Both:

The final plot compares both incubation and nestling stages.

```
grid.arrange(plotInc, plotNest)
```



References

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