

# Nest Provisioning in a Fire Disturbed Landscape

Eliza Stein

11/8/2020

## 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 (?). Before human intervention, Ponderosa Pine forests naturally underwent forest fires in 5-50 year intervals (?). Over the past century, however, tree planting initiatives and increased implementation of fire suppression have led to increased density of stands (?), making forest stands that are already drought stressed even more susceptible to high severity crown fires (?). 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 (?).

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 (?). The diet of the owl primarily consists of moths native to these regions (?). 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rather than emigration, explains most of the population declines following the Hayman Fire (Linkhart and Yanco, unpublished data).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 (?). 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) (?). 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.

## Initialization

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

## Required Packages

```
# 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
```

Working directory:

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)
}
```

## 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

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 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", "165", "180", "195", "210", "225", "240")

#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))

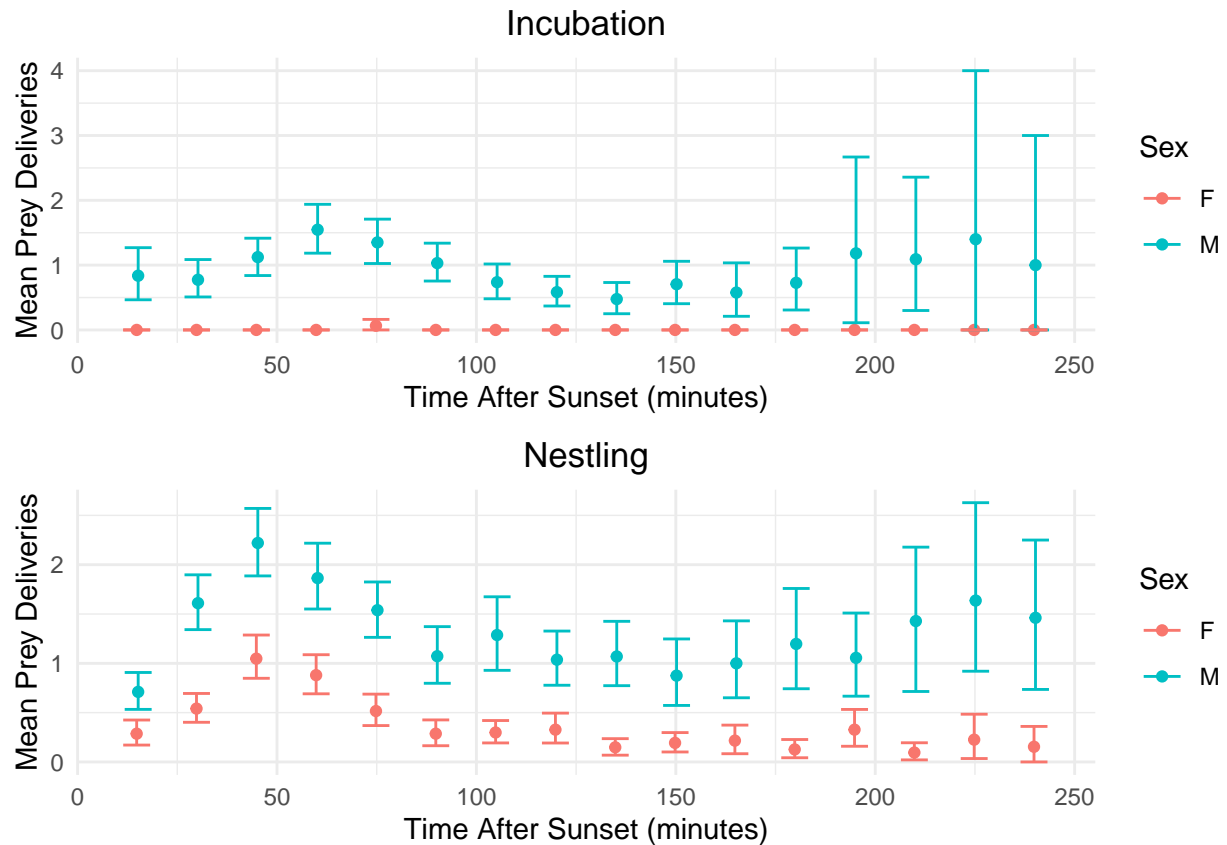
```

Plot both as separate plots, side by side:

```

grid.arrange(plotInc_sex, plotNest_sex)

```



## 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))

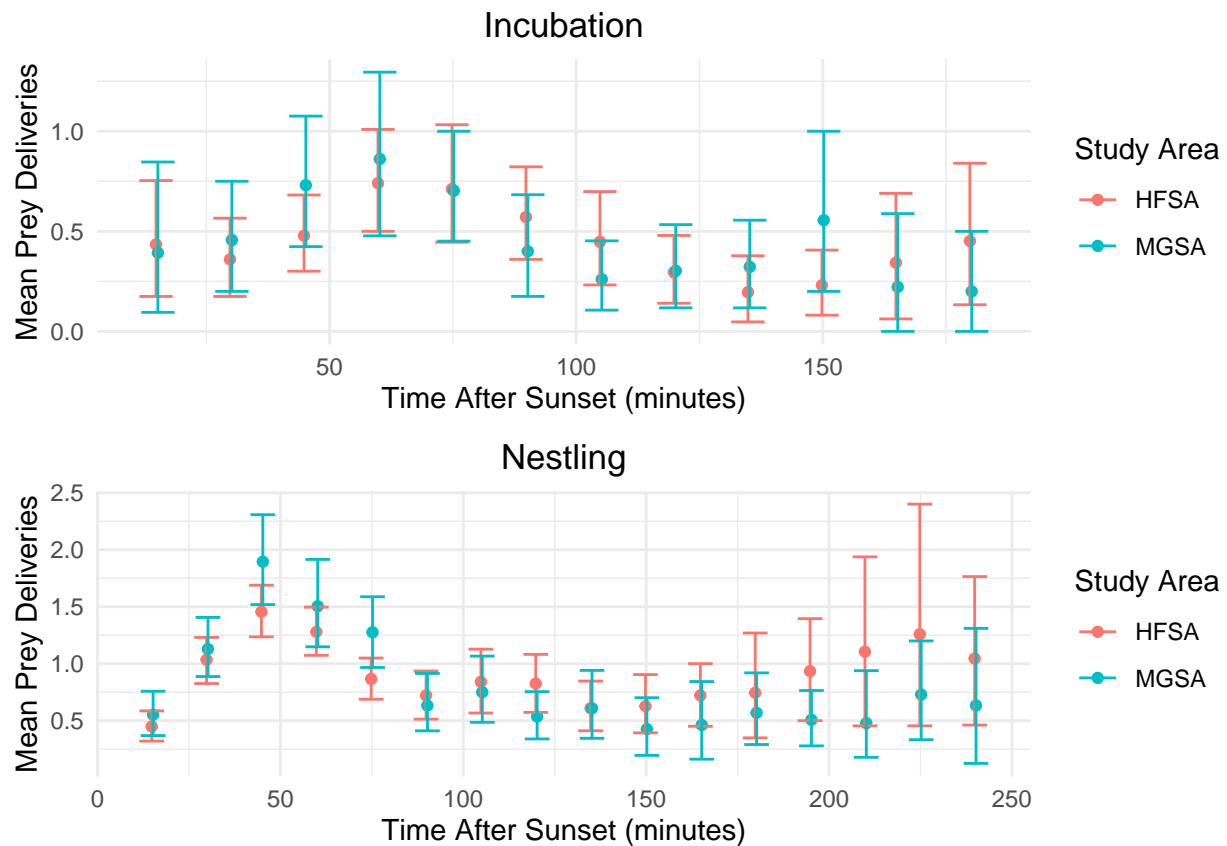
```

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:

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



## 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
```