

R-code for “Dancing in the moonlight: evidence that Killdeer foraging behavior varies with lunar cycle”

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In this document I provide all the necessary code for reproducing the analyses presented in my paper. To access the dataset and Rmarkdown file, please download this [GitHub](#) repository. Simply follow the link and click on *Download ZIP* on the right-hand side of the page. An explanation of the files in the repository can be found in the Readme file. Please don’t hesitate to contact me at [luke.eberhart\[at\]gmail.com](mailto:luke.eberhart[at]gmail.com) if you have any questions.

The structure of the code I present here follows the analyses presented in the *Results* section of the paper.

Prerequisites:

- For running the complete code you need a `files` subfolder containing the raw data downloaded from `Data_files` folder provided in the [GitHub](#) repository.
- The following packages are needed for analysis and can be easily installed from [CRAN](#) by uncommenting the `install.packages` functions:

```
# install.packages("dplyr")
# install.packages("gridExtra")
# install.packages("ggplot2")
# install.packages("RColorBrewer")
# install.packages("grid")
# install.packages("extrafont")
# install.packages("lme4")
# install.packages("AICcmodavg")
# install.packages("VGAM")
# install.packages("tidyr")
# install.packages("stringr")
# install.packages("scales")
# install.packages("multcomp")
# install.packages("Rmisc")
# install.packages("arm")
library(dplyr)
library(gridExtra)
library(ggplot2)
library(RColorBrewer)
library(grid)
library(extrafont)
library(lme4)
library(AICcmodavg)
library(VGAM)
library(tidyr)
library(stringr)
library(scales)
library(multcomp)
library(Rmisc)
library(arm)
library(reshape)
```

Loading and wrangling data

To start, please load the following datasets into your R environment:

- **behavior data** in which each row is a single observation of the behavior (i.e. foraging, roosting, alert, or preening) of an individual on a given date, time, and scan. Within each behavior, a “1” signifies the behavior the individual was engaged in, whereas a “0” signifies the behavior the individual was not engaged in.
- **lunar data** of the proportion of the moon’s disk that was illuminated the preceding night of the date specified in each row.
- **climate data** for the maximum precipitation (mm) and minimum temperature (°C) recorded during the preceding 12 hours of each survey session.

```
setwd("/Users/Luke/Documents/Academic_Projects/Killdeer/Killdeer_R_Project/Data_files")
Behavior <- read.csv("behavior_data_raw.csv")
Lunar <- read.csv("lunar_data_raw.csv")
Climate <- read.csv("climate_data_raw.csv")
```

Summarize the Behavior data such that each row reveals the total number of individuals engaged in a given behavior on each scan.

```
Behavior_totals <-
  Behavior %>%
  dplyr::group_by(Date, Time, Scan) %>%
  dplyr::summarise(Foraging = sum(Foraging),
                  Roosting = sum(Roosting),
                  Alert = sum(Alert),
                  Preening = sum(Preening))
```

Define the variables of the Behavior_totals correctly. Date needs to be recognized as a date, Time needs to be a factor with the order: Sunrise, Midday, and Sunset, and the behaviors need to be numeric.

```
Behavior_totals$Date <- as.Date(Behavior_totals$Date, "%Y-%m-%d")
Behavior_totals$Time <- factor(Behavior_totals$Time,
                              levels = c("Sunrise", "Midday", "Sunset"))
Behavior_totals[,c("Foraging", "Roosting", "Alert", "Preening")] <-
  lapply(Behavior_totals[,c("Foraging", "Roosting", "Alert", "Preening")], as.numeric)
```

Create a Total variable in the dataframe which sums the total number of birds observed on each scan

```
Behavior_totals$Total <- rowSums(Behavior_totals[,c(4:7)])
```

Define the variables of the Climate dataframe correctly. Date needs to be recognized as a date, Time needs to be a factor with the order: Sunrise, Midday, and Sunset, and Min12Temp and Max12Precip need to be numeric.

```
Climate$Date <- as.Date(Climate$Date, "%Y-%m-%d")
Climate[,c("Min12Temp", "Max12Precip")] <-
  lapply(Climate[,c("Min12Temp", "Max12Precip")], as.numeric)
Climate$Time <- factor(Climate$Time,
                      levels = c("Sunrise", "Midday", "Sunset"))
```

Define the variables of the Lunar dataframe correctly. Date needs to be recognized as a date and PropMoon need to be numeric.

```
Lunar$Date <- as.Date(Lunar$Date, "%Y-%m-%d")
Lunar[,c("PropMoon")] <- as.numeric(Lunar[,c("PropMoon")])
```

Join the three dataframes by Date and Time to create a collated dataframe henceforth referred to as Killdeer. Order the data according to Date, Time, and Scan.

```
Killdeer <- dplyr::left_join(Behavior_totals, Climate, by = c("Date", "Time"))
Killdeer <- dplyr::left_join(Killdeer, Lunar, by = c("Date"))
Killdeer <- Killdeer[with(Killdeer, order(Date, Time, Scan)), ]
head(Killdeer)
#> Source: local data frame [6 x 11]
#> Groups: Date, Time [1]
#>
#>      Date      Time  Scan Foraging Roosting Alert Preening Total
#>   (date)   (fctr) (int)   (dbl)   (dbl) (dbl)  (dbl) (dbl)
#> 1 2010-02-07 Sunrise     1      11      35     0       7    53
#> 2 2010-02-07 Sunrise     2      32      24     0       5    61
#> 3 2010-02-07 Sunrise     3      30      26     0       7    63
#> 4 2010-02-07 Sunrise     4      30      25     0       8    63
#> 5 2010-02-07 Sunrise     5      28      23     0       7    58
#> 6 2010-02-07 Sunrise     6      35      19     0       7    61
#> Variables not shown: Min12Temp (dbl), Max12Precip (dbl), PropMoon (dbl)
```

Subset dataset to include only scans that had at least one bird observed.

```
Killdeer <- dplyr::filter(Killdeer, Total != 0)
```

Create a Session variable that defines each unique visit to the study site

```
Killdeer$Session <- as.factor(paste(Killdeer$Date, Killdeer$Time, sep = "_"))
```

Create a Unique_scan variable that defines each unique scan made

```
Killdeer$Unique_scan <- as.factor(paste(Killdeer$Session, Killdeer$Scan, sep = "_"))
```

Add variables describing the number of individuals not engaged in the focal behavior

```
Killdeer$NonForaging <- Killdeer$Total - Killdeer$Foraging
Killdeer$NonRoosting <- Killdeer$Total - Killdeer$Roosting
Killdeer$NonPreening <- Killdeer$Total - Killdeer$Preening
Killdeer$NonAlert <- Killdeer$Total - Killdeer$Alert
```

Check sample sizes for Date, Session, and Unique_scan

```
length(levels(as.factor(Killdeer$Date)))
#> [1] 9
length(levels(as.factor(Killdeer$Session)))
#> [1] 22
length(levels(as.factor(Killdeer$Unique_scan)))
#> [1] 131
```

Temporal variation in killdeer abundance

Linear regression mixed model predicting variation in abundance across time of day (i.e. fixed effect: Time, random effects: Unique_scan, Session, Date).

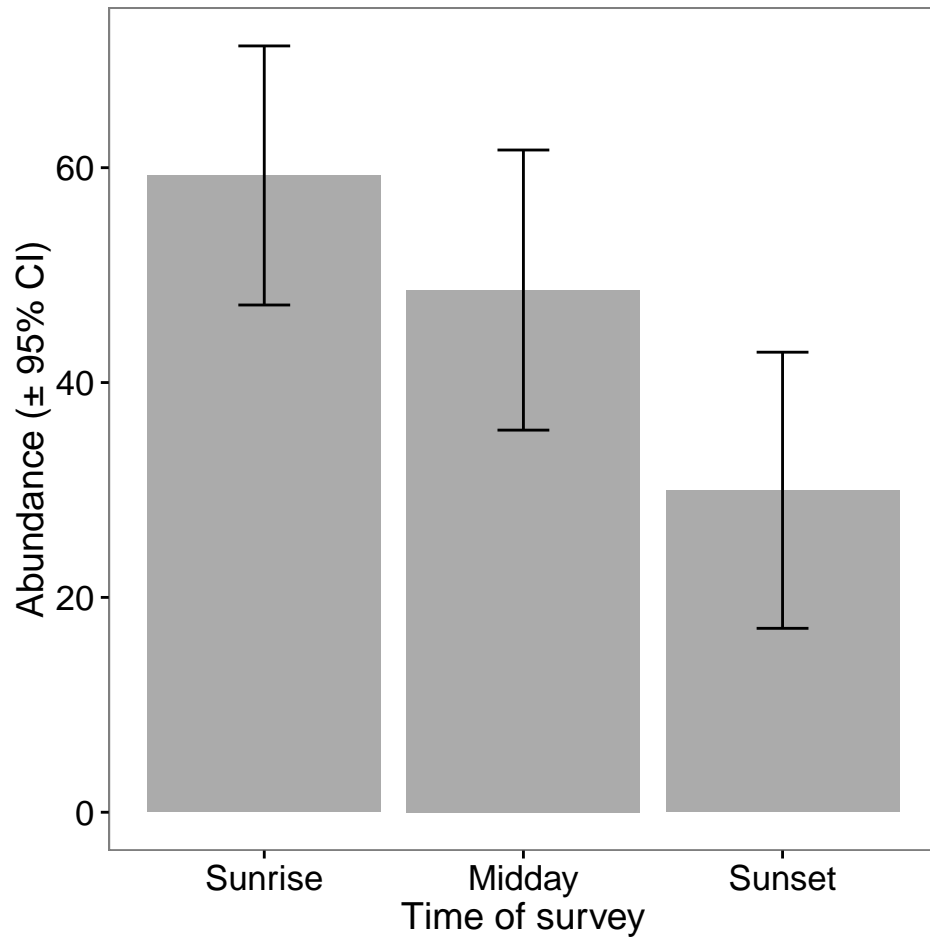
```
Abundance_Time_model <-  
  lme4::glmer(Total ~  
    Time + (1| Unique_scan) + (1 | Session) + (1| Date),  
    data = Killdeer, family = poisson)
```

Calculate the post hoc Tukey contrast statistics

```
summary(multcomp::glht(Abundance_Time_model, mcp(Time = "Tukey")))  
#>  
#> Simultaneous Tests for General Linear Hypotheses  
#>  
#> Multiple Comparisons of Means: Tukey Contrasts  
#>  
#>  
#> Fit: lme4::glmer(formula = Total ~ Time + (1 | Unique_scan) + (1 |  
#> Session) + (1 | Date), data = Killdeer, family = poisson)  
#>  
#> Linear Hypotheses:  
#>               Estimate Std. Error z value Pr(>|z|)  
#> Midday - Sunrise == 0 -0.3385     0.4702  -0.720  0.7509  
#> Sunset - Sunrise == 0 -1.2255     0.5191  -2.361  0.0476 *  
#> Sunset - Midday == 0  -0.8870     0.5508  -1.610  0.2401  
#> ---  
#> Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
#> (Adjusted p values reported -- single-step method)
```

Calculate summary statistics of abundance across the three times of day, then plot (Figure 2 in the paper).

```
Abundance <- Rmisc::summarySE(Killdeer, measurevar = "Total", groupvars = c("Time"))  
ggplot2::ggplot(data = Abundance, aes(x = Time, y = Total)) +  
  geom_bar(position = position_dodge(), stat = "identity", alpha = 0.5) +  
  geom_errorbar(aes(ymin = Total - ci, ymax = Total + ci),  
    width = .2, position = position_dodge(.9)) +  
  theme_bw() +  
  theme(axis.title.x = element_text(size = 14, vjust = -0.5),  
    axis.text.x = element_text(size = 13),  
    axis.title.y = element_text(size = 14, vjust = 1.5),  
    axis.text.y = element_text(size = 13),  
    panel.grid.major = element_blank(),  
    panel.grid.minor = element_blank()) +  
  ylab("Abundance ( $\pm$  95% CI)") +  
  xlab("Time of survey")
```



Foraging model selection, analysis, and plotting

Assign the *a priori* models to a list

```
Forage_models <- list()
```

- Model 1: Null model

```
Forage_models[[1]] <-  
  lme4::glmer(cbind(Foraging, NonForaging) ~  
    1 +  
    (1 | Unique_scan) + (1 | Session) + (1 | Date),  
    data = Killdeer, family = binomial)
```

- Model 2: Univariate model with proportion of moon illuminated

```
Forage_models[[2]] <-  
  lme4::glmer(cbind(Foraging, NonForaging) ~  
    PropMoon +
```

```
(1| Unique_scan) + (1 | Session) + (1| Date),
data = Killdeer, family = binomial)
```

- **Model 3: Univariate model with minimum 12 hour temperature**

```
Forage_models[[3]] <-
lme4::glmer(cbind(Foraging, NonForaging) ~
  Min12Temp +
  (1| Unique_scan) + (1 | Session) + (1| Date),
data = Killdeer, family = binomial)
```

- **Model 4: Univariate model with max 12 hour precipitation**

```
Forage_models[[4]] <-
lme4::glmer(cbind(Foraging, NonForaging) ~
  Max12Precip +
  (1| Unique_scan) + (1 | Session) + (1| Date),
data = Killdeer, family = binomial)
```

- **Model 5: Additive model of both lunar and temperature covariates**

```
Forage_models[[5]] <-
lme4::glmer(cbind(Foraging, NonForaging) ~
  Min12Temp + PropMoon +
  (1| Unique_scan) + (1 | Session) + (1| Date),
data = Killdeer, family = binomial)
```

- **Model 6: Additive model of both lunar and precipitation covariates**

```
Forage_models[[6]] <-
lme4::glmer(cbind(Foraging, NonForaging) ~
  Max12Precip + PropMoon +
  (1| Unique_scan) + (1 | Session) + (1| Date),
data = Killdeer, family = binomial)
```

- **Model 7: Additive model of both lunar, temperature, and precipitation covariates**

```
Forage_models[[7]] <-
lme4::glmer(cbind(Foraging, NonForaging) ~
  Min12Temp + Max12Precip + PropMoon +
  (1| Unique_scan) + (1 | Session) + (1| Date),
data = Killdeer, family = binomial)
```

Name models and create a ranked AIC table

```
Modnames <- paste("Model", 1:length(Forage_models), sep = " ")
Forage_models_table <- AICcmodavg::aictab(cand.set = Forage_models,
  modnames = Modnames, sort = TRUE)
```

Calculate evidence ratios and add them to the AIC table

```

Evidence_Ratios <- function(AIC_table){
  ER <- vector( , nrow(AIC_table))
  for(i in 1:nrow(AIC_table)) {
    ER[i] <- AIC_table$AICcWt[1]/AIC_table$AICcWt[i]
  }
  ER[1] <- NA
  table <- cbind(AIC_table, ER)
  out <- cbind(table[, c(1:2)], round(table[, c(3:9)], 2))
}

Forage_models_table <- Evidence_Ratios(Forage_models_table)

```

Estimate the marginal R-squared of each model following Nakagawa and Schielzeth (Equ. 29 and 30 and Table 2; 2013) and add them to the AIC table to produce Table 1 presented in the paper.

```

r2_m_glm <- function(mod){
  v <- var(as.vector(fixef(mod) %*% t(model.matrix(mod))))
  r2_m <- v/(v + VarCorr(mod)$Unique_scan[1] +
    VarCorr(mod)$Session[1] + VarCorr(mod)$Date[1] + pi^2/3)
  out <- unlist(list(r2_m = r2_m))
}

r2_m <- data.frame(round(t(as.data.frame(t(sapply(Forage_models, r2_m_glm))))), 3))
r2_m$Modnames <-
  c("Model 1", "Model 2", "Model 3", "Model 4", "Model 5", "Model 6", "Model 7")
colnames(r2_m) <- c("r2_m", "Modnames")
Forage_models_table <- dplyr::left_join(Forage_models_table, r2_m[,c(1,2,4,6,9,10)])
Forage_models_table

```

#>	Modnames	K	Delta_AICc	AICcWt	ER	r2_m
#> 1	Model 2	5	0.00	0.55	NA	0.431
#> 2	Model 5	6	2.19	0.18	2.99	0.432
#> 3	Model 6	6	2.19	0.18	2.99	0.431
#> 4	Model 7	7	4.41	0.06	9.08	0.433
#> 5	Model 1	4	7.56	0.01	43.73	0.000
#> 6	Model 3	5	8.82	0.01	82.39	0.021
#> 7	Model 4	5	9.42	0.00	111.03	0.006

Calculate the 95% confidence interval of the top model by creating a function which applies varying steps of the predictor (i.e., PropMoon) to the model and returns the coefficients of the intercept and beta.

```

CI_foraging <- function(off) {
  model <- lme4::glmer(cbind(Foraging, NonForaging) ~
    I(PropMoon-off) + (1| Unique_scan) + (1 | Session) + (1| Date),
    data = Killdeer, family = binomial)
  ests <- summary(model)$coefficients[1,1:2]
  # backlink the coefficients to the probability scale
  return(c(off,ests,invlogit(ests[1]+c(-1,0,1)*1.96*ests[2])))
}

# specify the off (i.e., vector of numbers from 0 to 1 stepped by 0.05)
offs_foraging <- seq(0,1,0.05)
# apply the off vector to the function (returning a matrix)
result_foraging <- sapply(offs_foraging,CI_foraging)
# transpose the matrix
result_foraging <- t(result_foraging)

```

```

# convert the matrix to a data.frame
result_foraging <- data.frame(result_foraging)
# define the column names
colnames(result_foraging) <-
  c("PropMoon", "Coefficient", "Std. Error", "Upper", "Mean", "Lower")
# Create proportional variable for plotting
Killdeer$prop_Forage <- Killdeer$Foraging/Killdeer$Total

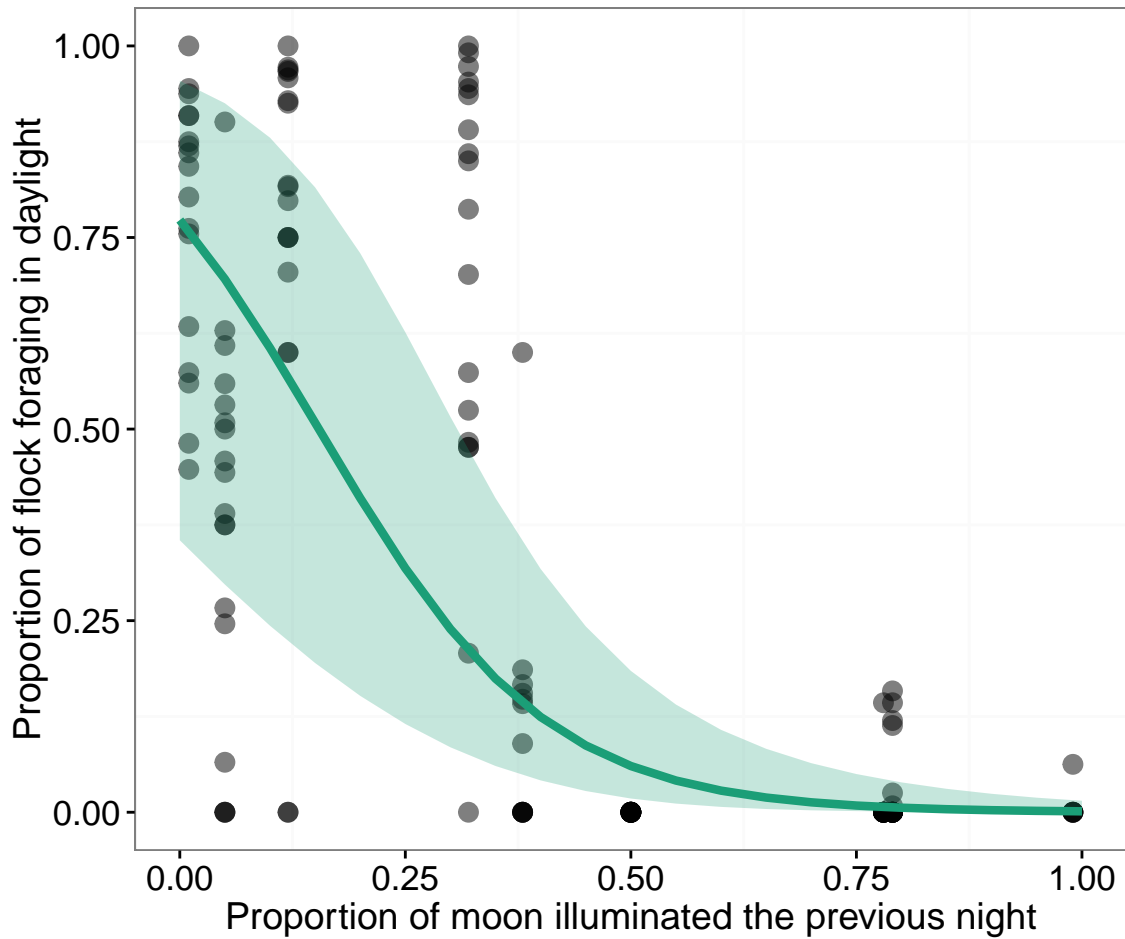
```

Plot the top model with confidence intervals

```

ggplot2::ggplot() +
  geom_point(data = Killdeer,
    aes(x = PropMoon, y = prop_Forage), size = 3, alpha = 0.5) +
  geom_ribbon(data = result_foraging,
    aes(x = PropMoon, y = Mean, ymin = Lower, ymax = Upper),
    fill = "#1B9E77", alpha = 0.25) +
  geom_line(data = result_foraging,
    aes(x = PropMoon, y = Mean), size = 1.5, colour = "#1B9E77") +
  theme_bw() +
  theme(legend.position = c(1, 1),
    legend.justification = c(1, 1),
    legend.text=element_text(size=11),
    legend.title=element_blank(),
    legend.key.height=unit(0.8,"line"),
    legend.key.width=unit(0.8,"line"),
    legend.background = element_rect(fill=NA),
    axis.title.x = element_text(size = 14, vjust = -0.5),
    axis.text.x = element_text(size = 13),
    axis.title.y = element_text(size = 14, vjust = 1.5),
    axis.text.y = element_text(size = 13),
    panel.grid.major = element_blank()) +
  scale_y_continuous(limits=c(0,1)) +
  ylab("Proportion of flock foraging in daylight") +
  xlab("Proportion of moon illuminated the previous night")

```

Roosting model selection, analysis, and plotting

Assign the *a priori* models to a list

```
Roosting_models <- list()
```

- Model 1: Null model

```
Roosting_models[[1]] <-  
  lme4::glmer(cbind(Roosting, NonRoosting) ~  
    1 +  
    (1| Unique_scan) + (1 | Session) + (1| Date),  
    data = Killdeer, family = binomial)
```

- Model 2: Univariate model with proportion of moon illuminated

```
Roosting_models[[2]] <-  
  lme4::glmer(cbind(Roosting, NonRoosting) ~  
    PropMoon +
```

```
(1| Unique_scan) + (1 | Session) + (1| Date),
data = Killdeer, family = binomial)
```

- **Model 3: Univariate model with minimum 12 hour temperature**

```
Roosting_models[[3]] <-
lme4::glmer(cbind(Roosting, NonRoosting) ~
  Min12Temp +
  (1| Unique_scan) + (1 | Session) + (1| Date),
data = Killdeer, family = binomial)
```

- **Model 4: Univariate model with max 12 hour precipitation**

```
Roosting_models[[4]] <-
lme4::glmer(cbind(Roosting, NonRoosting) ~
  Max12Precip +
  (1| Unique_scan) + (1 | Session) + (1| Date),
data = Killdeer, family = binomial)
```

- **Model 5: Additive model of both lunar and temperature covariates**

```
Roosting_models[[5]] <-
lme4::glmer(cbind(Roosting, NonRoosting) ~
  Min12Temp + PropMoon +
  (1| Unique_scan) + (1 | Session) + (1| Date),
data = Killdeer, family = binomial)
```

- **Model 6: Additive model of both lunar and precipitation covariates**

```
Roosting_models[[6]] <-
lme4::glmer(cbind(Roosting, NonRoosting) ~
  Max12Precip + PropMoon +
  (1| Unique_scan) + (1 | Session) + (1| Date),
data = Killdeer, family = binomial)
```

- **Model 7: Additive model of both lunar, temperature, and precipitation covariates**

```
Roosting_models[[7]] <-
lme4::glmer(cbind(Roosting, NonRoosting) ~
  Min12Temp + Max12Precip + PropMoon +
  (1| Unique_scan) + (1 | Session) + (1| Date),
data = Killdeer, family = binomial)
```

Name models, create a ranked AIC table, calculate evidence ratios and marginal r-squared, and produce Table 2 presented in the paper.

```

Modnames <- paste("Model", 1:length(Roosting_models), sep = " ")
Roost_models_table <- AICcmmodavg::aictab(cand.set = Roosting_models,
                                         modnames = Modnames, sort = TRUE)
Roost_models_table <- Evidence_Ratios(Roost_models_table)
r2_m <- data.frame(round(t(as.data.frame(t(sapply(Roosting_models, r2_m_glm))), 3))
r2_m$Modnames <-
  c("Model 1", "Model 2", "Model 3", "Model 4", "Model 5", "Model 6", "Model 7")
colnames(r2_m) <- c("r2_m", "Modnames")
Roost_models_table <- dplyr::left_join(Roost_models_table, r2_m)[,c(1,2,4,6,9,10)]
Roost_models_table
#>   Modnames K Delta_AICc AICcWt   ER r2_m
#> 1 Model 2 5      0.00   0.49   NA 0.364
#> 2 Model 6 6      1.63   0.22  2.25 0.374
#> 3 Model 5 6      2.19   0.16  2.99 0.365
#> 4 Model 7 7      3.77   0.07  6.59 0.378
#> 5 Model 1 4      5.95   0.02 19.58 0.000
#> 6 Model 4 5      6.28   0.02 23.05 0.057
#> 7 Model 3 5      7.57   0.01 44.10 0.018

```

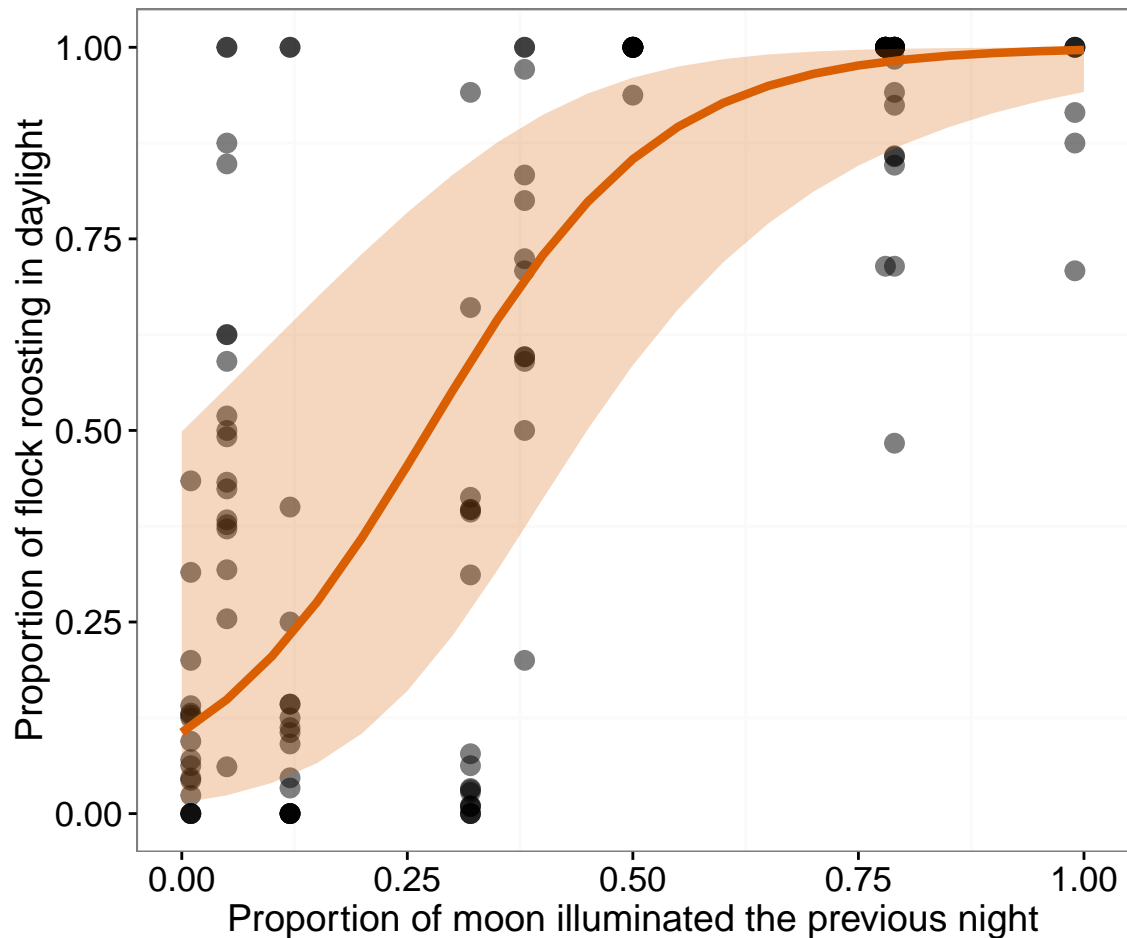
Plot the top model with confidence intervals

```

CI_roosting <- function(off) {
  model <- lme4::glmer(cbind(Roosting, NonRoosting) ~
    I(PropMoon-off) + (1| Unique_scan) + (1 | Session) + (1| Date),
    data = Killdeer, family = binomial)
  ests <- summary(model)$coefficients[1,1:2]
  return(c(off,ests,invlogit(ests[1]+c(-1,0,1)*1.96*ests[2])))
}
offs_roosting <- seq(0,1,0.05)
result_roosting <- sapply(offs_roosting,CI_roosting)
result_roosting <- t(result_roosting)
result_roosting <- data.frame(result_roosting)
colnames(result_roosting) <-
  c("PropMoon", "Coefficient", "Std. Error", "Upper", "Mean", "Lower")
Killdeer$prop_Roost <- Killdeer$Roosting/Killdeer$Total
ggplot2::ggplot() +
  geom_point(data = Killdeer,
    aes(x = PropMoon, y = prop_Roost), size = 3, alpha = 0.5) +
  geom_ribbon(data = result_roosting,
    aes(x = PropMoon, y = Mean, ymin = Lower, ymax = Upper),
    fill = "#D95F02", alpha = 0.25) +
  geom_line(data = result_roosting,
    aes(x = PropMoon, y = Mean), size = 1.5, colour = "#D95F02") +
  theme_bw() +
  theme(legend.position = c(1, 1),
    legend.justification = c(1, 1),
    legend.text=element_text(size=11),
    legend.title=element_blank(),
    legend.key.height=unit(0.8,"line"),
    legend.key.width=unit(0.8,"line"),
    legend.background = element_rect(fill=NA),
    axis.title.x = element_text(size = 14, vjust = -0.5),
    axis.text.x = element_text(size = 13),

```

```
axis.title.y = element_text(size = 14, vjust = 1.5),
axis.text.y = element_text(size = 13),
panel.grid.major = element_blank() +
scale_y_continuous(limits=c(0,1)) +
ylab("Proportion of flock roosting in daylight") +
xlab("Proportion of moon illuminated the previous night")
```



Preening model selection, analysis, and plotting

Assign the *a priori* models to a list

```
Preening_models <- list()
```

- Model 1: Null model

```
Preening_models[[1]] <-
  lme4::glmer(cbind(Preening, NonPreening) ~
    1 +
    (1| Unique_scan) + (1 | Session) + (1| Date),
    data = Killdeer, family = binomial)
```

- **Model 2: Univariate model with proportion of moon illuminated**

```
Preening_models[[2]] <-
  lme4::glmer(cbind(Preening, NonPreening) ~
    PropMoon +
    (1| Unique_scan) + (1 | Session) + (1| Date),
    data = Killdeer, family = binomial)
```

- **Model 3: Univariate model with minimum 12 hour temperature**

```
Preening_models[[3]] <-
  lme4::glmer(cbind(Preening, NonPreening) ~
    Min12Temp +
    (1| Unique_scan) + (1 | Session) + (1| Date),
    data = Killdeer, family = binomial)
```

- **Model 4: Univariate model with max 12 hour precipitation**

```
Preening_models[[4]] <-
  lme4::glmer(cbind(Preening, NonPreening) ~
    Max12Precip +
    (1| Unique_scan) + (1 | Session) + (1| Date),
    data = Killdeer, family = binomial)
```

- **Model 5: Additive model of both lunar and temperature covariates**

```
Preening_models[[5]] <-
  lme4::glmer(cbind(Preening, NonPreening) ~
    Min12Temp + PropMoon +
    (1| Unique_scan) + (1 | Session) + (1| Date),
    data = Killdeer, family = binomial)
```

- **Model 6: Additive model of both lunar and precipitation covariates**

```
Preening_models[[6]] <-
  lme4::glmer(cbind(Preening, NonPreening) ~
    Max12Precip + PropMoon +
    (1| Unique_scan) + (1 | Session) + (1| Date),
    data = Killdeer, family = binomial)
```

- **Model 7: Additive model of both lunar, temperature, and precipitation covariates**

```
Preening_models[[7]] <-
  lme4::glmer(cbind(Preening, NonPreening) ~
    Min12Temp + Max12Precip + PropMoon +
    (1| Unique_scan) + (1 | Session) + (1| Date),
    data = Killdeer, family = binomial)
```

Name models, create a ranked AIC table, calculate evidence ratios and marginal r-squared, and produce Table 3 presented in the paper.

```

Modnames <- paste("Model", 1:length(Preening_models), sep = " ")
Preen_models_table <- AICcmodavg::aictab(cand.set = Preening_models,
                                         modnames = Modnames, sort = TRUE)
Preen_models_table <- Evidence_Ratios(Preen_models_table)
r2_m <- data.frame(round(t(as.data.frame(t(sapply(Preening_models, r2_m_glm))), 3))
r2_m$Modnames <-
  c("Model 1", "Model 2", "Model 3", "Model 4", "Model 5", "Model 6", "Model 7")
colnames(r2_m) <- c("r2_m", "Modnames")
Preen_models_table <- dplyr::left_join(Preen_models_table, r2_m)[,c(1,2,4,6,9,10)]
Preen_models_table
#>   Modnames K Delta_AICc AICcWt   ER  r2_m
#> 1 Model 4 5      0.00   0.35  NA 0.040
#> 2 Model 2 5      1.25   0.19 1.86 0.039
#> 3 Model 6 6      1.35   0.18 1.96 0.051
#> 4 Model 1 4      2.27   0.11 3.11 0.000
#> 5 Model 7 7      3.22   0.07 4.99 0.053
#> 6 Model 5 6      3.42   0.06 5.52 0.040
#> 7 Model 3 5      4.08   0.05 7.67 0.005

```