#couldn't figure out how to get RMarkdown to work on my computer, so I copied and pasted my script into Word instead…

```
# load libraries

library(tidyverse)

library(readr)

library(lubridate)

library(magrittr)

library(ggplot2)

library(car)

library(emmeans)

library(lme4)


#read in data

prelim_tidy <- read_csv("_data/_tidy/prelim_data_tidycols.csv")

View(prelim_tidy)


bipedal_data <- read_csv("_summary/bipedal_table.csv")

View(bipedal_data)


#Omit any missing values:

summary(is.na(prelim_tidy))


prelim_temp<-na.omit(prelim_tidy)

View(prelim_temp)


#Combine positional behaviors into smaller categories

# suspensory = Cb, Br & QM

#Vertical climb and cling together

prelim_temp$pos_beh[prelim_temp$pos_beh == "Cb"] <- "Su"
```

```
prelim_temp$pos_beh[prelim_temp$pos_beh == "Br"] <- "Su"

prelim_temp$pos_beh[prelim_temp$pos_beh == "QM"] <- "Su"

prelim_temp$pos_beh[prelim_temp$pos_beh == "Vci"] <- "VC"

prelim_temp$pos_beh[prelim_temp$pos_beh == "Abp"] <- "Bp"

prelim_temp$pos_beh[prelim_temp$pos_beh == "BpS"] <- "Bp"

prelim_temp$pos_beh[prelim_temp$pos_beh == "BpW"] <- "Bp"


############

##re-order levels

prelim_temp$time_od <- factor(prelim_temp$time_od, levels = c("e_morning", "l_morning",
"e_afternoon", "l_afternoon", "evening"))

prelim_temp$pos_beh <- factor(prelim_temp$pos_beh, levels = c("St","Ly", "Sq", "QS", "QW", "Bp",
"Su", "VC"))


##change to factor & numeric

factor_cols <- c("pos_beh","context", "substrate", "hab_type", "individual")

numeric_cols <- c("sun", "therm_t", "t_lo", "t_hi")


prelim_temp[factor_cols] <- lapply(prelim_temp[factor_cols], as.factor)


prelim_temp[numeric_cols] <- lapply(prelim_temp[numeric_cols], as.numeric)



###

hist(prelim_temp$therm_t)

dotchart(prelim_temp$therm_t)

boxplot(prelim_temp$therm_t ~ prelim_temp$pos_beh,  ylab="body temp")


# Plot response against each predictor and random effect.
```

```
ggplot(prelim_temp, aes(pos_beh, therm_t, color=context))+
  geom_boxplot()

ggplot(prelim_temp, aes(pos_beh, therm_t, color=time_od))+
  geom_boxplot()+
  facet_grid(.~individual)

##
with(prelim_temp, table(pos_beh, hab_type))
with(prelim_temp, table(pos_beh, time_od))
with(prelim_temp, table(pos_beh, hab_type, time_od))

## choosing models
##GLMER

### full model
therm_mod <- lmer(therm_t ~ pos_beh + time_od + sun + date + hab_type + context +
                  (1|individual) + pos_beh*hab_type + pos_beh*sun + time_od*sun,
                  data = prelim_temp)

##minus pos_beh/sun interaction
therm_mod2 <- lmer(therm_t ~ pos_beh + time_od + sun + date + hab_type + context +
                   (1|individual) + pos_beh*hab_type + time_od*sun,
                 data = prelim_temp)

##plus pos_beh*sun, minus pos_beh*hab_type
therm_mod3 <- lmer(therm_t ~ pos_beh + time_od + sun + date + hab_type + context +
                   (1|individual) + pos_beh*sun + time_od*sun,
                  data = prelim_temp)
```

```
##minus interactions with pos_beh
therm_mod4 <- lmer(therm_t ~ pos_beh + time_od + sun + date + hab_type + context +
                     (1|individual) + time_od*sun,
                   data = prelim_temp)

##minus time_od interaction
therm_mod5 <- lmer(therm_t ~ pos_beh + time_od + sun + date + hab_type + context +
                     (1|individual) + pos_beh*sun,
                   data = prelim_temp)

##minus all interactions
therm_mod6 <- lmer(therm_t ~ pos_beh + time_od + sun + date + hab_type + context +
                     (1|individual),
                   data = prelim_temp)

####compare interaction models
AIC(therm_mod3, therm_mod4, therm_mod5, therm_mod6) ###lowest AIC is with no interaction
(3226.904; DF: 23)
                                ###second lowest is time_od*sun (3255.461, DF: 27)
                                ###continue forward with time_od*sun & no interactions
#####################################################################
##time_od*sun models
## minus context
therm_mod7 <- lmer(therm_t ~ pos_beh + time_od + sun + date + hab_type +
                     (1|individual) + time_od*sun,
                   data = prelim_temp)

##minus hab_type
```

```
therm_mod8 <- lmer(therm_t ~ pos_beh + time_od + sun + date + context +
                     (1|individual) + time_od*sun,
                   data = prelim_temp)

##minus date
therm_mod9 <- lmer(therm_t ~ pos_beh + time_od + sun + hab_type + context +
                     (1|individual) + time_od*sun,
                   data = prelim_temp)

##minus hab_type & context
therm_mod10 <- lmer(therm_t ~ pos_beh + time_od + sun + date +
                     (1|individual) + time_od*sun,
                   data = prelim_temp)
###Compare models
AIC(therm_mod7, therm_mod8, therm_mod9, therm_mod10) ##model 7 and 10 are lowest (3247.068 & 3248.205, resp.)
                          ##model 8 isn't far off, though, (3255. 603)
                        ##and it may be important to include context

################################################################################
###no interactions
## minus context
therm_mod11 <- lmer(therm_t ~ pos_beh + time_od + sun + date + hab_type +
                     (1|individual), data = prelim_temp)

##minus hab_type
therm_mod12 <- lmer(therm_t ~ pos_beh + time_od + sun + date + context +
                     (1|individual), data = prelim_temp)
```

```
##minus date
therm_mod13 <- lmer(therm_t ~ pos_beh + time_od + sun + hab_type + context +
                    (1|individual), data = prelim_temp)

##minus hab_type & context
therm_mod14 <- lmer(therm_t ~ pos_beh + time_od + sun + date +
                     (1|individual), data = prelim_temp)

###Compare models
AIC(therm_mod11, therm_mod12, therm_mod13, therm_mod14) ##models 11 and 14 are lowest (3218.163 & 3218.819, resp.)

###compare between types of models
AIC(therm_mod4, therm_mod6, therm_mod7, therm_mod10, therm_mod8, therm_mod11, therm_mod14)
    ##best models (11, 14, 6) exclude context and exclude interactions
    ##run a few more tests and include one with the interaction still (model 7)

### more comparison #########
anova(therm_mod6, therm_mod7) ##not nested, so can't run
anova(therm_mod6, therm_mod11) ##no signif
anova(therm_mod6, therm_mod14) ##no signif
anova(therm_mod11, therm_mod14) ##significance, so model 11 better than 14
                  #####think I'll choose model 11 since it includes habitat type
                 ##### and it's AIC value is best (3218.163 vs. 3226.904 (model 6) & 3218.819 (model 14))

#########################################################################
#extract residuals
###model 6
```

```
E1 <- resid(therm_mod6, type = "pearson")

#plot fitted vs residuals
F1 <- fitted(therm_mod6, type = "response")

plot(x = F1,
    y = E1,
    xlab = "Fitted values",
    ylab = "Pearson residuals",
    main = "Model 6",
    cex.lab = 1.5)
abline(h = 0, lty = 2)

### model 11 ############
E2 <- resid(therm_mod11, type = "pearson")

#plot fitted vs residuals
F2 <- fitted(therm_mod11, type = "response")

plot(x = F2,
    y = E2,
    xlab = "Fitted values",
    ylab = "Pearson residuals",
    main = "Model 11",
    cex.lab = 1.5)
abline(h = 0, lty = 2)

### model 14 ############
E3 <- resid(therm_mod14, type = "pearson")
```

```
#plot fitted vs residuals
F3 <- fitted(therm_mod14, type = "response")

plot(x = F3,
    y = E3,
    xlab = "Fitted values",
    ylab = "Pearson residuals",
    main = "Model 14",
    cex.lab = 1.5)
abline(h = 0, lty = 2)

### model 7 ############
E4 <- resid(therm_mod7, type = "pearson")

#plot fitted vs residuals
F4 <- fitted(therm_mod7, type = "response")

plot(x = F4,
    y = E4,
    xlab = "Fitted values",
    ylab = "Pearson residuals",
    main = "Model 7",
    cex.lab = 1.5)
abline(h = 0, lty = 2)

### residual plots all seem relatively normal; cloud around horizontal axis, indicating a good fit
#########################################################################
##Model 11 - includes pos_beh, time_od, sun, date, hab_type and (1|individual)
```

```
E2 <- resid(therm_mod11, type = "pearson")

#plot fitted vs residuals
F2 <- fitted(therm_mod11, type = "response")

plot(x = F2,
    y = E2,
    xlab = "Fitted values",
    ylab = "Pearson residuals",
    main = "Model 11",
    cex.lab = 1.5)
abline(h = 0, lty = 2)

boxplot(E2 ~ pos_beh, data=prelim_temp)
boxplot(E2 ~ time_od, data=prelim_temp)
plot(x=prelim_temp$sun, y=E2)
boxplot(E2 ~ hab_type, data=prelim_temp)
plot(x=prelim_temp$date, y=E2)

model.matrix(therm_mod11)

##summary
summary(therm_mod11)

##confidence intervals
confint(therm_mod11) ##maybe I don't need habitat in there because none of the levels are significant

##model 14
summary(therm_mod14)
```

```
confint(therm_mod14)



##### OMIT OUTLIERS ###

prelim_temp2 <- prelim_temp

prelim_temp2$therm_t[prelim_temp2$therm_t >= 42] <- NA


View(prelim_temp2)


prelim_temp3<-na.omit(prelim_temp2)

View(prelim_temp3)


#Vertical climb and cling together

prelim_temp3$pos_beh[prelim_temp3$pos_beh == "Cb"] <- "Su"

prelim_temp3$pos_beh[prelim_temp3$pos_beh == "Br"] <- "Su"

prelim_temp3$pos_beh[prelim_temp3$pos_beh == "QM"] <- "Su"

prelim_temp3$pos_beh[prelim_temp3$pos_beh == "Vci"] <- "VC"

prelim_temp3$pos_beh[prelim_temp3$pos_beh == "Abp"] <- "Bp"

prelim_temp3$pos_beh[prelim_temp3$pos_beh == "BpS"] <- "Bp"

prelim_temp3$pos_beh[prelim_temp3$pos_beh == "BpW"] <- "Bp"


#############

##re-order levels

prelim_temp3$time_od <- factor(prelim_temp3$time_od, levels = c("e_morning", "l_morning",
"e_afternoon", "l_afternoon", "evening"))

prelim_temp3$pos_beh <- factor(prelim_temp3$pos_beh, levels = c("St","Ly", "Sq", "QS", "QW", "Bp",
"Su", "VC"))


###change to factor & numeric
```

```
factor_cols <- c("pos_beh","context", "substrate", "hab_type", "individual")
numeric_cols <- c("sun", "therm_t", "t_lo", "t_hi")

prelim_temp3[factor_cols] <- lapply(prelim_temp3[factor_cols], as.factor)

prelim_temp3[numeric_cols] <- lapply(prelim_temp3[numeric_cols], as.numeric)

str(prelim_temp3)

###check model minus outliers
##model 11 with outliers
therm_mod11 <- lmer(therm_t ~ pos_beh + time_od + sun + date + hab_type +
                    (1|individual), data = prelim_temp)
summary(therm_mod11)
confint(therm_mod11)

##model minus outliers
mod_2 <- lmer(therm_t ~ pos_beh + time_od + sun + date + hab_type +
                (1|individual), data = prelim_temp3)
summary(mod_2)
confint(mod_2)


##plotting residuals
##model 11
E2 <- resid(therm_mod11, type = "pearson")

#plot fitted vs residuals
F2 <- fitted(therm_mod11, type = "response")
```

```
plot(x = F2,
    y = E2,
    xlab = "Fitted values",
    ylab = "Pearson residuals",
    main = "Model 11",
    cex.lab = 1.5)
abline(h = 0, lty = 2)

##mod_2
E5 <- resid(mod_2, type = "pearson")

#plot fitted vs residuals
F5 <- fitted(mod_2, type = "response")

plot(x = F5,
    y = E5,
    xlab = "Fitted values",
    ylab = "Pearson residuals",
    main = "Model",
    cex.lab = 1.5)
abline(h = 0, lty = 2)

#HSR: post-hoc test to compare between levels of position behavior. Will want to do this in the analysis file not graphics file.
library(emmeans)
emmeans(mod_2, list(pairwise ~ pos_beh), adjust = "tukey")
```