

Cal Poly Herpetology CURE - Capture Data Analyses

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Packages

Background and Goals

This data was collected April - May 2021 during a course-based undergraduate research experience (CURE) in Dr. Emily Taylor's Herpetology class of Spring Quarter 2021 at Cal Poly, San Luis Obispo. This part of the study was conducted to describe the variation of osmoregulation (cutaneous evaporative water loss) and osmotic balance (plasma osmolality and hematocrit) in *Sceloporus occidentalis* and to investigate what drives that variation. Please refer to **doi:** for full details.

Data

Morphometrics and Blood Data

This data was collected upon capture of each lizard.

Variables in this dataframe: - date - collection/capture time for each lizard - individual ID for each lizard - sock ID used to capture each lizard (removed, not relevant to analyses) - SVL = snout-vent length - mass in

grams - sex - if female, whether or not gravid (with eggs) - which eye the blood sample was taken from - percent hematocrit = percent of blood that's red blood cells - osmolality = the concentration of solutes in the blood (this is the average of 1-3 replicates) - cloacal temperature at the time of CEWL measurement - processing time for each lizard, when all measurements were finished - hemolyzed = whether or not red blood cells burst and contaminated plasma

Before loading in this data, some incorrectly-measured hematocrit and osmolality were omitted: - hematocrit for individuals 1-16, due to observer error - osmolality for individual 19, due to instrumental error

```
# load and format data
morpho_blood_dat <- read.csv("./data/Herpetology_Data.csv", # filename
                             na.strings=c("", "NA") # fix empty cells
                             ) %>%

dplyr::mutate(# put date and time together
              collect_date_time = (paste(date, collect_time)),
              # replace some date-time values that have missing times
              collect_date_time = replace(collect_date_time,
                                           collect_date_time == "4/5/21 NA", NA),
              # correctly format date-time variable
              collect_date_time = as.POSIXct(collect_date_time,
                                              format = "%m/%d/%y %H:%M"),
              # correctly format date-only variable
              date = as.Date(date, format = "%m/%d/%y"),
              # correctly format collection time variable
              # format extracts just time after posix adds arbitrary date
              collect_time = (as.POSIXct(collect_time, format = "%H:%M")),
              # correctly format processing time variable
              processing_time = (as.POSIXct(processing_time, format = "%H:%M")),
              # set individual_ID variable as a factor, not numeric
              individual_ID = as.factor(individual_ID),
              # set sex variable as a factor, not character
              sex_M_F = as.factor(sex_M_F),
              # set gravidity variable as a factor, not character
              gravid_Y_N = as.factor(gravid_Y_N),
              # set blood sample eye variable as a factor, not character
              blood_sample_eye = as.factor(blood_sample_eye),
              # set hemolyzed variable as a factor, not character
              hemolyzed = as.factor(hemolyzed),
              # compute holding time as capture time - cloacal measurement time:
              hold_time = as.numeric(processing_time - collect_time)
              ) %>%

# remove two columns not relevant for statistics
dplyr::select(-sock_ID, -notes)

# check
summary(morpho_blood_dat)
```

##	date	collect_time	individual_ID
##	Min. :2021-04-05	Min. :2021-12-19 10:17:00	1 : 1
##	1st Qu.:2021-04-19	1st Qu.:2021-12-19 12:36:00	2 : 1
##	Median :2021-04-26	Median :2021-12-19 12:48:00	3 : 1
##	Mean :2021-04-27	Mean :2021-12-19 12:51:12	4 : 1
##	3rd Qu.:2021-05-10	3rd Qu.:2021-12-19 13:03:00	5 : 1
##	Max. :2021-05-17	Max. :2021-12-19 15:57:00	6 : 1
##		NA's :3	(Other):142

```
##      SVL_mm      mass_g      sex_M_F gravid_Y_N blood_sample_eye
## Min.   :42.00   Min.    : 2.300   F: 48   N    : 22   both:  2
## 1st Qu.:63.00   1st Qu.: 9.125   M:100   Y    : 26   L    :  4
## Median :67.00   Median :11.200           NA's:100   R    :142
## Mean   :64.97   Mean    :10.586
## 3rd Qu.:69.00   3rd Qu.:12.725
## Max.   :73.00   Max.    :15.000
##
## hematocrit_percent osmolality_mmol_kg cloacal_temp_C
## Min.   :16.00      Min.    :293      Min.    :20.00
## 1st Qu.:33.00      1st Qu.:341      1st Qu.:22.00
## Median :35.00      Median :366      Median :23.00
## Mean   :35.36      Mean    :365      Mean    :23.48
## 3rd Qu.:38.00      3rd Qu.:387      3rd Qu.:25.00
## Max.   :54.00      Max.    :436      Max.    :28.00
## NA's   :27         NA's     :3         NA's    :7
## processing_time      hemolyzed collect_date_time
## Min.   :2021-12-19 12:44:00   N    :85   Min.    :2021-04-05 10:17:00
## 1st Qu.:2021-12-19 14:09:00   Y    :39   1st Qu.:2021-04-19 12:49:00
## Median :2021-12-19 15:17:30   NA's:24   Median :2021-04-26 15:34:00
## Mean   :2021-12-19 15:12:09           Mean    :2021-04-28 20:28:01
## 3rd Qu.:2021-12-19 16:15:15           3rd Qu.:2021-05-10 12:44:00
## Max.   :2021-12-19 17:38:00           Max.    :2021-05-17 13:01:00
## NA's   :8                         NA's    :3
## hold_time
## Min.   : 21.0
## 1st Qu.: 95.0
## Median :141.5
## Mean   :143.8
## 3rd Qu.:197.5
## Max.   :268.0
## NA's   :10
```

```
unique(morpho_blood_dat$date)
```

```
## [1] "2021-04-05" "2021-04-19" "2021-04-26" "2021-05-03" "2021-05-10"
## [6] "2021-05-17"
```

```
# get info
morpho_blood_dat %>%
  dplyr::filter(complete.cases(hold_time)) %>%
  summarise(mean_hold_time_minutes = mean(hold_time),
            mean_hold_time_hrs = mean_hold_time_minutes/60)
```

```
##   mean_hold_time_minutes mean_hold_time_hrs
## 1                143.8333                2.397222
```

```
# export
#write.csv(morpho_blood_dat, "exported_data/capture_hydration.csv")
```

I want to test if any IDs are missing, and which ones if so.

```
test <- c(seq(1, 150, by = 1))
lost <- test[test %nin% morpho_blood_dat$individual_ID]
lost
```

```
## [1] 23 56
```

Individuals 23 and 56 actually both do not exist because those numbers were skipped when assigning IDs, so we have all the individuals measured in the dataframe.

CEWL Data

First, load it all in and merge.

Variables in this dataframe are: - date - time - date_time combined variable - individual_ID for each lizard measured - region = where on the body CEWL was measured - TEWL_g_m2h = CEWL measurement value in grams/sq-meter/hour - ambient_temp_C = temperature when and where measurement was taken - ambient_RH_percent = relative humidity when and where measurement was taken - e_s_kPa = saturation vapor pressure at a given temperature (calculated using the Clausius-Clapeyron equation from Riddell et al. 2017, cited in the published paper using this data) - e_a_kPa = actual ambient vapor pressure ($e_a = e_s * RH$ proportion) - VPD_kPa = vapor pressure deficit, which is essentially the drying power of the air ($VPD = e_s - e_a$)

```
# week 1
CEWL_April_05 <- read.csv("../data/capture_CEWL/4-5-21-CEWL.csv", # filename
                          na.strings=c("", "NA")) %>% # fix empty cells

# rename and select the pertinent variables/cols
# I have to do this for each one
# so they all have the same number of columns for joining
dplyr::select(date = Date,
              Time, Status,
              ID = Comments,
              TEWL_g_m2h = TEWL..g..m2h.., # rename
              ambient_temp_C = AmbT..C., # rename
              ambient_RH_percent = AmbRH....
            )

# week 2
CEWL_April_19 <- read.csv("../data/capture_CEWL/4-19-21-CEWL.csv",
                          na.strings=c("", "NA")) %>%

dplyr::select(date = Date,
              Time, Status,
              ID = Comments,
              TEWL_g_m2h = TEWL..g..m2h.., # rename
              ambient_temp_C = AmbT..C., # rename
              ambient_RH_percent = AmbRH....
            )

# week 3
CEWL_April_26 <- read.csv("../data/capture_CEWL/4-26-21-CEWL.csv",
                          na.strings=c("", "NA")) %>%

dplyr::select(date = Date,
              Time, Status,
              ID = Comments,
              TEWL_g_m2h = TEWL..g..m2h.., # rename
              ambient_temp_C = AmbT..C., # rename
              ambient_RH_percent = AmbRH....
            )

# week 4
CEWL_May_3 <- read.csv("../data/capture_CEWL/5-3-21-CEWL.csv",
                       na.strings=c("", "NA")) %>%
```

```

dplyr::select(date = Date,
              Time, Status,
              ID = Comments,
              TEWL_g_m2h = TEWL..g..m2h.., # rename
              ambient_temp_C = AmbT..C., # rename
              ambient_RH_percent = AmbRH....
            )

# week 5
CEWL_May_10 <- read.csv("../data/capture_CEWL/5-10-21-CEWL.csv",
                       na.strings=c("", "NA")) %>%
  dplyr::select(date = Date,
                Time, Status,
                ID = Comments,
                TEWL_g_m2h = TEWL..g..m2h.., # rename
                ambient_temp_C = AmbT..C., # rename
                ambient_RH_percent = AmbRH....
              )

# week 6
CEWL_May_17 <- read.csv("../data/capture_CEWL/5-17-21-CEWL.csv",
                       na.strings=c("", "NA")) %>%
  dplyr::select(date = Date,
                Time, Status,
                ID = Comments,
                TEWL_g_m2h = TEWL..g..m2h.., # rename
                ambient_temp_C = AmbT..C., # rename
                ambient_RH_percent = AmbRH....
              )

# merge all CEWL datafiles & reformat
CEWL <- CEWL_April_05 %>% # week 1
  # join with weeks 2-6
  rbind(., CEWL_April_19,
         CEWL_April_26,
         CEWL_May_3,
         CEWL_May_10,
         CEWL_May_17
        ) %>%
  # remove any unsuccessful measurements
  dplyr::filter(Status == "Normal") %>%
  # extract individual_ID and region separately from the "ID" variable
  separate(ID, c("individual_ID", "region")) %>%
  # reformat data
  dplyr::mutate(# paste and format date-time variable
                CEWL_date_time = as.POSIXct(paste(date, Time),
                                                format = "%m/%d/%y %I:%M:%S %p"),
                # reformat date only
                date = as.Date(date, format = "%m/%d/%y"),
                # reformat time
                # format extracts just time after posix adds arbitrary date
                # but then it's a character again...
                Time = format(as.POSIXct(Time, format = "%I:%M:%S %p"),

```

```

        format = "%H:%M:%S"),
# format individual ID as a factor
individual_ID = as.factor(individual_ID),
# set body region as a factor variable after getting only the consistent characters due
region = as.factor(substring(region, 1, 4)),
# calculate VPD
ambient_temp_K = ambient_temp_C + 273.15,
e_s_kPa = 0.611*exp((2500000/461.5)*
                    ((1/273)-(1/ambient_temp_K))),
e_a_kPa = e_s_kPa * (ambient_RH_percent/100),
VPD_kPa = e_s_kPa - e_a_kPa
) %>%
# remove cols not relevant to stats
dplyr::select(-Status) %>%
# remove any rows with missing values
dplyr::filter(complete.cases())
summary(CEWL)

```

```

##      date                Time      individual_ID  region
##  Min.   :2021-04-05   Length:699      01      : 5    dewl:139
##  1st Qu.:2021-04-19   Class :character 02      : 5    dors:141
##  Median :2021-04-26   Mode  :character 03      : 5    head:141
##  Mean   :2021-04-28                                     04      : 5    mite:137
##  3rd Qu.:2021-05-10                                     05      : 5    vent:141
##  Max.   :2021-05-17                                     06      : 5
##                                     (Other):669
##      TEWL_g_m2h    ambient_temp_C  ambient_RH_percent
##  Min.   : 3.41    Min.   :22.30    Min.   :34.00
##  1st Qu.:17.09    1st Qu.:23.00    1st Qu.:41.30
##  Median :22.00    Median :23.20    Median :45.20
##  Mean   :25.87    Mean   :23.44    Mean   :43.56
##  3rd Qu.:32.59    3rd Qu.:23.80    3rd Qu.:46.30
##  Max.   :96.16    Max.   :25.30    Max.   :53.10
##
##  CEWL_date_time      ambient_temp_K    e_s_kPa      e_a_kPa
##  Min.   :2021-04-05 13:24:15    Min.   :295.4    Min.   :2.760    Min.   :0.9779
##  1st Qu.:2021-04-19 14:07:34    1st Qu.:296.1    1st Qu.:2.882    1st Qu.:1.2086
##  Median :2021-04-26 17:10:23    Median :296.4    Median :2.918    Median :1.3315
##  Mean   :2021-04-28 23:39:45    Mean   :296.6    Mean   :2.964    Mean   :1.2910
##  3rd Qu.:2021-05-10 16:03:10    3rd Qu.:296.9    3rd Qu.:3.028    3rd Qu.:1.3948
##  Max.   :2021-05-17 17:22:31    Max.   :298.4    Max.   :3.318    Max.   :1.4956
##
##      VPD_kPa
##  Min.   :1.297
##  1st Qu.:1.541
##  Median :1.683
##  Mean   :1.673
##  3rd Qu.:1.779
##  Max.   :2.055
##

```

Write CEWL dataframe as a csv for use in other analyses:

```
#write.csv(CEWL, "exported_data/capture_CEWL.csv")
```

Weather Data

This data was obtained from <http://www.itrc.org/databases/precip/> (Adcon Server Data) to test the effect of ambient conditions on CEWL. This is different from the ambient conditions already measured with CEWL, which are the temperature and humidity around the measurement device at the time of measurement. We think that the temperature, humidity, wind speed, and solar radiation the lizard was exposed to prior to capture may also affect CEWL.

We didn't have a daylight savings time switchover during this study, so we don't need to worry about incorporating.

```
# load in csvs and put all in one dataframe
weather <- read.csv("./data/weather/4_5Weather.csv", sep = ';') %>%
  rbind(read.csv("./data/weather/4_19Weather.csv", sep = ';')) %>%
  rbind(read.csv("./data/weather/5_3Weather.csv", sep = ';')) %>%
  rbind(read.csv("./data/weather/5_10Weather.csv", sep = ';')) %>%
  rbind(read.csv("./data/weather/5_17Weather.csv", sep = ';')) %>%
  # add a variable for combined date-time
  mutate(collect_date_time = as.POSIXct(paste(Date, Time),
                                          format = "%m/%d/%y %I:%M:%S %p")) %>%
  # remove lonely date and time
  dplyr::select(-Date, -Time)
```

The weather data is only every 15 minutes, but I want to match it to any minute measurement, so I need to interpolate the values for each minute.

First, make a separate dataframe with every minute for each of those days.

```
all_times <- data.frame(collect_date_time = c(# April 5
  seq(from = as.POSIXct("2021-04-05 10:00"),
    to = as.POSIXct("2021-04-05 16:00"),
    by="min"),
  # April 19
  seq(from = as.POSIXct("2021-04-19 10:00"),
    to = as.POSIXct("2021-04-19 16:00"),
    by="min"),
  # April 26
  seq(from = as.POSIXct("2021-04-26 10:00"),
    to = as.POSIXct("2021-04-26 16:00"),
    by="min"),
  # May 3
  seq(from = as.POSIXct("2021-05-03 10:00"),
    to = as.POSIXct("2021-05-03 16:00"),
    by="min"),
  # May 10
  seq(from = as.POSIXct("2021-05-10 10:00"),
    to = as.POSIXct("2021-05-10 16:00"),
    by="min"),
  # May 17
  seq(from = as.POSIXct("2021-05-17 10:00"),
    to = as.POSIXct("2021-05-17 16:00"),
    by="min")
))
```

Next, merge the weather data into the times dataframe and interpolate the temperature and humidity between measurements.

```
all_times_weather <- all_times %>% # time only dataframe
# add weather measurements based on matching date-time
left_join(weather, by = 'collect_date_time') %>%
# convert temperature units, thanks America
mutate(temp_C = fahrenheit.to.celsius(Temperature_F, round = 2),
# interpolate temperatures
temp_C_interpol = na.approx(temp_C),
# interpolate humidities
RH_percent_interpol = na.approx(RH_percent),
# interpolate Wind Speeds
Wind_mph_interpol = na.approx(Wind_Speed_mph),
# interpolate solar radiation
Solar_rad_Wm2_interpol = na.approx(Pyranometer_W_m),
# compute VPD
temp_K_interpol = temp_C_interpol + 273.15,
e_s_kPa_int = 0.611*exp((2500000/461.5)*
((1/273)-(1/temp_K_interpol))),
e_a_kPa_int = e_s_kPa_int * (RH_percent_interpol/100),
VPD_kPa_int = e_s_kPa_int - e_a_kPa_int
) %>%
# keep only the relevant variables
dplyr::select(collect_date_time,
temp_C_interpol,
RH_percent_interpol,
VPD_kPa_int,
Wind_mph_interpol,
Solar_rad_Wm2_interpol)
summary(all_times_weather)
```

```
## collect_date_time      temp_C_interpol RH_percent_interpol
## Min.   :2021-04-05 10:00:00   Min.   :13.28   Min.   :38.20
## 1st Qu.:2021-04-19 13:00:15   1st Qu.:16.54   1st Qu.:56.77
## Median :2021-04-30 01:00:00   Median :17.78   Median :67.65
## Mean   :2021-04-28 21:00:00   Mean   :18.78   Mean   :65.52
## 3rd Qu.:2021-05-10 12:59:45   3rd Qu.:20.48   3rd Qu.:72.30
## Max.   :2021-05-17 16:00:00   Max.   :25.78   Max.   :92.10
## VPD_kPa_int      Wind_mph_interpol Solar_rad_Wm2_interpol
## Min.   :0.1224    Min.   :0.100    Min.   : 356.9
## 1st Qu.:0.5578    1st Qu.:4.340    1st Qu.: 743.2
## Median :0.6430    Median :4.567    Median : 882.6
## Mean   :0.8248    Mean   :4.574    Mean   : 860.2
## 3rd Qu.:1.0401    3rd Qu.:5.020    3rd Qu.: 979.5
## Max.   :2.1079    Max.   :7.100    Max.   :1037.5
```

Compute Scaled Mass Index

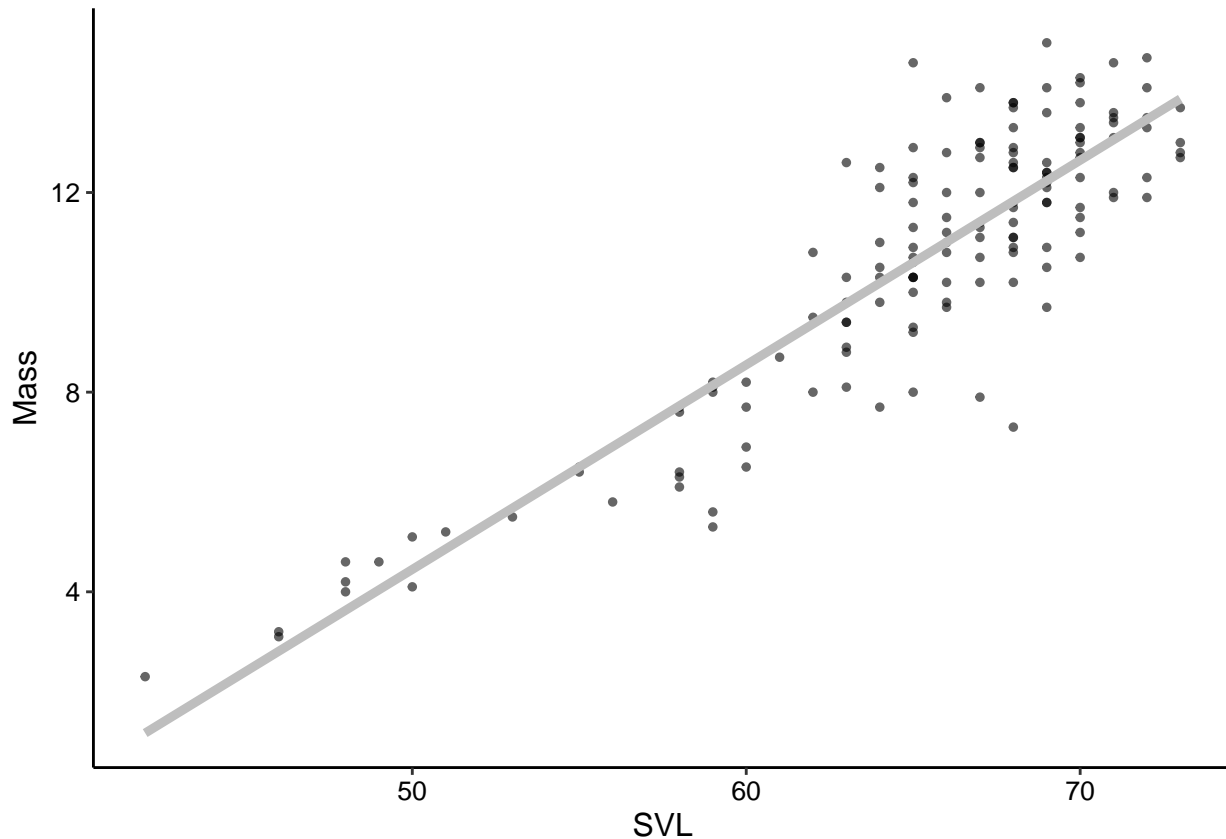
This is also known as the body condition index, or log-log residuals.

I calculate as described by: Peig, J., & Green, A. J. (2009). New perspectives for estimating body condition from mass/length data: The scaled mass index as an alternative method. *Oikos*, 118(12), 1883–1891. <https://doi.org/10.1111/j.1600-0706.2009.17643.x>

Step 1: mass ~ SVL

plot:

```
morpho_blood_dat %>%  
  ggplot(data = .) +  
  geom_point(aes(x = SVL_mm,  
                 y = mass_g,  
                 ),  
            size = 1,  
            alpha = 0.6) +  
  stat_smooth(aes(x = SVL_mm,  
                  y = mass_g,  
                  ),  
             formula = y ~ x,  
             method = "lm",  
             color = "gray",  
             se = F,  
             size = 1.6,  
             alpha = 1 ) +  
  theme_classic() +  
  xlab("SVL") +  
  ylab("Mass") +  
  theme(text = element_text(color = "black",  
                             family = "sans",  
                             size = 12),  
        axis.text = element_text(color = "black",  
                                   family = "sans",  
                                   size = 10),  
        legend.text.align = 0  
  )
```



create a simple linear regression

```
mass_SVL_SLR <- lm(data = morpho_blood_dat, mass_g ~ SVL_mm)
summary(mass_SVL_SLR)
```

```
##
## Call:
## lm(formula = mass_g ~ SVL_mm, data = morpho_blood_dat)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4.5265 -0.8762 -0.0024  0.6735  4.0031
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -16.04514    1.14303  -14.04  <2e-16 ***
## SVL_mm       0.40988    0.01751   23.40  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.316 on 146 degrees of freedom
## Multiple R-squared:  0.7895, Adjusted R-squared:  0.7881
## F-statistic: 547.7 on 1 and 146 DF, p-value: < 2.2e-16
```

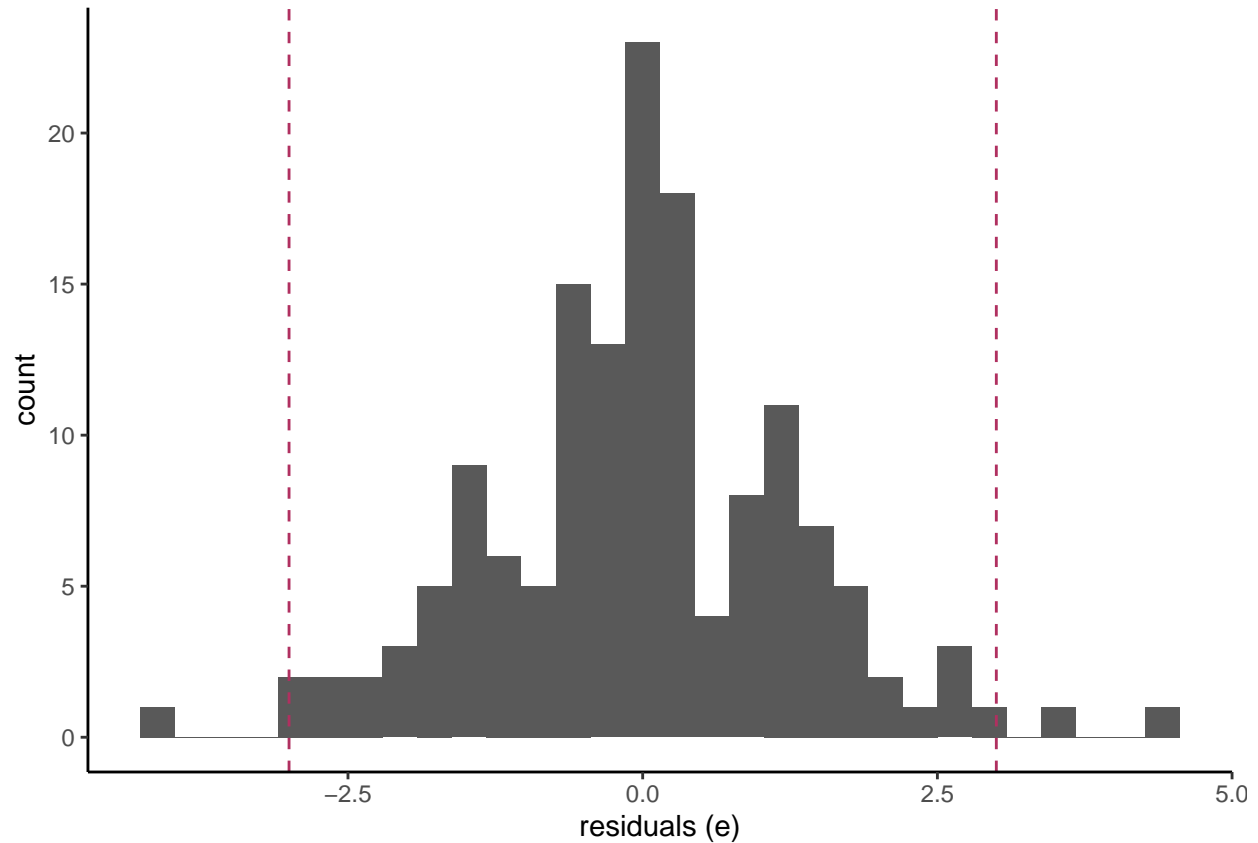
look for outliers by calculating residuals

```
mass_SVL_SLR_residuals <- morpho_blood_dat %>%
  mutate(y_hat = 0.40988*SVL_mm - 16.04514,
         e = y_hat - mass_g)
```

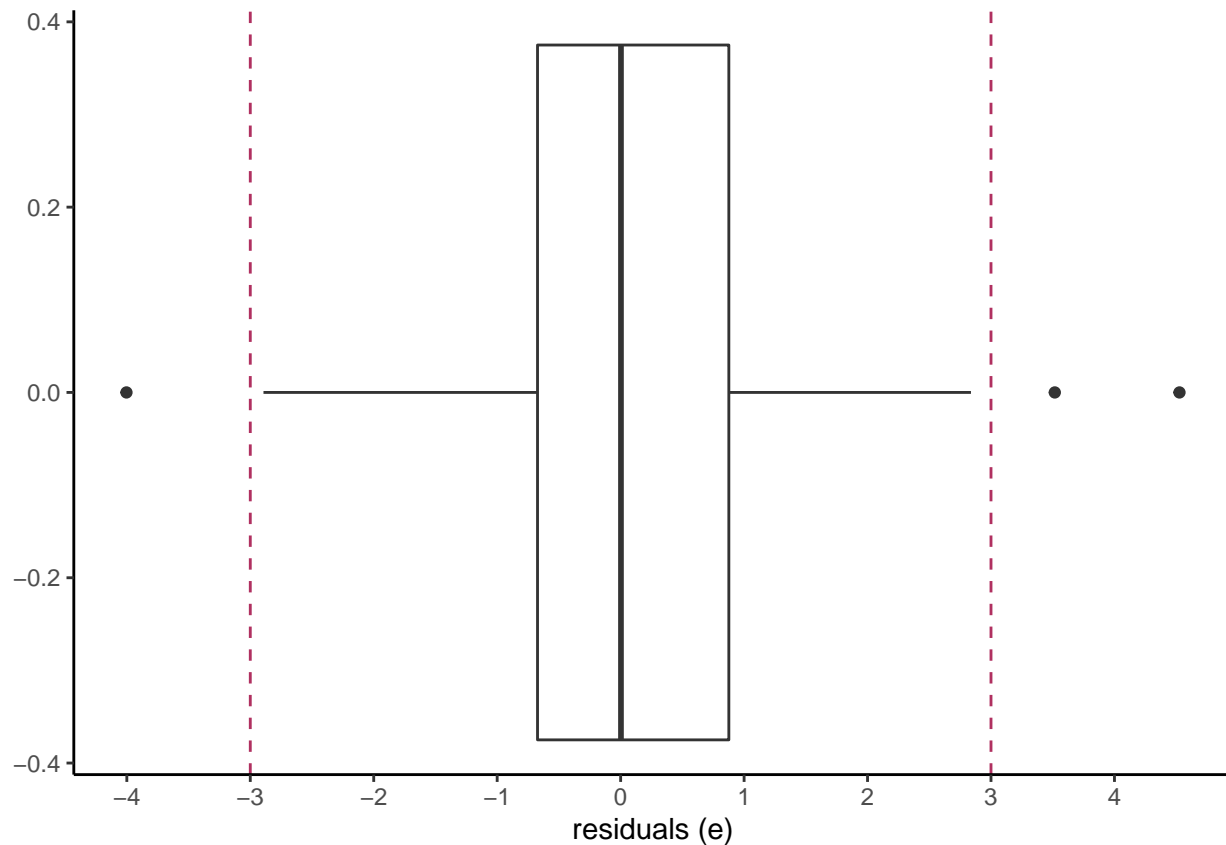
plot residuals

```
ggplot(data = mass_SVL_SLR_residuals,  
       aes(x = e)) +  
  geom_histogram() +  
  theme_classic() +  
  xlab("residuals (e)") +  
  geom_vline(xintercept = -3, linetype = "dashed", color = "maroon") +  
  geom_vline(xintercept = 3, linetype = "dashed", color = "maroon")
```

`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.



```
ggplot(data = mass_SVL_SLR_residuals,  
       aes(x = e)) +  
  geom_boxplot() +  
  theme_classic() +  
  scale_x_continuous(breaks = c(seq(-5, 5, 1))) +  
  xlab("residuals (e)") +  
  geom_vline(xintercept = -3, linetype = "dashed", color = "maroon") +  
  geom_vline(xintercept = 3, linetype = "dashed", color = "maroon")
```



From the histogram, there are clearly points disconnected from the main curve. In the boxplot, we can distinguish that those outlying points have residuals <-3.5 and >3 , so I'll go back and filter those out in the code chunk before making the distribution plots. Now the boxplot has no dots outside the main distribution.

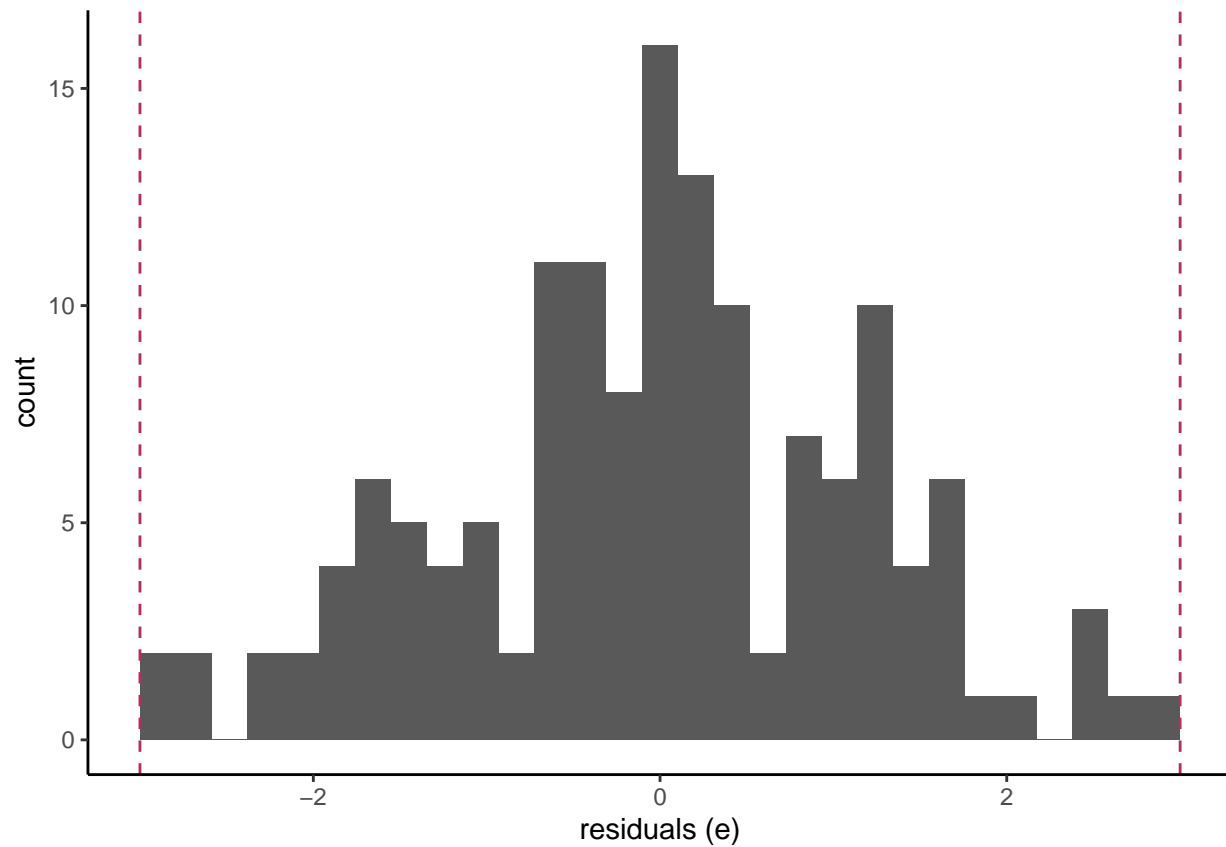
calculating residuals with outliers excluded

```
mass_SVL_SLR_residuals2 <- morpho_blood_dat %>%
  mutate(y_hat = 0.40988*SVL_mm - 16.04514,
         e = y_hat - mass_g) %>%
  dplyr::filter(e < 3 & e > -3)
```

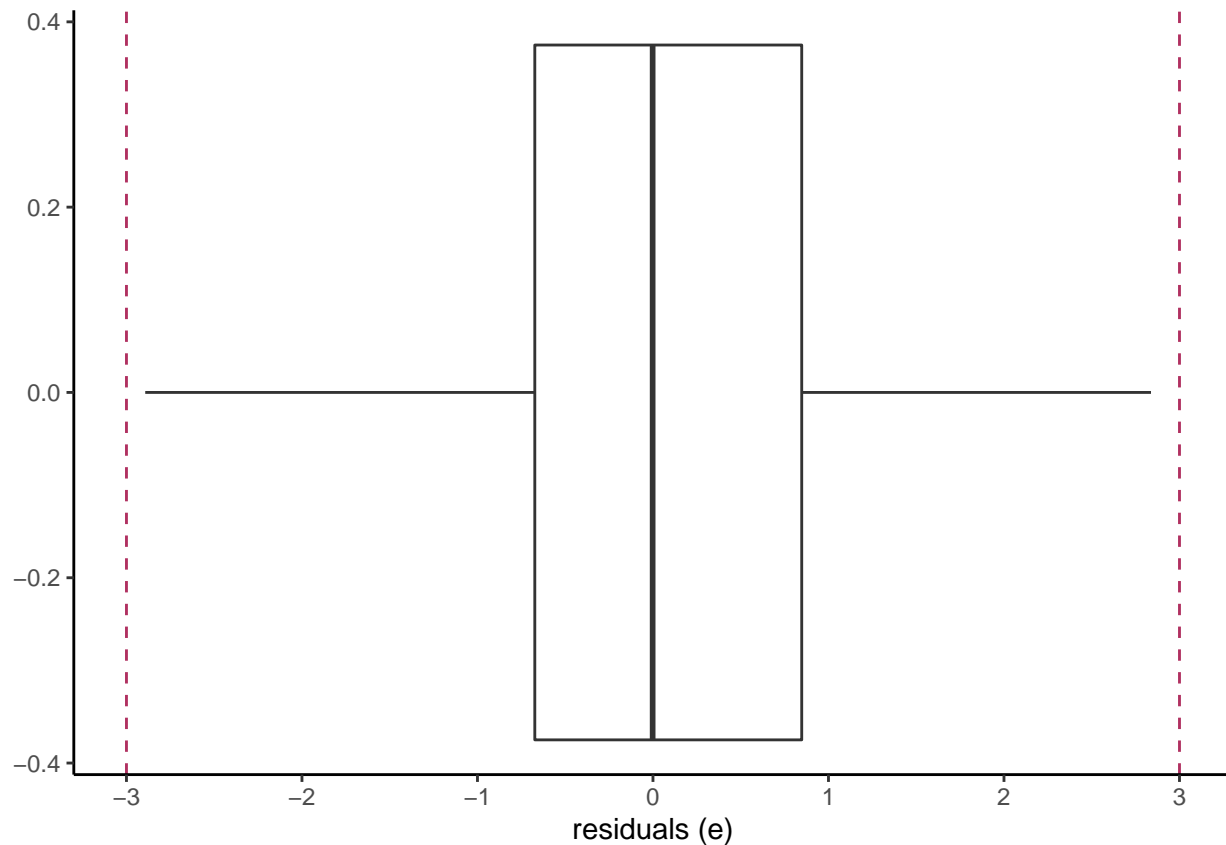
plot new residuals

```
ggplot(data = mass_SVL_SLR_residuals2,
      aes(x = e)) +
  geom_histogram() +
  theme_classic() +
  xlab("residuals (e)") +
  geom_vline(xintercept = -3, linetype = "dashed", color = "maroon") +
  geom_vline(xintercept = 3, linetype = "dashed", color = "maroon")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



```
ggplot(data = mass_SVL_SLR_residuals2,
  aes(x = e)) +
  geom_boxplot() +
  theme_classic() +
  scale_x_continuous(breaks = c(seq(-5, 5, 1))) +
  xlab("residuals (e)") +
  geom_vline(xintercept = -3, linetype = "dashed", color = "maroon") +
  geom_vline(xintercept = 3, linetype = "dashed", color = "maroon")
```



And, check mean residual value:

```
mass_SVL_SLR_residuals2 %>%
  summarise(mean_res = mean(e),
            med = median(e))
```

```
##      mean_res      med
## 1 -0.02769117 -0.00174
```

Not zero, which is not ideal, but pretty close.

Next, check for high leverage points:

```
# compute values for observations
high_leverage <- data.frame(H = hatvalues(mass_SVL_SLR)
                           ) %>% mutate(row = rownames(.))

# compute cutoff value
h_bar <- (3*sum(high_leverage$H))/nrow(high_leverage)

# add to original dataframe
# see which observations have extremely high leverage (if any)
high_leverage_dat <- mass_SVL_SLR_residuals %>%
  mutate(row = rownames(.)) %>%
  left_join(., high_leverage, by = "row") %>%
  dplyr::filter(H > h_bar)
high_leverage_dat
```

```
##      date      collect_time individual_ID SVL_mm mass_g sex_M_F
## 1 2021-04-05 2021-12-19 10:38:00          4    48    4.2      M
```

```
## 2 2021-04-05 2021-12-19 10:17:00      5      50      4.1      M
## 3 2021-04-05 2021-12-19 10:47:00      6      48      4.6      M
## 4 2021-04-05 2021-12-19 10:42:00      8      42      2.3      M
## 5 2021-04-05 2021-12-19 13:27:00      9      46      3.1      F
## 6 2021-04-26 2021-12-19 12:32:00     55      46      3.2      F
## 7 2021-04-26 2021-12-19 12:47:00     62      51      5.2      M
## 8 2021-04-26 2021-12-19 12:40:00     65      48      4.0      M
## 9 2021-05-03 2021-12-19 12:36:00     85      49      4.6      M
## 10 2021-05-10 2021-12-19 13:10:00    120      50      5.1      M
##   gravid_Y_N blood_sample_eye hematocrit_percent osmolality_mmol_kg
## 1      <NA>              R              NA              341
## 2      <NA>              R              NA              354
## 3      <NA>              L              NA              355
## 4      <NA>              R              NA              304
## 5      N              L              NA              NA
## 6      N              R              37              373
## 7      <NA>              R              40              400
## 8      <NA>              R              40              394
## 9      <NA>              R              34              380
## 10     <NA>              R              33              371
##   cloacal_temp_C   processing_time hemolyzed   collect_date_time hold_time
## 1             26 2021-12-19 14:02:00      Y 2021-04-05 10:38:00      204
## 2             25 2021-12-19 13:59:00      Y 2021-04-05 10:17:00      222
## 3             24 2021-12-19 14:06:00      N 2021-04-05 10:47:00      199
## 4             23 2021-12-19 14:20:00      N 2021-04-05 10:42:00      218
## 5             23 2021-12-19 14:43:00    <NA> 2021-04-05 13:27:00       76
## 6             27 2021-12-19 13:16:00      N 2021-04-26 12:32:00       44
## 7             26 2021-12-19 14:28:00      N 2021-04-26 12:47:00      101
## 8             25 2021-12-19 15:26:00    <NA> 2021-04-26 12:40:00      166
## 9             24 2021-12-19 14:13:00      Y 2021-05-03 12:36:00       97
## 10            21 2021-12-19 17:15:00      Y 2021-05-10 13:10:00      245
##   y_hat      e row      H
## 1 3.62910 -0.57090   4 0.05776372
## 2 4.44886  0.34886   5 0.04645120
## 3 3.62910 -0.97090   6 0.05776372
## 4 1.16982 -1.13018   8 0.10020003
## 5 2.80934 -0.29066   9 0.07049270
## 6 2.80934 -0.39066  54 0.07049270
## 7 4.85874 -0.34126  60 0.04132611
## 8 3.62910 -0.37090  63 0.05776372
## 9 4.03898 -0.56102  83 0.05193040
## 10 4.44886 -0.65114 118 0.04645120
```

The points for individuals 4, 5, 6, 8, 9, 57, 64, 67, 87, and 123 seem to be high-leverage, so we will try removing them.

Check for influential points based on Cook's distance:

```
# get Cook's distance
cooks <- data.frame(c = cooks.distance(mass_SVL_SLR) # specify model name
) %>% mutate(row = rownames(.))

# add to original dataframe
influential <- mass_SVL_SLR_residuals2 %>%
  mutate(row = rownames(.)) %>%
```

```

left_join(., cooks, by = "row")

# see moderately influential points
cook_mod_inf <- influential %>%
  dplyr::filter(c>0.5)
cook_mod_inf

## [1] date          collect_time    individual_ID    SVL_mm
## [5] mass_g          sex_M_F        gravid_Y_N       blood_sample_eye
## [9] hematocrit_percent osmolality_mmol_kg cloacal_temp_C   processing_time
## [13] hemolyzed       collect_date_time hold_time        y_hat
## [17] e              row           c
## <0 rows> (or 0-length row.names)

```

There are no even moderately-influential points, at least based on Cook's distance, so there's nothing to potentially remove.

Create new SLR and check mean residual value after removing outliers and high leverage points:

```

# create new dataframe with filtered data
cleaned_SMI_dat <- mass_SVL_SLR_residuals2 %>% # already w outliers removed
  mutate(row = rownames(.)) %>%
  # add high leverage point info
  left_join(., high_leverage, by = "row") %>%
  # remove high leverage points
  dplyr::filter(H < h_bar)

# model
mass_SVL_SLR2 <- lm(data = cleaned_SMI_dat, mass_g ~ SVL_mm)
summary(mass_SVL_SLR2)

```

```

##
## Call:
## lm(formula = mass_g ~ SVL_mm, data = cleaned_SMI_dat)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.72134 -0.88611  0.00146  0.70819  2.87193
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -17.32109     1.28410  -13.49  <2e-16 ***
## SVL_mm       0.42953     0.01953   21.99  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.209 on 133 degrees of freedom
## Multiple R-squared:  0.7843, Adjusted R-squared:  0.7827
## F-statistic: 483.6 on 1 and 133 DF, p-value: < 2.2e-16

```

```

# compute residuals
mass_SVL_SLR2_residuals <- cleaned_SMI_dat %>%
  mutate(y_hat = predict(mass_SVL_SLR2),
         e = residuals(mass_SVL_SLR2))

# check residuals values

```



```
mass_SVL_SLR2_residuals %>%
  summarise(mean_res = mean(e),
            med = median(e))
```

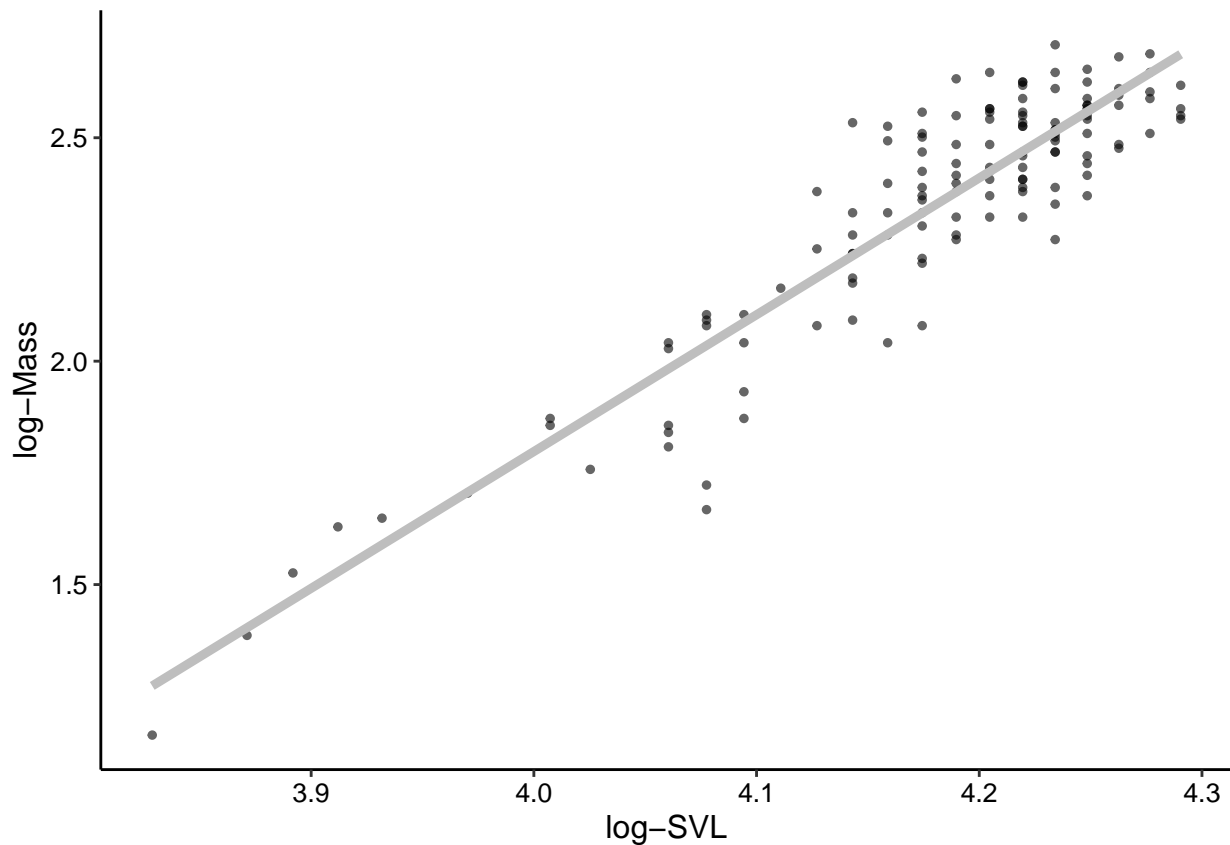
```
##           mean_res           med
## 1 4.654038e-17 0.001458016
```

The residuals are much much smaller, so I believe it is the right choice to remove the high leverage points. The “cleaned_SMI_dat” will be used to calculate the equation for SMI.

Step 2: make log-log relationship

plot and calculate SLR for filtered data

```
cleaned_SMI_dat %>%
  ggplot(data = .) +
  geom_point(aes(x = log(SVL_mm),
                y = log(mass_g),
                ),
            size = 1,
            alpha = 0.6) +
  stat_smooth(aes(x = log(SVL_mm),
                  y = log(mass_g),
                  ),
              formula = y ~ x,
              method = "lm",
              color = "gray",
              se = F,
              size = 1.6,
              alpha = 1 ) +
  theme_classic() +
  xlab("log-SVL") +
  ylab("log-Mass") +
  theme(text = element_text(color = "black",
                            family = "sans",
                            size = 12),
        axis.text = element_text(color = "black",
                                  family = "sans",
                                  size = 10),
        legend.text.align = 0
  )
```



SLR

```
log_mass_SVL_SLR <- lm(data = cleaned_SMI_dat,
                        log(mass_g) ~ log(SVL_mm))
summary(log_mass_SVL_SLR)
```

```
##
## Call:
## lm(formula = log(mass_g) ~ log(SVL_mm), data = cleaned_SMI_dat)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.36738 -0.07518  0.00334  0.06423  0.29781
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -10.4465     0.4858  -21.50  <2e-16 ***
## log(SVL_mm)   3.0611     0.1162   26.34  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1175 on 133 degrees of freedom
## Multiple R-squared:  0.8391, Adjusted R-squared:  0.8379
## F-statistic: 693.6 on 1 and 133 DF,  p-value: < 2.2e-16
```

compute standardized major axis using this regression equation:

```
r <- sqrt(0.8391) # Pearson's correlection coefficient (sqrt of R-squared)
b_OLS <- 3.0611 # regression slope
```

```
b_SMA <- b_OLS/r
```

also get a value for L0:

```
L0 <- mean(cleaned_SMI_dat$SVL_mm)
```

Step 3: calculate scaled mass index

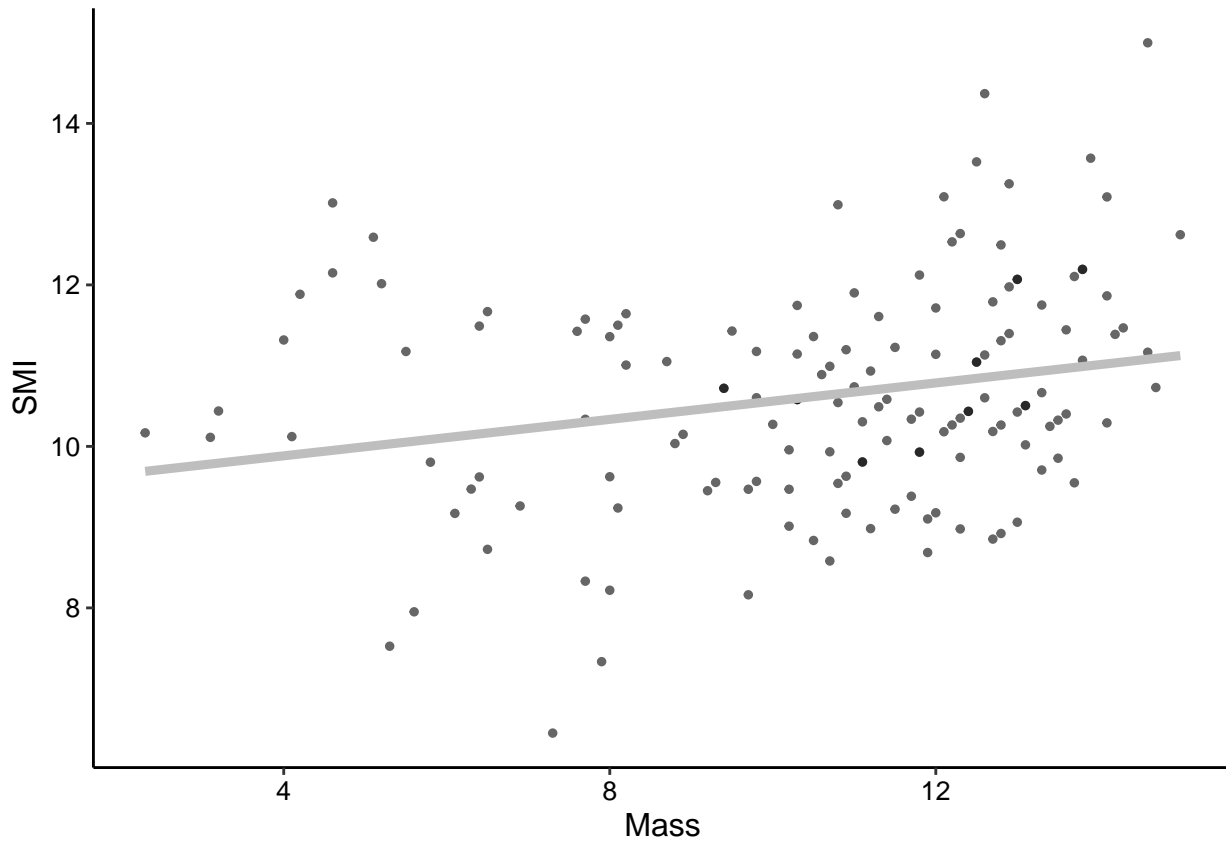
(And join weather data.)

```
morpho_blood_SMI <- morpho_blood_dat %>%  
  mutate(SMI = mass_g * ((L0/SVL_mm) ^ b_SMA)) %>%  
  left_join(all_times_weather,  
    by = c("collect_date_time")  
  )
```

Check

Look at the difference between regular mass and SMI:

```
morpho_blood_SMI %>%  
  ggplot(data = .) +  
  geom_point(aes(x = mass_g,  
    y = SMI,  
    ),  
    size = 1,  
    alpha = 0.6) +  
  stat_smooth(aes(x = mass_g,  
    y = SMI,  
    ),  
    formula = y ~ x,  
    method = "lm",  
    color = "gray",  
    se = F,  
    size = 1.6,  
    alpha = 1 ) +  
  theme_classic() +  
  xlab("Mass") +  
  ylab("SMI") +  
  theme(text = element_text(color = "black",  
    family = "sans",  
    size = 12),  
    axis.text = element_text(color = "black",  
    family = "sans",  
    size = 10),  
    legend.text.align = 0  
  )
```



Join Data

Add CEWL and morpho_blood_SMI data together.

```
CEWL_data_full <- CEWL %>%
  left_join(morpho_blood_SMI,
            by = c("date", "individual_ID")
            )
summary(CEWL_data_full)
```

```
##      date           Time      individual_ID  region
##  Min.   :2021-04-05   Length:699      01      : 5   dewl:139
##  1st Qu.:2021-04-19   Class :character  02      : 5   dors:141
##  Median :2021-04-26   Mode  :character  03      : 5   head:141
##  Mean   :2021-04-28                                     04      : 5   mite:137
##  3rd Qu.:2021-05-10                                     05      : 5   vent:141
##  Max.   :2021-05-17                                     06      : 5
##                                                         (Other):669
##      TEWL_g_m2h  ambient_temp_C  ambient_RH_percent
##  Min.   : 3.41   Min.   :22.30   Min.   :34.00
##  1st Qu.:17.09   1st Qu.:23.00   1st Qu.:41.30
##  Median :22.00   Median :23.20   Median :45.20
##  Mean   :25.87   Mean   :23.44   Mean   :43.56
##  3rd Qu.:32.59   3rd Qu.:23.80   3rd Qu.:46.30
##  Max.   :96.16   Max.   :25.30   Max.   :53.10
##
##  CEWL_date_time      ambient_temp_K  e_s_kPa  e_a_kPa
##  Min.   :2021-04-05 13:24:15   Min.   :295.4   Min.   :2.760   Min.   :0.9779
```

```

## 1st Qu.:2021-04-19 14:07:34 1st Qu.:296.1 1st Qu.:2.882 1st Qu.:1.2086
## Median :2021-04-26 17:10:23 Median :296.4 Median :2.918 Median :1.3315
## Mean :2021-04-28 23:39:45 Mean :296.6 Mean :2.964 Mean :1.2910
## 3rd Qu.:2021-05-10 16:03:10 3rd Qu.:296.9 3rd Qu.:3.028 3rd Qu.:1.3948
## Max. :2021-05-17 17:22:31 Max. :298.4 Max. :3.318 Max. :1.4956
##
## VPD_kPa collect_time SVL_mm mass_g
## Min. :1.297 Min. :2021-12-19 11:29:00 Min. :46.00 Min. : 3.20
## 1st Qu.:1.541 1st Qu.:2021-12-19 12:37:00 1st Qu.:64.00 1st Qu.: 9.70
## Median :1.683 Median :2021-12-19 12:48:00 Median :67.00 Median :11.40
## Mean :1.673 Mean :2021-12-19 12:55:48 Mean :65.81 Mean :10.88
## 3rd Qu.:1.779 3rd Qu.:2021-12-19 13:02:15 3rd Qu.:69.00 3rd Qu.:12.80
## Max. :2.055 Max. :2021-12-19 15:44:00 Max. :73.00 Max. :15.00
## NA's :59 NA's :44 NA's :44
## sex_M_F gravid_Y_N blood_sample_eye hematocrit_percent osmolality_mmol_kg
## F :216 N : 91 both: 10 Min. :16.0 Min. :293.0
## M :439 Y :125 L : 0 1st Qu.:33.0 1st Qu.:347.0
## NA's: 44 NA's:483 R :645 Median :36.0 Median :368.0
## NA's: 44 Mean :35.4 Mean :366.8
## 3rd Qu.:38.0 3rd Qu.:387.0
## Max. :54.0 Max. :436.0
## NA's :119 NA's :49
## cloacal_temp_C processing_time hemolyzed
## Min. :20.0 Min. :2021-12-19 12:44:00 N :368
## 1st Qu.:22.0 1st Qu.:2021-12-19 14:14:00 Y :179
## Median :23.0 Median :2021-12-19 15:25:00 NA's:152
## Mean :23.4 Mean :2021-12-19 15:16:48
## 3rd Qu.:25.0 3rd Qu.:2021-12-19 16:18:00
## Max. :28.0 Max. :2021-12-19 17:38:00
## NA's :49 NA's :59
## collect_date_time hold_time SMI temp_C_interpol
## Min. :2021-04-05 13:25:00 Min. : 21.0 Min. : 6.450 Min. :15.67
## 1st Qu.:2021-04-19 13:09:30 1st Qu.: 91.0 1st Qu.: 9.624 1st Qu.:16.66
## Median :2021-05-03 12:40:00 Median :132.0 Median :10.505 Median :18.68
## Mean :2021-05-01 01:04:48 Mean :140.5 Mean :10.573 Mean :18.77
## 3rd Qu.:2021-05-10 12:52:00 3rd Qu.:189.0 3rd Qu.:11.444 3rd Qu.:19.96
## Max. :2021-05-17 13:01:00 Max. :268.0 Max. :14.999 Max. :23.61
## NA's :59 NA's :69 NA's :44 NA's :59
## RH_percent_interpol VPD_kPa_int Wind_mph_interpol Solar_rad_Wm2_interpol
## Min. :44.29 Min. :0.3424 Min. :3.773 Min. : 587.0
## 1st Qu.:57.51 1st Qu.:0.5533 1st Qu.:4.577 1st Qu.: 741.9
## Median :68.10 Median :0.6986 Median :5.000 Median : 951.3
## Mean :66.53 Mean :0.7837 Mean :4.945 Mean : 892.3
## 3rd Qu.:72.54 3rd Qu.:1.0127 3rd Qu.:5.233 3rd Qu.:1032.9
## Max. :81.10 Max. :1.5691 Max. :6.200 Max. :1037.5
## NA's :59 NA's :59 NA's :59 NA's :59

```

Final Formatting

redo the levels for body region:

```

CEWL_data_full$region <- factor(CEWL_data_full$region,
                                levels = c("dors", "vent",
                                             "head", "dewl", "mite"),
                                labels = c("Dorsum", "Ventrum", "Head",

```

```

    "Dewlap", "Mite Patch")
  )
unique(CEWL_data_full$region)

```

```

## [1] Dorsum      Ventrurn    Dewlap      Head        Mite Patch
## Levels: Dorsum Ventrurn Head Dewlap Mite Patch

```

NOTE: running this more than once overrides things, so be careful

Check Data Distributions

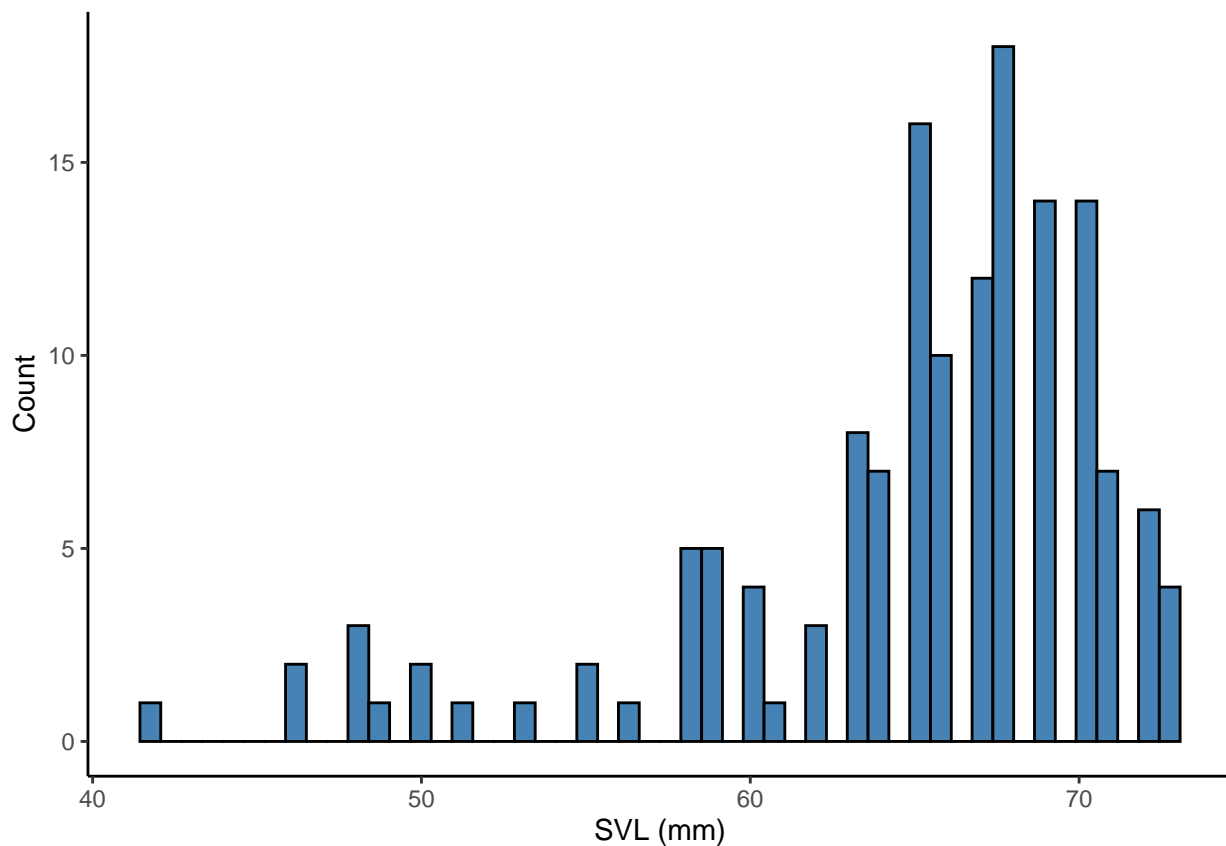
Histograms & Q-Q Plots

SVL

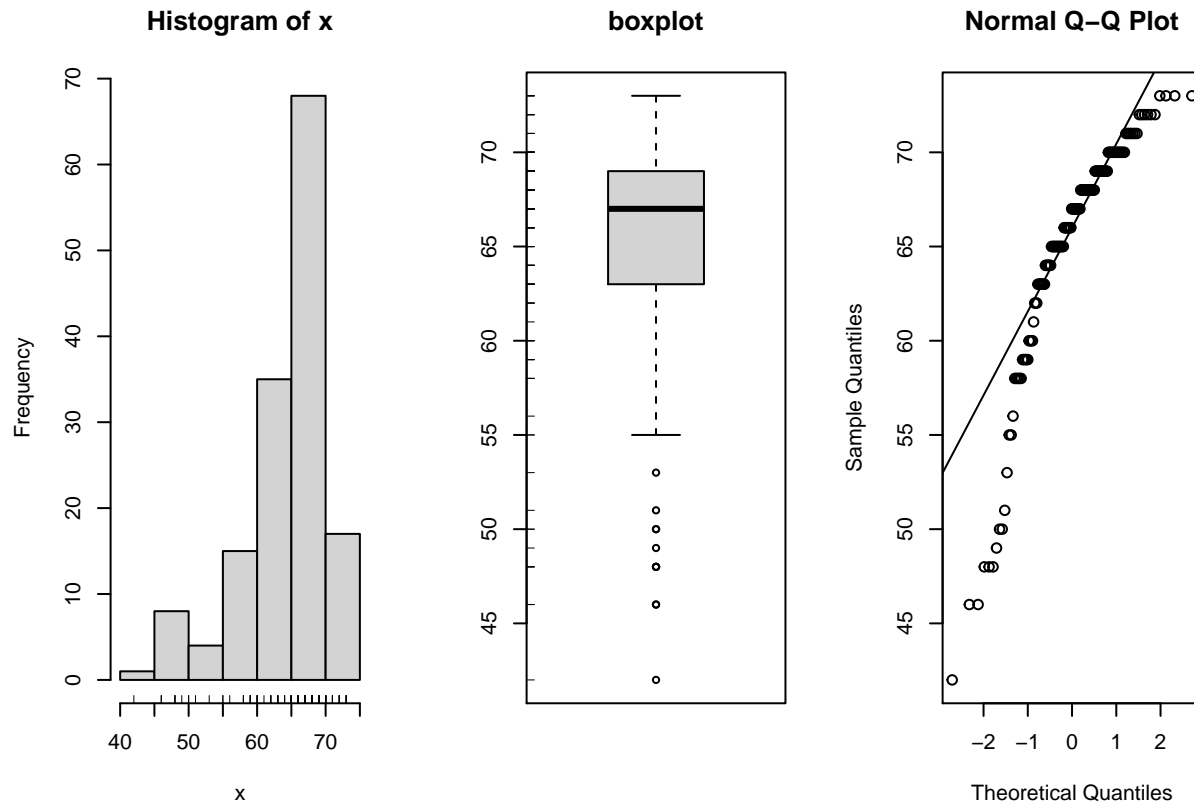
```

morpho_blood_SMI %>%
  ggplot(., aes(x = SVL_mm)) +
  geom_histogram(color = "black", fill="steelblue", bins=50) +
  theme_classic() +
  xlab("SVL (mm)") +
  ylab("Count")

```



```
simple.eda(morpho_blood_SMI$SVL_mm)
```



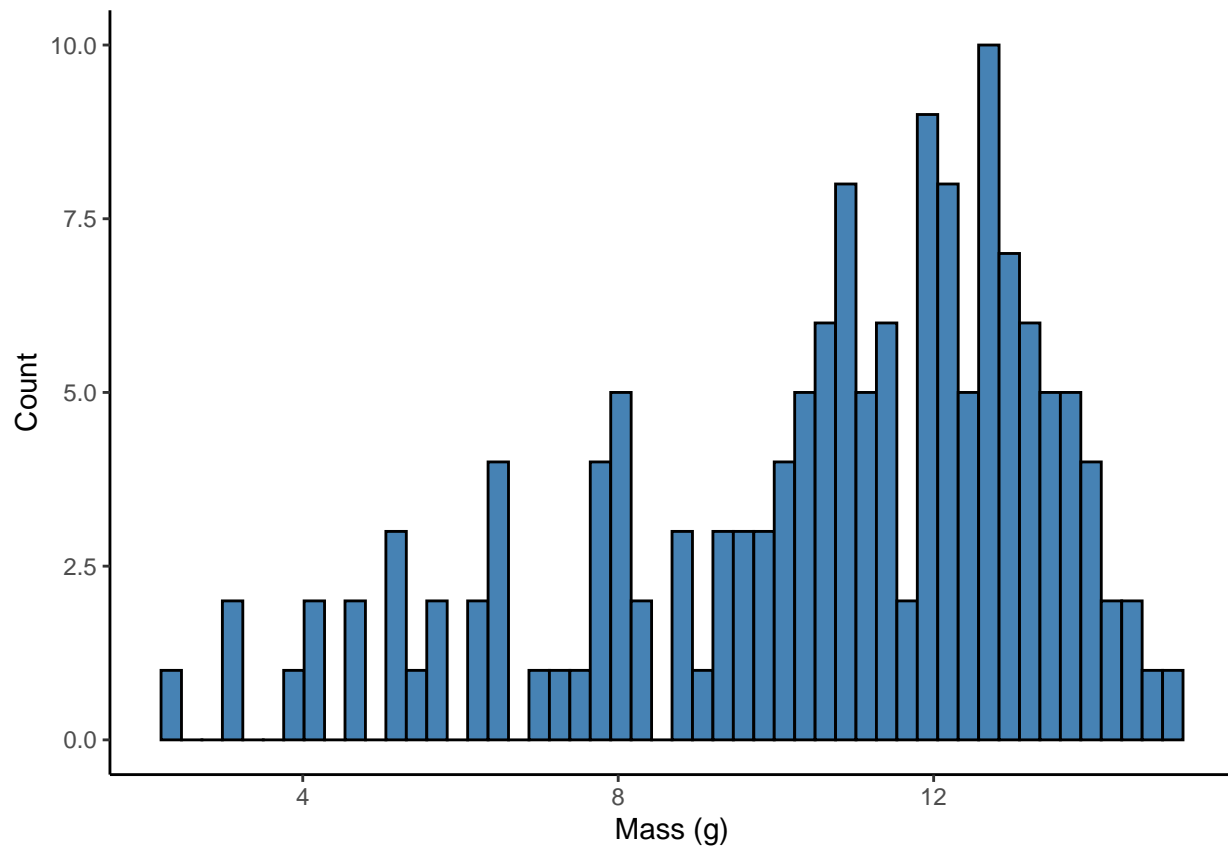
```
# Normality test if p > .05, data is normal. Data is not normal.
```

```
shapiro.test(morpho_blood_SMI$SVL_mm)
```

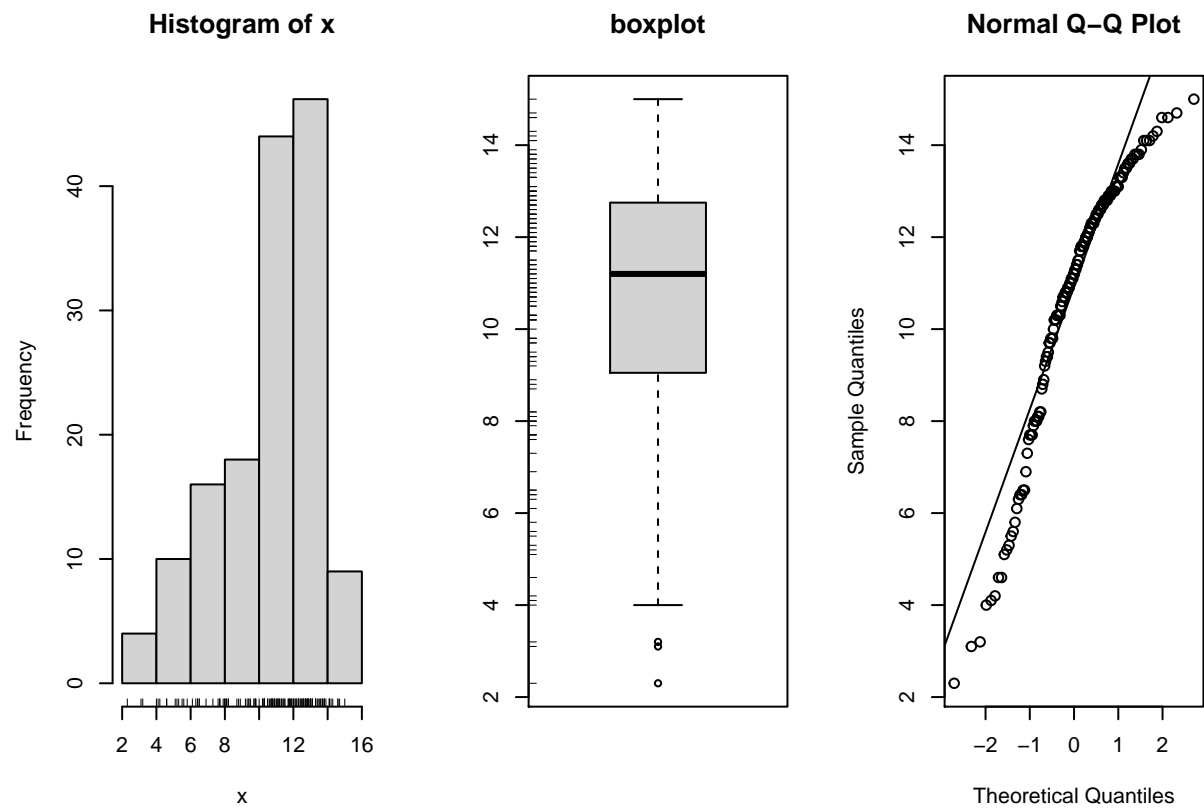
```
##
##  Shapiro-Wilk normality test
##
## data:  morpho_blood_SMI$SVL_mm
## W = 0.85469, p-value = 8.85e-11
```

Mass

```
morpho_blood_SMI %>%
  ggplot(., aes(x = mass_g)) +
  geom_histogram(color = "black", fill="steelblue", bins=50) +
  theme_classic() +
  xlab("Mass (g)") +
  ylab("Count")
```



```
simple.eda(morpho_blood_SMI$mass_g)
```

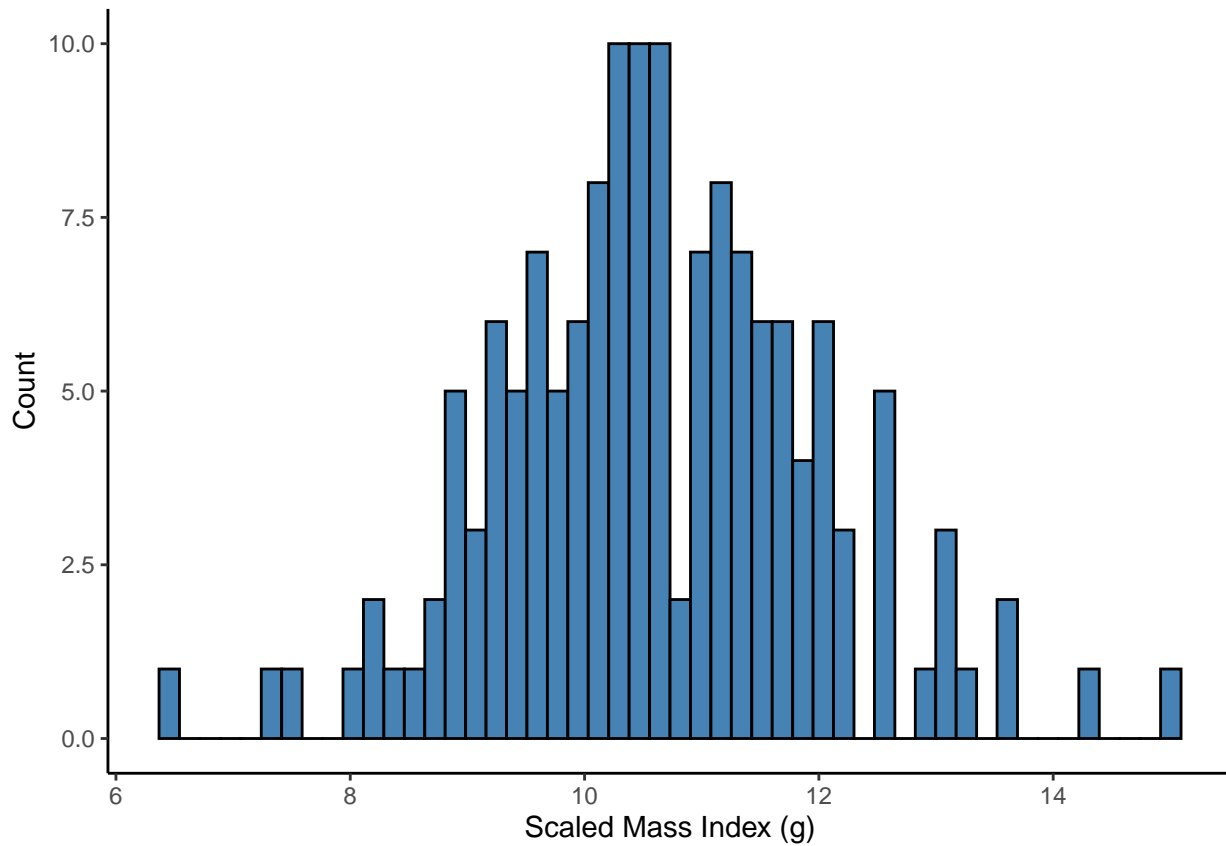



```
# Normality test if  $p > .05$ , data is normal. Data is not normal.  
shapiro.test(morpho_blood_SMI$mass_g)
```

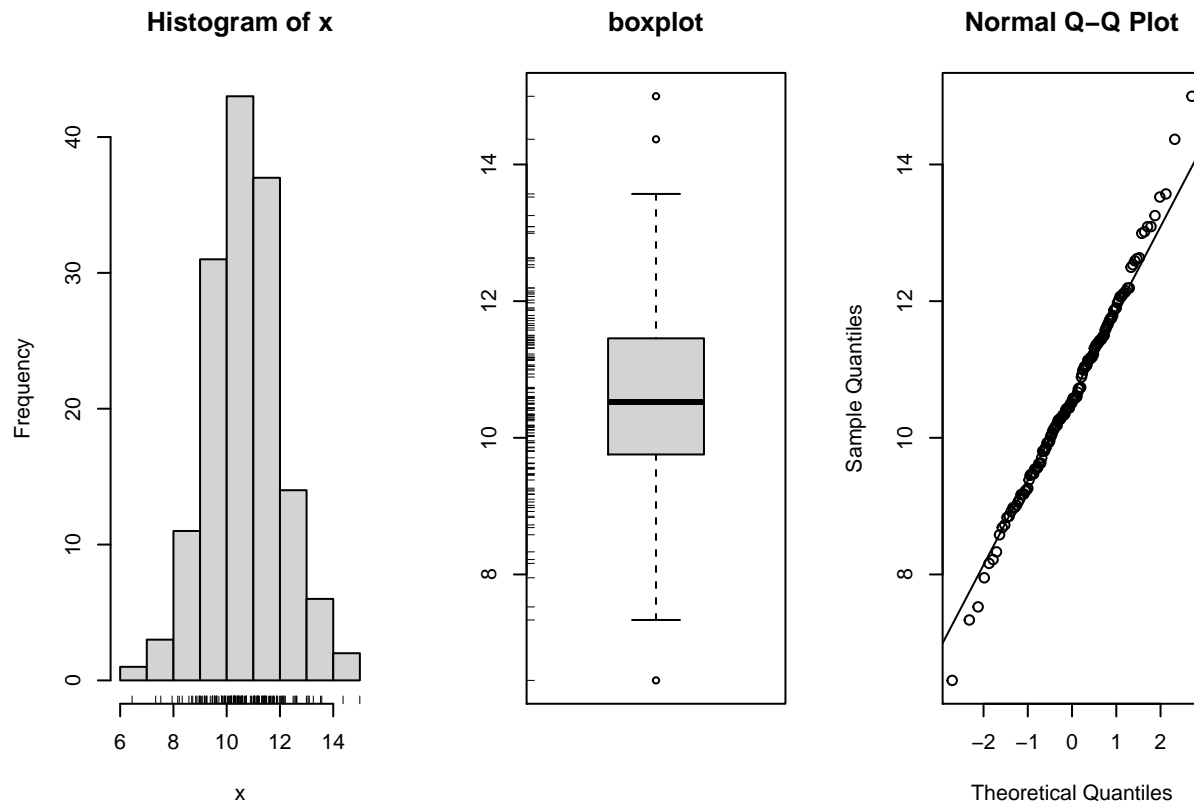
```
##  
## Shapiro-Wilk normality test  
##  
## data: morpho_blood_SMI$mass_g  
## W = 0.92517, p-value = 5.397e-07
```

SMI

```
morpho_blood_SMI %>%  
  ggplot(., aes(x = SMI)) +  
  geom_histogram(color = "black", fill="steelblue", bins=50) +  
  theme_classic() +  
  xlab("Scaled Mass Index (g)") +  
  ylab("Count")
```



```
simple.eda(morpho_blood_SMI$SMI)
```



```
# Normality test if p > .05, data is normal. Data is not normal.
shapiro.test(morpho_blood_SMI$SMI)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  morpho_blood_SMI$SMI
## W = 0.9937, p-value = 0.7667
```

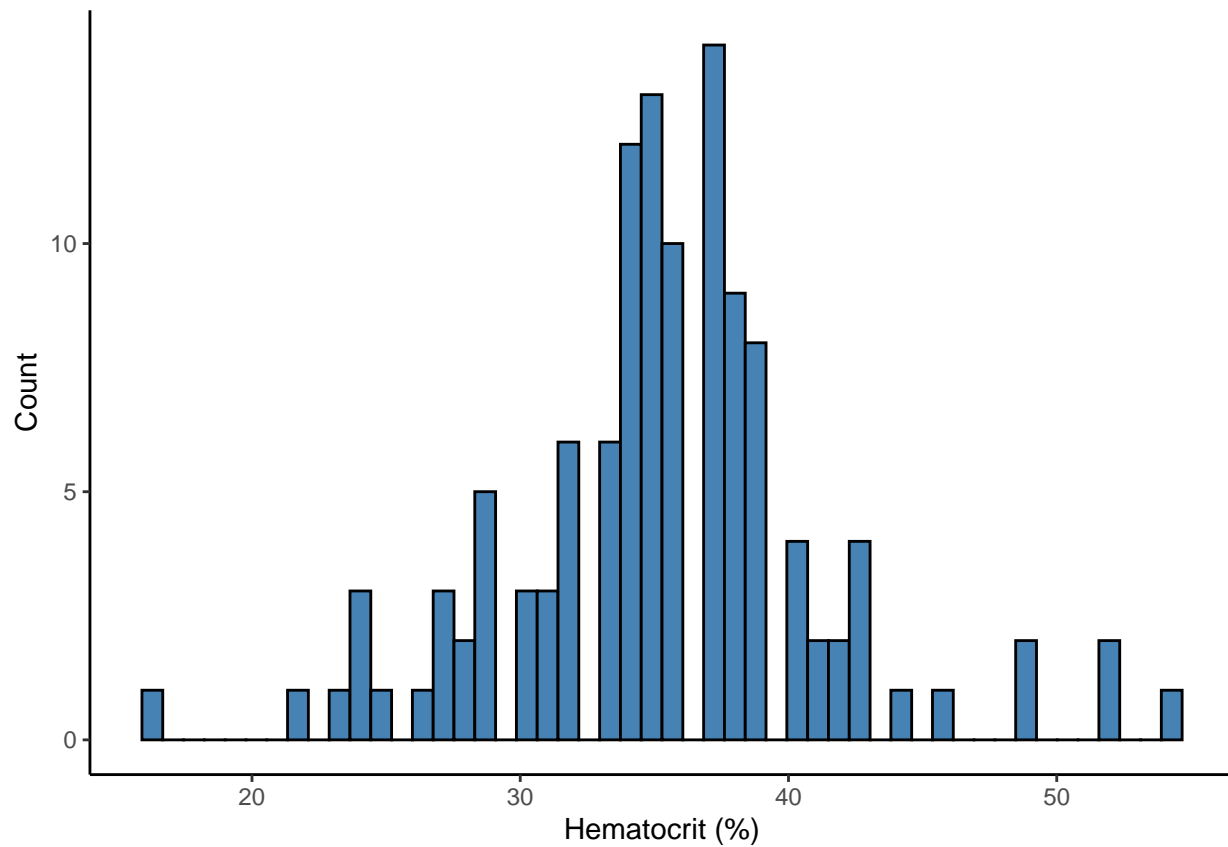
SMI is one of the few variables actually normally distributed!

Hematocrit

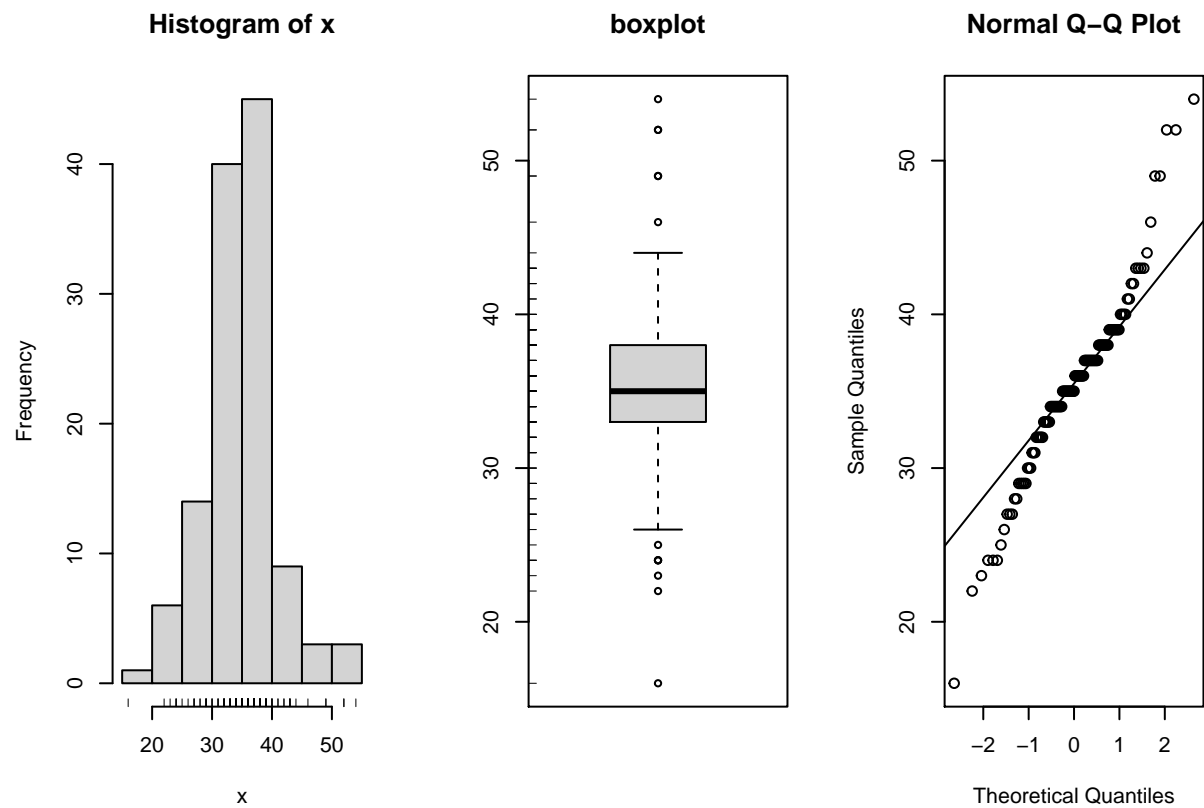
looks pretty normally distributed around ~35%, but not statistically normal

```
morpho_blood_SMI %>%
  ggplot(., aes(x = hematocrit_percent)) +
  geom_histogram(color = "black", fill="steelblue", bins=50) +
  theme_classic() +
  xlab("Hematocrit (%)") +
  ylab("Count")
```

```
## Warning: Removed 27 rows containing non-finite values (stat_bin).
```



```
simple.eda(morpho_blood_SMI$hematocrit_percent)
```



```
# Normality test if  $p > .05$ , data is normal. Data is not normal
shapiro.test(morpho_blood_SMI$hematocrit_percent)
```

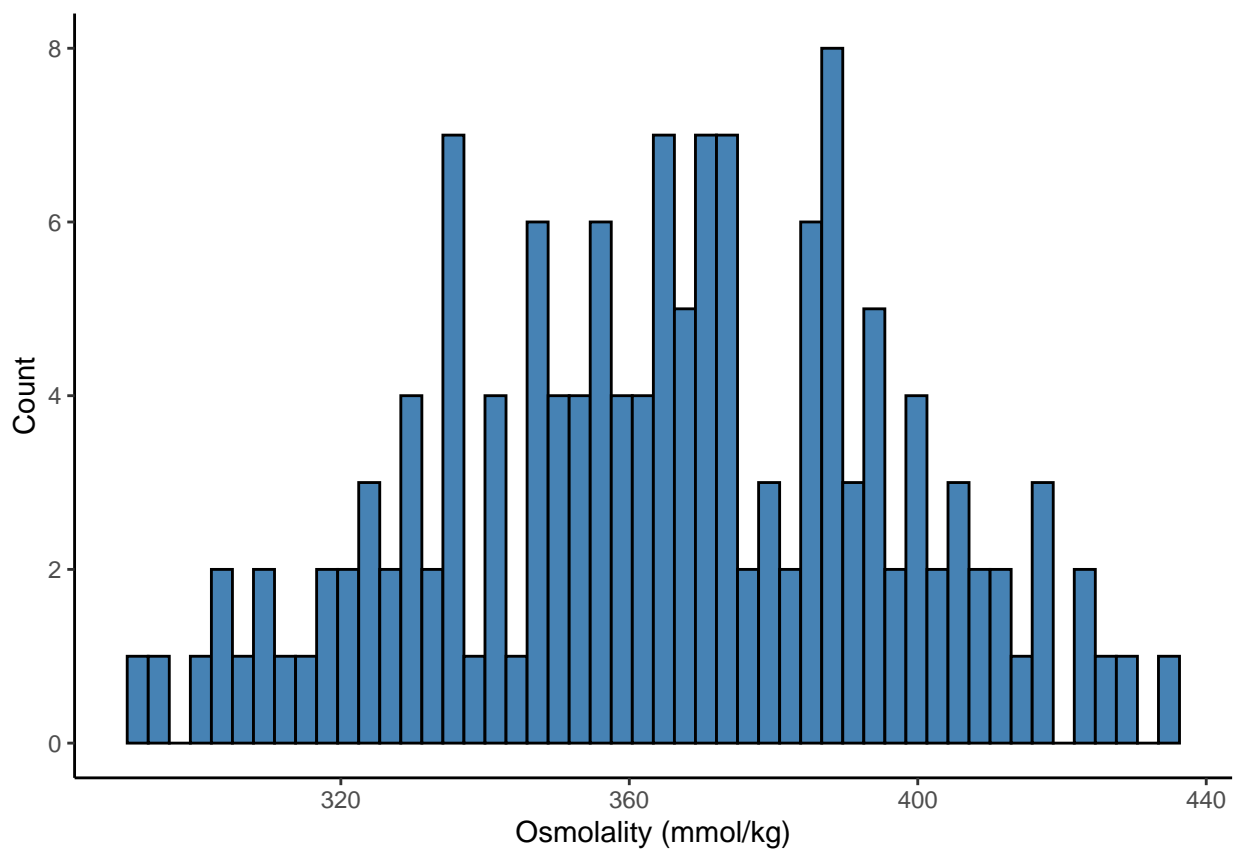
```
##
## Shapiro-Wilk normality test
##
## data: morpho_blood_SMI$hematocrit_percent
## W = 0.95933, p-value = 0.001056
```

Osmolality

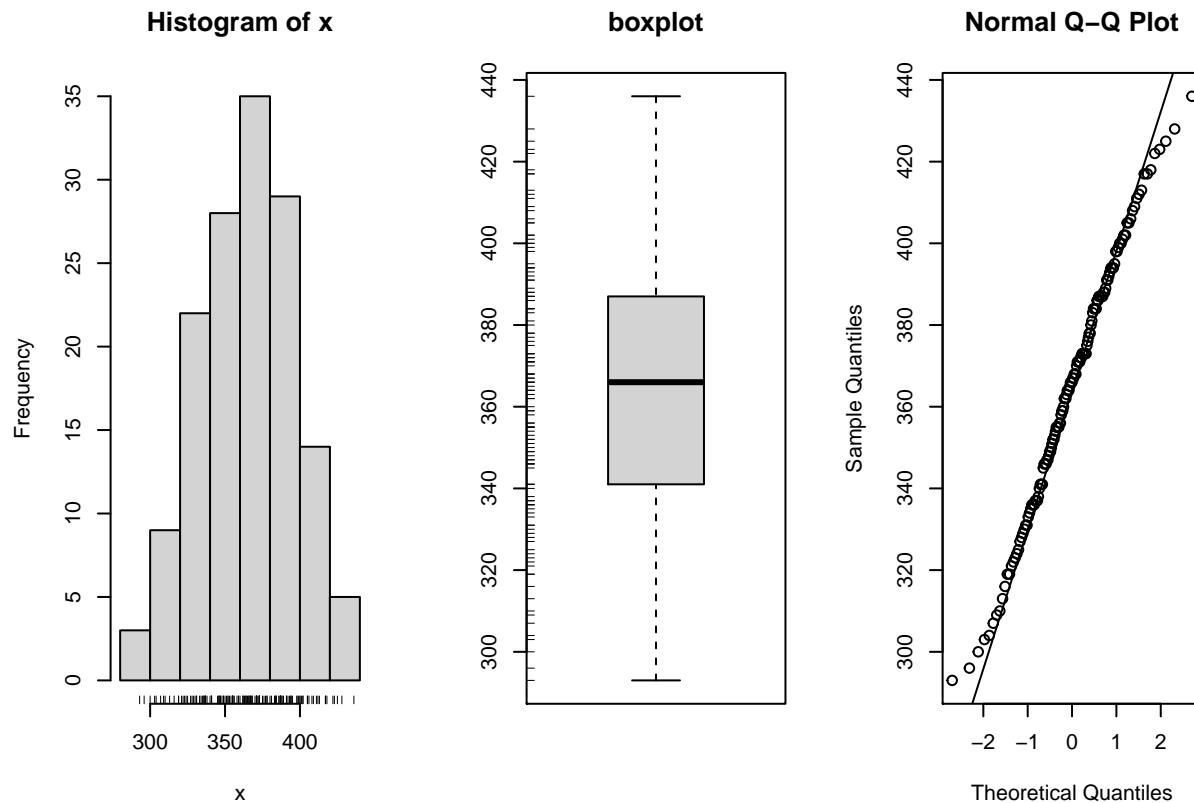
pretty normally distributed around ~370! :D

```
morpho_blood_SMI %>%
  ggplot(., aes(x = osmolality_mmol_kg)) +
  geom_histogram(color = "black", fill="steelblue", bins=50) +
  theme_classic() +
  xlab("Osmolality (mmol/kg)") +
  ylab("Count")
```

```
## Warning: Removed 3 rows containing non-finite values (stat_bin).
```



```
simple.eda(morpho_blood_SMI$osmolality_mmol_kg)
```



```
# Normality test if  $p > .05$ , data is normal. Data is normal
shapiro.test(morpho_blood_SMI$osmolality_mmol_kg)
```

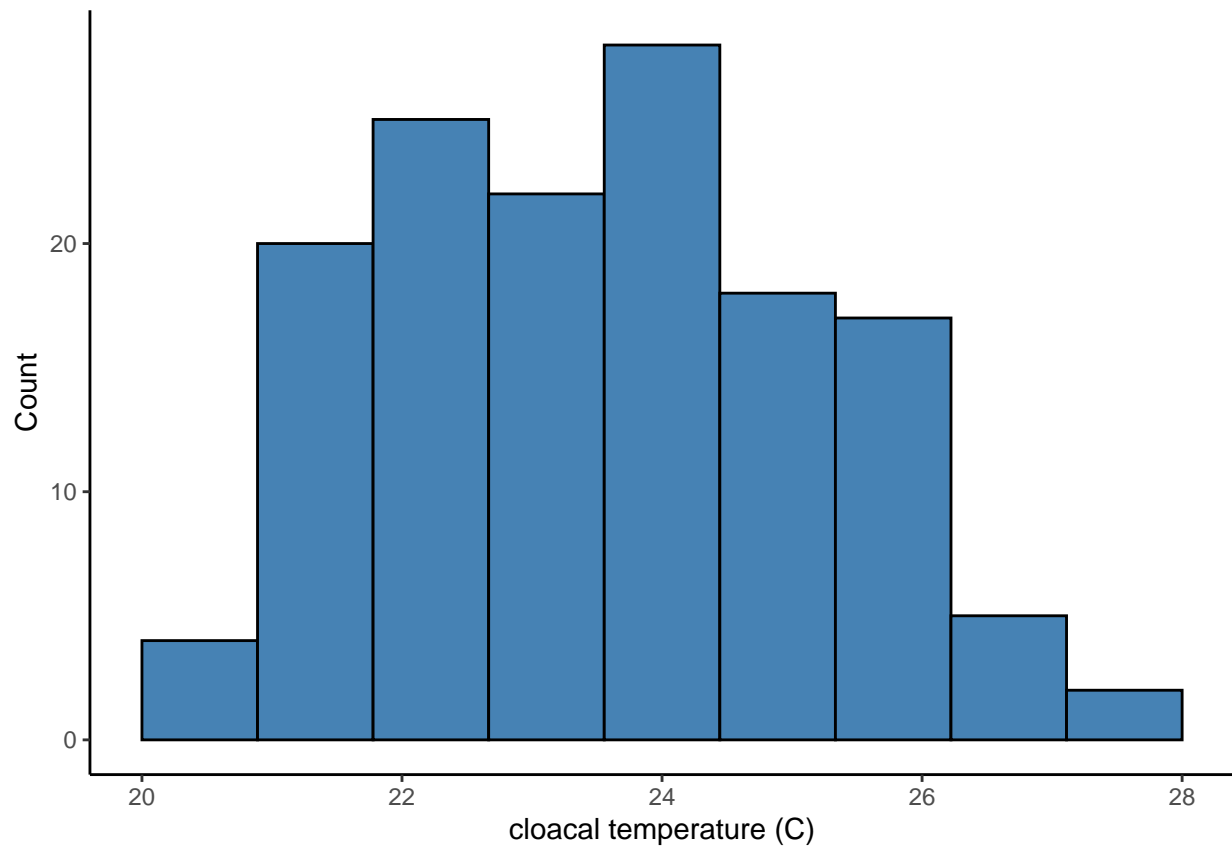
```
##
## Shapiro-Wilk normality test
##
## data: morpho_blood_SMI$osmolality_mmol_kg
## W = 0.99198, p-value = 0.5876
```

Cloacal Temperature

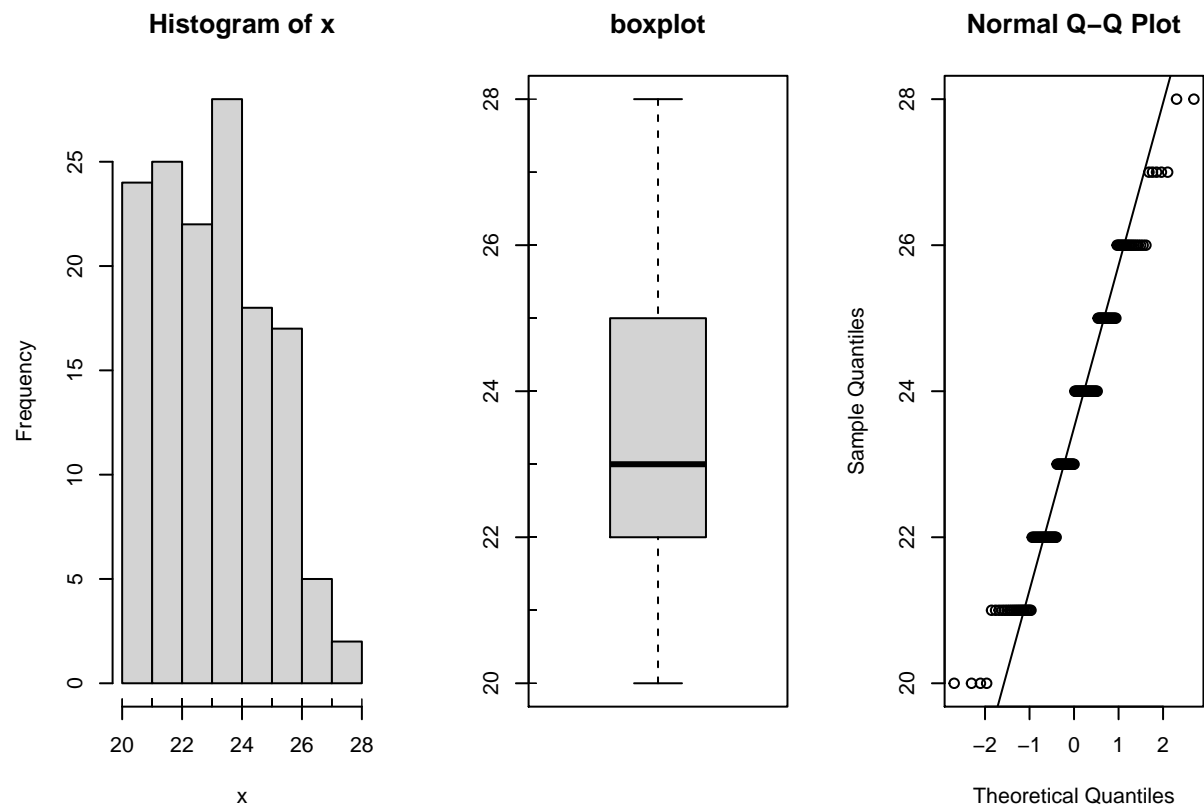
seems normally distributed, but not normal

```
morpho_blood_SMI %>%
  ggplot(., aes(x = cloacal_temp_C)) +
  geom_histogram(color = "black", fill="steelblue", bins=10) +
  theme_classic() +
  xlab("cloacal temperature (C)") +
  ylab("Count")
```

```
## Warning: Removed 7 rows containing non-finite values (stat_bin).
```



```
simple.eda(morpho_blood_SMI$cloacal_temp_C)
```

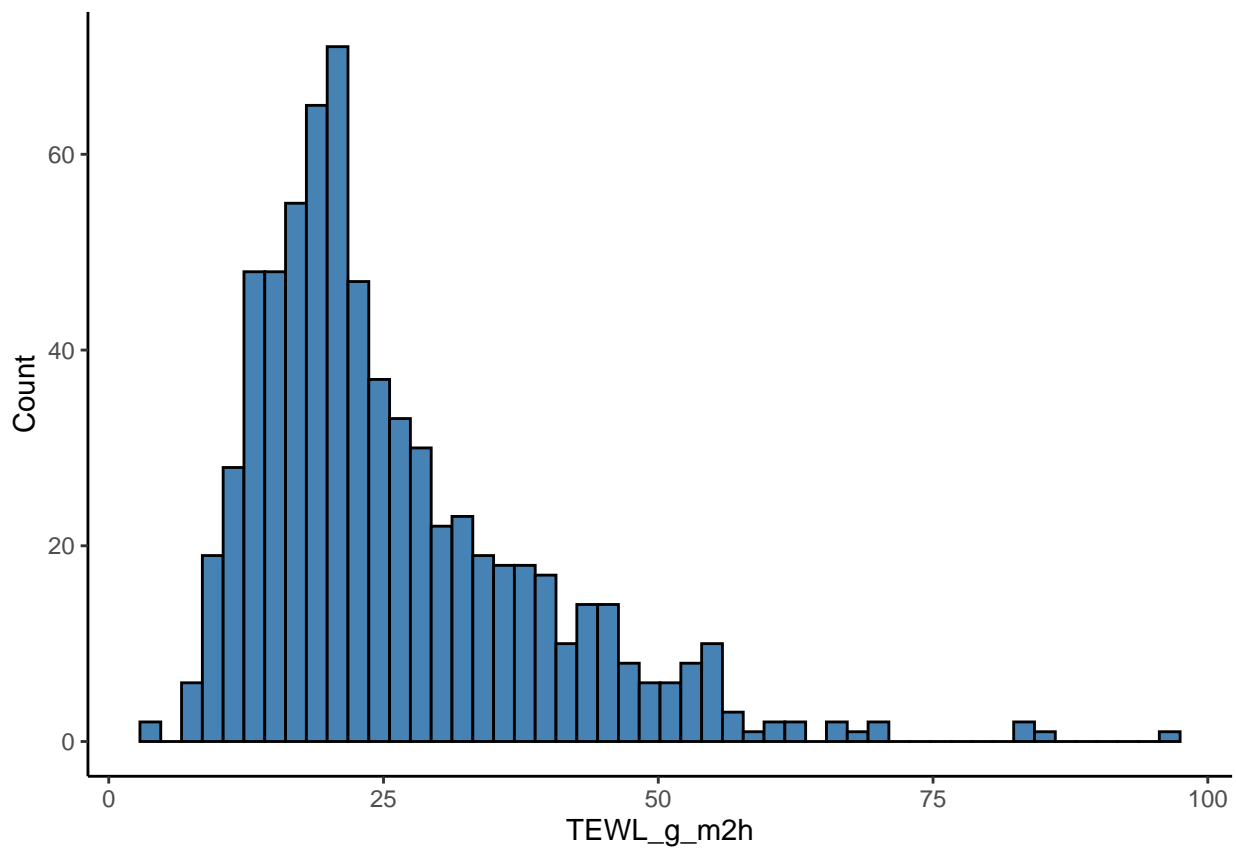


```
# Normality test if p > .05, data is normal. Data is not normal
shapiro.test(morpho_blood_SMI$cloacal_temp_C)
```

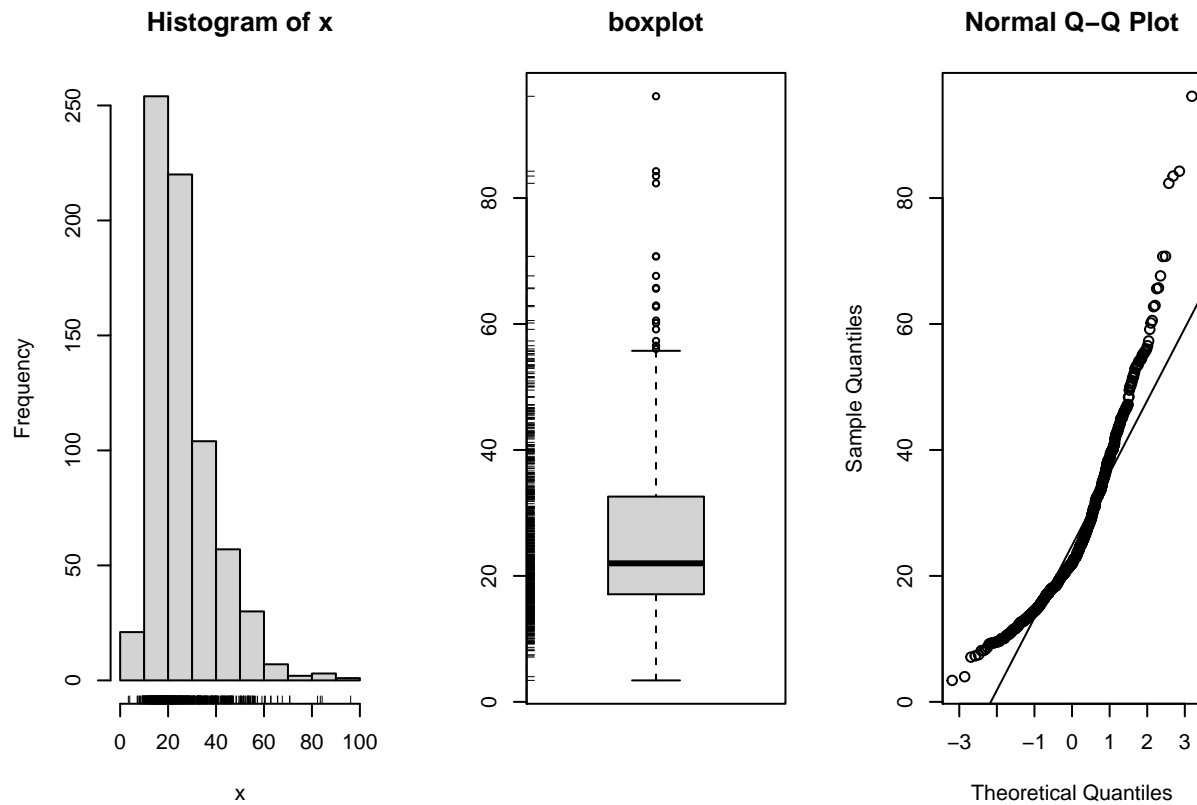
```
##
## Shapiro-Wilk normality test
##
## data: morpho_blood_SMI$cloacal_temp_C
## W = 0.95661, p-value = 0.0002007
```

CEWL

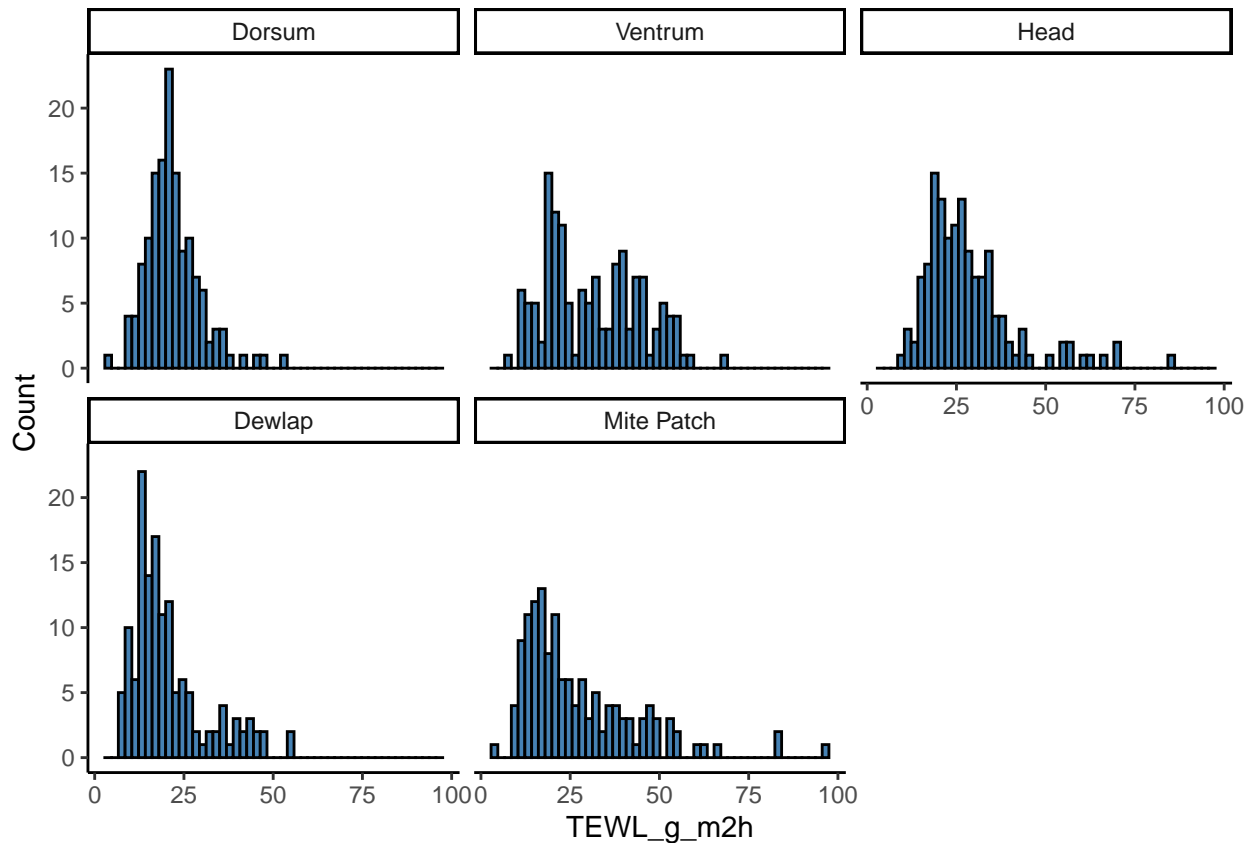
```
CEWL_data_full %>%
  ggplot(., aes(x = TEWL_g_m2h)) +
  geom_histogram(color = "black", fill="steelblue", bins=50) +
  theme_classic() +
  xlab("TEWL_g_m2h") +
  ylab("Count")
```



```
simple.eda(CEWL_data_full$TEWL_g_m2h)
```



```
CEWL_data_full %>%
  ggplot(., aes(x = TEWL_g_m2h)) +
  geom_histogram(color = "black", fill="steelblue", bins=50) +
  theme_classic() +
  xlab("TEWL_g_m2h") +
  ylab("Count") +
  facet_wrap(~region)
```

```
# Normality test if  $p > .05$ , data is normal. Data is not normal
shapiro.test(CEWL_data_full$TEWL_g_m2h)
```

```
##
## Shapiro-Wilk normality test
##
## data: CEWL_data_full$TEWL_g_m2h
## W = 0.89548, p-value < 2.2e-16
```

```
# Log transformation
shapiro.test(log(CEWL_data_full$TEWL_g_m2h))
```

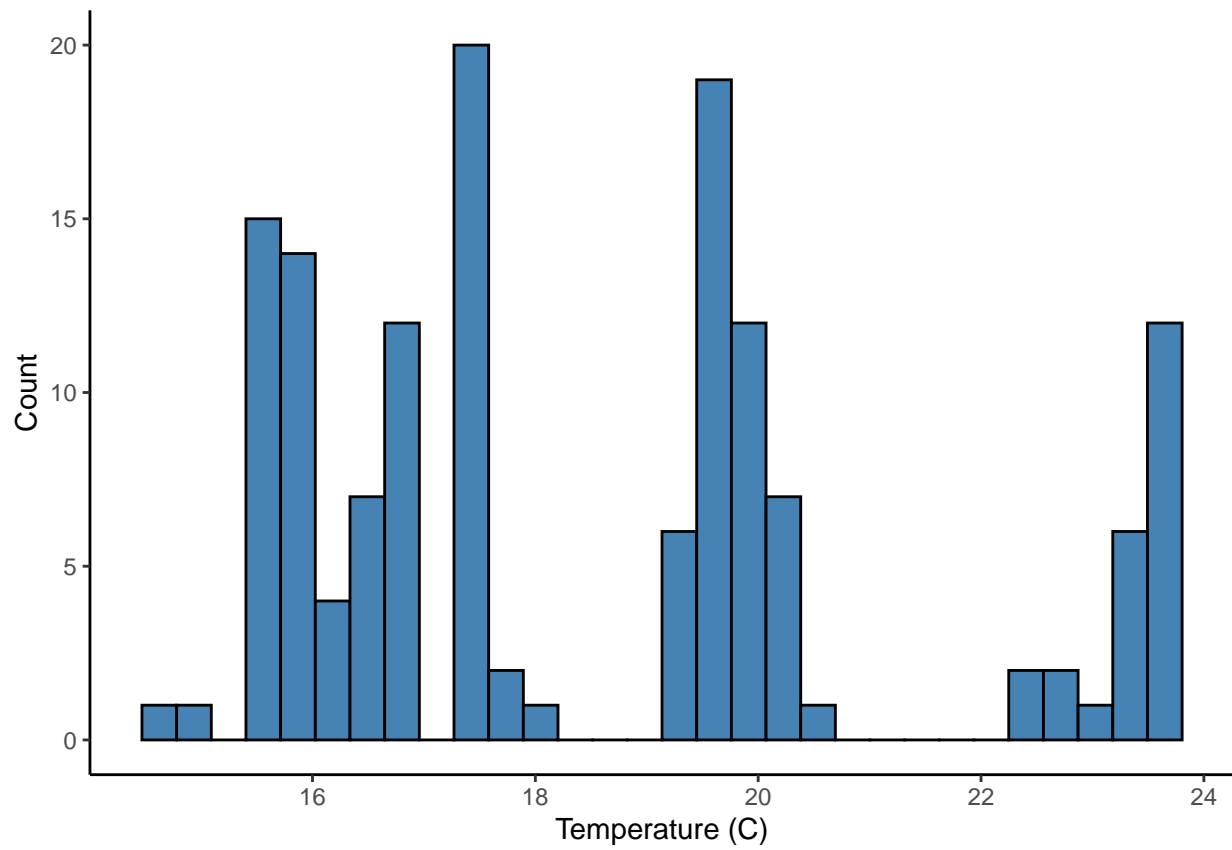
```
##
## Shapiro-Wilk normality test
##
## data: log(CEWL_data_full$TEWL_g_m2h)
## W = 0.99368, p-value = 0.004976
```

```
# p-value improves to 0.00548, but is still significant
```

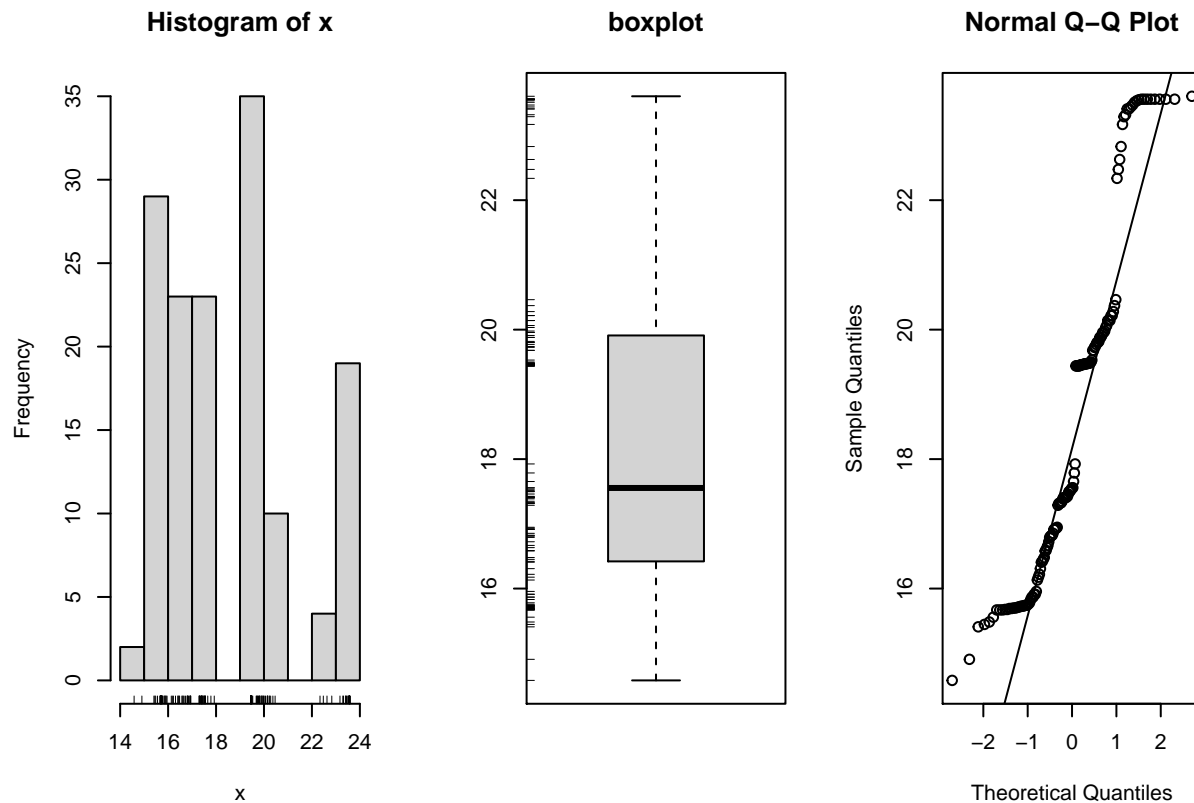
Capture Temperature

```
morpho_blood_SMI %>%
  ggplot(., aes(x = temp_C_interpol)) +
  geom_histogram(color = "black", fill="steelblue", bins=30) +
  theme_classic() +
  xlab("Temperature (C)") +
  ylab("Count")
```

```
## Warning: Removed 3 rows containing non-finite values (stat_bin).
```



```
simple.eda(morpho_blood_SMI$temp_C_interpol)
```



```
# Normality test if p > .05, data is normal. Data is not normal
shapiro.test(morpho_blood_SMI$temp_C_interpol)
```

```
##
## Shapiro-Wilk normality test
##
## data: morpho_blood_SMI$temp_C_interpol
## W = 0.89272, p-value = 8.162e-09
```

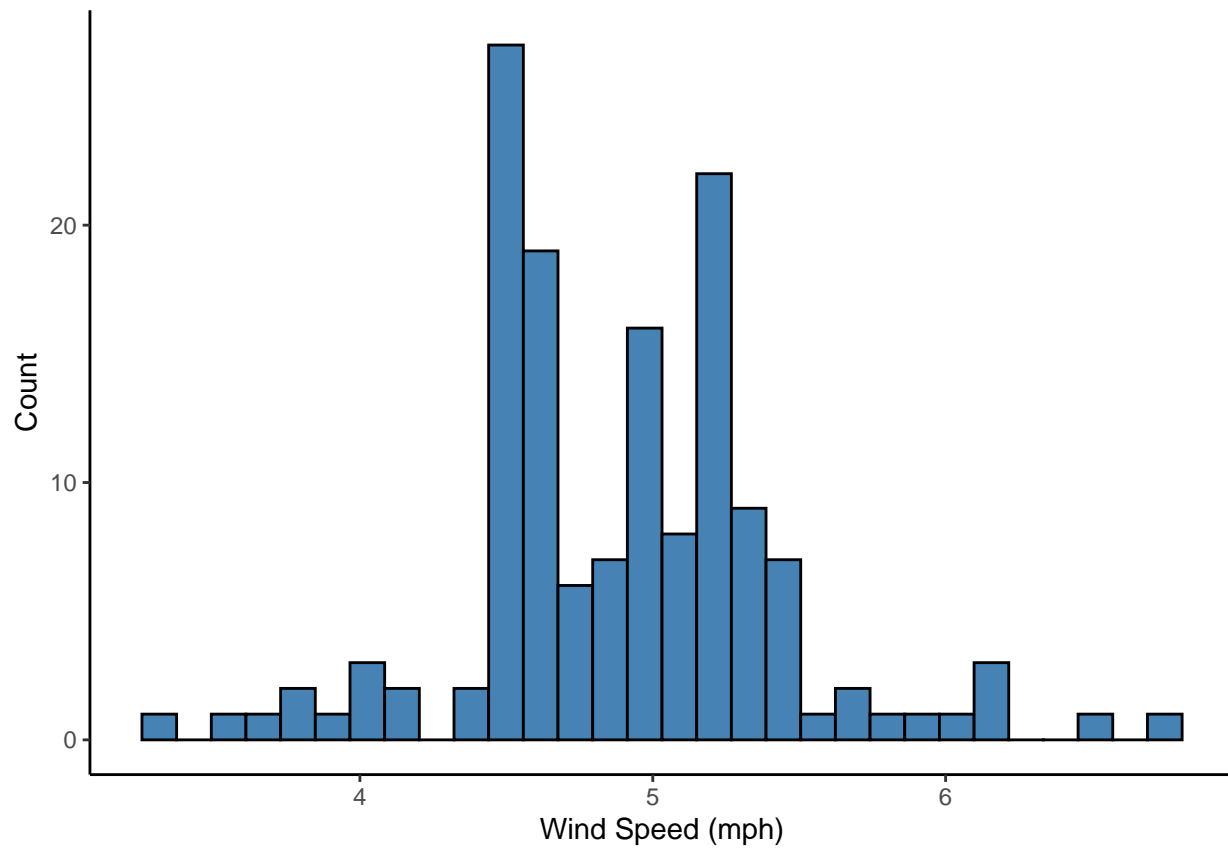
```
# log transform
shapiro.test(log(morpho_blood_SMI$temp_C_interpol))
```

```
##
## Shapiro-Wilk normality test
##
## data: log(morpho_blood_SMI$temp_C_interpol)
## W = 0.91155, p-value = 9.439e-08
```

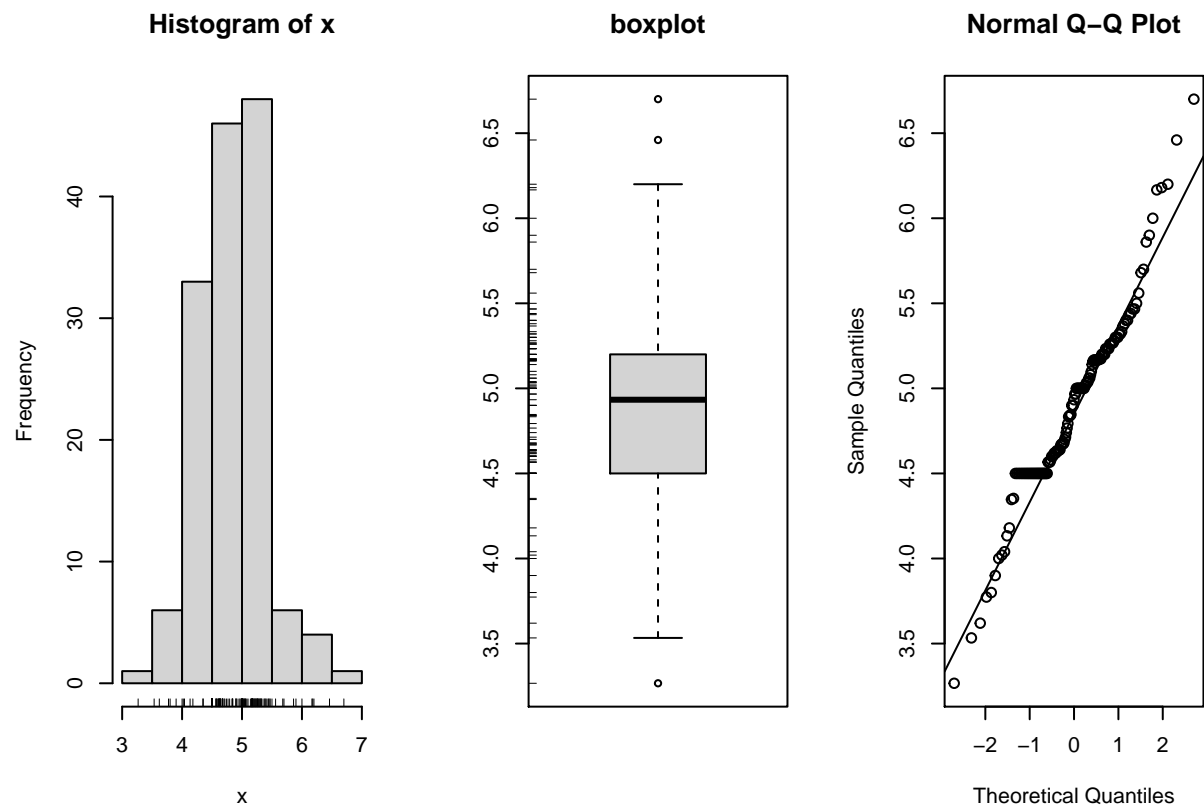
Wind Speed at Capture

```
morpho_blood_SMI %>%
  ggplot(., aes(x = Wind_mph_interpol)) +
  geom_histogram(color = "black", fill="steelblue", bins=30) +
  theme_classic() +
  xlab("Wind Speed (mph)") +
  ylab("Count")
```

```
## Warning: Removed 3 rows containing non-finite values (stat_bin).
```



```
simple.eda(morpho_blood_SMI$Wind_mph_interpol)
```



```
# Normality test if p > .05, data is normal. Data is not normal  
shapiro.test(morpho_blood_SMI$Wind_mph_interpol)
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: morpho_blood_SMI$Wind_mph_interpol  
## W = 0.96149, p-value = 0.0004364
```

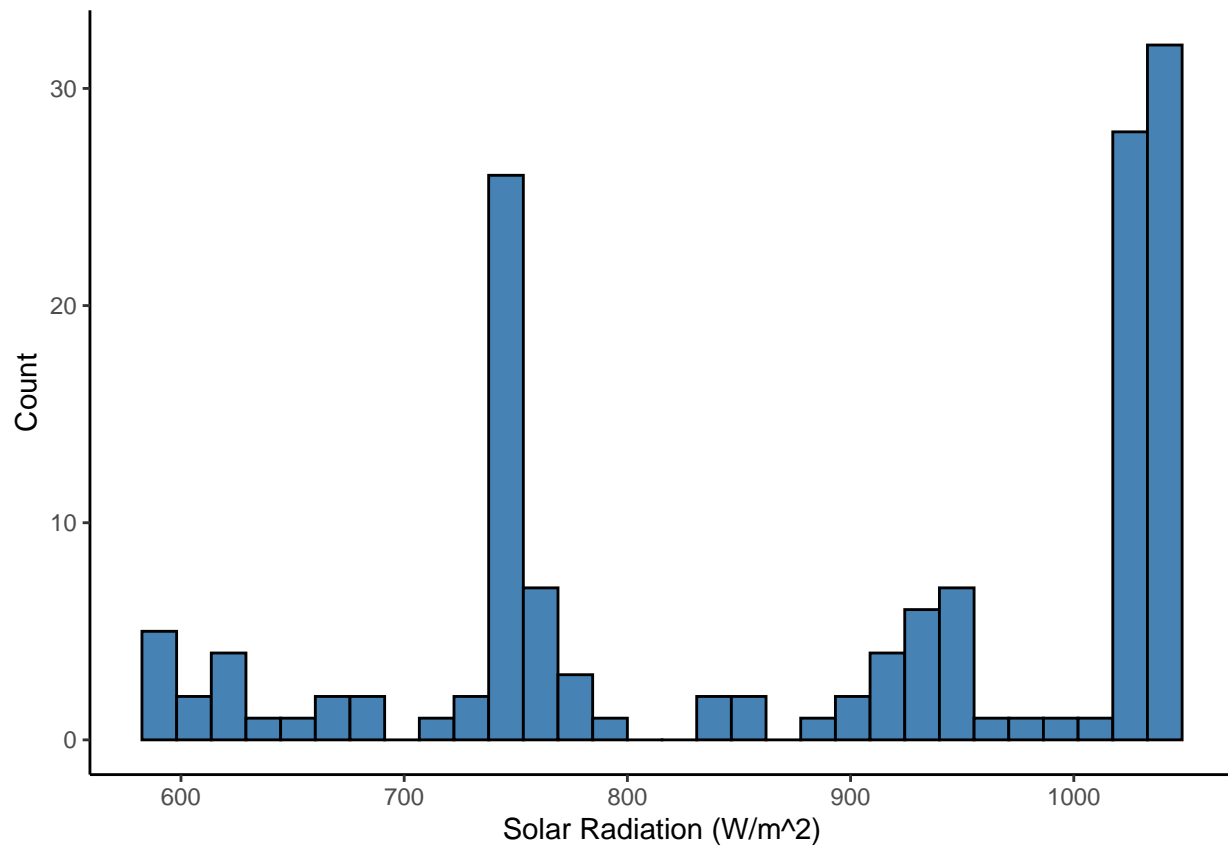
```
# ln transformation doesn't fix non normality  
shapiro.test(log(morpho_blood_SMI$Wind_mph_interpol))
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: log(morpho_blood_SMI$Wind_mph_interpol)  
## W = 0.95827, p-value = 0.0002241
```

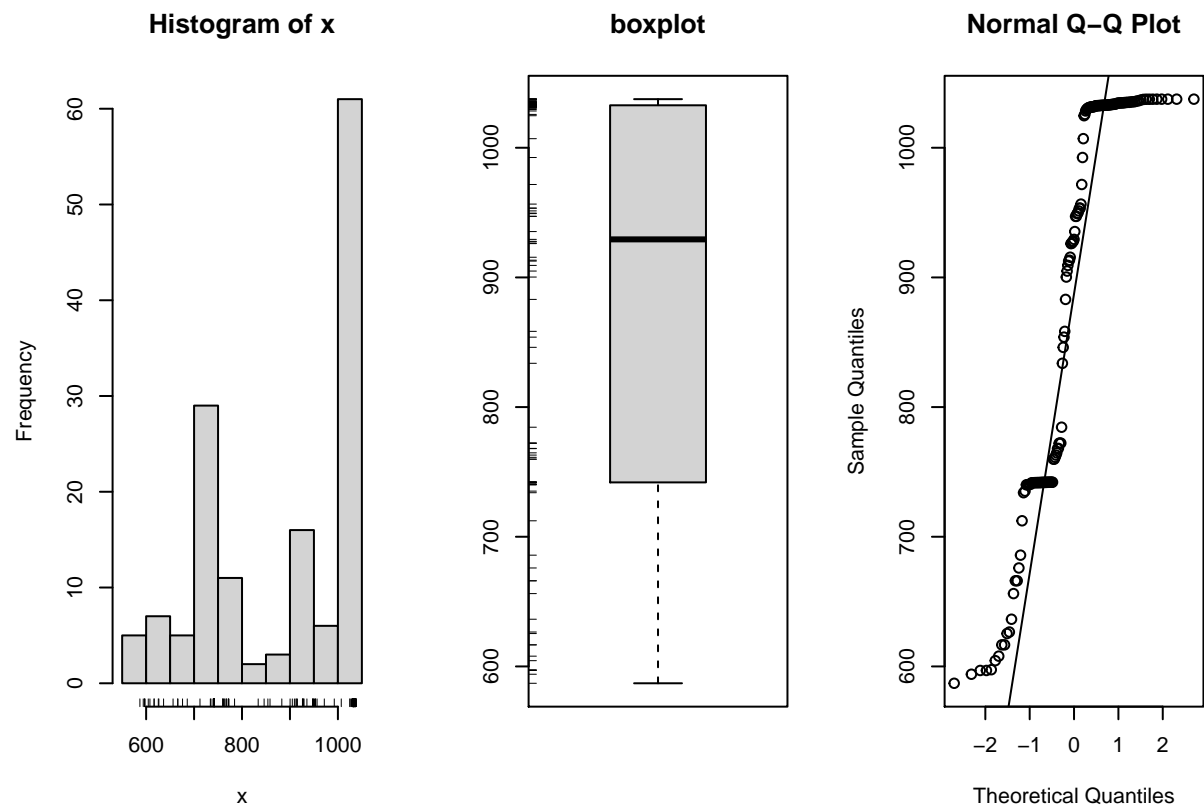
Solar Radiation at Capture

```
morpho_blood_SMI %>%  
  ggplot(., aes(x = Solar_rad_Wm2_interpol)) +  
  geom_histogram(color = "black", fill="steelblue", bins=30) +  
  theme_classic() +  
  xlab("Solar Radiation (W/m^2)") +  
  ylab("Count")
```

```
## Warning: Removed 3 rows containing non-finite values (stat_bin).
```



```
simple.eda(morpho_blood_SMI$Solar_rad_Wm2_interpol)
```



```
# Normality test if p > .05, data is normal. Data is not normal
shapiro.test(morpho_blood_SMI$Solar_rad_Wm2_interpol)
```

```
##
## Shapiro-Wilk normality test
##
## data: morpho_blood_SMI$Solar_rad_Wm2_interpol
## W = 0.82946, p-value = 1.072e-11
```

```
# Doesn't fix non normality
shapiro.test(log(morpho_blood_SMI$Solar_rad_Wm2_interpol))
```

```
##
## Shapiro-Wilk normality test
##
## data: log(morpho_blood_SMI$Solar_rad_Wm2_interpol)
## W = 0.829, p-value = 1.028e-11
```

Conclusion

Osmolality and SMI were the only normally distributed variables.

The following variables each had non-normal distributions: - SVL (skewed left) - mass (skewed left) - hct (looks like a bell curve, but not very pretty) - cloacal temp (skewed right) - CEWL (skewed right, overall and for each region individually) - capture temp (multimodal) - wind speed (multimodal but sorta bell curve) - solar radiation (multimodal)

All of the non-normal variables are likely to need transformation if they're included in the final model.

Basic Figures

osmolality & hematocrit

Hct ~ SVL

```
morpho_blood_SMI %>%
  ggplot(data = .) +
  geom_point(aes(x = SVL_mm,
                 y = hematocrit_percent,
                 ),
             size = 1,
             alpha = 0.6) +
  stat_smooth(aes(x = SVL_mm,
                  y = hematocrit_percent,
                  ),
              formula = y ~ x,
              method = "lm",
              color = "gray",
              se = F,
              size = 1.6,
              alpha = 1 ) +
  theme_classic() +
  xlab("SVL") +
  ylab("Hct") +
  theme(text = element_text(color = "black",
```

```

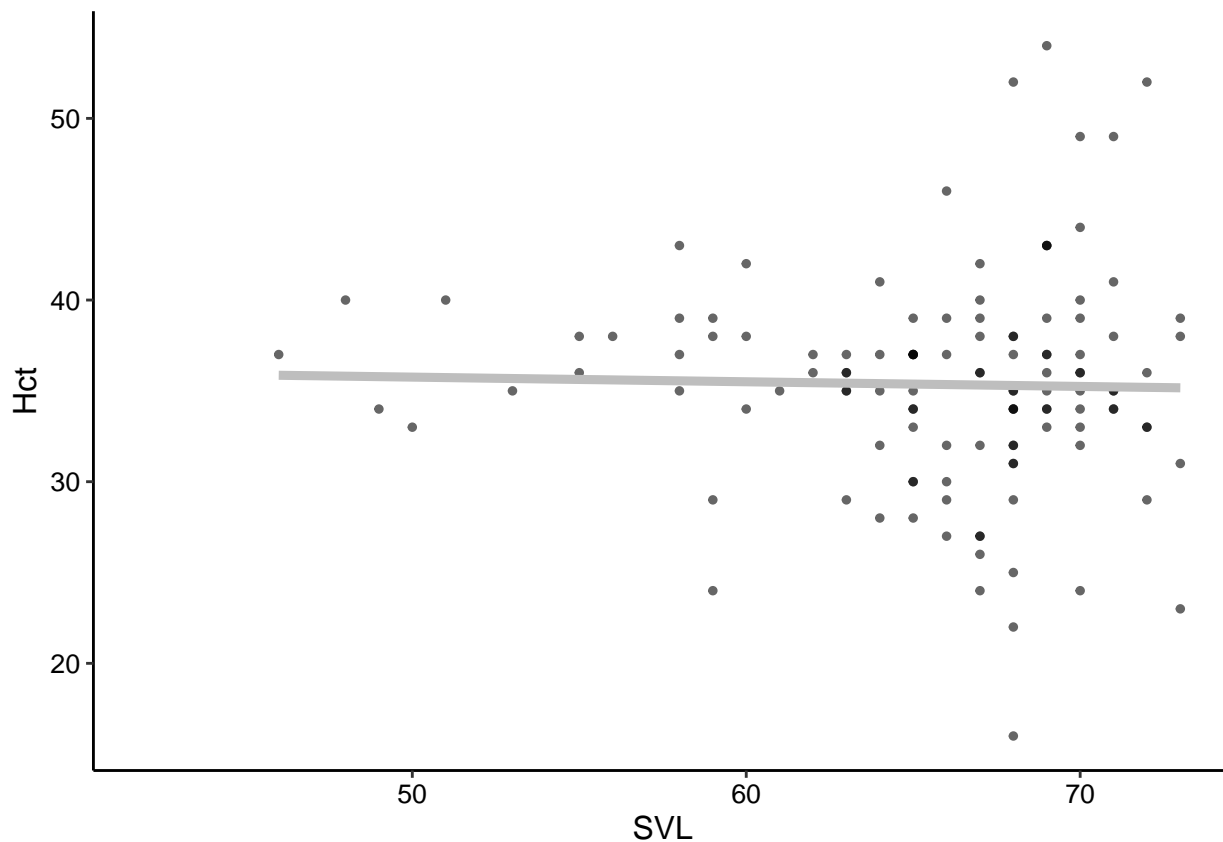
        family = "sans",
        size = 12),
axis.text = element_text(color = "black",
        family = "sans",
        size = 10),

legend.text.align = 0)

```

Warning: Removed 27 rows containing non-finite values (stat_smooth).

Warning: Removed 27 rows containing missing values (geom_point).



Osml ~ SVL

```

morpho_blood_SMI %>%
  ggplot(data = .) +
  geom_point(aes(x = SVL_mm,
    y = osmolality_mmol_kg,
    ),
    size = 1,
    alpha = 0.6) +
  stat_smooth(aes(x = SVL_mm,
    y = osmolality_mmol_kg,
    ),
    formula = y ~ x,
    method = "lm",
    color = "gray",
    se = F,

```



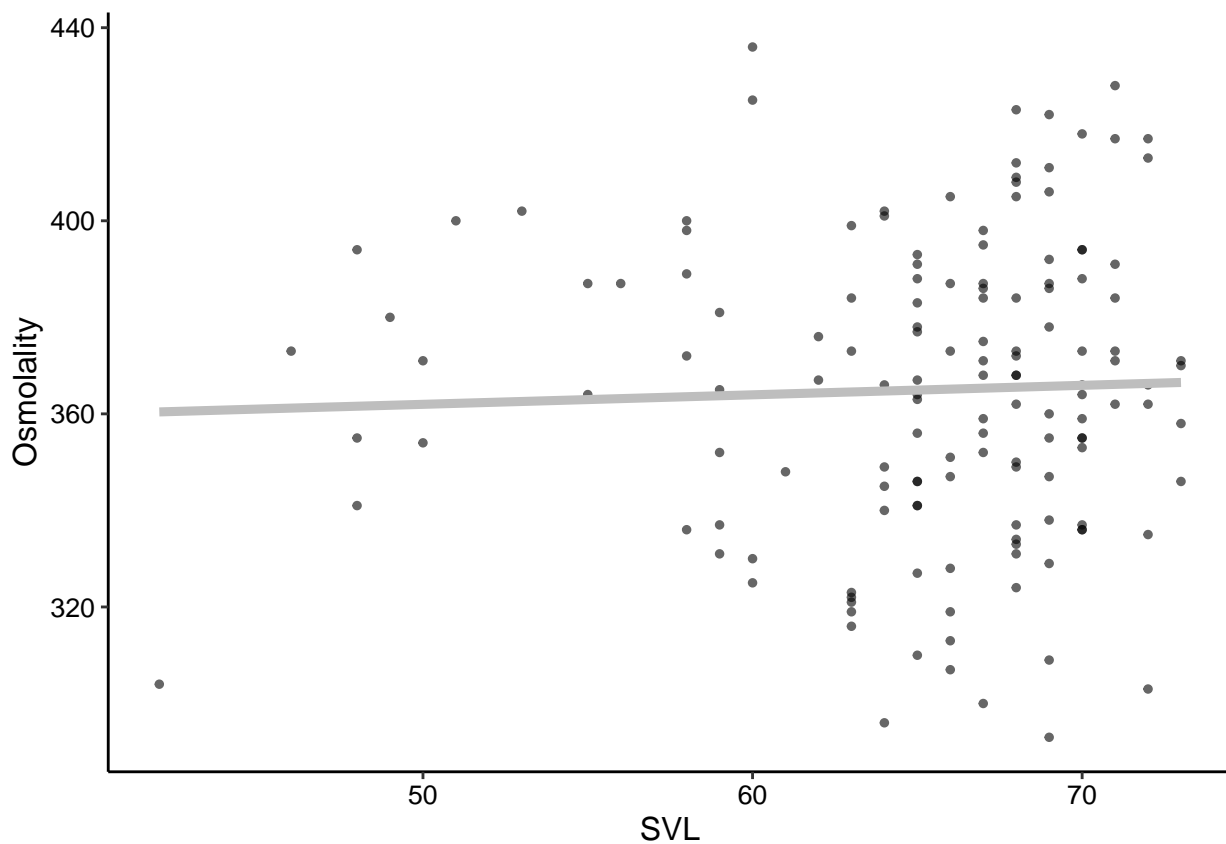
```

        size = 1.6,
        alpha = 1 ) +
theme_classic() +
xlab("SVL") +
ylab("Osmolality") +
theme(text = element_text(color = "black",
                           family = "sans",
                           size = 12),
      axis.text = element_text(color = "black",
                                family = "sans",
                                size = 10),
      legend.text.align = 0)

```

Warning: Removed 3 rows containing non-finite values (stat_smooth).

Warning: Removed 3 rows containing missing values (geom_point).



Hct ~ SMI

```

morpho_blood_SMI %>%
  ggplot(data = .) +
  geom_point(aes(x = SMI,
                 y = hematocrit_percent,
                 ),
            size = 1,
            alpha = 0.6) +
  stat_smooth(aes(x = SMI,

```

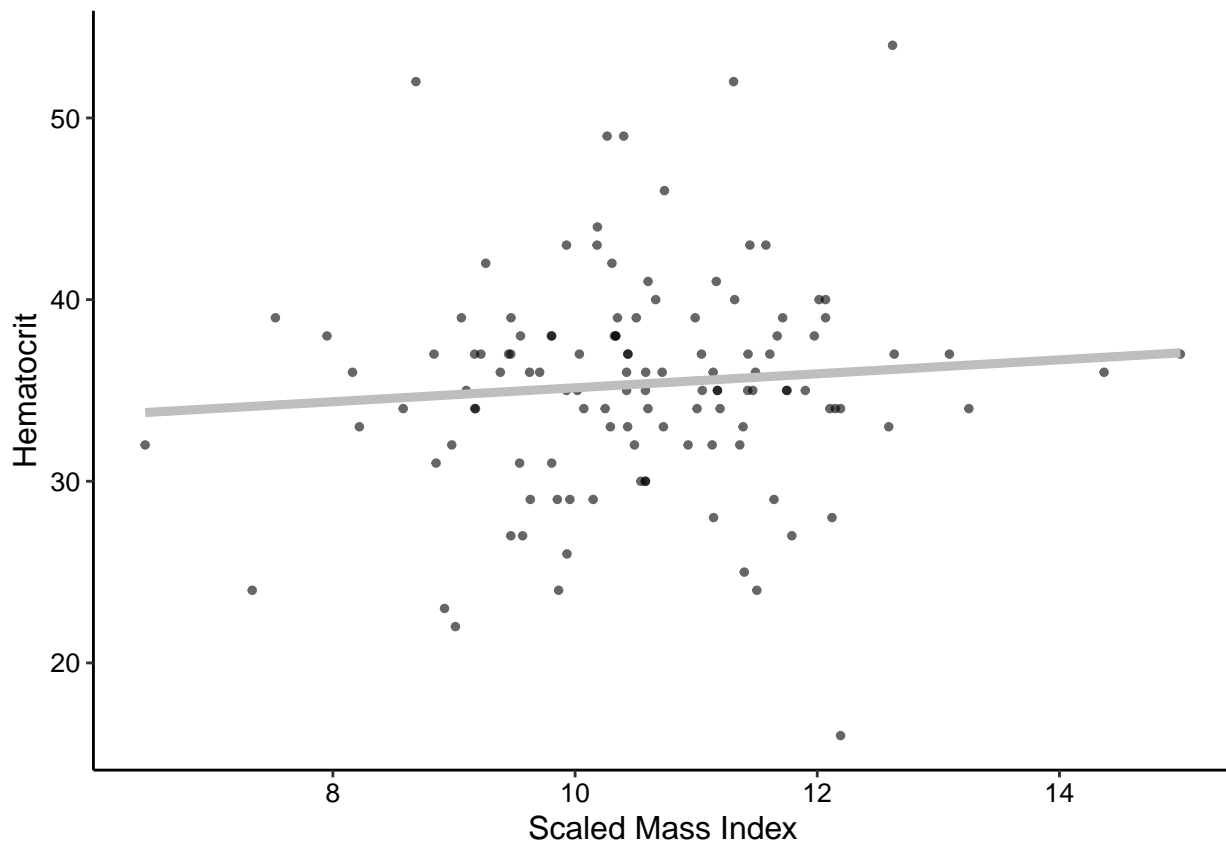
```

    y = hematocrit_percent,
  ),
  formula = y ~ x,
  method = "lm",
  color = "gray",
  se = F,
  size = 1.6,
  alpha = 1 ) +
theme_classic() +
xlab("Scaled Mass Index") +
ylab("Hematocrit") +
theme(text = element_text(color = "black",
                           family = "sans",
                           size = 12),
      axis.text = element_text(color = "black",
                                family = "sans",
                                size = 10),
      legend.text.align = 0)

```

Warning: Removed 27 rows containing non-finite values (stat_smooth).

Warning: Removed 27 rows containing missing values (geom_point).



Osml ~ SMI

```

morpho_blood_SMI %>%
  ggplot(data = .) +

```

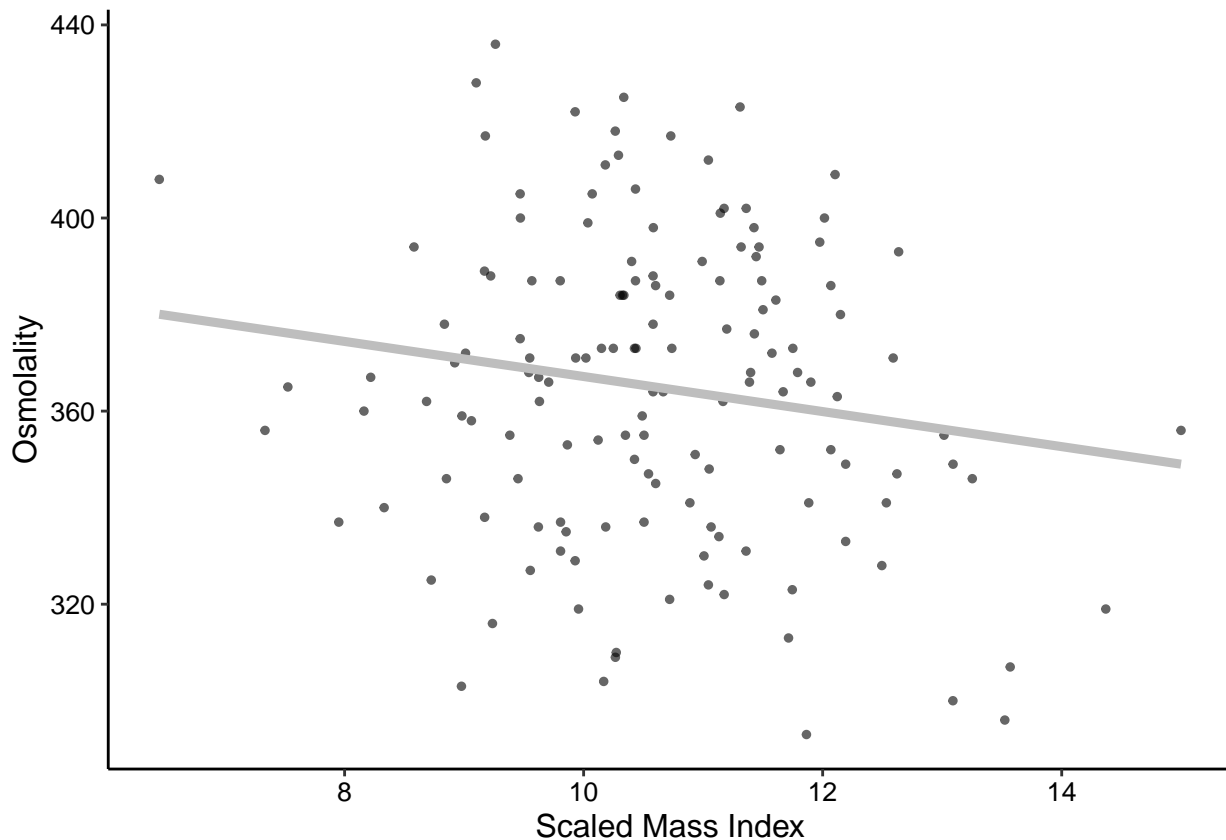
```

geom_point(aes(x = SMI,
               y = osmolality_mmol_kg,
               ),
           size = 1,
           alpha = 0.6) +
stat_smooth(aes(x = SMI,
               y = osmolality_mmol_kg),
           formula = y ~ x,
           method = "lm",
           se = F,
           color = "gray",
           size = 1.6,
           alpha = 1 ) +
theme_classic() +
xlab("Scaled Mass Index") +
ylab("Osmolality") +
theme(text = element_text(color = "black",
                          family = "sans",
                          size = 12),
      axis.text = element_text(color = "black",
                              family = "sans",
                              size = 10),
      legend.text.align = 0)

```

Warning: Removed 3 rows containing non-finite values (stat_smooth).

Warning: Removed 3 rows containing missing values (geom_point).

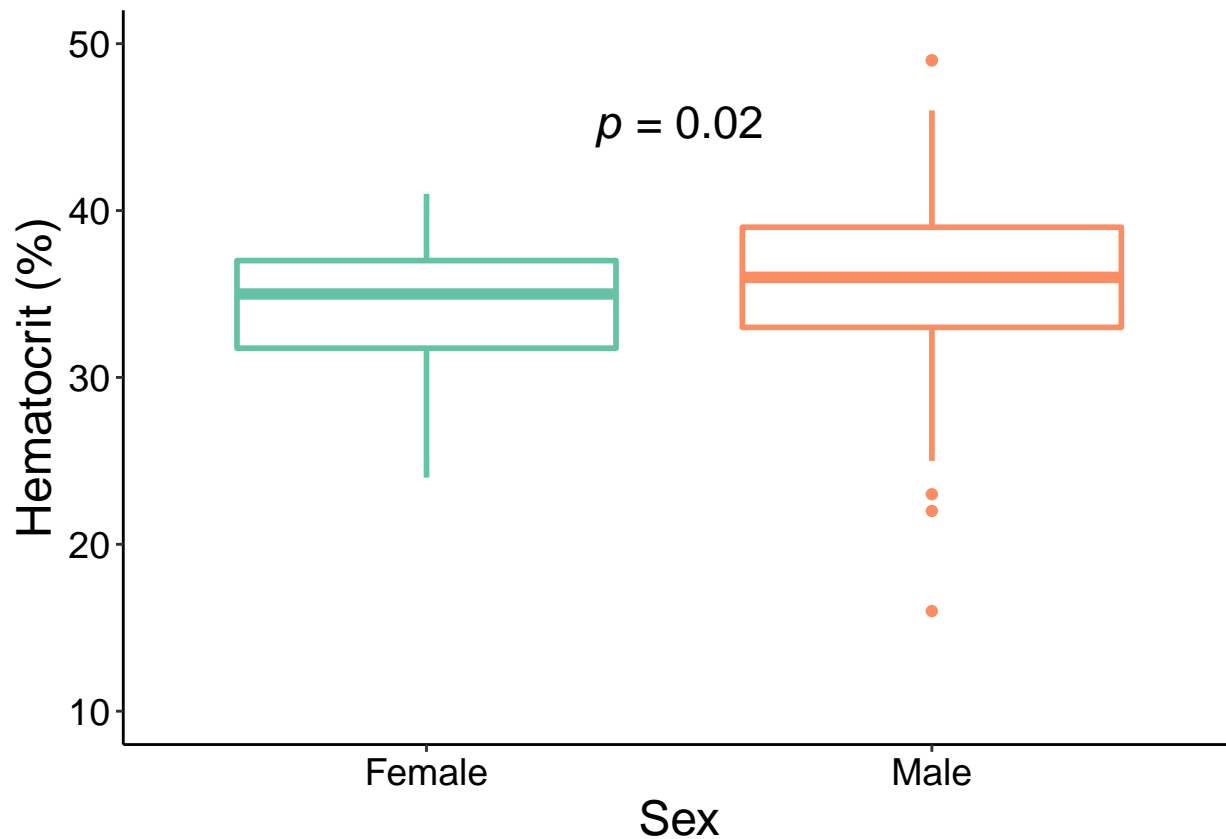


Hct ~ Sex

males have significantly higher hematocrit %

```
morpho_blood_SMI %>%
  ggplot(data = .) +
  geom_boxplot(aes(x = sex_M_F,
                    y = hematocrit_percent,
                    color = sex_M_F
                  ),
               size = 1,
               alpha = 1) +
  theme_classic() +
  xlab("Sex") +
  ylab("Hematocrit (%)") +
  annotate("text", x = 1.5, y = 45,
            label = "paste(italic(p), \" = 0.02\\")",
            parse = TRUE,
            size = 6) +
  ylim(10, 50) +
  scale_x_discrete(labels = c("F" = "Female",
                              "M" = "Male")) +
  scale_color_brewer(palette = "Set2") +
  theme(text = element_text(color = "black",
                              family = "sans",
                              size = 18),
        axis.text = element_text(color = "black",
                                    family = "sans",
                                    size = 14),
        legend.text.align = 0,
        legend.position = "none"
  ) -> hct_sex_fig
hct_sex_fig
```

```
## Warning: Removed 30 rows containing non-finite values (stat_boxplot).
```



```
# export figure
#ggsave(filename = "hct_sex_fig.jpeg",
#       plot = hct_sex_fig,
#       path = "./final_figures",
#       device = "jpeg",
#       dpi = 1200,
#       width = 6, height = 4)

# lms
lm_hct_sex_mass <- lm(hematocrit_percent ~ sex_M_F*mass_g - mass_g,
                     data = morpho_blood_SMI)
summary(lm_hct_sex_mass)
```

```
##
## Call:
## lm(formula = hematocrit_percent ~ sex_M_F * mass_g - mass_g,
##     data = morpho_blood_SMI)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -20.6306  -2.6187   0.6422   3.1481  17.2271
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    35.9163     3.7236   9.646  <2e-16 ***
## sex_M_FM        -0.9224     4.7553  -0.194    0.847
## sex_M_FF:mass_g -0.2244     0.3596  -0.624    0.534
## sex_M_FM:mass_g  0.1186     0.2568   0.462    0.645
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5.847 on 117 degrees of freedom
## (27 observations deleted due to missingness)
## Multiple R-squared:  0.05203,    Adjusted R-squared:  0.02772
## F-statistic: 2.141 on 3 and 117 DF,  p-value: 0.09884

lm_hct_sex <- lm(hematocrit_percent ~ sex_M_F,
                 data = morpho_blood_SMI)
summary(lm_hct_sex)

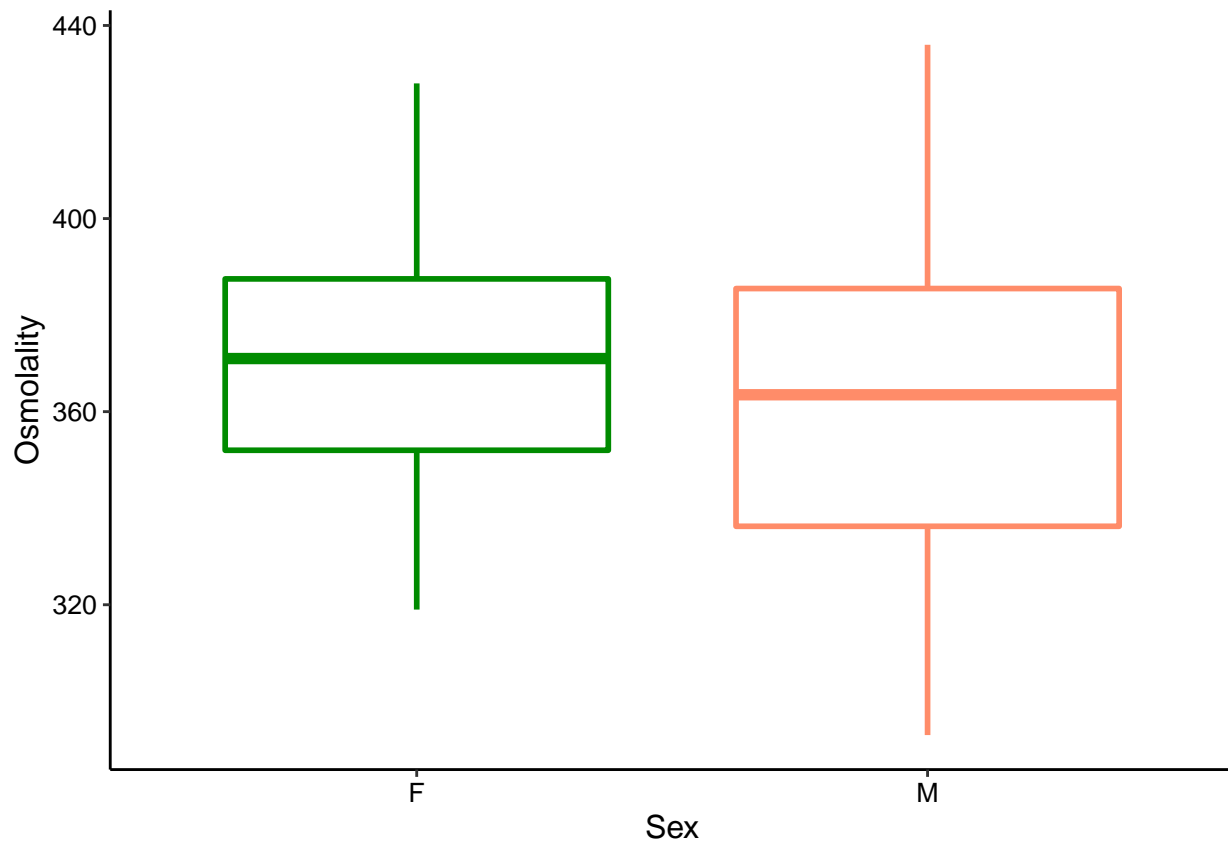
##
## Call:
## lm(formula = hematocrit_percent ~ sex_M_F, data = morpho_blood_SMI)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -20.3247  -3.3247   0.6753   3.3409  17.6753
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  33.6591     0.8763  38.410  <2e-16 ***
## sex_M_FM      2.6656     1.0985   2.427   0.0167 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5.813 on 119 degrees of freedom
## (27 observations deleted due to missingness)
## Multiple R-squared:  0.04715,    Adjusted R-squared:  0.03914
## F-statistic: 5.888 on 1 and 119 DF,  p-value: 0.01674
```

Hematocrit is significantly predicted by sex, but the interaction between sex and mass is ~nonexistent.

Osml ~ Sex

```
morpho_blood_SMI %>%
  ggplot(data = .) +
  geom_boxplot(aes(x = sex_M_F,
                  y = osmolality_mmol_kg,
                  color = sex_M_F
                  ),
              size = 1,
              alpha = 0.6) +
  scale_colour_manual(name = "Sex",
                     values = c("green4", "salmon1")) +
  theme_classic() +
  xlab("Sex") +
  ylab("Osmolality") +
  theme(text = element_text(color = "black", family = "sans", size = 12),
        axis.text = element_text(color = "black", family = "sans", size = 10),
        legend.text.align = 0,
        legend.position = "none")
```

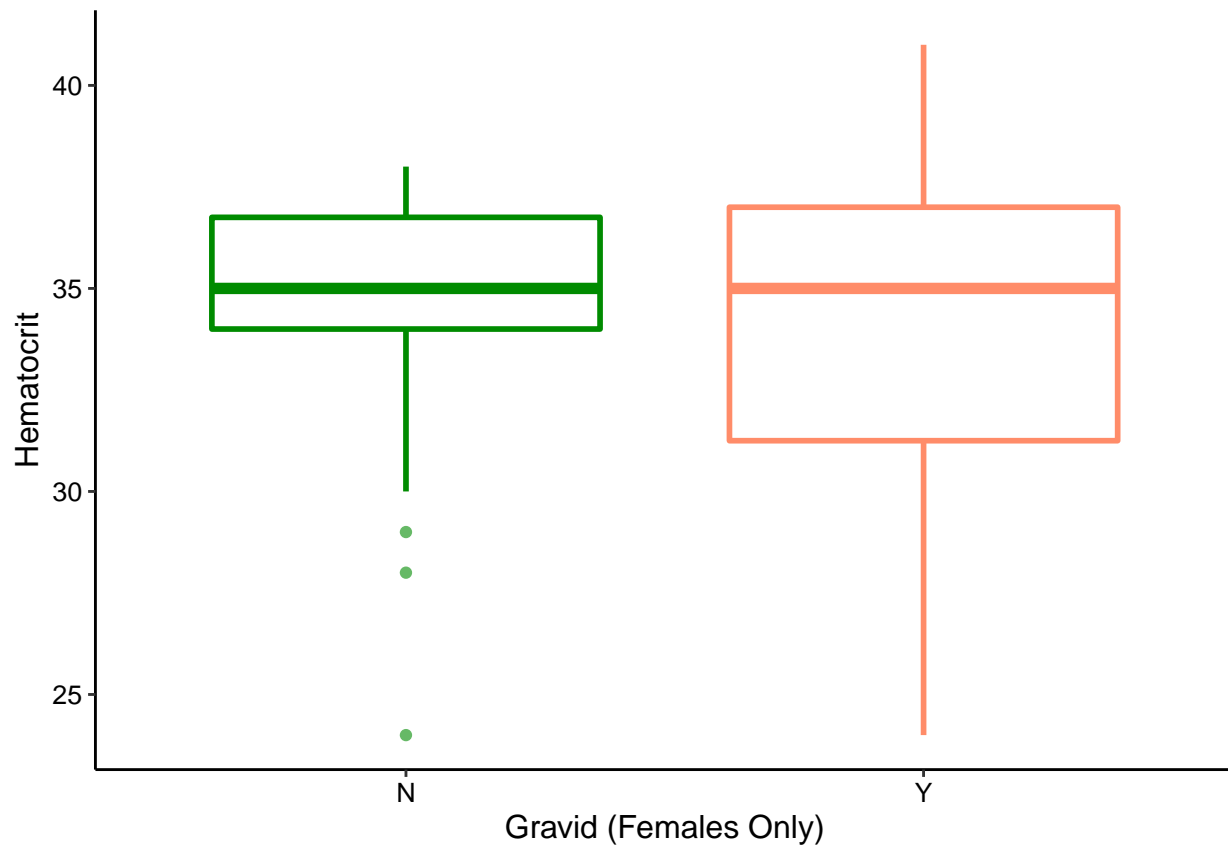
```
## Warning: Removed 3 rows containing non-finite values (stat_boxplot).
```



Hct ~ Gravidity

```
morpho_blood_SMI %>%
  dplyr::filter(sex_M_F == 'F') %>%
  ggplot(data = .) +
  geom_boxplot(aes(x = gravid_Y_N,
                    y = hematocrit_percent,
                    color = gravid_Y_N
                  ),
               size = 1,
               alpha = 0.6) +
  scale_colour_manual(name = "Gravid",
                      values = c("green4", "salmon1") ) +
  theme_classic() +
  xlab("Gravid (Females Only)") +
  ylab("Hematocrit") +
  theme(text = element_text(color = "black", family = "sans", size = 12),
        axis.text = element_text(color = "black", family = "sans", size = 10),
        legend.text.align = 0,
        legend.position = "none")
```

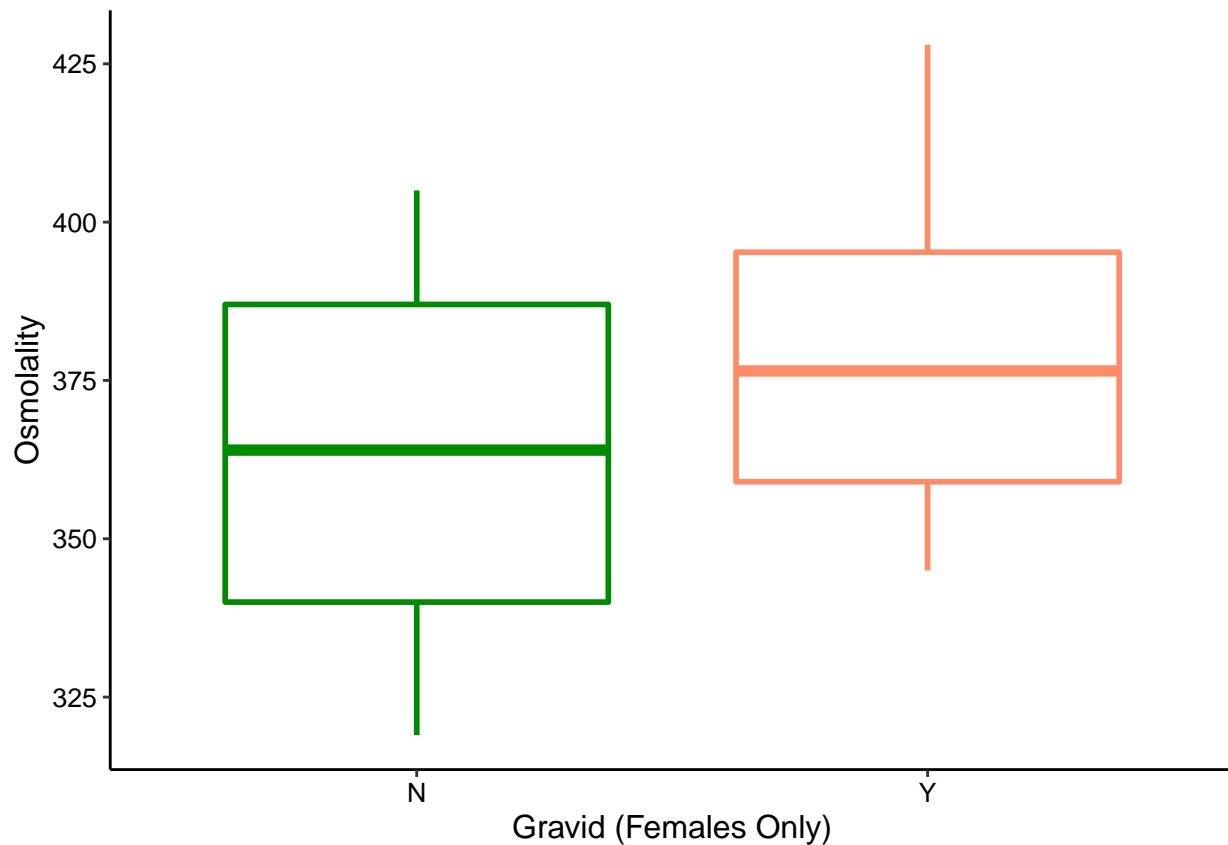
Warning: Removed 4 rows containing non-finite values (stat_boxplot).



Osml ~ Gravidity

```
morpho_blood_SMI %>%
  dplyr::filter(sex_M_F == 'F') %>%
  ggplot(data = .) +
    geom_boxplot(aes(x = gravid_Y_N,
                     y = osmolality_mmol_kg,
                     color = gravid_Y_N
                    ),
                size = 1,
                alpha = 0.6) +
    scale_colour_manual(name = "Gravid",
                       values = c("green4", "salmon1") ) +
    theme_classic() +
    xlab("Gravid (Females Only)") +
    ylab("Osmolality") +
    theme(text = element_text(color = "black", family = "sans", size = 12),
          axis.text = element_text(color = "black", family = "sans", size = 10),
          legend.text.align = 0,
          legend.position = "none")
```

Warning: Removed 1 rows containing non-finite values (stat_boxplot).

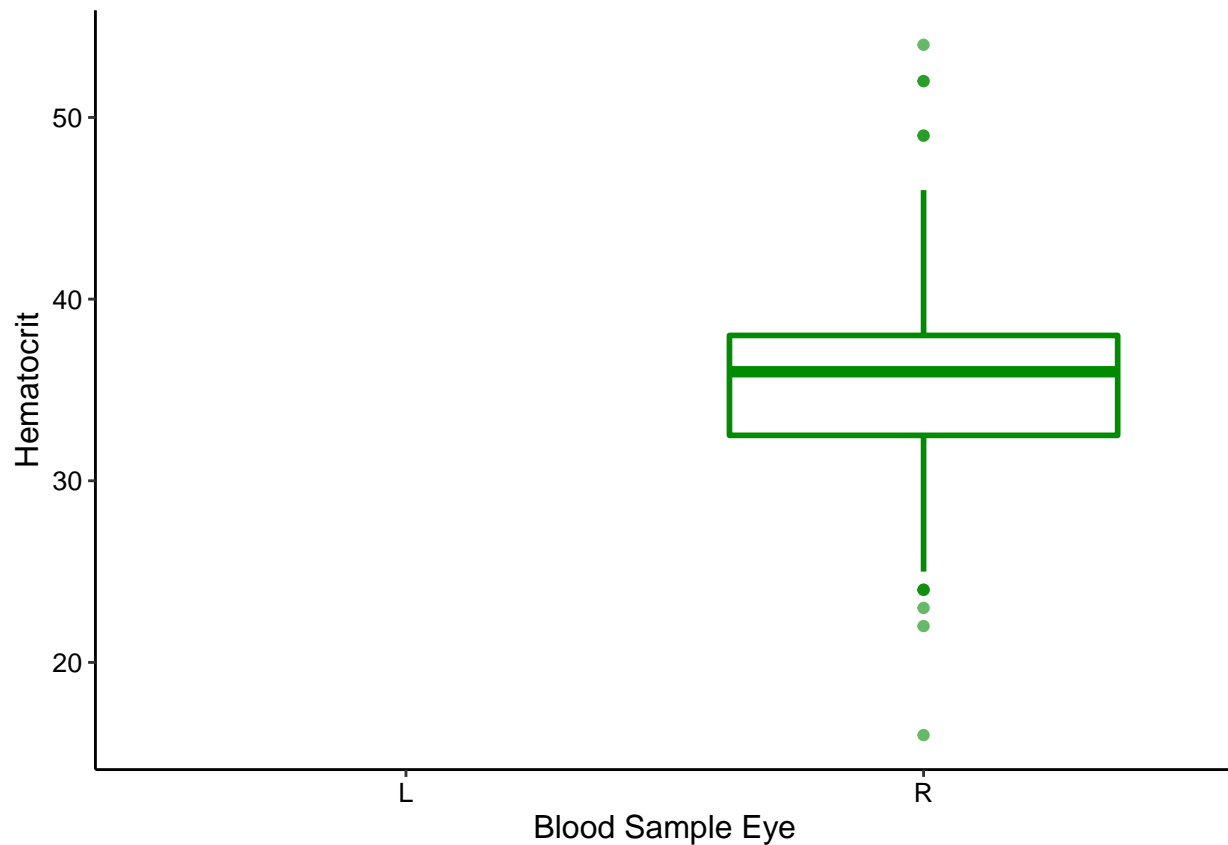


Hct ~ Sample Eye

Actually, any blood samples not taken from the right eye ended up being excluded or didn't have hematocrit values, so we can't test this difference.

```
morpho_blood_SMI %>%
  dplyr::filter(blood_sample_eye %in% c("R", "L")) %>%
  ggplot(data = .) +
  geom_boxplot(aes(x = blood_sample_eye,
                   y = hematocrit_percent,
                   color = blood_sample_eye
                  ),
               size = 1,
               alpha = 0.6) +
  scale_colour_manual(name = "Blood Sample Eye",
                     values = c("green4", "salmon1") ) +
  theme_classic() +
  xlab("Blood Sample Eye") +
  ylab("Hematocrit") +
  theme(text = element_text(color = "black", family = "sans", size = 12),
        axis.text = element_text(color = "black", family = "sans", size = 10),
        legend.text.align = 0,
        legend.position = "none"
  )
```

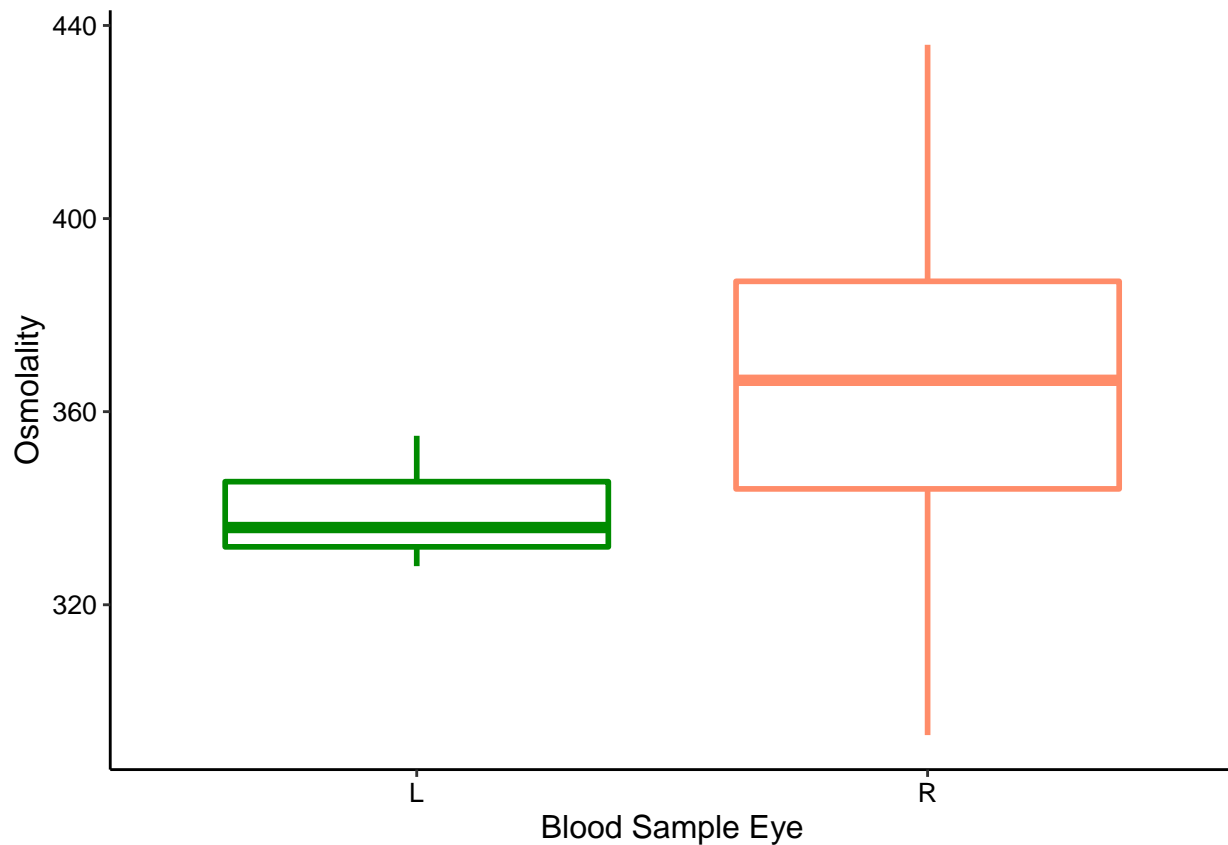
Warning: Removed 27 rows containing non-finite values (stat_boxplot).



Osml ~ Sample Eye

```
morpho_blood_SMI %>%
  dplyr::filter(blood_sample_eye %in% c("R", "L")) %>%
  ggplot(data = .) +
  geom_boxplot(aes(x = blood_sample_eye,
                   y = osmolality_mmol_kg,
                   color = blood_sample_eye
                  ),
               size = 1,
               alpha = 0.6) +
  scale_colour_manual(name = "Blood Sample Eye",
                     values = c("green4", "salmon1") ) +
  theme_classic() +
  xlab("Blood Sample Eye") +
  ylab("Osmolality") +
  theme(text = element_text(color = "black", family = "sans", size = 12),
        axis.text = element_text(color = "black", family = "sans", size = 10),
        legend.text.align = 0,
        legend.position = "none")
```

Warning: Removed 3 rows containing non-finite values (stat_boxplot).

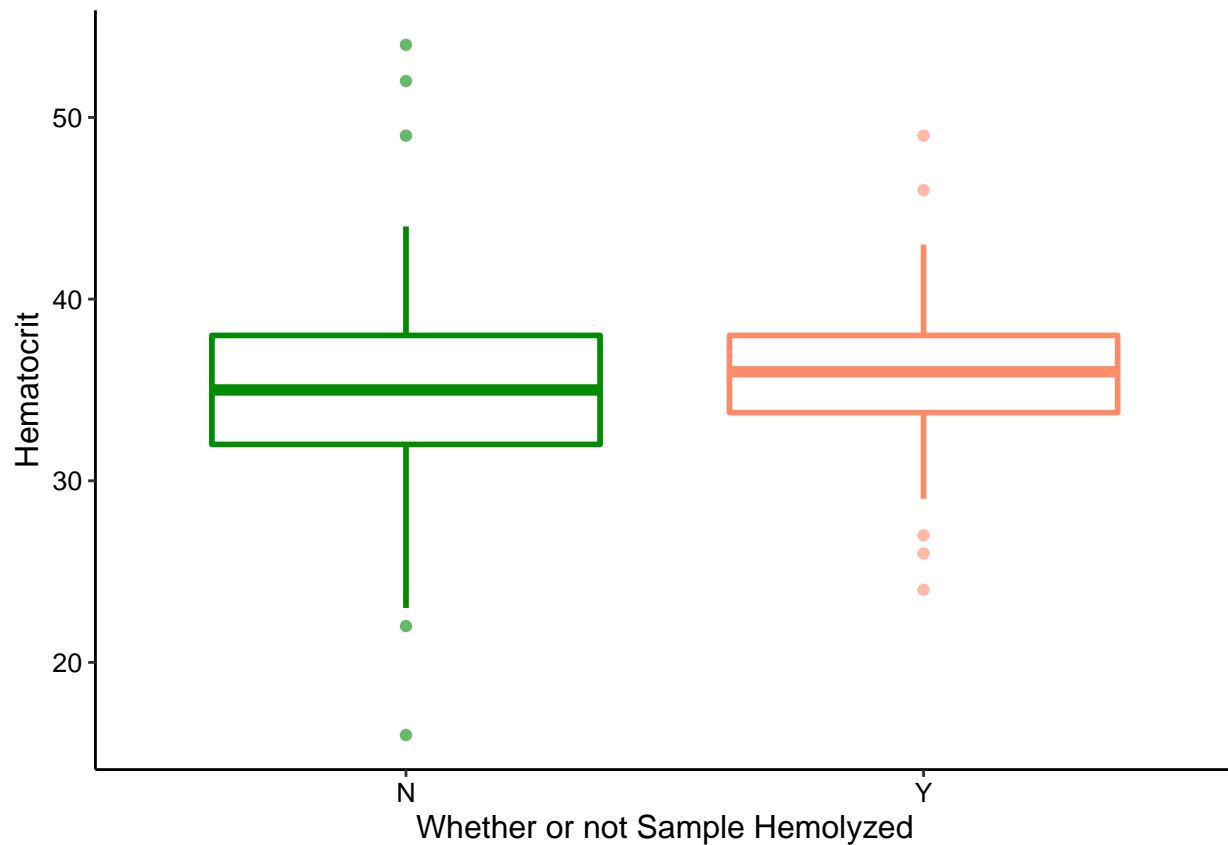


There IS a significant difference, but upon further inspection, the number of blood draws taken from the right postorbital sinus vs left or both is so uneven, this would be unhelpful in the actual model.

Hct ~ Hemolyzed/Not

```
morpho_blood_SMI %>%
  dplyr::filter(hemolyzed %in% c("Y", "N")) %>%
  ggplot(data = .) +
  geom_boxplot(aes(x = hemolyzed,
                    y = hematocrit_percent,
                    color = hemolyzed
                  ),
               size = 1,
               alpha = 0.6) +
  scale_colour_manual(name = "Blood Sample Eye",
                      values = c("green4", "salmon1", "green4", "salmon1") ) +
  theme_classic() +
  xlab("Whether or not Sample Hemolyzed") +
  ylab("Hematocrit") +
  theme(text = element_text(color = "black", family = "sans", size = 12),
        axis.text = element_text(color = "black", family = "sans", size = 10),
        legend.text.align = 0,
        legend.position = "none")
```

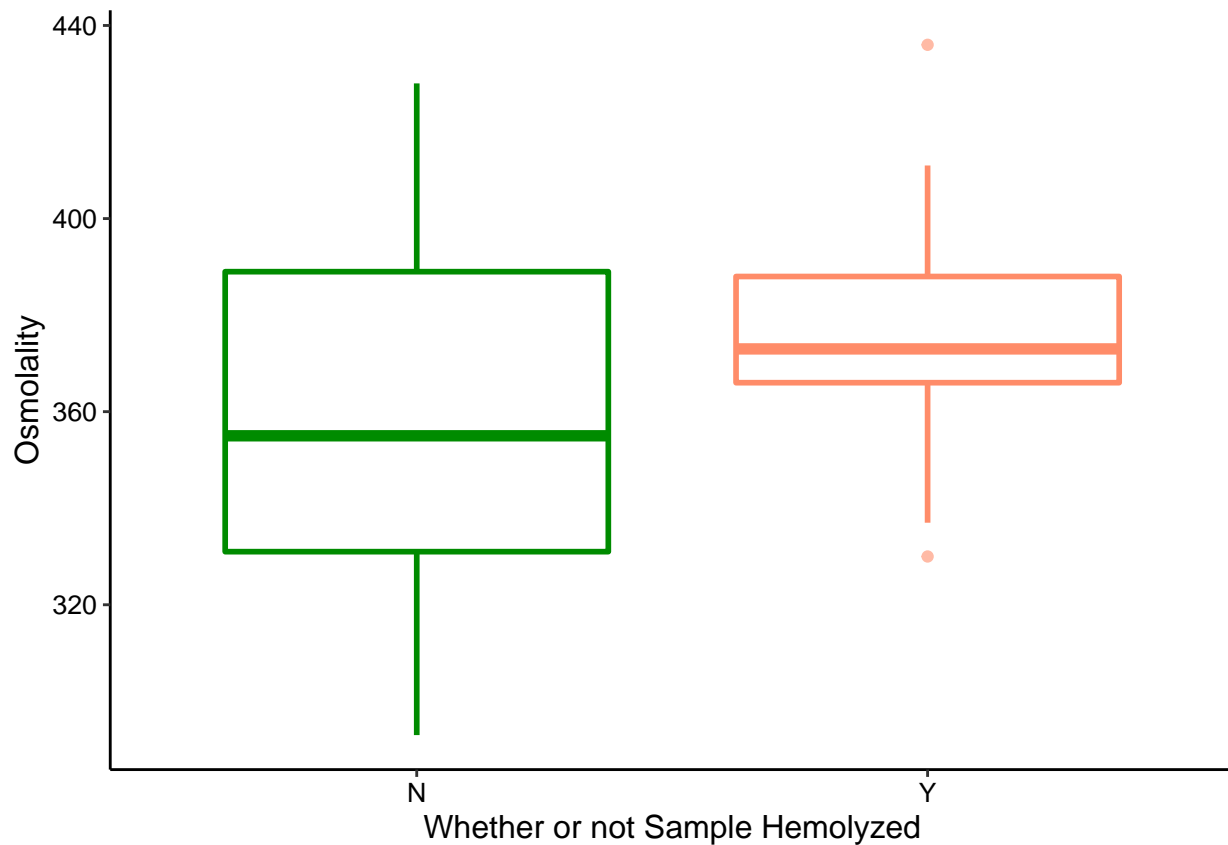
Warning: Removed 25 rows containing non-finite values (stat_boxplot).



Osml ~ Hemolyzed/Not

```
morpho_blood_SMI %>%
  dplyr::filter(hemolyzed %in% c("Y", "N")) %>%
  ggplot(data = .) +
  geom_boxplot(aes(x = hemolyzed,
                    y = osmolality_mmol_kg,
                    color = hemolyzed
                  ),
               size = 1,
               alpha = 0.6) +
  scale_colour_manual(name = "Blood Sample Eye",
                      values = c("green4", "salmon1", "green4", "salmon1") ) +
  theme_classic() +
  xlab("Whether or not Sample Hemolyzed") +
  ylab("Osmolality") +
  theme(text = element_text(color = "black", family = "sans", size = 12),
        axis.text = element_text(color = "black", family = "sans", size = 10),
        legend.text.align = 0,
        legend.position = "none")
```

Warning: Removed 1 rows containing non-finite values (stat_boxplot).

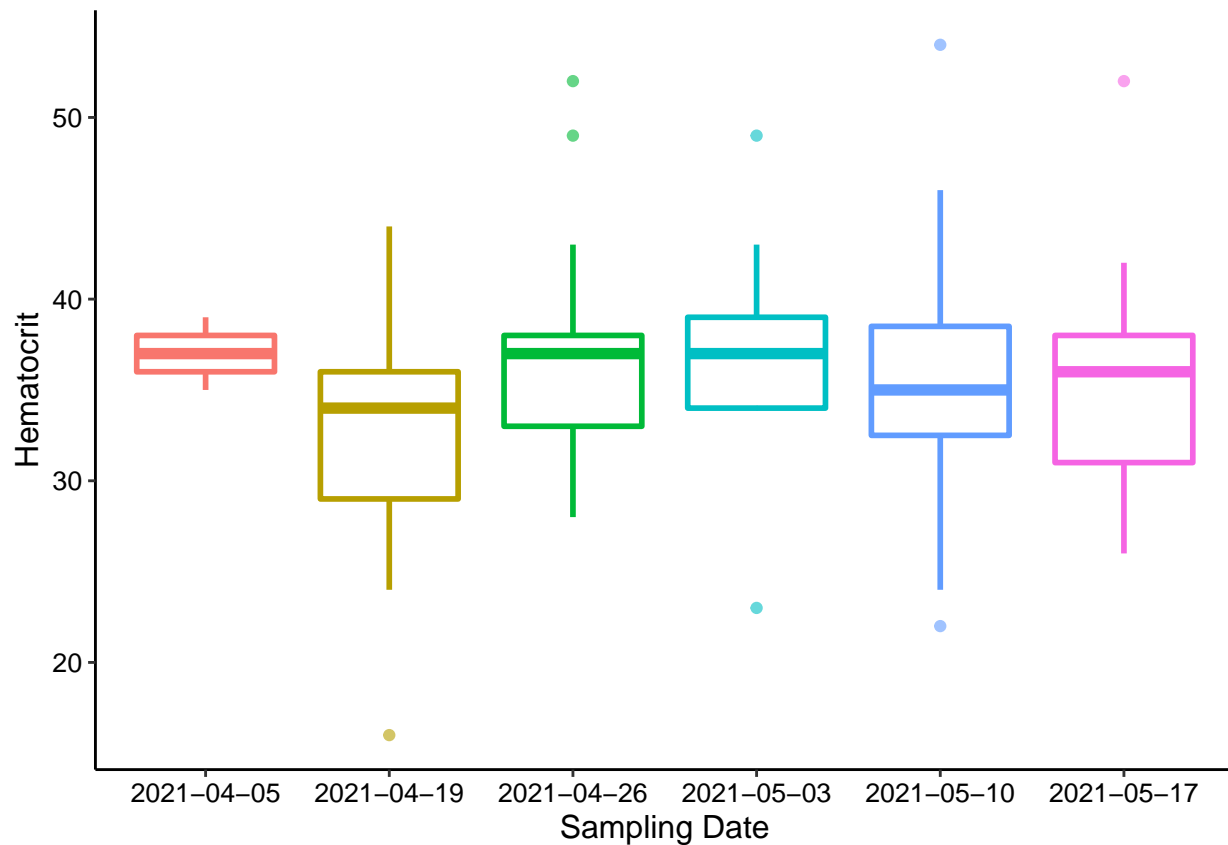


Osmolality in hemolyzed samples versus not are significantly different! This is an unfortunate trait of the dataset, and not something we are specifically interested in testing, so we will include it as a random factor in the LMM.

Hct ~ Week

```
morpho_blood_SMI %>%
  ggplot(data = .) +
  geom_boxplot(aes(x = as.factor(date),
                    y = hematocrit_percent,
                    color = as.factor(date)
                  ),
              size = 1,
              alpha = 0.6) +
  theme_classic() +
  xlab("Sampling Date") +
  ylab("Hematocrit") +
  theme(text = element_text(color = "black", family = "sans", size = 12),
        axis.text = element_text(color = "black", family = "sans", size = 10),
        legend.text.align = 0,
        legend.position = "none")
```

Warning: Removed 27 rows containing non-finite values (stat_boxplot).



Osml ~ Week

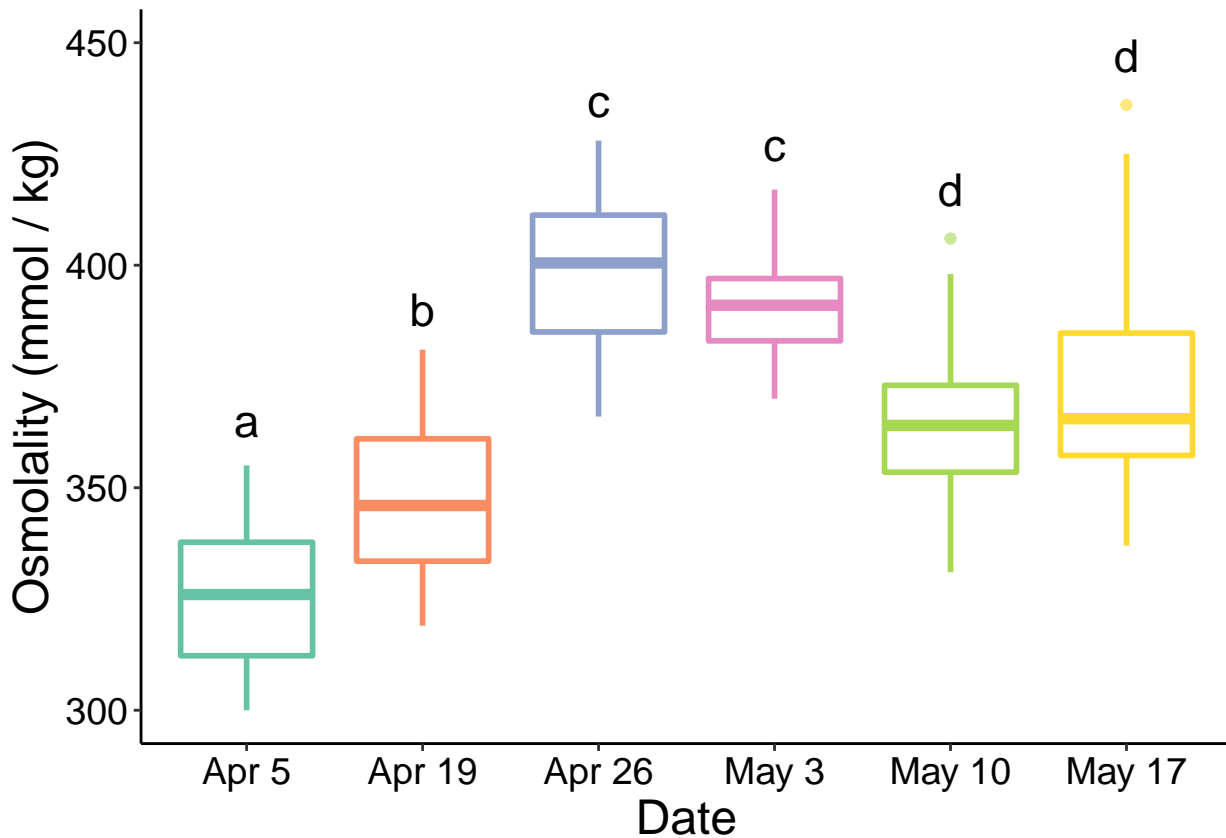
```
morpho_blood_SMI %>%
  ggplot(data = .) +
  geom_boxplot(aes(x = as.factor(date),
                    y = osmolality_mmol_kg,
                    color = as.factor(date)
                  ),
              size = 1,
              alpha = 0.6) +
  theme_classic() +
  xlab("Date") +
  ylab("Osmolality (mmol / kg)") +
  annotate("text", x = 1, y = 365, label = "a", size = 6) +
  annotate("text", x = 2, y = 390, label = "b", size = 6) +
  annotate("text", x = 3, y = 437, label = "c", size = 6) +
  annotate("text", x = 4, y = 427, label = "c", size = 6) +
  annotate("text", x = 5, y = 417, label = "d", size = 6) +
  annotate("text", x = 6, y = 447, label = "d", size = 6) +
  scale_x_discrete(labels = c("2021-04-05" = "Apr 5",
                              "2021-04-19" = "Apr 19",
                              "2021-04-26" = "Apr 26",
                              "2021-05-03" = "May 3",
                              "2021-05-10" = "May 10",
                              "2021-05-17" = "May 17")) +
  scale_color_brewer(palette = "Set2") +
```

```

ylim(300, 450) +
  theme(text = element_text(color = "black",
                             family = "sans",
                             size = 18),
        axis.text = element_text(color = "black",
                                   family = "sans",
                                   size = 14),
        legend.text.align = 0,
        legend.position = "none"
  ) -> osml_date_fig
osml_date_fig

```

```
## Warning: Removed 5 rows containing non-finite values (stat_boxplot).
```



```

# export figure
#ggsave(filename = "osml_date_fig.tiff",
#        plot = osml_date_fig,
#        path = "./final_figures",
#        device = "tiff",
#        dpi = 1200,
#        width = 6, height = 4)

# lm
lm_osml_wk <- glm(osmolality_mmol_kg ~ date,
                  data = morpho_blood_SMI)
summary(lm_osml_wk)

```

```
##
```

```
## Call:
## glm(formula = osmolality_mmol_kg ~ date, data = morpho_blood_SMI)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -48.236  -21.636   -2.635   20.364   65.564
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -1.999e+04  2.954e+03  -6.766 3.15e-10 ***
## date         1.086e+00  1.576e-01   6.889 1.65e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 735.2172)
##
##      Null deviance: 140031  on 144  degrees of freedom
## Residual deviance: 105136  on 143  degrees of freedom
## (3 observations deleted due to missingness)
## AIC: 1372.5
##
## Number of Fisher Scoring iterations: 2
```

Osmolality was VERY different by week, and that was not easily attributable to climate factors (see below). We also experienced technical difficulties with the osmometer between some weeks, so some of the variation may be attributable to technical error. Thus date/week will be a good random factor to include in the LMM. distinguish pairwise differences using an ANOVA:

```
osml_date_aov <- aov(osmolality_mmol_kg ~ as.factor(date),
                     data = morpho_blood_SMI)
TukeyHSD(osml_date_aov)
```

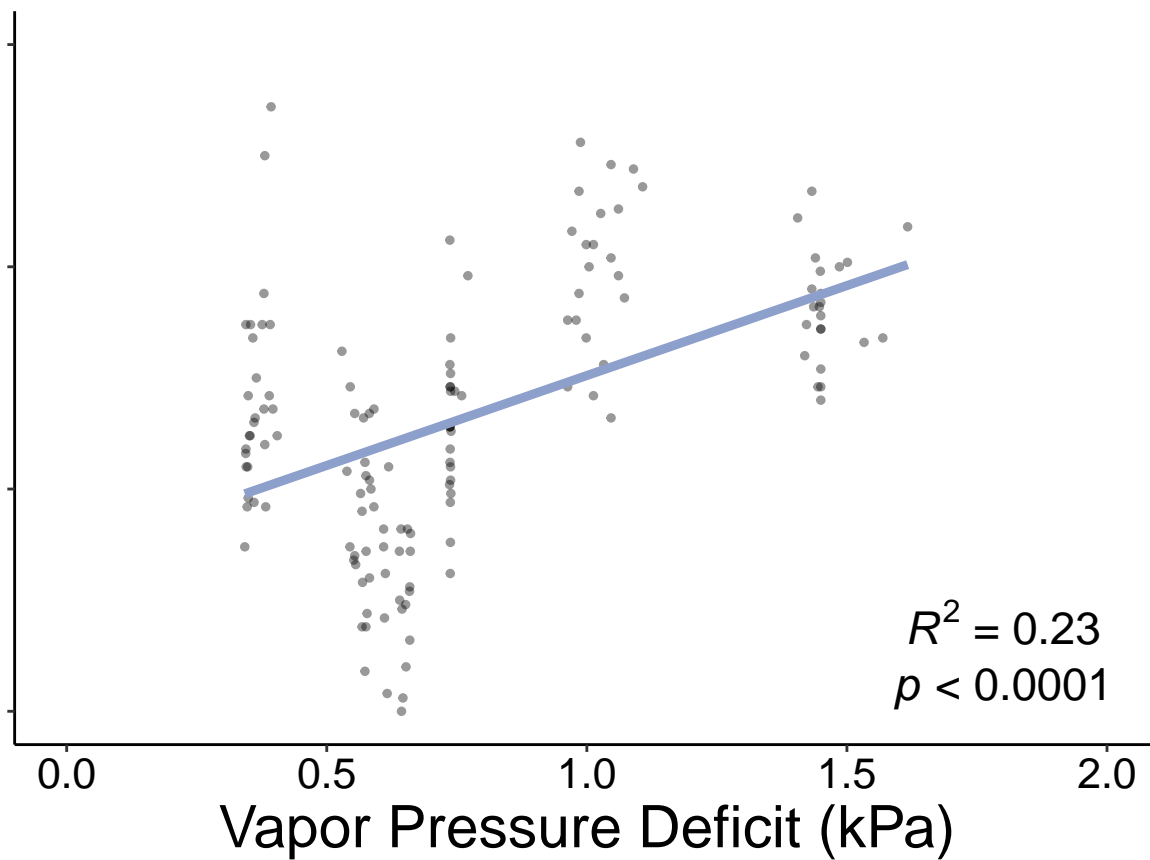
```
##      Tukey multiple comparisons of means
##      95% family-wise confidence level
##
## Fit: aov(formula = osmolality_mmol_kg ~ as.factor(date), data = morpho_blood_SMI)
##
## $`as.factor(date)`
##              diff          lwr          upr      p adj
## 2021-04-19-2021-04-05 22.891304   7.979417  37.803191 0.0002634
## 2021-04-26-2021-04-05 75.076923  60.628732  89.525114 0.0000000
## 2021-05-03-2021-04-05 66.657895  50.935165  82.380624 0.0000000
## 2021-05-10-2021-04-05 41.543478  26.631591  56.455365 0.0000000
## 2021-05-17-2021-04-05 46.785714  32.597872  60.973557 0.0000000
## 2021-04-26-2021-04-19 52.185619  37.273732  67.097506 0.0000000
## 2021-05-03-2021-04-19 43.766590  27.616718  59.916462 0.0000000
## 2021-05-10-2021-04-19 18.652174   3.290581  34.013766 0.0078361
## 2021-05-17-2021-04-19 23.894410   9.234635  38.554185 0.0000857
## 2021-05-03-2021-04-26 -8.419028 -24.141758   7.303701 0.6342961
## 2021-05-10-2021-04-26 -33.533445 -48.445332 -18.621558 0.0000000
## 2021-05-17-2021-04-26 -28.291209 -42.479051 -14.103367 0.0000008
## 2021-05-10-2021-05-03 -25.114416 -41.264289  -8.964544 0.0002088
## 2021-05-17-2021-05-03 -19.872180 -35.356006  -4.388355 0.0039942
## 2021-05-17-2021-05-10  5.242236  -9.417539  19.902011 0.9059063
```


Osmol ~ VPD

```
my_blue <- RColorBrewer::brewer.pal(8, "Set2")[3]
morpho_blood_SMI %>%
  ggplot(data = .) +
    geom_point(aes(x = VPD_kPa_int,
                  y = osmolality_mmol_kg,
                  ),
              size = 1,
              alpha = 0.4) +
    stat_smooth(aes(x = VPD_kPa_int,
                  y = osmolality_mmol_kg),
                formula = y ~ x,
                method = "lm",
                se = F,
                color = my_blue,
                size = 1.6,
                alpha = 1 ) +
    theme_classic() +
    xlab("Vapor Pressure Deficit (kPa)") +
    #ylab("Osmolality (mmol/kg)") +
    ylab("") +
    xlim(0, 2) +
    ylim(300, 450) +
    annotate("text", x = 1.8, y = 320,
            label = "paste(italic(R) ^ 2, \" = 0.23\\")",
            parse = TRUE,
            size = 6) +
    annotate("text", x = 1.8, y = 305,
            label = "paste(italic(p), \" < 0.0001\\")",
            parse = TRUE,
            size = 6) +
    theme(text = element_text(color = "black",
                              family = "sans",
                              size = 22),
          axis.text = element_text(color = "black",
                                    family = "sans",
                                    size = 16),
          axis.text.y = element_blank(),
          legend.text.align = 0,
          plot.margin = unit(c(0.1,0,0.1,0.45), "cm"),
    ) -> osml_vpd_fig
osml_vpd_fig
```

Warning: Removed 7 rows containing non-finite values (stat_smooth).

Warning: Removed 7 rows containing missing values (geom_point).



```
# export figure
#ggsave(filename = "osml_abhum_fig.jpeg",
#       plot = osml_abhum_fig,
#       path = "./final_figures",
#       device = "jpeg",
#       dpi = 1200,
#       width = 6, height = 4)
```

Hct ~ VPD

```
morpho_blood_SMI %>%
  ggplot(data = .) +
  geom_point(aes(x = VPD_kPa_int,
                 y = hematocrit_percent,
                 ),
            size = 1,
            alpha = 0.6) +
  stat_smooth(aes(x = VPD_kPa_int,
                  y = hematocrit_percent),
             formula = y ~ x,
             method = "lm",
             se = F,
             color = "blue",
             size = 1.6,
             alpha = 1 ) +
  theme_classic() +
```

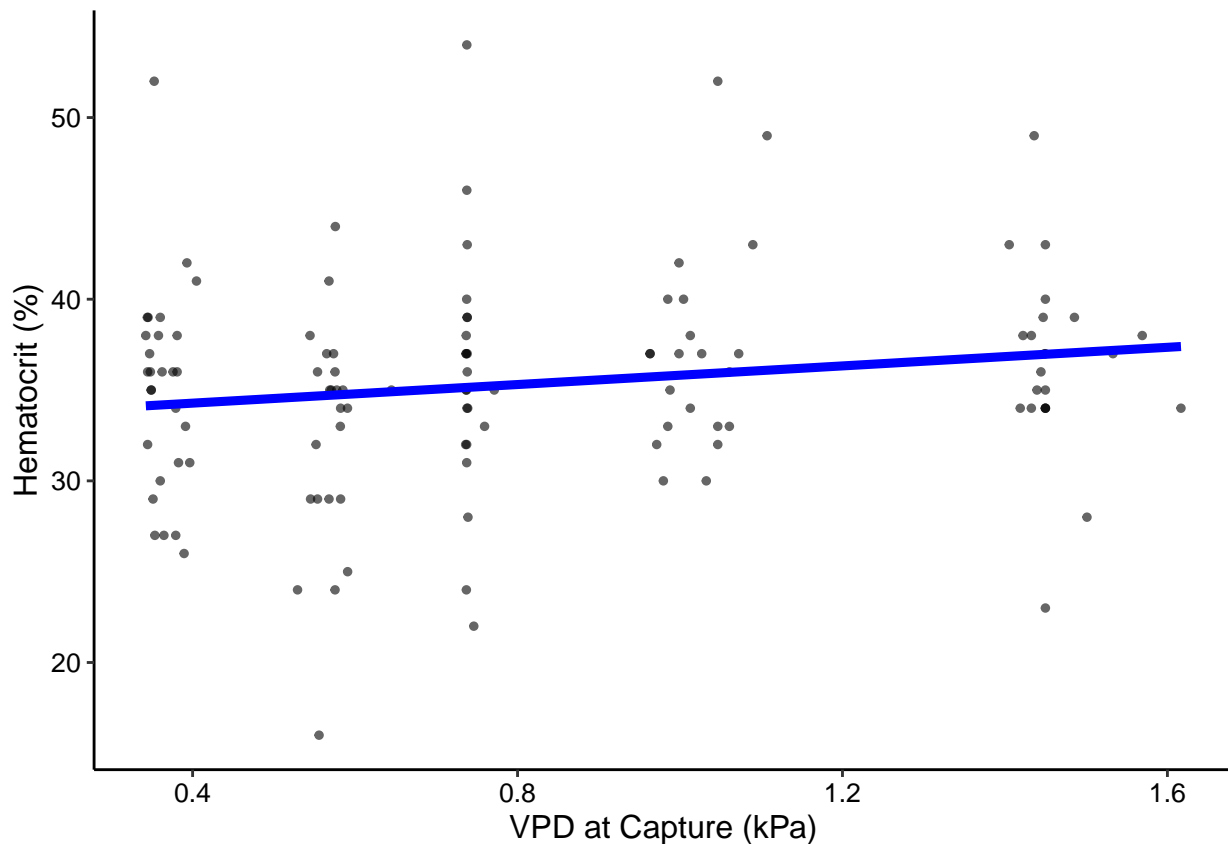
```

xlab("VPD at Capture (kPa)") +
ylab("Hematocrit (%)") +
theme(text = element_text(color = "black",
                           family = "sans",
                           size = 12),
      axis.text = element_text(color = "black",
                                family = "sans",
                                size = 10),
      legend.text.align = 0)

```

```
## Warning: Removed 28 rows containing non-finite values (stat_smooth).
```

```
## Warning: Removed 28 rows containing missing values (geom_point).
```



Hct ~ Temperature

```

morpho_blood_SMI %>%
  ggplot(data = .) +
  geom_point(aes(x = temp_C_interpol,
                 y = hematocrit_percent,
                 ),
            size = 1,
            alpha = 0.6) +
  stat_smooth(aes(x = temp_C_interpol,
                  y = hematocrit_percent),
             formula = y ~ x,
             method = "lm",

```

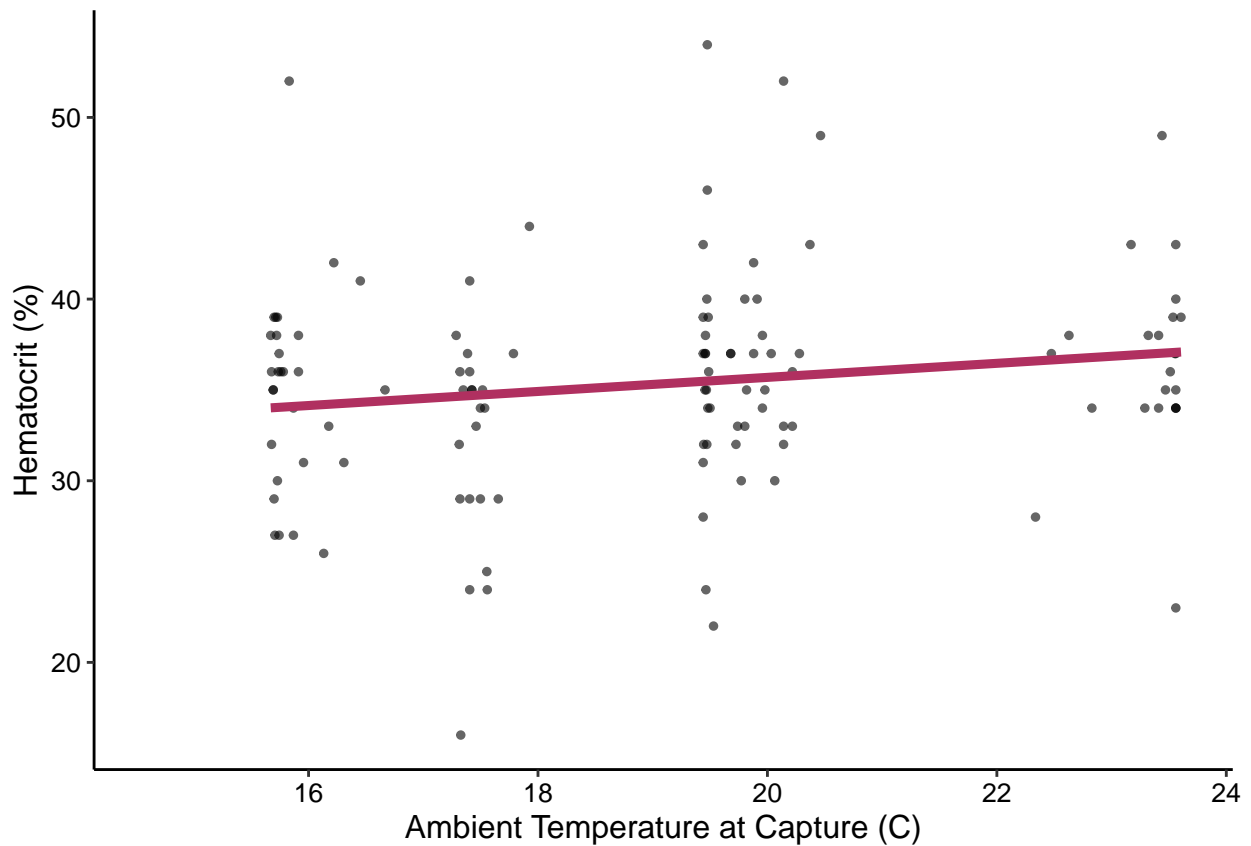
```

    se = F,
    color = "maroon",
    size = 1.6,
    alpha = 1 ) +
theme_classic() +
xlab("Ambient Temperature at Capture (C)") +
ylab("Hematocrit (%)") +
theme(text = element_text(color = "black",
                           family = "sans",
                           size = 12),
      axis.text = element_text(color = "black",
                               family = "sans",
                               size = 10),
      legend.text.align = 0)

```

Warning: Removed 28 rows containing non-finite values (stat_smooth).

Warning: Removed 28 rows containing missing values (geom_point).



Osml ~ Temperature

```

my_red <- RColorBrewer::brewer.pal(8, "Set2")[4]

morpho_blood_SMI %>%
  ggplot(data = .) +
  geom_point(aes(x = temp_C_interpol,
                 y = osmolality_mmol_kg,

```

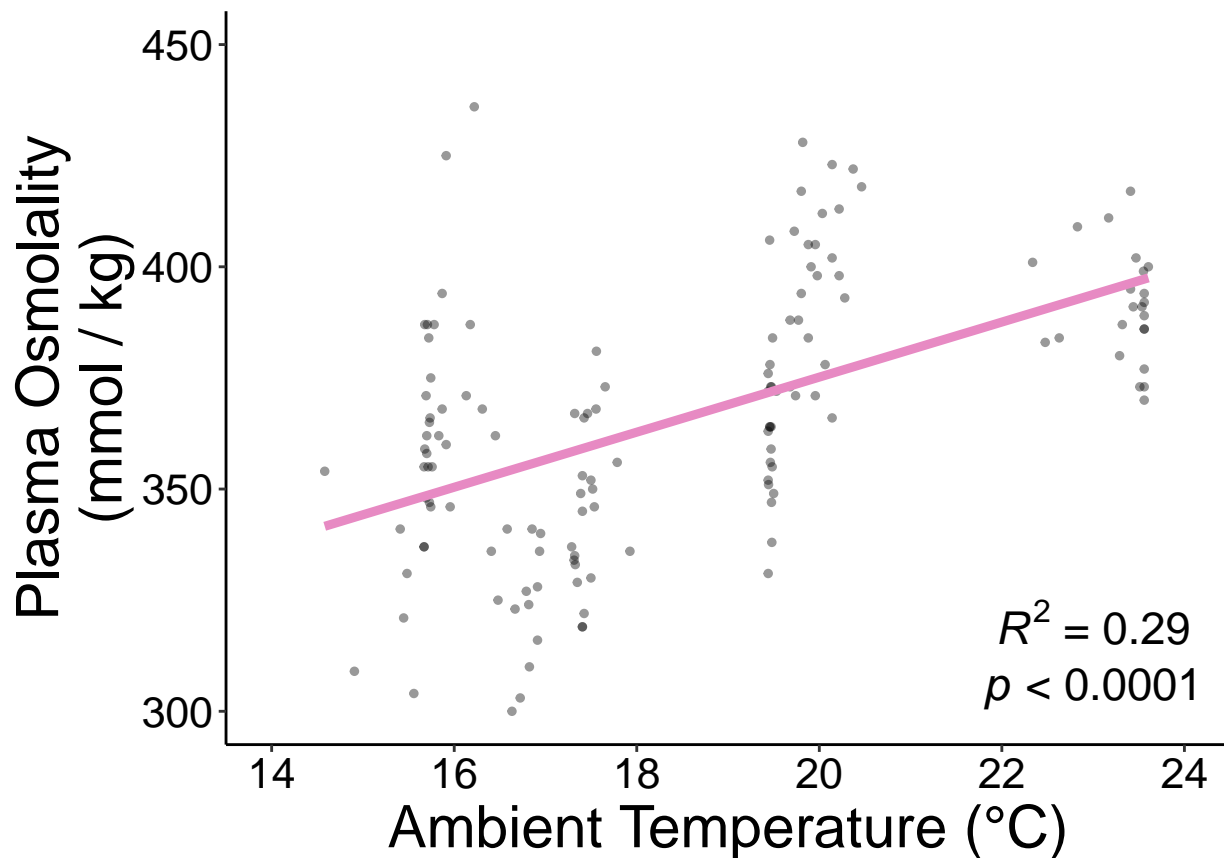
```

    ),
    size = 1,
    alpha = 0.4) +
stat_smooth(aes(x = temp_C_interpol,
                 y = osmolality_mmol_kg),
             formula = y ~ x,
             method = "lm",
             se = F,
             color = my_red,
             size = 1.6,
             alpha = 1 ) +
theme_classic() +
xlab("Ambient Temperature (°C)") +
ylab("Plasma Osmolality\n(mmol / kg)") +
annotate("text", x = 23, y = 320,
          label = "paste(italic(R) ^ 2, \" = 0.29\\")",
          parse = TRUE,
          size = 6) +
annotate("text", x = 23, y = 305,
          label = "paste(italic(p), \" < 0.0001\\")",
          parse = TRUE,
          size = 6) +
xlim(14, 24) +
ylim(300,450) +
theme(text = element_text(color = "black",
                           family = "sans",
                           size = 22),
      axis.text = element_text(color = "black",
                                family = "sans",
                                size = 16),
      legend.text.align = 0,
      plot.margin = unit(c(0.1,0,0.1,0.45), "cm")
) -> osml_temp_fig
osml_temp_fig

```

```
## Warning: Removed 7 rows containing non-finite values (stat_smooth).
```

```
## Warning: Removed 7 rows containing missing values (geom_point).
```



```
# export figure
#ggsave(filename = "osml_temp_fig.jpeg",
#       plot = osml_temp_fig,
#       path = "./final_figures",
#       device = "jpeg",
#       dpi = 1200,
#       width = 6, height = 4)
```

Hct ~ Individual

```
morpho_blood_SMI %>%
  ggplot(data = .) +
  geom_point(aes(x = individual_ID,
                 y = hematocrit_percent,
                 ),
            size = 1,
            alpha = 0.6) +
  stat_smooth(aes(x = individual_ID,
                  y = hematocrit_percent,
                  ),
            formula = y ~ x,
            method = "lm",
            color = "gray",
            se = F,
            size = 1.6,
            alpha = 1 ) +
```

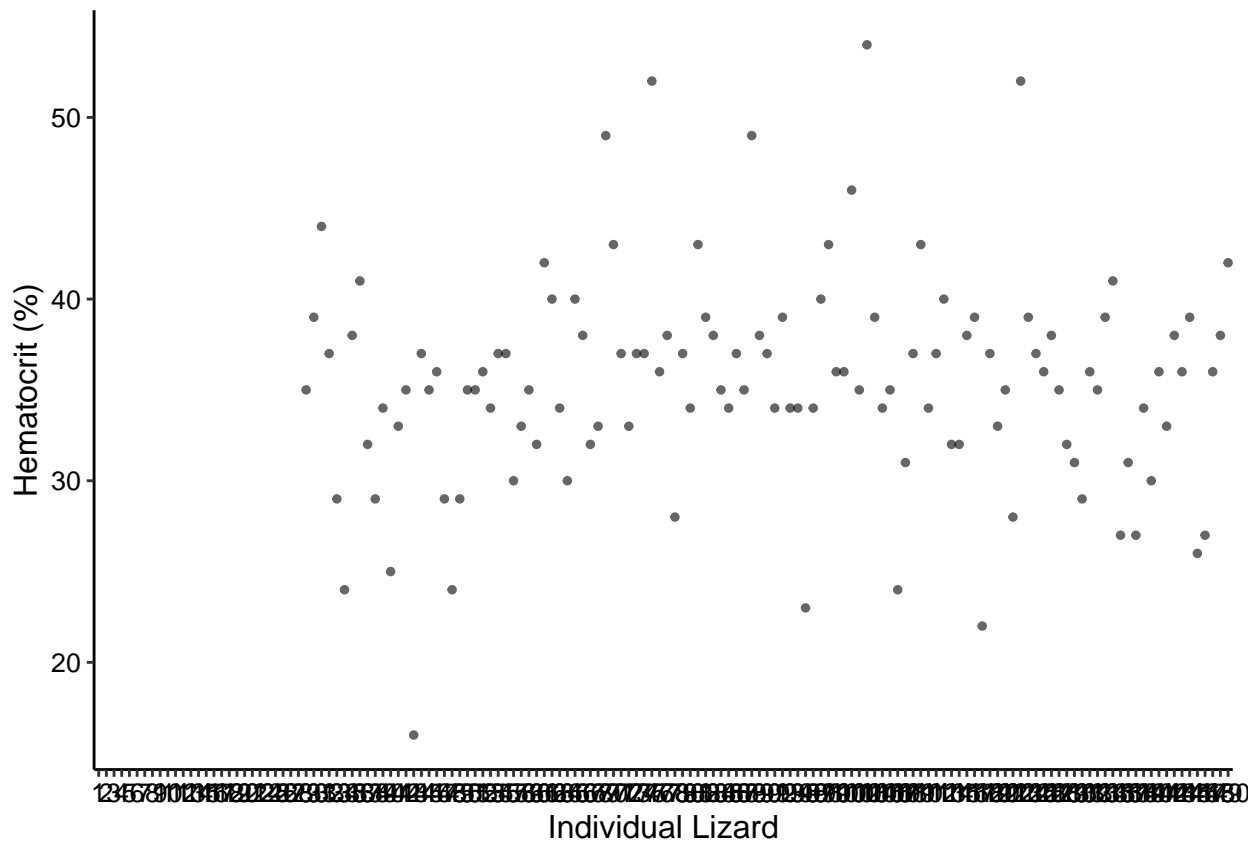
```

theme_classic() +
xlab("Individual Lizard") +
ylab("Hematocrit (%)") +
theme(text = element_text(color = "black",
                           family = "sans",
                           size = 12),
      axis.text = element_text(color = "black",
                                family = "sans",
                                size = 10),
      legend.text.align = 0)

```

Warning: Removed 27 rows containing non-finite values (stat_smooth).

Warning: Removed 27 rows containing missing values (geom_point).



Osml ~ Individual

```

morpho_blood_SMI %>%
  ggplot(data = .) +
  geom_point(aes(x = individual_ID,
                 y = osmolality_mmol_kg,
                 size = 1,
                 alpha = 0.6)) +
  stat_smooth(aes(x = individual_ID,
                  y = osmolality_mmol_kg,
                  ),

```

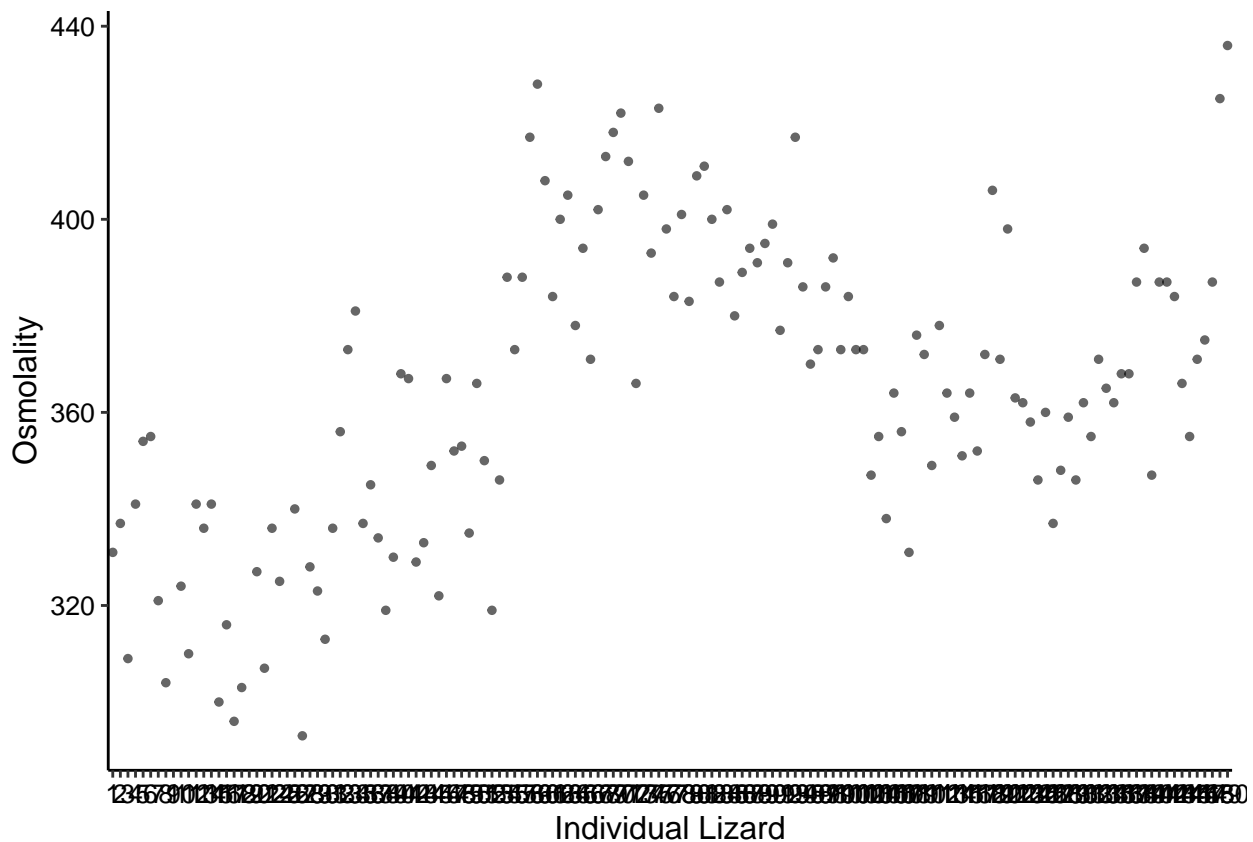
```

    formula = y ~ x,
    method = "lm",
    color = "gray",
    se = F,
    size = 1.6,
    alpha = 1 ) +
theme_classic() +
xlab("Individual Lizard") +
ylab("Osmolality") +
theme(text = element_text(color = "black",
                           family = "sans",
                           size = 12),
      axis.text = element_text(color = "black",
                                family = "sans",
                                size = 10),
      legend.text.align = 0)

```

Warning: Removed 3 rows containing non-finite values (stat_smooth).

Warning: Removed 3 rows containing missing values (geom_point).



Osmolality Multi-Figure

```

ggarrange(osml_temp_fig, osml_vpd_fig,
  ncol = 2, nrow = 1,
  labels = c("A", "B", "C", "D", "E", "F"),
  hjust = c(-2, -0.5),

```



```
font.label = list(size = 24, face = "bold", color = "black")
) -> osml_multi_fig
```

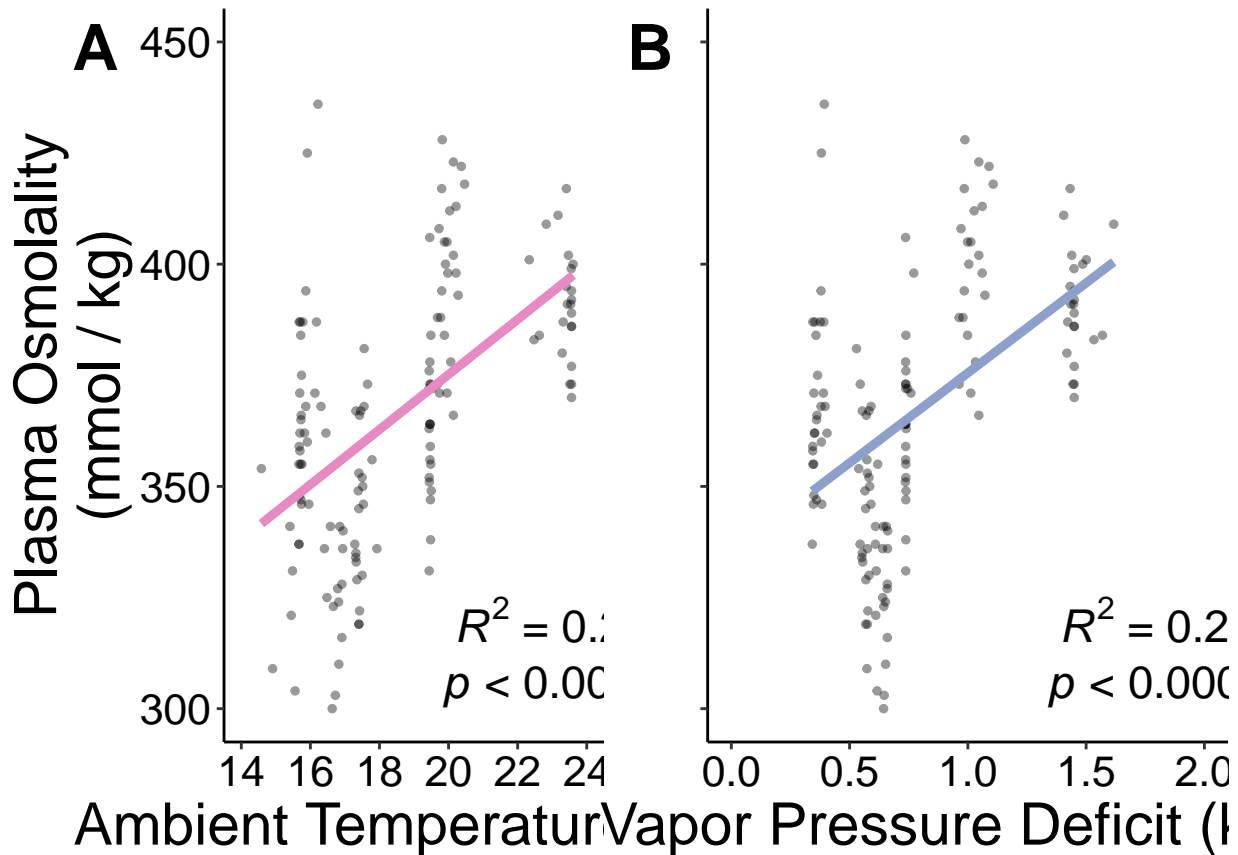
```
## Warning: Removed 7 rows containing non-finite values (stat_smooth).
```

```
## Warning: Removed 7 rows containing missing values (geom_point).
```

```
## Warning: Removed 7 rows containing non-finite values (stat_smooth).
```

```
## Warning: Removed 7 rows containing missing values (geom_point).
```

```
osml_multi_fig
```



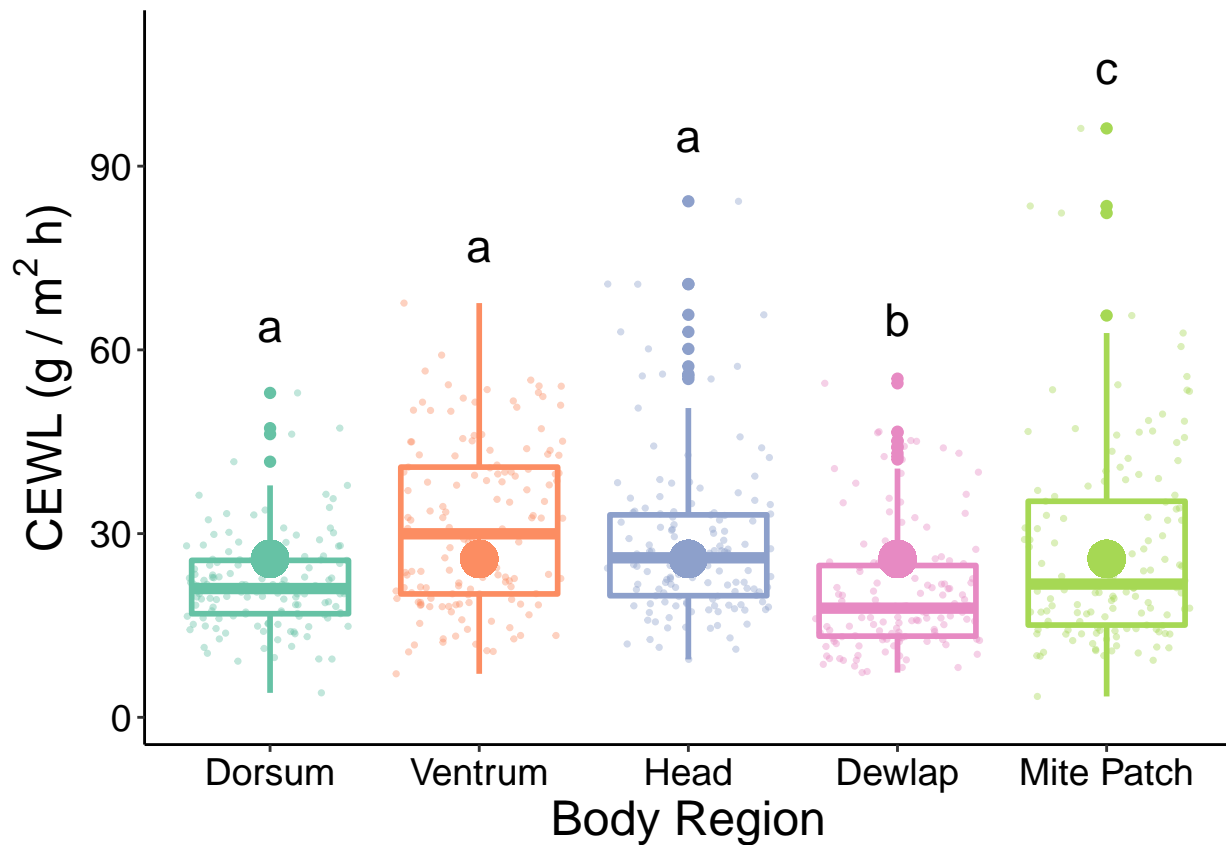
```
# export figure
ggsave(filename = "osml_multi_fig.jpeg",
  plot = osml_multi_fig,
  path = "./final_figures",
  device = "jpeg",
  dpi = 1200,
  width = 12, height = 4)
```

What affects evaporative water loss?

Potential relationships: - CEWL ~ date/week, individual, SVL, SMI, gravidity, hct, osml, cloacal temp, ambient temp, ambient RH, measurement temp, measurement RH, **body region**

CEWL ~ Body Region

```
CEWL_data_full %>%
  ggplot(data = .) +
  geom_boxplot(aes(x = (region),
                  y = (TEWL_g_m2h),
                  color = region
                  ),
              size = 1,
              alpha = 1) +
  geom_jitter(aes(x = (region),
                  y = TEWL_g_m2h,
                  color = region
                  ),
              size = 0.6,
              alpha = 0.4) +
  geom_point(aes(x = (region),
                  y = mean(TEWL_g_m2h),
                  color = region,
                  ),
              size = 6,
              alpha = 1) +
  theme_classic() +
  xlab("Body Region") +
  ylab(bquote('CEWL (g / '*m^2~h*')')) +
  annotate("text", x = 1, y = 64, label = "a", size = 6) +
  annotate("text", x = 2, y = 77, label = "a", size = 6) +
  annotate("text", x = 3, y = 95, label = "a", size = 6) +
  annotate("text", x = 4, y = 65, label = "b", size = 6) +
  annotate("text", x = 5, y = 106, label = "c", size = 6) +
  scale_color_brewer(palette = "Set2") +
  ylim(1, 110) +
  theme(text = element_text(color = "black",
                             family = "sans",
                             size = 18),
        axis.text = element_text(color = "black",
                                   family = "sans",
                                   size = 14),
        legend.text.align = 0,
        legend.position = "none"
  ) -> CEWL_region_fig
CEWL_region_fig
```



```
# export figure
ggsave(filename = "CEWL_region_fig.jpeg",
        plot = CEWL_region_fig,
        path = "./final_figures",
        device = "jpeg",
        dpi = 1200,
        width = 6, height = 4)
```

Body Region Ratios

```
CEWL_mite <- CEWL_data_full %>%
  dplyr::filter(region == "Mite Patch") %>%
  dplyr::select(mite_CEWL = TEWL_g_m2h, individual_ID)
CEWL_dewl <- CEWL_data_full %>%
  dplyr::filter(region == "Dewlap") %>%
  dplyr::select(dewl_CEWL = TEWL_g_m2h, individual_ID)
CEWL_head <- CEWL_data_full %>%
  dplyr::filter(region == "Head") %>%
  dplyr::select(head_CEWL = TEWL_g_m2h, individual_ID)
CEWL_vent <- CEWL_data_full %>%
  dplyr::filter(region == "Ventrurn") %>%
  dplyr::select(vent_CEWL = TEWL_g_m2h, individual_ID)
CEWL_dors <- CEWL_data_full %>%
  dplyr::filter(region == "Dorsum") %>%
  dplyr::select(dors_CEWL = TEWL_g_m2h, individual_ID)

by_region_CEWL <- CEWL_mite %>%
```

```

left_join(CEWL_dewl, by = "individual_ID") %>%
left_join(CEWL_head, by = "individual_ID") %>%
left_join(CEWL_vent, by = "individual_ID") %>%
left_join(CEWL_dors, by = "individual_ID") %>%
mutate(mite_dors = mite_CEWL/dors_CEWL,
       dewl_dors = mite_CEWL/dors_CEWL,
       head_dors = mite_CEWL/dors_CEWL,
       vent_dors = mite_CEWL/dors_CEWL,
       dors_dors = mite_CEWL/dors_CEWL,
       )

ratio_mite <- by_region_CEWL %>%
  dplyr::select(individual_ID, ratio_to_dors = mite_dors) %>%
  mutate(region = "Mite Patch")
ratio_dewl <- by_region_CEWL %>%
  dplyr::select(individual_ID, ratio_to_dors = dewl_dors) %>%
  mutate(region = "Dewlap")
ratio_head <- by_region_CEWL %>%
  dplyr::select(individual_ID, ratio_to_dors = head_dors) %>%
  mutate(region = "Head")
ratio_vent <- by_region_CEWL %>%
  dplyr::select(individual_ID, ratio_to_dors = vent_dors) %>%
  mutate(region = "Ventrums")
ratio_dors <- by_region_CEWL %>%
  dplyr::select(individual_ID, ratio_to_dors = dors_dors) %>%
  mutate(region = "Dorsum")

vert_ratios <- ratio_mite %>%
  rbind(ratio_dewl) %>%
  rbind(ratio_head) %>%
  rbind(ratio_vent) %>%
  rbind(ratio_dors)

vert_ratios %>%
  ggplot(data = .) +
  geom_boxplot(aes(x = (region),
                  y = ratio_to_dors,
                  color = region
                  ),
              size = 1,
              alpha = 1) +
  geom_jitter(aes(x = (region),
                  y = ratio_to_dors,
                  color = region
                  ),
              size = 1,
              alpha = 0.3) +
  geom_point(aes(x = (region),
                  y = mean(ratio_to_dors),
                  color = region
                  ),
              size = 5,
              alpha = 1) +
  theme_classic() +

```

```

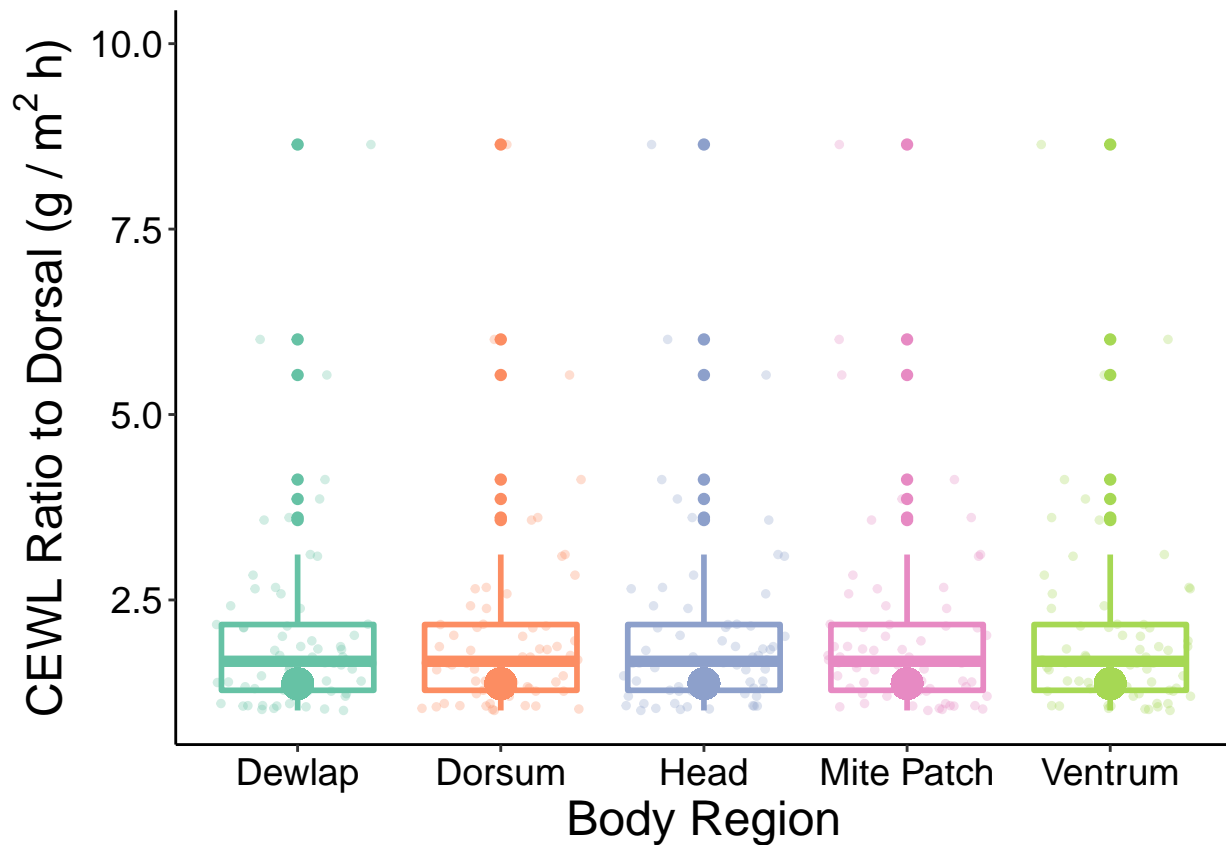
xlab("Body Region") +
ylab(bquote('CEWL Ratio to Dorsal (g / '*m^2~h*')')) +
annotate("text", x = 1, y = 64, label = "a", size = 6) +
annotate("text", x = 2, y = 77, label = "b", size = 6) +
annotate("text", x = 3, y = 95, label = "b", size = 6) +
annotate("text", x = 4, y = 65, label = "a", size = 6) +
annotate("text", x = 5, y = 106, label = "b", size = 6) +
scale_color_brewer(palette = "Set2") +
ylim(1, 10) +
theme(text = element_text(color = "black",
                           family = "sans",
                           size = 18),
      axis.text = element_text(color = "black",
                                family = "sans",
                                size = 14),
      legend.text.align = 0,
      legend.position = "none"
) -> CEWL_region_fig3
CEWL_region_fig3

```

```

## Warning: Removed 360 rows containing non-finite values (stat_boxplot).
## Warning: Removed 360 rows containing missing values (geom_point).
## Warning: Removed 1 rows containing missing values (geom_text).
## Warning: Removed 1 rows containing missing values (geom_text).
## Warning: Removed 1 rows containing missing values (geom_text).
## Warning: Removed 1 rows containing missing values (geom_text).
## Warning: Removed 1 rows containing missing values (geom_text).

```



```
# export figure
ggsave(filename = "CEWL_region_fig3.jpeg",
        plot = CEWL_region_fig3,
        path = "./final_figures",
        device = "jpeg",
        dpi = 1200,
        width = 6, height = 4)
```

```
## Warning: Removed 360 rows containing non-finite values (stat_boxplot).
```

```
## Warning: Removed 360 rows containing missing values (geom_point).
```

```
## Warning: Removed 1 rows containing missing values (geom_text).
```

```
## Warning: Removed 1 rows containing missing values (geom_text).
```

```
## Warning: Removed 1 rows containing missing values (geom_text).
```

```
## Warning: Removed 1 rows containing missing values (geom_text).
```

```
## Warning: Removed 1 rows containing missing values (geom_text).
```

CEWL ~ Osmolality

```
CEWL_data_full %>%
  ggplot(data = .) +
  geom_point(aes(x = osmolality_mmol_kg,
                 y = TEWL_g_m2h,
```

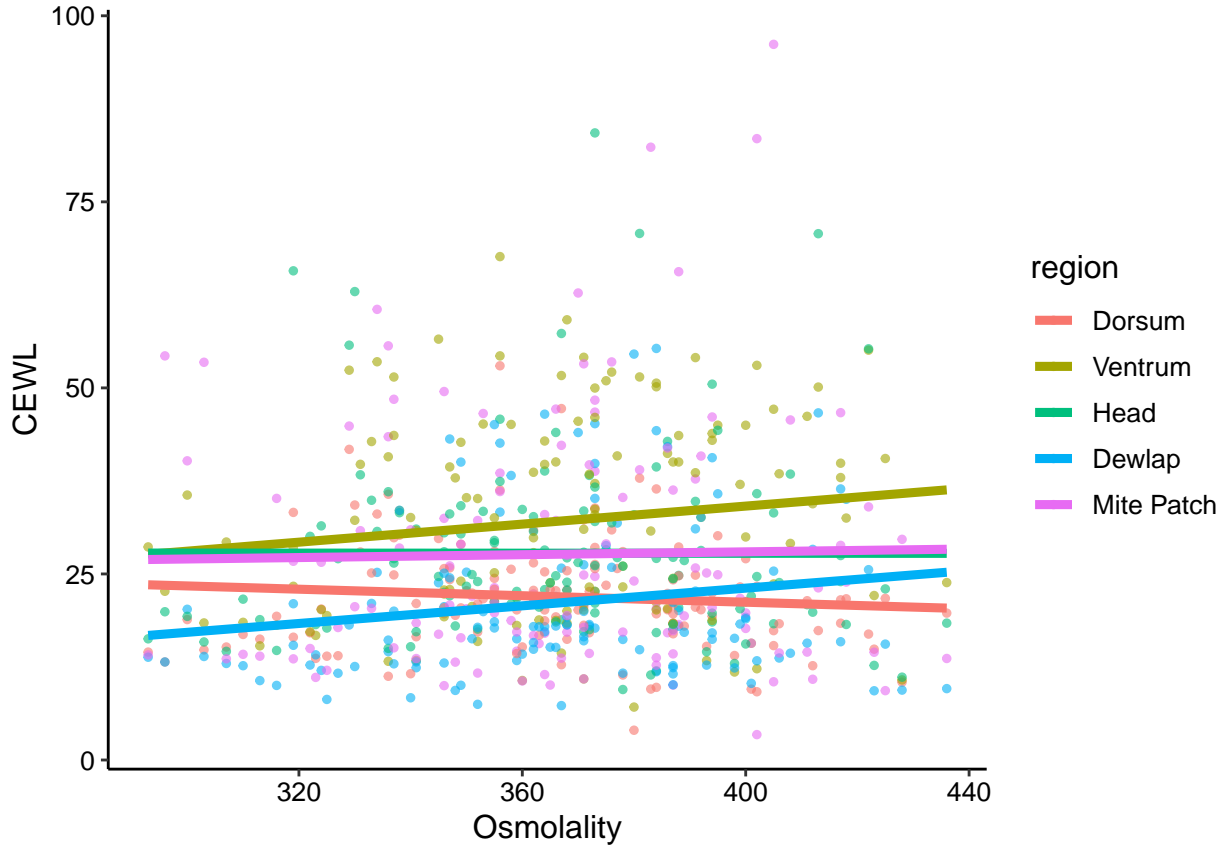
```

        color = region
      ),
      size = 1,
      alpha = 0.6) +
stat_smooth(aes(x = osmolality_mmol_kg,
                y = TEWL_g_m2h,
                color = region
                ),
            formula = y ~ x,
            method = "lm",
            se = F,
            size = 1.6,
            alpha = 1 ) +
theme_classic() +
xlab("Osmolality") +
ylab("CEWL") +
theme(text = element_text(color = "black",
                          family = "sans",
                          size = 12),
      axis.text = element_text(color = "black",
                              family = "sans",
                              size = 10),
      legend.text.align = 0)

```

Warning: Removed 49 rows containing non-finite values (stat_smooth).

Warning: Removed 49 rows containing missing values (geom_point).



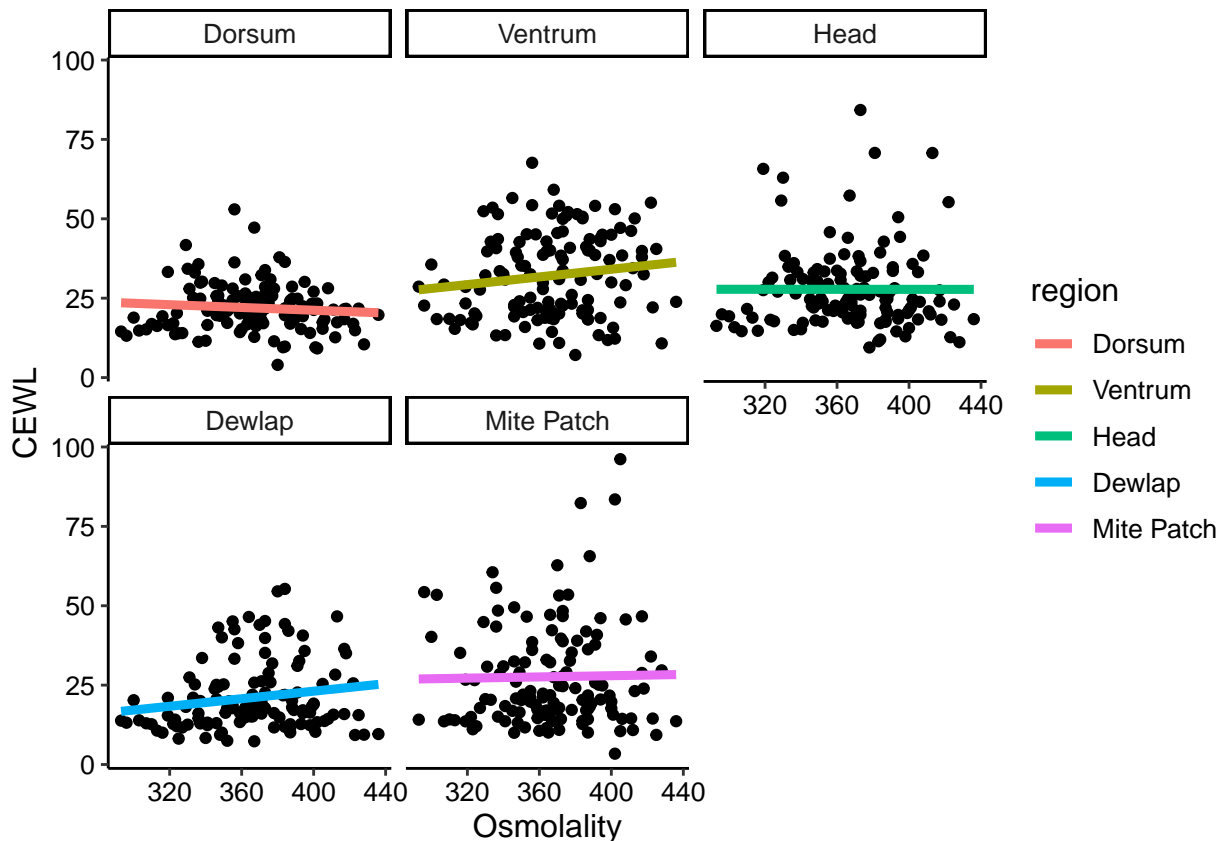
```

# Facet ggplot
ggplot(aes(osmolality_mmol_kg, TEWL_g_m2h), data = CEWL_data_full) +
  geom_point() +
  stat_smooth(aes(x = osmolality_mmol_kg,
                  y = TEWL_g_m2h,
                  color = region
                  ),
              formula = y ~ x,
              method = "lm",
              se = F,
              size = 1.6,
              alpha = 1 )+
  theme_classic() +
  xlab("Osmolality") +
  ylab("CEWL") +
  theme(text = element_text(color = "black",
                             family = "sans",
                             size = 12),
        axis.text = element_text(color = "black",
                                   family = "sans",
                                   size = 10),
        legend.text.align = 0) +
  facet_wrap(~ region) # create a facet for each body region

```

Warning: Removed 49 rows containing non-finite values (stat_smooth).

Warning: Removed 49 rows containing missing values (geom_point).

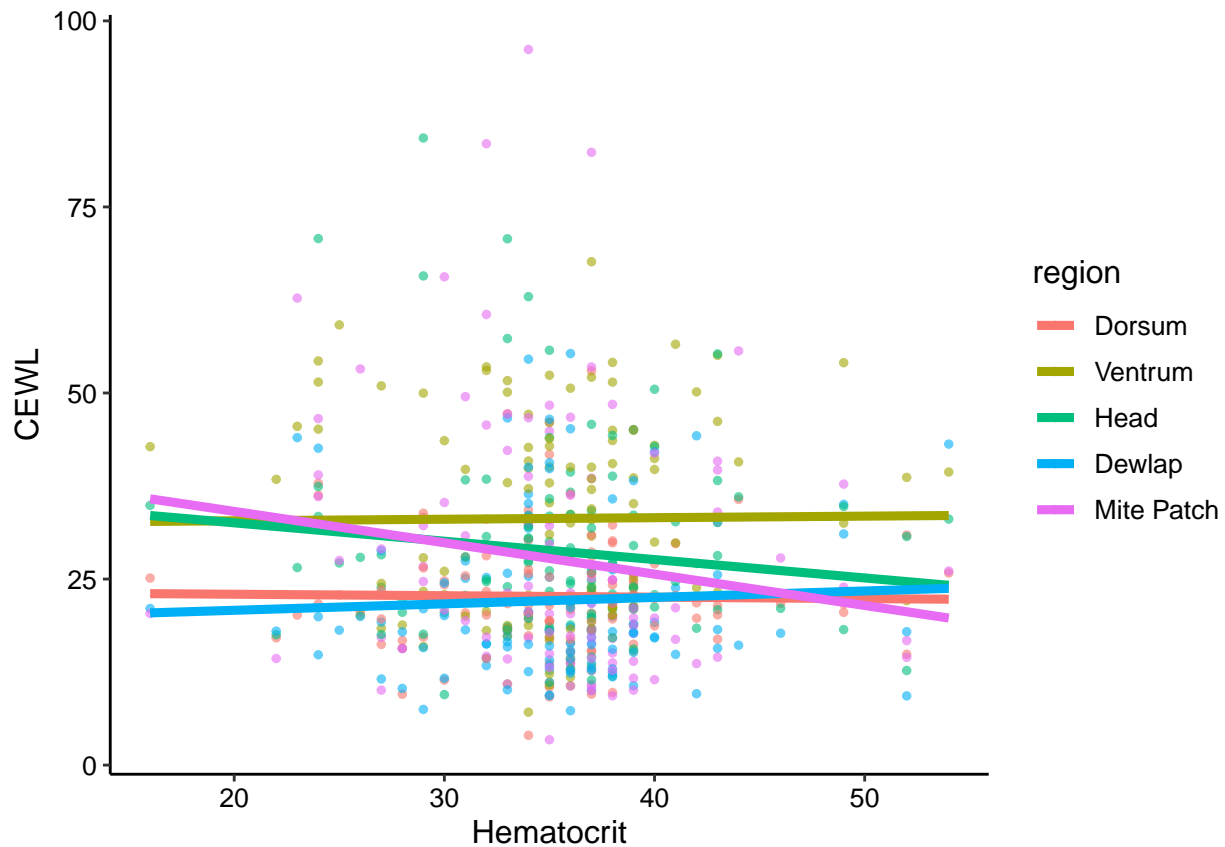


CEWL ~ Hematocrit

```
CEWL_data_full %>%
  ggplot(data = .) +
  geom_point(aes(x = hematocrit_percent,
                 y = TEWL_g_m2h,
                 color = region
                 ),
             size = 1,
             alpha = 0.6) +
  stat_smooth(aes(x = hematocrit_percent,
                  y = TEWL_g_m2h,
                  color = region
                  ),
              formula = y ~ x,
              method = "lm",
              se = F,
              size = 1.6,
              alpha = 1 ) +
  theme_classic() +
  xlab("Hematocrit") +
  ylab("CEWL") +
  theme(text = element_text(color = "black",
                             family = "sans",
                             size = 12),
        axis.text = element_text(color = "black",
                                   family = "sans",
                                   size = 10),
        legend.text.align = 0)
```

```
## Warning: Removed 119 rows containing non-finite values (stat_smooth).
```

```
## Warning: Removed 119 rows containing missing values (geom_point).
```



CEWL ~ Cloacal Temperature

```
CEWL_data_full %>%
  ggplot(data = .) +
  geom_point(aes(x = cloacal_temp_C,
                 y = TEWL_g_m2h,
                 color = region
                 ),
            size = 1,
            alpha = 0.4) +
  stat_smooth(aes(x = cloacal_temp_C,
                  y = TEWL_g_m2h,
                  color = region
                  ),
             formula = y ~ x,
             method = "lm",
             se = F,
             size = 1.6,
             alpha = 1) +
  theme_classic() +
  xlab("Cloacal Temperature (°C)") +
  ylab("") +
  #ylab(bquote('CEWL (g/'*m^2*'h)')) +
  #annotate("text", x = 1, y = 65, label = "a", size = 6) +
  scale_color_brewer(palette = "Set2",
                    name = "") +
```

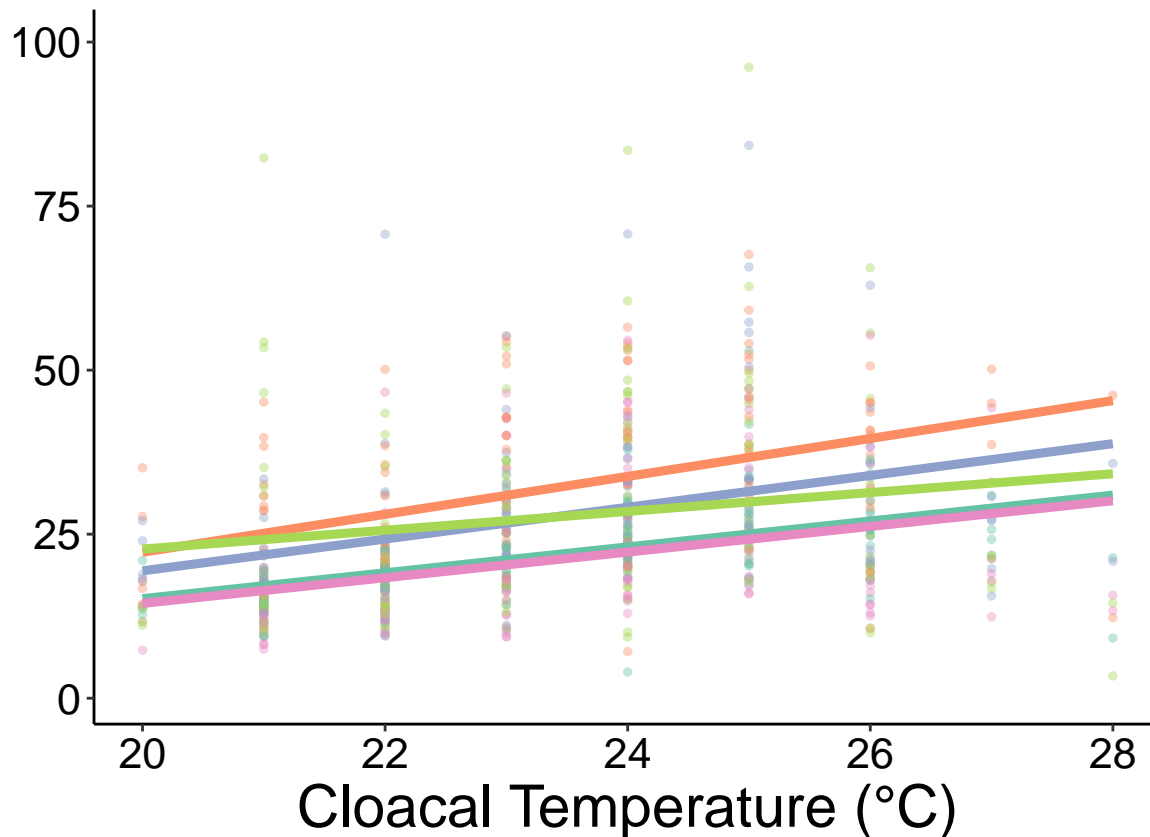
```

ylim(1, 100) +
xlim(20, 28) +
theme(text = element_text(color = "black",
                             family = "sans",
                             size = 22),
      axis.text = element_text(color = "black",
                                family = "sans",
                                size = 16),
      legend.text = element_text(color = "black",
                                  family = "sans",
                                  size = 26),
      plot.margin = unit(c(0.1,0,0.35,0.45), "cm"),
      legend.text.align = 0,
      legend.position = "none") -> CEWL_ctemp_fig
CEWL_ctemp_fig

```

Warning: Removed 49 rows containing non-finite values (stat_smooth).

Warning: Removed 49 rows containing missing values (geom_point).



```

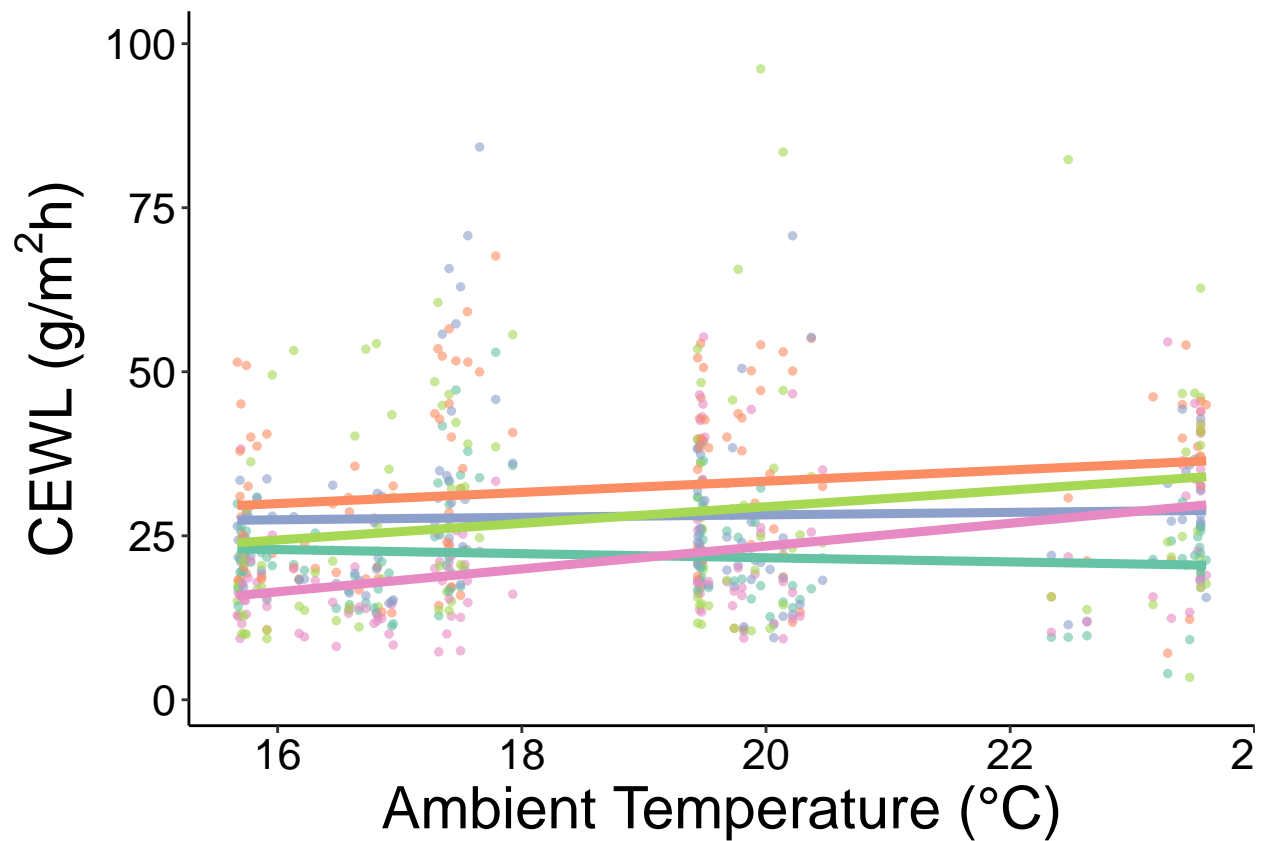
# export figure
#ggsave(filename = "CEWL_ctemp_fig.tiff",
#        plot = CEWL_ctemp_fig,
#        path = "./final_figures",
#        device = "tiff",
#        dpi = 1200,
#        width = 6, height = 4)

```

CEWL ~ Capture Temperature

```
CEWL_data_full %>%
  ggplot(data = .) +
  geom_point(aes(x = temp_C_interpol,
                 y = TEWL_g_m2h,
                 color = region
                ),
            size = 1,
            alpha = 0.6) +
  stat_smooth(aes(x = temp_C_interpol,
                  y = TEWL_g_m2h,
                  color = region
                 ),
             formula = y ~ x,
             method = "lm",
             se = F,
             size = 1.6,
             alpha = 1 ) +
  scale_color_brewer(palette = "Set2") +
  theme_classic() +
  xlab("Ambient Temperature (°C)") +
  #ylab("") +
  ylim(1, 100) +
  ylab(bquote('CEWL (g/*m2*h)')) +
  theme(text = element_text(color = "black",
                             family = "sans",
                             size = 22),
        axis.text = element_text(color = "black",
                                   family = "sans",
                                   size = 16),
        legend.text = element_text(color = "black",
                                     family = "sans",
                                     size = 26),
        plot.margin = unit(c(0.1,0,0.35,0.1), "cm"),
        legend.text.align = 0,
        legend.position = "none"
  ) -> cap_temp_CEWL
cap_temp_CEWL

## Warning: Removed 59 rows containing non-finite values (stat_smooth).
## Warning: Removed 59 rows containing missing values (geom_point).
```



CEWL ~ Capture VPD

```
CEWL_data_full %>%
  ggplot(data = .) +
  geom_jitter(aes(x = VPD_kPa_int,
                  y = TEWL_g_m2h,
                  color = region
                ),
             size = 1,
             alpha = 0.4) +
  stat_smooth(aes(x = VPD_kPa_int,
                  y = TEWL_g_m2h,
                  color = region
                ),
             formula = y ~ x,
             method = "lm",
             se = F,
             size = 1.6,
             alpha = 1 ) +
  theme_classic() +
  xlab("Vapor Pressure Deficit (kPa)") +
  #ylab(bquote('CEWL (g/'*m^2*'h)')) +
  ylab("") +
  #annotate("text", x = 1, y = 65, label = "a", size = 6) +
  scale_color_brewer(palette = "Set2",
                    name = "") +
```

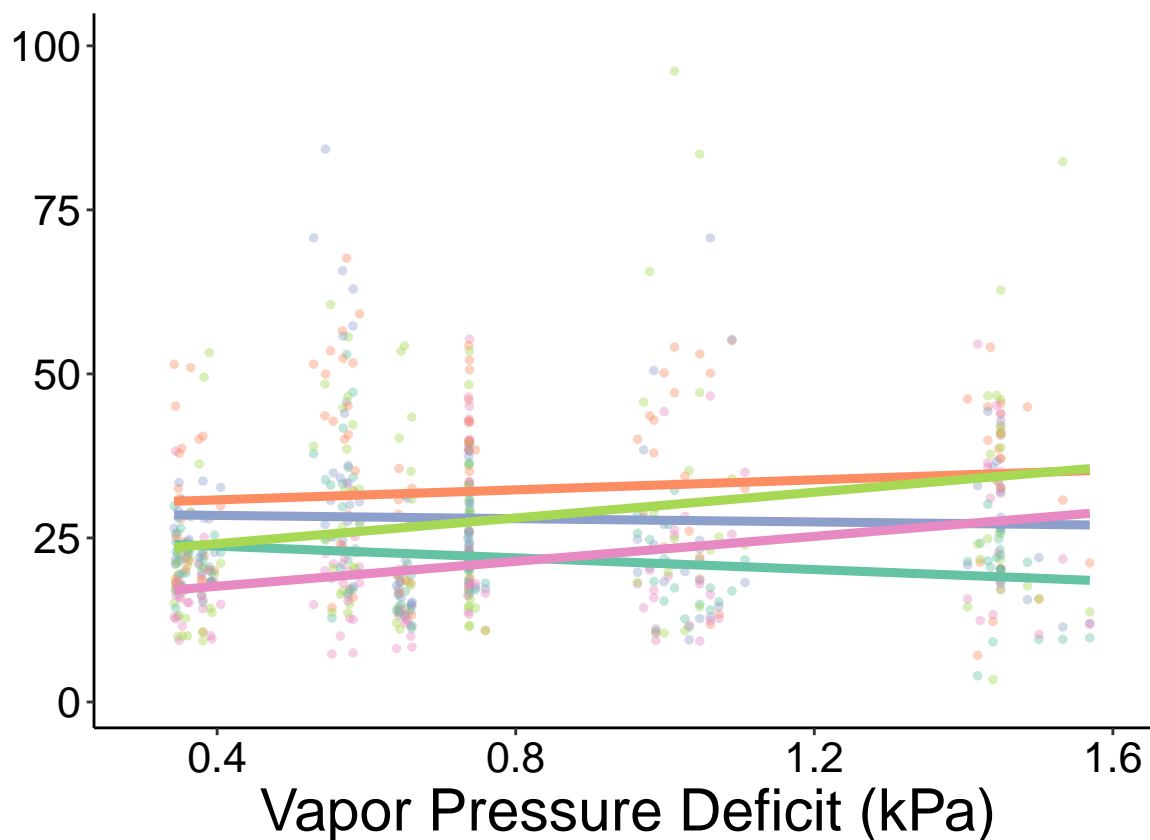
```

ylim(1, 100) +
xlim(0.3, 1.6) +
theme(text = element_text(color = "black",
                           family = "sans",
                           size = 22),
      axis.text = element_text(color = "black",
                                family = "sans",
                                size = 16),
      legend.text = element_text(color = "black",
                                  family = "sans",
                                  size = 26),
      legend.text.align = 0,
      plot.margin = unit(c(0.1,0,0.35,0.45), "cm"),
      legend.position = "none"
      #legend.position = c(0.15, 0.85)
    ) -> CEWL_vpd_fig
CEWL_vpd_fig

```

Warning: Removed 59 rows containing non-finite values (stat_smooth).

Warning: Removed 59 rows containing missing values (geom_point).



```

# export figure
#ggsave(filename = "CEWL_vpd_fig.tiff",
#       plot = CEWL_vpd_fig,
#       path = "./final_figures",
#       device = "tiff",
#       dpi = 1200,

```

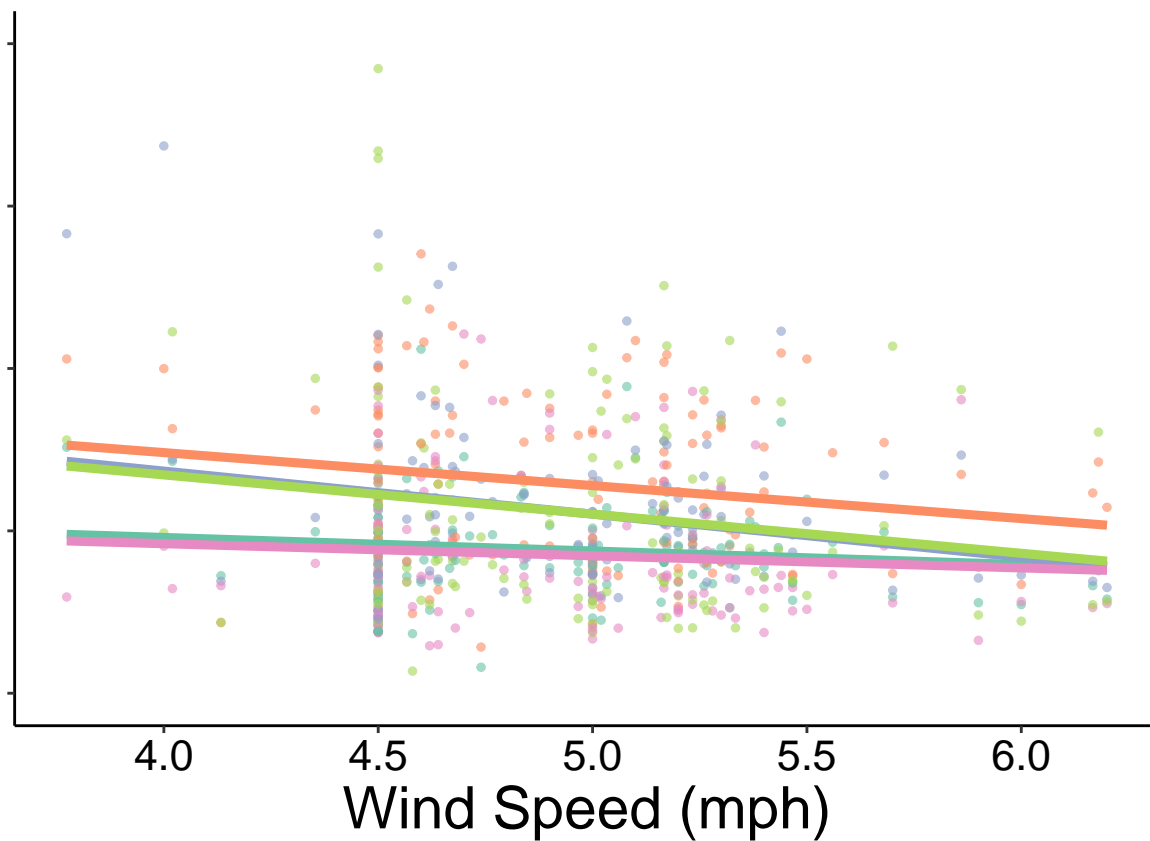
```
# width = 6, height = 4)
```

CEWL ~ Wind Speed

```
CEWL_data_full %>%
  ggplot(data = .) +
  geom_point(aes(x = Wind_mph_interpol,
                 y = TEWL_g_m2h,
                 color = region
                 ),
            size = 1,
            alpha = 0.6) +
  stat_smooth(aes(x = Wind_mph_interpol,
                  y = TEWL_g_m2h,
                  color = region
                  ),
             formula = y ~ x,
             method = "lm",
             se = F,
             size = 1.6,
             alpha = 1 ) +
  theme_classic() +
  scale_color_brewer(palette = "Set2") +
  xlab("Wind Speed (mph)") +
  #ylab(bquote('CEWL (g/'*m~2*'h)')) +
  ylab("") +
  ylim(0,100) +
  theme(text = element_text(color = "black",
                             family = "sans",
                             size = 22),
        axis.text = element_text(color = "black",
                                   family = "sans",
                                   size = 16),
        legend.text = element_text(color = "black",
                                    family = "sans",
                                    size = 26),
        axis.text.y = element_blank(),
        plot.margin = unit(c(0.1,0,0.35,0.45), "cm"),
        legend.text.align = 0,
        legend.position = "none"
  ) -> wind_CEWL_plot
wind_CEWL_plot
```

```
## Warning: Removed 59 rows containing non-finite values (stat_smooth).
```

```
## Warning: Removed 59 rows containing missing values (geom_point).
```



CEWL ~ Solar Rad

```
CEWL_data_full %>%
  ggplot(data = .) +
  geom_point(aes(x = Solar_rad_Wm2_interpol,
                 y = TEWL_g_m2h,
                 color = region
                ),
            size = 1,
            alpha = 0.6) +
  stat_smooth(aes(x = Solar_rad_Wm2_interpol,
                  y = TEWL_g_m2h,
                  color = region
                 ),
             formula = y ~ x,
             method = "lm",
             se = F,
             size = 1.6,
             alpha = 1 ) +
  theme_classic() +
  scale_color_brewer(palette = "Set2") +
  xlab(bquote('Solar Radiation (W/'*m^2*')')) +
  #ylab(bquote('CEWL (g/'*m^2*'h)')) +
  ylab("") +
  ylim(0,100) +
  theme(text = element_text(color = "black",
```



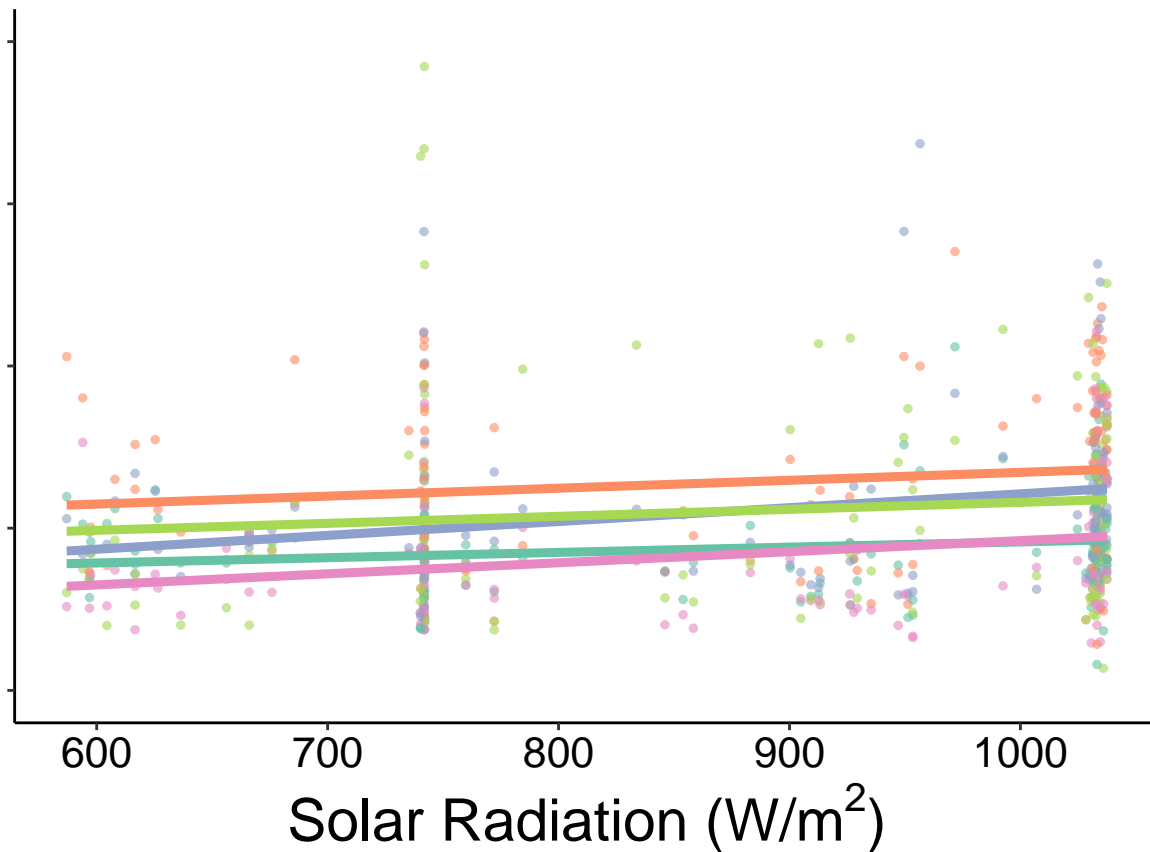
```

        family = "sans",
        size = 22),
axis.text = element_text(color = "black",
                          family = "sans",
                          size = 16),
legend.text = element_text(color = "black",
                           family = "sans",
                           size = 26),
axis.text.y = element_blank(),
plot.margin = unit(c(0.1,0,0,0.45), "cm"),
legend.text.align = 0,
legend.position = "none"
) -> sorad_CEWL_plot
sorad_CEWL_plot

```

Warning: Removed 59 rows containing non-finite values (stat_smooth).

Warning: Removed 59 rows containing missing values (geom_point).



CEWL ~ Measurement Temperature

```

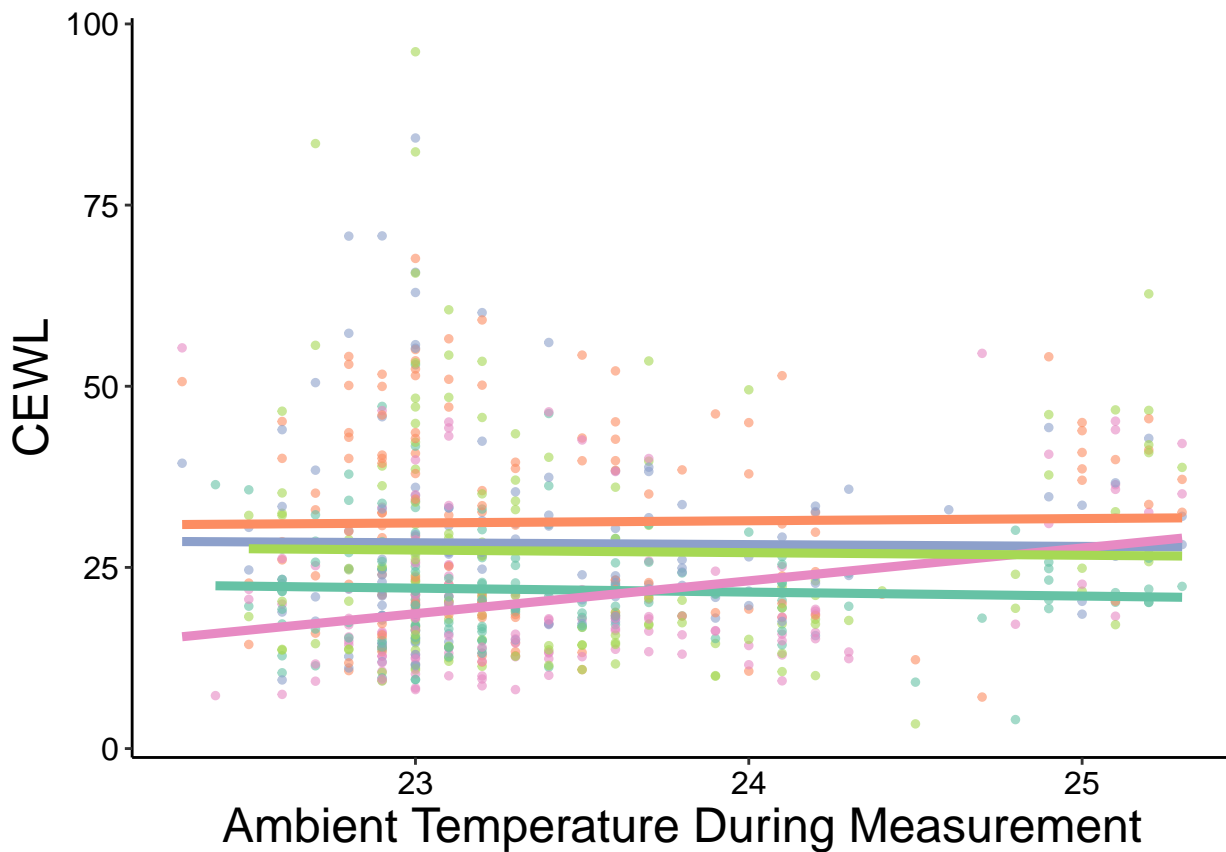
CEWL_data_full %>%
  ggplot(data = .) +
  geom_point(aes(x = ambient_temp_C,
                 y = TEWL_g_m2h,
                 color = region
                 ),

```

```

    size = 1,
    alpha = 0.6) +
stat_smooth(aes(x = ambient_temp_C,
  y = TEWL_g_m2h,
  color = region
),
  formula = y ~ x,
  method = "lm",
  se = F,
  size = 1.6,
  alpha = 1 ) +
theme_classic() +
scale_color_brewer(palette = "Set2") +
xlab("Ambient Temperature During Measurement") +
ylab("CEWL") +
theme(text = element_text(color = "black",
  family = "sans",
  size = 18),
  axis.text = element_text(color = "black",
    family = "sans",
    size = 12),
  legend.text.align = 0,
  legend.position = "none"
)

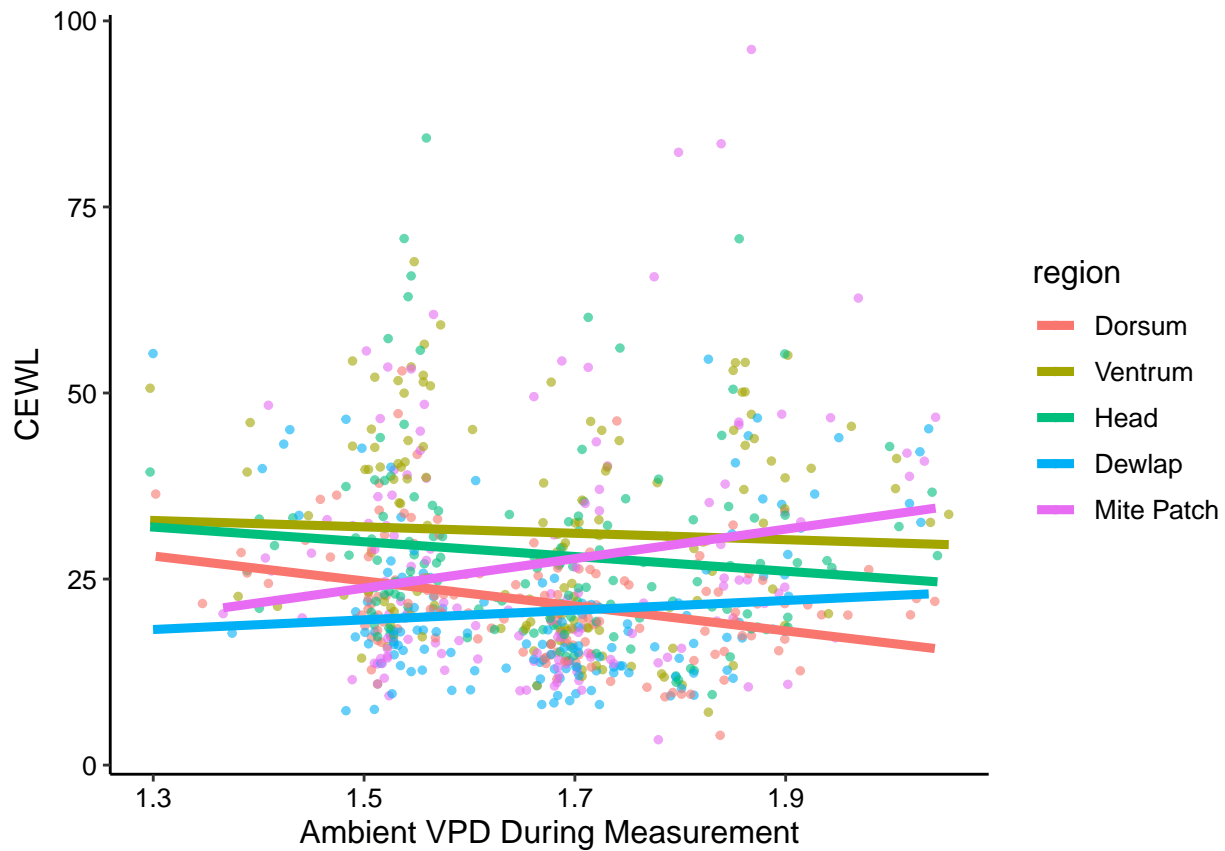
```



CEWL ~ Measurement VPD

Very interesting relationship! Mite patch CEWL decreases as VPD increases, but every other location appears to increase. In this case, an interaction term is warranted.

```
CEWL_data_full %>%
  ggplot(data = .) +
  geom_point(aes(x = VPD_kPa,
                 y = TEWL_g_m2h,
                 color = region
                ),
            size = 1,
            alpha = 0.6) +
  stat_smooth(aes(x = VPD_kPa,
                  y = TEWL_g_m2h,
                  color = region
                 ),
             formula = y ~ x,
             method = "lm",
             se = F,
             size = 1.6,
             alpha = 1 ) +
  theme_classic() +
  xlab("Ambient VPD During Measurement") +
  ylab("CEWL") +
  theme(text = element_text(color = "black",
                             family = "sans",
                             size = 12),
        axis.text = element_text(color = "black",
                                   family = "sans",
                                   size = 10),
        legend.text.align = 0)
```



CEWL ~ Individual

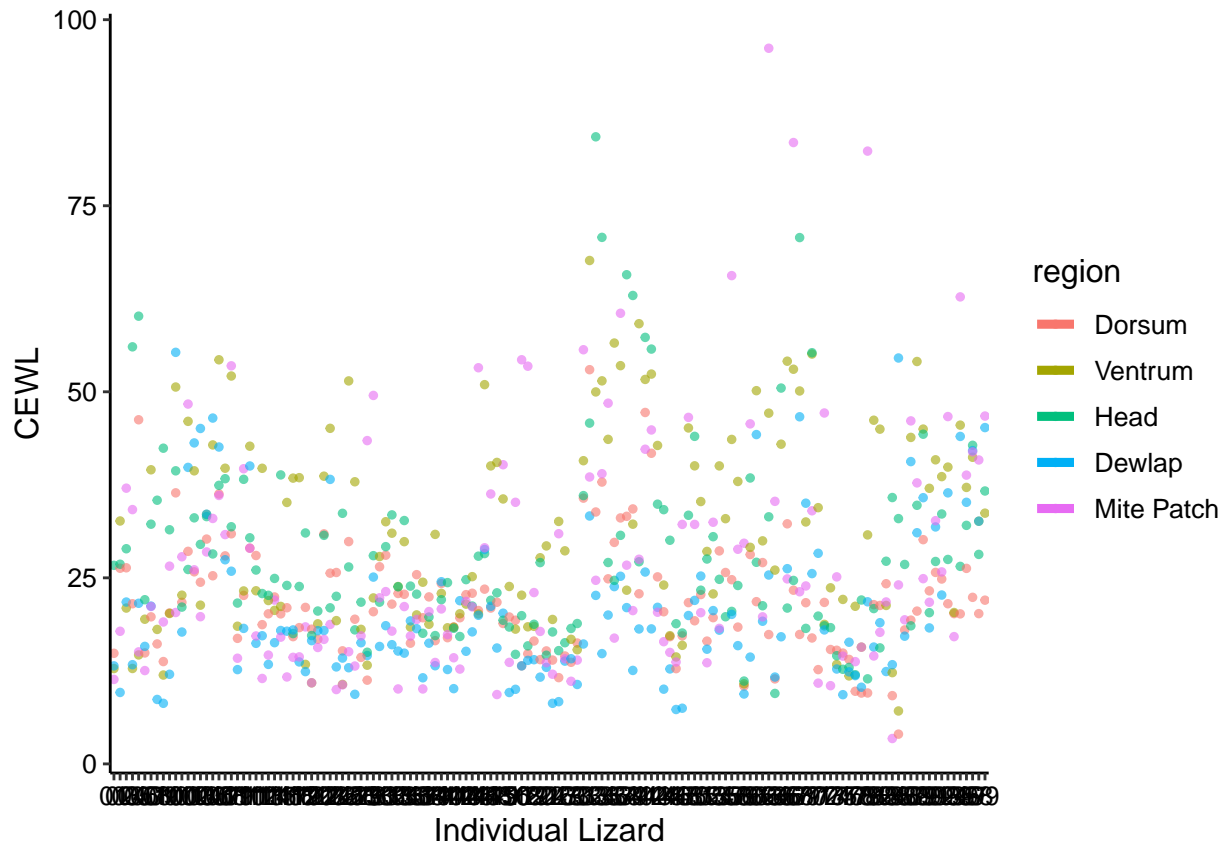
```
CEWL_data_full %>%
  ggplot(data = .) +
  geom_point(aes(x = individual_ID,
                 y = TEWL_g_m2h,
                 color = region
                 ),
            size = 1,
            alpha = 0.6) +
  stat_smooth(aes(x = individual_ID,
                  y = TEWL_g_m2h,
                  color = region
                  ),
             formula = y ~ x,
             method = "lm",
             se = F,
             size = 1.6,
             alpha = 1 ) +
  theme_classic() +
  xlab("Individual Lizard") +
  ylab("CEWL") +

  # just to get a better look
  # ylim(5, 40) +
```

```

theme(text = element_text(color = "black",
                             family = "sans",
                             size = 12),
      axis.text = element_text(color = "black",
                                family = "sans",
                                size = 10),
      legend.text.align = 0)

```



CEWL ~ SVL

```

CEWL_data_full %>%
  ggplot(data = .) +
  geom_point(aes(x = SVL_mm,
                  y = TEWL_g_m2h,
                  color = region
                ),
            size = 1,
            alpha = 0.6) +
  stat_smooth(aes(x = SVL_mm,
                   y = TEWL_g_m2h,
                   color = region
                 ),
            formula = y ~ x,
            method = "lm",
            se = F,
            size = 1.6,

```

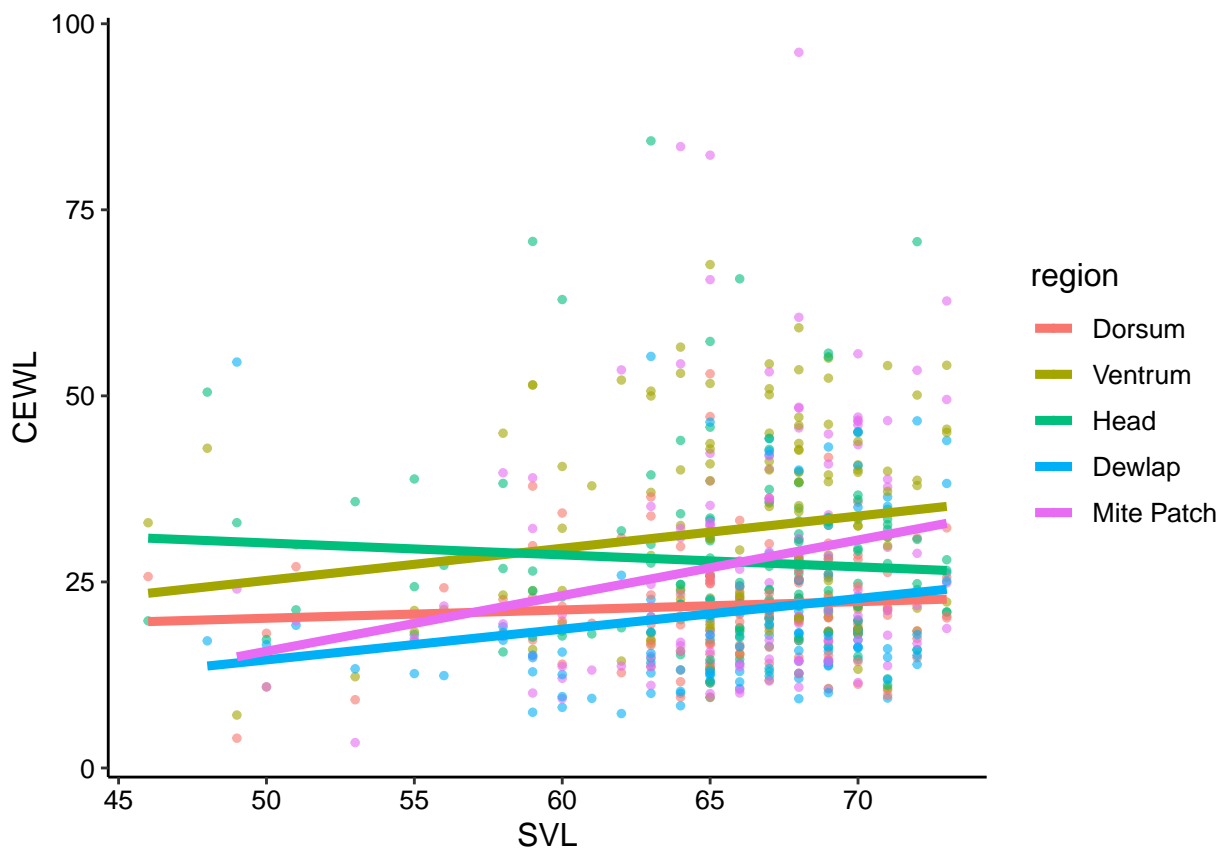
```

    alpha = 1 ) +
  theme_classic() +
  xlab("SVL") +
  ylab("CEWL") +
  theme(text = element_text(color = "black",
                             family = "sans",
                             size = 12),
        axis.text = element_text(color = "black",
                                   family = "sans",
                                   size = 10),
        legend.text.align = 0)

```

Warning: Removed 44 rows containing non-finite values (stat_smooth).

Warning: Removed 44 rows containing missing values (geom_point).



CEWL ~ SMI

```

CEWL_data_full %>%
  ggplot(data = .) +
  geom_point(aes(x = SMI,
                 y = TEWL_g_m2h,
                 color = region
                 ),
            size = 1,
            alpha = 0.4) +
  stat_smooth(aes(x = SMI,

```

```

        y = TEWL_g_m2h,
        color = region
      ),
      formula = y ~ x,
      method = "lm",
      se = F,
      size = 1.6,
      alpha = 1 ) +
  theme_classic() +
  xlab("Scaled Mass Index (g)") +
  ylab(bquote('CEWL (g / '*m^2~h*')')) +
  #annotate("text", x = 1, y = 65, label = "a", size = 6) +
  scale_color_brewer(palette = "Set2",
                     name = "") +

  ylim(1, 100) +
  xlim(2, 16) +
  scale_x_continuous(breaks = c(seq(2, 16, by = 2))) +
  theme(text = element_text(color = "black",
                             family = "sans",
                             size = 18),
        axis.text = element_text(color = "black",
                                   family = "sans",
                                   size = 14),
        legend.text = element_text(color = "black",
                                     family = "sans",
                                     size = 12),
        plot.margin = unit(c(0.1,0.5,0.1,0.1), "cm"),
        legend.text.align = 0,
        legend.position = c(0.15, 0.85)
  ) -> CEWL_SMI_fig

```

```

## Scale for 'x' is already present. Adding another scale for 'x', which will
## replace the existing scale.

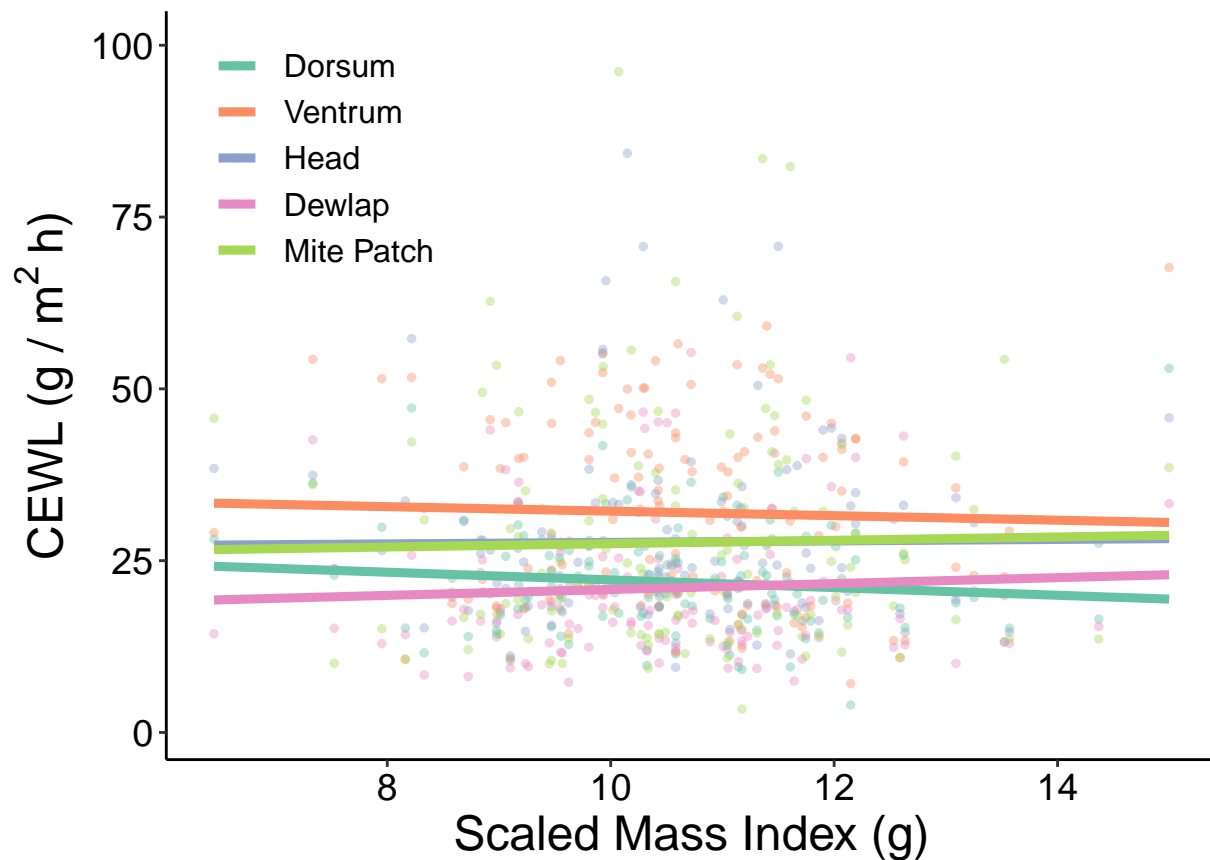
```

```
CEWL_SMI_fig
```

```

## Warning: Removed 44 rows containing non-finite values (stat_smooth).
## Warning: Removed 44 rows containing missing values (geom_point).

```



```
# export figure
#ggsave(filename = "CEWL_mass_fig.tiff",
#       plot = CEWL_mass_fig,
#       path = "./final_figures",
#       device = "tiff",
#       dpi = 1200,
#       width = 6, height = 4)
```

CEWL ~ Mass

Head has an opposite trend from all the other body regions, so we need an interaction term.

```
CEWL_data_full %>%
  ggplot(data = .) +
  geom_point(aes(x = mass_g,
                 y = TEWL_g_m2h,
                 color = region
                 ),
            size = 1,
            alpha = 0.4) +
  stat_smooth(aes(x = mass_g,
                  y = TEWL_g_m2h,
                  color = region
                  ),
             formula = y ~ x,
             method = "lm",
             se = F,
```



```

        size = 1.6,
        alpha = 1 ) +
theme_classic() +
xlab("Mass (g)") +
ylab("") +
#ylab(bquote('CEWL (g/'*m^2*'h)')) +
#annotate("text", x = 1, y = 65, label = "a", size = 6) +
scale_color_brewer(palette = "Set2",
                   name = "") +
ylim(1, 100) +
xlim(2, 16) +
scale_x_continuous(breaks = c(seq(2, 16, by = 2))) +
theme(text = element_text(color = "black",
                           family = "sans",
                           size = 22),
      axis.text = element_text(color = "black",
                                family = "sans",
                                size = 16),
      axis.text.y = element_blank(),
      legend.text = element_text(color = "black",
                                  family = "sans",
                                  size = 26),
      plot.margin = unit(c(0.1,0,0.35,0.45), "cm"),
      legend.text.align = 0,
      legend.position = "none"
      #legend.position = c(0.5, 0.5)
      ) -> CEWL_mass_fig

```

```

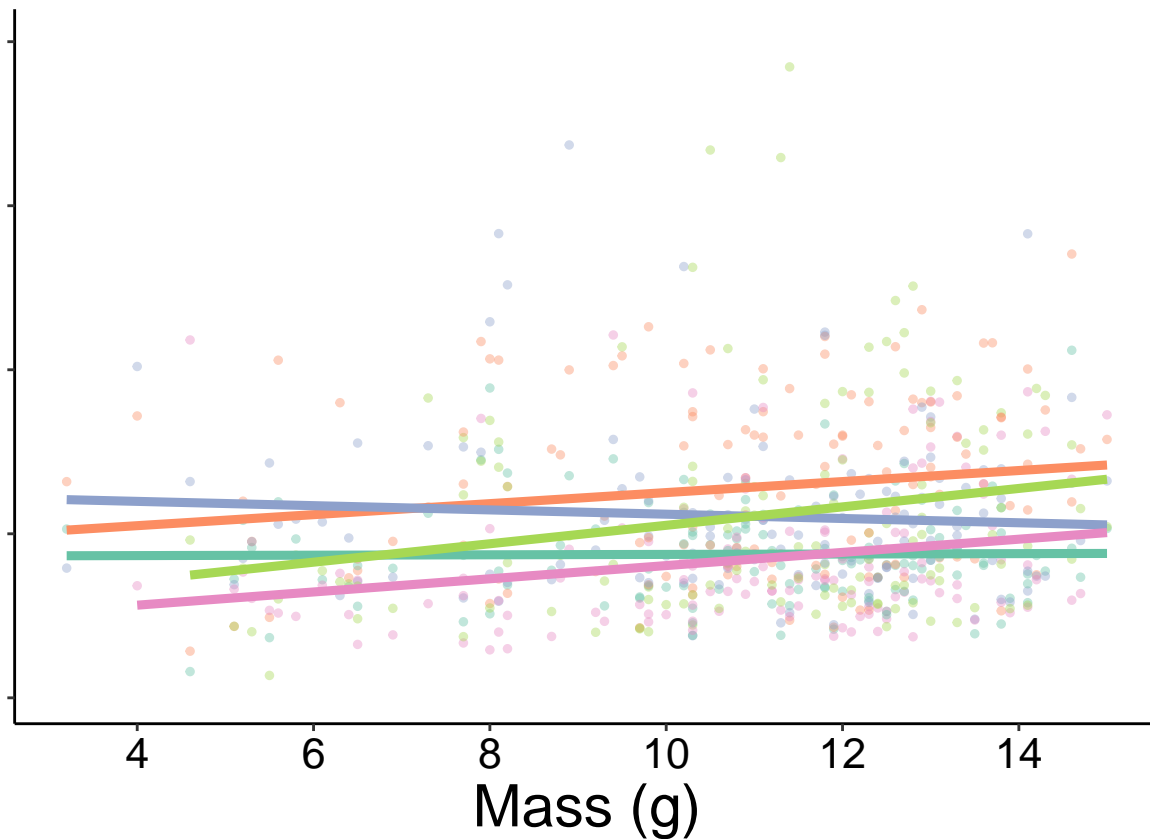
## Scale for 'x' is already present. Adding another scale for 'x', which will
## replace the existing scale.

```

```
CEWL_mass_fig
```

```
## Warning: Removed 44 rows containing non-finite values (stat_smooth).
```

```
## Warning: Removed 44 rows containing missing values (geom_point).
```



```
# MUST CHANGE COMMENTS ABOVE to produce this
CEWL_legend <- as_ggplot(get_legend(CEWL_mass_fig))
```

```
## Warning: Removed 44 rows containing non-finite values (stat_smooth).
```

```
## Warning: Removed 44 rows containing missing values (geom_point).
```

```
# export figure
#ggsave(filename = "CEWL_mass_fig.tiff",
#       plot = CEWL_mass_fig,
#       path = "./final_figures",
#       device = "tiff",
#       dpi = 1200,
#       width = 6, height = 4)
```

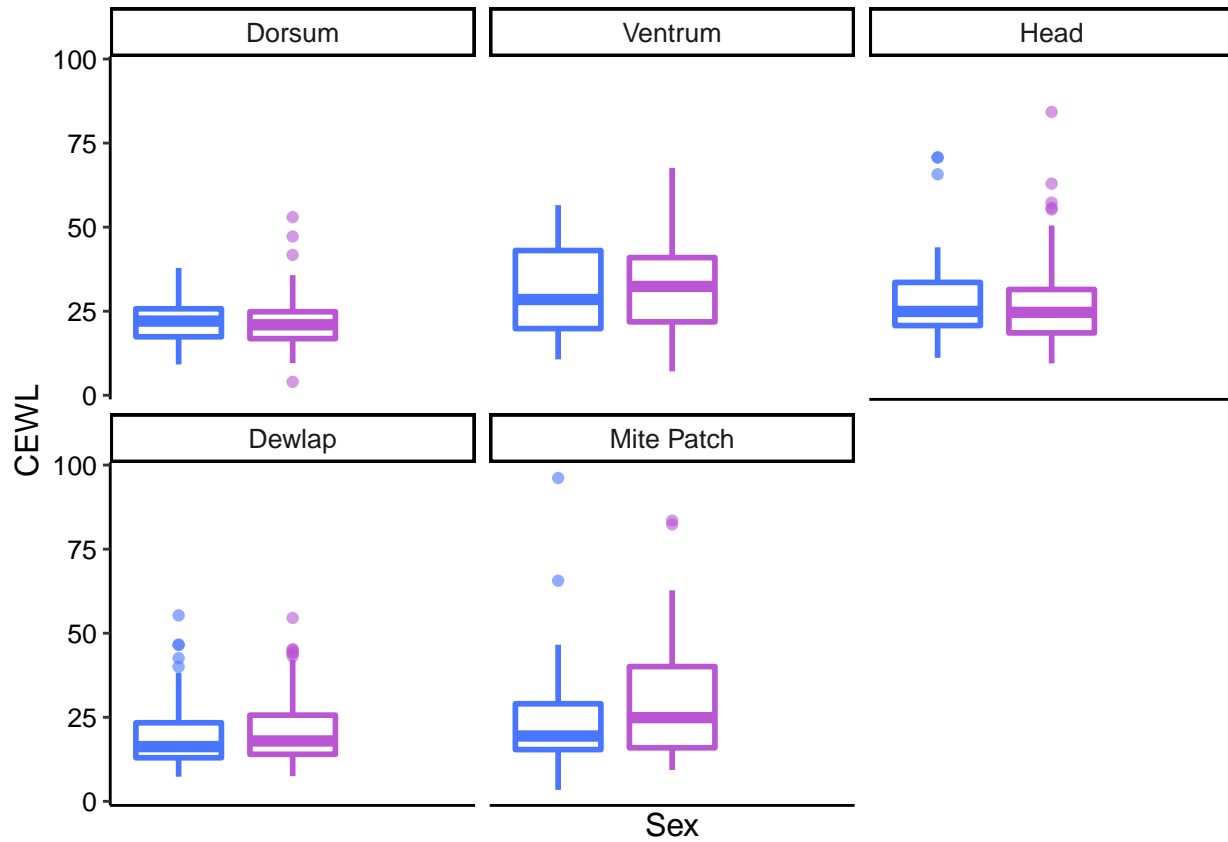
CEWL ~ Sex

```
CEWL_data_full %>%
  ggplot(data = .) +
  geom_boxplot(aes(x = sex_M_F,
                  y = TEWL_g_m2h,
                  color = sex_M_F
                  ),
              size = 1,
              alpha = 0.6) +
  facet_wrap(~region) +
  scale_color_manual(values = c("royalblue1", "mediumorchid")) +
```

```

scale_x_discrete(breaks = c(1,2,3)) +
theme_classic() +
xlab("Sex") +
ylab("CEWL") +
theme(text = element_text(color = "black", family = "sans", size = 12),
      axis.text = element_text(color = "black", family = "sans", size = 10),
      legend.text.align = 0,
      legend.position = "none")

```



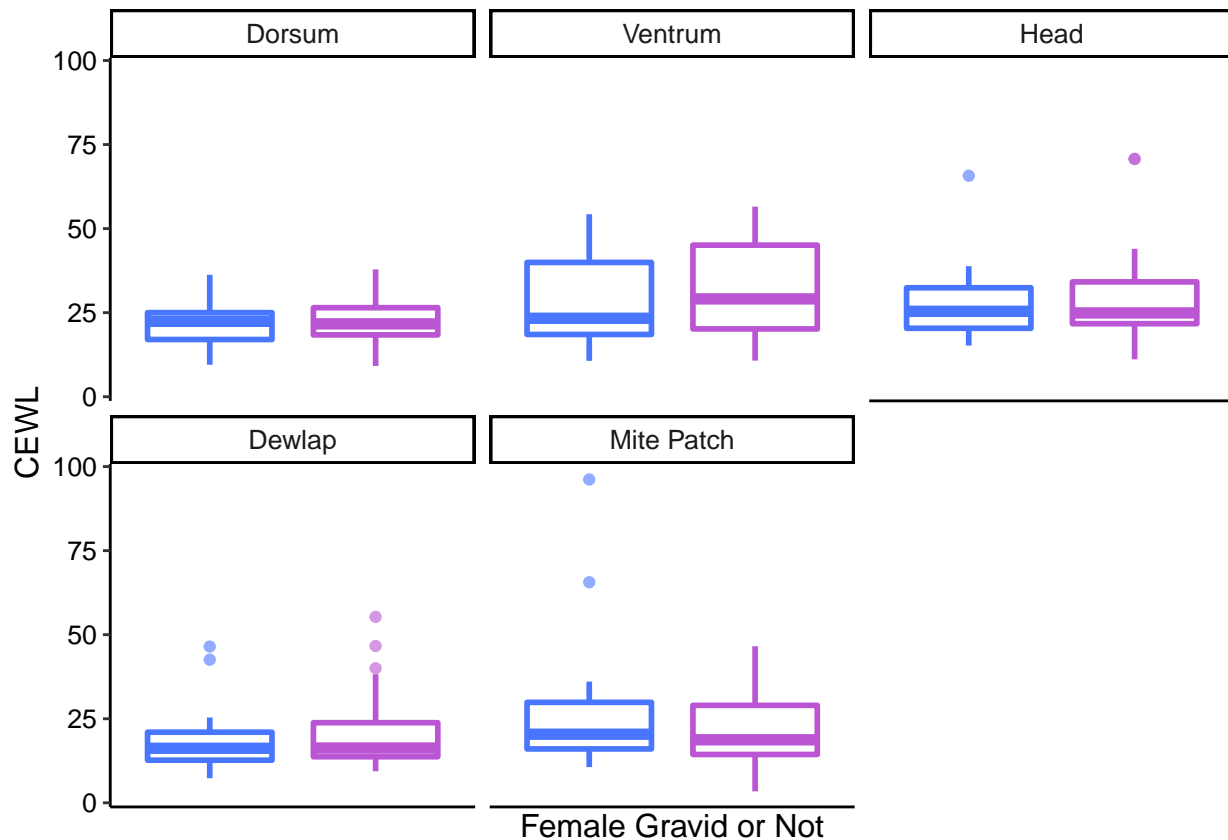
CEWL ~ Gravity

```

CEWL_data_full %>%
  dplyr::filter(sex_M_F == "F") %>%
  ggplot(data = .) +
  geom_boxplot(aes(x = gravid_Y_N,
                  y = TEWL_g_m2h,
                  color = gravid_Y_N
                  ),
              size = 1,
              alpha = 0.6) +
  facet_wrap(~region) +
  scale_color_manual(values = c("royalblue1", "mediumorchid")) +
  scale_x_discrete(breaks = c(1,2,3)) +
  theme_classic() +
  xlab("Female Gravid or Not") +
  ylab("CEWL") +

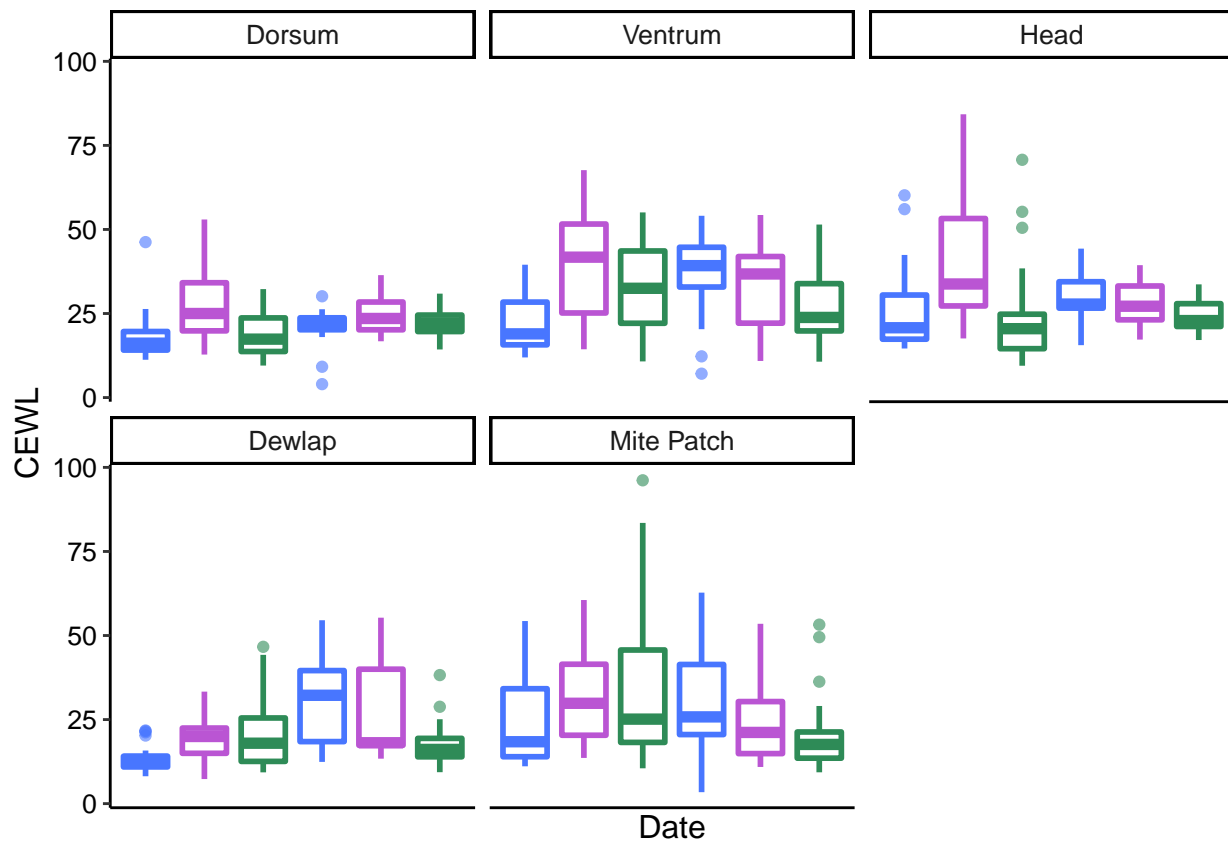
```

```
theme(text = element_text(color = "black", family = "sans", size = 12),
      axis.text = element_text(color = "black", family = "sans", size = 10),
      legend.text.align = 0,
      legend.position = "none")
```



CEWL ~ Week

```
CEWL_data_full %>%
  ggplot(data = .) +
  geom_boxplot(aes(x = as.factor(date),
                  y = TEWL_g_m2h,
                  color = as.factor(date)
                  ),
              size = 1,
              alpha = 0.6) +
  facet_wrap(~region) + # could not figure out how to change facet labels without changing underlying d
  scale_color_manual(values = c("royalblue1", "mediumorchid", "seagreen4",
                                "royalblue1", "mediumorchid", "seagreen4")) +
  scale_x_discrete(breaks = c(1,2,3)) +
  theme_classic() +
  xlab("Date") +
  ylab("CEWL") +
  theme(text = element_text(color = "black", family = "sans", size = 12),
        axis.text = element_text(color = "black", family = "sans", size = 10),
        legend.text.align = 0,
        legend.position = "none")
```



CEWL ~ holding time

```
CEWL_data_full %>%
  ggplot(data = .) +
  geom_point(aes(x = hold_time,
                 y = TEWL_g_m2h,
                 color = region
                 ),
            size = 1,
            alpha = 0.6) +
  stat_smooth(aes(x = hold_time,
                  y = TEWL_g_m2h,
                  color = region
                  ),
             formula = y ~ x,
             method = "lm",
             se = F,
             size = 1.6,
             alpha = 1 ) +
  theme_classic() +
  xlab("Holding Time (minutes)") +
  ylab("CEWL (g/m²/hr)") +
  theme(text = element_text(color = "black",
                             family = "sans",
                             size = 12),
        axis.text = element_text(color = "black",
```

```

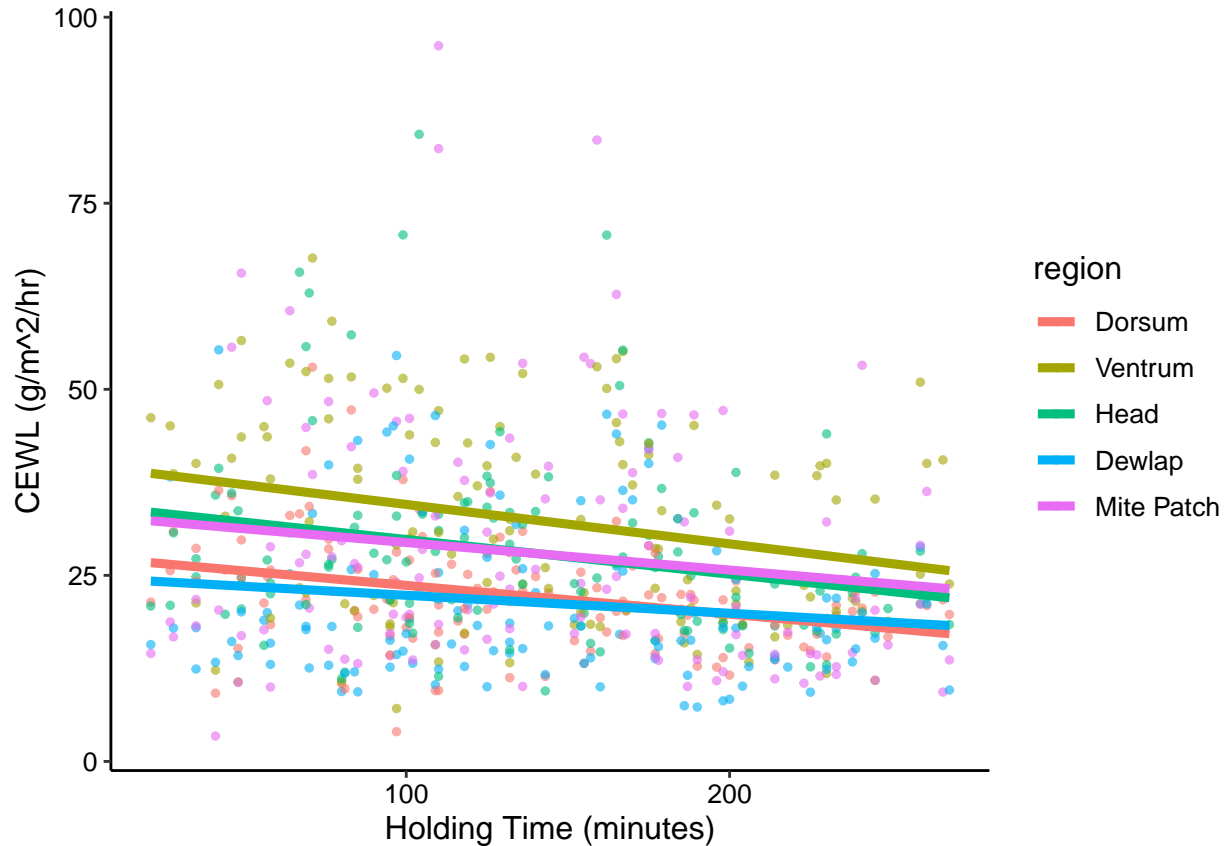
family = "sans",
size = 10),

legend.text.align = 0)

```

```
## Warning: Removed 69 rows containing non-finite values (stat_smooth).
```

```
## Warning: Removed 69 rows containing missing values (geom_point).
```



CEWL Multi-Figure

```

ggarrange(CEWL_vpd_fig, wind_CEWL_plot,
  cap_temp_CEWL, sorad_CEWL_plot,
  CEWL_ctemp_fig, CEWL_mass_fig,
  labels = c("A", "B", "C", "D", "E", "F"),
  font.label = list(size = 24, face = "bold", color = "black"),
  ncol = 2, nrow = 3,
  common.legend = TRUE,
  legend = "bottom"
) -> CEWL_multi_fig

```

```
## Warning: Removed 59 rows containing non-finite values (stat_smooth).
```

```
## Warning: Removed 59 rows containing missing values (geom_point).
```

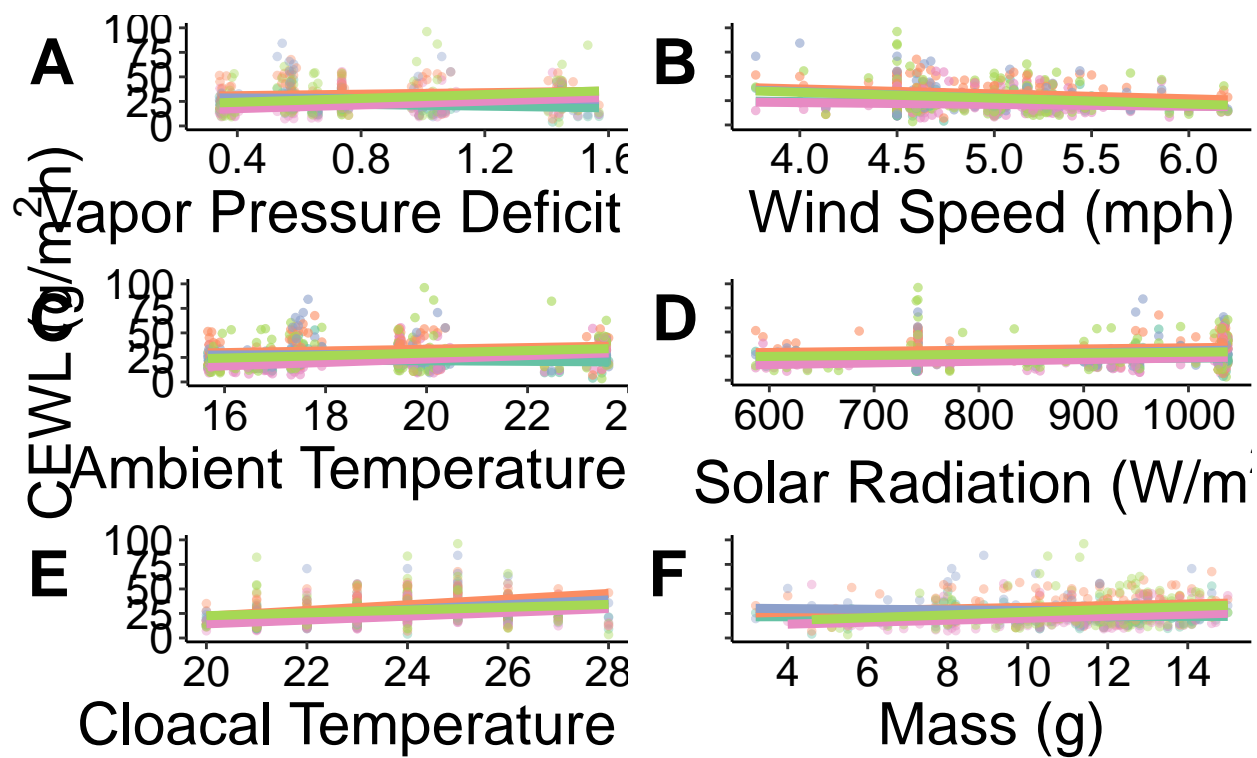
```
## Warning: Removed 59 rows containing non-finite values (stat_smooth).
```

```
## Warning: Removed 59 rows containing missing values (geom_point).
```

```
## Warning: Removed 59 rows containing non-finite values (stat_smooth).
```

```
## Warning: Removed 59 rows containing missing values (geom_point).
## Warning: Removed 59 rows containing non-finite values (stat_smooth).
## Warning: Removed 59 rows containing missing values (geom_point).
## Warning: Removed 59 rows containing non-finite values (stat_smooth).
## Warning: Removed 59 rows containing missing values (geom_point).
## Warning: Removed 49 rows containing non-finite values (stat_smooth).
## Warning: Removed 49 rows containing missing values (geom_point).
## Warning: Removed 44 rows containing non-finite values (stat_smooth).
## Warning: Removed 44 rows containing missing values (geom_point).
```

CEWL_multi_fig



um — Ventrums — Heads — Dewlaps — Mism

```
# export figure
ggsave(filename = "CEWL_multi_fig.jpeg",
        plot = CEWL_multi_fig,
        path = "./final_figures",
        device = "jpeg",
        dpi = 1200,
        width = 12, height = 14)
```

LMMs

Hematocrit

Models

Start with all the variables that may explain hematocrit. Female gravidity cannot be included because of the low sample size and number of contrasts.

FULL model:

```
hct_mod1 <- lm(data = morpho_blood_SMI,
               # response variable
               hematocrit_percent ~
               # predictor variables
               VPD_kPa_int*temp_C_interpol +
               Wind_mph_interpol + Solar_rad_Wm2_interpol +
               SMI + SVL_mm + mass_g + sex_M_F +
               date + hemolyzed)

summary(hct_mod1)
```

```
##
## Call:
## lm(formula = hematocrit_percent ~ VPD_kPa_int * temp_C_interpol +
##   Wind_mph_interpol + Solar_rad_Wm2_interpol + SMI + SVL_mm +
##   mass_g + sex_M_F + date + hemolyzed, data = morpho_blood_SMI)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -18.1941  -3.6239   0.3462   2.5602  14.9818
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -3.286e+01  2.811e+03  -0.012   0.991
## VPD_kPa_int      9.555e+00  4.315e+01   0.221   0.825
## temp_C_interpol  2.666e+00  2.943e+00   0.906   0.368
## Wind_mph_interpol 1.731e+00  1.776e+00   0.975   0.333
## Solar_rad_Wm2_interpol -1.039e-02  1.229e-02  -0.846   0.400
## SMI             -2.031e+00  1.887e+00  -1.076   0.285
## SVL_mm          -1.339e+00  9.095e-01  -1.472   0.145
## mass_g           2.792e+00  1.879e+00   1.486   0.141
## sex_M_FM         1.504e+00  1.358e+00   1.108   0.271
## date            5.479e-03  1.514e-01   0.036   0.971
## hemolyzedY       1.512e+00  1.424e+00   1.062   0.291
## VPD_kPa_int:temp_C_interpol -9.041e-01  1.192e+00  -0.759   0.450
##
## Residual standard error: 5.903 on 86 degrees of freedom
## (50 observations deleted due to missingness)
## Multiple R-squared:  0.1585, Adjusted R-squared:  0.05081
## F-statistic: 1.472 on 11 and 86 DF,  p-value: 0.157
```

use VIF to look for multicollinearity:

```
hct_mod1_VIFs <- data.frame(VIF = car::vif(hct_mod1)) %>%
  arrange(desc(VIF))
hct_mod1_VIFs
```



```
##                                VIF
## VPD_kPa_int                   686.831736
## VPD_kPa_int:temp_C_interpol 365.719539
## temp_C_interpol              133.547720
## mass_g                       68.600937
## SVL_mm                      68.241245
## SMI                          17.763173
## Solar_rad_Wm2_interpol       8.447012
## date                         5.456239
## Wind_mph_interpol            1.467925
## hemolyzed                    1.325258
## sex_M_F                      1.190854
```

drop VPD*temp interaction:

```
hct_mod2 <- lm(data = morpho_blood_SMI,
               # response variable
               hematocrit_percent ~
               # predictor variables
               VPD_kPa_int + temp_C_interpol +
               Wind_mph_interpol + Solar_rad_Wm2_interpol +
               SMI + SVL_mm + mass_g + sex_M_F +
               date + hemolyzed)
hct_mod2_VIFs <- data.frame(VIF = car::vif(hct_mod2)) %>%
  arrange(desc(VIF))
hct_mod2_VIFs
```

```
##                                VIF
## temp_C_interpol              105.990349
## VPD_kPa_int                 100.623056
## mass_g                      67.495792
## SVL_mm                     66.954120
## SMI                        17.401124
## Solar_rad_Wm2_interpol      5.014458
## date                       3.722299
## Wind_mph_interpol           1.458918
## sex_M_F                    1.184101
## hemolyzed                   1.182898
```

drop temp:

```
hct_mod3 <- lm(data = morpho_blood_SMI,
               # response variable
               hematocrit_percent ~
               # predictor variables
               VPD_kPa_int +
               Wind_mph_interpol + Solar_rad_Wm2_interpol +
               SMI + SVL_mm + mass_g + sex_M_F +
               date + hemolyzed)
hct_mod3_VIFs <- data.frame(VIF = car::vif(hct_mod3)) %>%
  arrange(desc(VIF))
hct_mod3_VIFs
```

```
##                                VIF
## mass_g                      67.463103
## SVL_mm                     66.913125
```

```
## SMI                17.396694
## date               1.267231
## Wind_mph_interpol  1.204614
## sex_M_F            1.183867
## hemolyzed          1.159591
## VPD_kPa_int        1.147005
## Solar_rad_Wm2_interpol 1.117964
```

drop SVL:

```
hct_mod4 <- lm(data = morpho_blood_SMI,
               # response variable
               hematocrit_percent ~
               # predictor variables
               VPD_kPa_int +
               Wind_mph_interpol + Solar_rad_Wm2_interpol +
               SMI + mass_g + sex_M_F +
               date + hemolyzed)
hct_mod4_VIFs <- data.frame(VIF = car::vif(hct_mod4)) %>%
  arrange(desc(VIF))
hct_mod4_VIFs
```

```
##                VIF
## date           1.249210
## mass_g         1.235449
## Wind_mph_interpol 1.195602
## sex_M_F        1.182238
## SMI            1.158255
## hemolyzed       1.156377
## Solar_rad_Wm2_interpol 1.103715
## VPD_kPa_int     1.072780
```

Now things are not badly collinear and we can carry out model selection based on t-values and AIC.

```
summary(hct_mod4)
```

```
##
## Call:
## lm(formula = hematocrit_percent ~ VPD_kPa_int + Wind_mph_interpol +
##   Solar_rad_Wm2_interpol + SMI + mass_g + sex_M_F + date +
##   hemolyzed, data = morpho_blood_SMI)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -18.0943  -3.4510   0.1912   2.9314  16.9078
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -1.766e+03  1.368e+03  -1.291   0.2002
## VPD_kPa_int      2.999e+00  1.720e+00   1.743   0.0847 .
## Wind_mph_interpol  3.905e-01  1.617e+00   0.242   0.8097
## Solar_rad_Wm2_interpol -5.334e-03  4.480e-03  -1.191   0.2369
## SMI              6.870e-01  4.861e-01   1.413   0.1610
## mass_g           5.480e-02  2.543e-01   0.216   0.8299
## sex_M_FM         1.626e+00  1.365e+00   1.192   0.2366
## date             9.560e-02  7.307e-02   1.308   0.1941
```

```
## hemolyzedY          7.940e-01  1.342e+00  0.592  0.5555
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5.954 on 89 degrees of freedom
## (50 observations deleted due to missingness)
## Multiple R-squared:  0.1139, Adjusted R-squared:  0.03427
## F-statistic:  1.43 on 8 and 89 DF,  p-value: 0.195
```

```
drop1(hct_mod4)
```

```
## Single term deletions
##
## Model:
## hematocrit_percent ~ VPD_kPa_int + Wind_mph_interpol + Solar_rad_Wm2_interpol +
## SMI + mass_g + sex_M_F + date + hemolyzed
##
```

	Df	Sum of Sq	RSS	AIC
<none>			3155.2	358.24
VPD_kPa_int	1	107.753	3262.9	359.53
Wind_mph_interpol	1	2.069	3157.3	356.30
Solar_rad_Wm2_interpol	1	50.273	3205.5	357.79
SMI	1	70.827	3226.0	358.42
mass_g	1	1.646	3156.8	356.29
sex_M_F	1	50.339	3205.5	357.79
date	1	60.685	3215.9	358.11
hemolyzed	1	12.418	3167.6	356.62

```
drop mass:
```

```
hct_mod5 <- lm(data = morpho_blood_SMI,
               # response variable
               hematocrit_percent ~
               # predictor variables
               VPD_kPa_int +
               Wind_mph_interpol + Solar_rad_Wm2_interpol +
               SMI + sex_M_F +
               date + hemolyzed)
summary(hct_mod5)
```

```
##
## Call:
## lm(formula = hematocrit_percent ~ VPD_kPa_int + Wind_mph_interpol +
## Solar_rad_Wm2_interpol + SMI + sex_M_F + date + hemolyzed,
## data = morpho_blood_SMI)
##
## Residuals:
```

	Min	1Q	Median	3Q	Max
	-18.0089	-3.3923	0.1318	2.6035	17.0617

```
##
## Coefficients:
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	-1.747e+03	1.358e+03	-1.286	0.2017
VPD_kPa_int	3.011e+00	1.710e+00	1.761	0.0816
Wind_mph_interpol	4.224e-01	1.601e+00	0.264	0.7925
Solar_rad_Wm2_interpol	-5.368e-03	4.453e-03	-1.205	0.2312
SMI	7.074e-01	4.743e-01	1.491	0.1394

```
## sex_M_FM          1.694e+00  1.321e+00  1.282  0.2031
## date              9.461e-02  7.254e-02  1.304  0.1955
## hemolyzedY        7.243e-01  1.295e+00  0.559  0.5774
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5.922 on 90 degrees of freedom
## (50 observations deleted due to missingness)
## Multiple R-squared:  0.1135, Adjusted R-squared:  0.0445
## F-statistic: 1.645 on 7 and 90 DF,  p-value: 0.1329
```

```
drop1(hct_mod5)
```

```
## Single term deletions
##
## Model:
## hematocrit_percent ~ VPD_kPa_int + Wind_mph_interpol + Solar_rad_Wm2_interpol +
## SMI + sex_M_F + date + hemolyzed
##
```

	Df	Sum of Sq	RSS	AIC
<none>			3156.8	356.29
VPD_kPa_int	1	108.778	3265.6	357.61
Wind_mph_interpol	1	2.441	3159.3	354.37
Solar_rad_Wm2_interpol	1	50.973	3207.8	355.86
SMI	1	78.018	3234.8	356.68
sex_M_F	1	57.662	3214.5	356.06
date	1	59.666	3216.5	356.13
hemolyzed	1	10.970	3167.8	354.63

drop wind:

```
hct_mod6 <- lm(data = morpho_blood_SMI,
               # response variable
               hematocrit_percent ~
               # predictor variables
               VPD_kPa_int +
               Solar_rad_Wm2_interpol +
               SMI + sex_M_F +
               date + hemolyzed)
```

```
summary(hct_mod6)
```

```
##
## Call:
## lm(formula = hematocrit_percent ~ VPD_kPa_int + Solar_rad_Wm2_interpol +
## SMI + sex_M_F + date + hemolyzed, data = morpho_blood_SMI)
##
## Residuals:
```

	Min	1Q	Median	3Q	Max
	-18.0303	-3.3830	0.0463	2.5747	17.0149

```
##
## Coefficients:
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	-1.859e+03	1.283e+03	-1.449	0.1509
VPD_kPa_int	2.982e+00	1.698e+00	1.757	0.0823
Solar_rad_Wm2_interpol	-5.099e-03	4.312e-03	-1.182	0.2401
SMI	7.038e-01	4.717e-01	1.492	0.1391
sex_M_FM	1.698e+00	1.314e+00	1.292	0.1997

```
## date                1.007e-01  6.842e-02  1.472  0.1446
## hemolyzedY          7.156e-01  1.288e+00  0.556  0.5799
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5.892 on 91 degrees of freedom
## (50 observations deleted due to missingness)
## Multiple R-squared:  0.1128, Adjusted R-squared:  0.05427
## F-statistic: 1.928 on 6 and 91 DF,  p-value: 0.08464
```

```
drop1(hct_mod6)
```

```
## Single term deletions
##
## Model:
## hematocrit_percent ~ VPD_kPa_int + Solar_rad_Wm2_interpol + SMI +
##   sex_M_F + date + hemolyzed
##
```

	Df	Sum of Sq	RSS	AIC
<none>			3159.3	354.37
VPD_kPa_int	1	107.130	3266.4	355.63
Solar_rad_Wm2_interpol	1	48.538	3207.8	353.86
SMI	1	77.298	3236.6	354.74
sex_M_F	1	57.933	3217.2	354.15
date	1	75.188	3234.5	354.67
hemolyzed	1	10.716	3170.0	352.70

```
drop hemolyzed:
```

```
hct_mod7 <- lm(data = morpho_blood_SMI,
               # response variable
               hematocrit_percent ~
               # predictor variables
               VPD_kPa_int +
               Solar_rad_Wm2_interpol +
               SMI + sex_M_F +
               date)
```

```
summary(hct_mod7)
```

```
##
## Call:
## lm(formula = hematocrit_percent ~ VPD_kPa_int + Solar_rad_Wm2_interpol +
##   SMI + sex_M_F + date, data = morpho_blood_SMI)
##
## Residuals:
```

	Min	1Q	Median	3Q	Max
	-18.2297	-3.7562	0.2711	3.1142	17.1619

```
##
## Coefficients:
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	-1.632e+03	1.057e+03	-1.544	0.1254
VPD_kPa_int	3.066e+00	1.484e+00	2.066	0.0411 *
Solar_rad_Wm2_interpol	-4.453e-03	3.582e-03	-1.243	0.2164
SMI	4.487e-01	4.306e-01	1.042	0.2997
sex_M_FM	2.262e+00	1.129e+00	2.003	0.0476 *
date	8.866e-02	5.627e-02	1.576	0.1179

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5.754 on 114 degrees of freedom
## (28 observations deleted due to missingness)
## Multiple R-squared:  0.1026, Adjusted R-squared:  0.06327
## F-statistic: 2.607 on 5 and 114 DF,  p-value: 0.02849
```

```
drop1(hct_mod7)
```

```
## Single term deletions
##
## Model:
## hematocrit_percent ~ VPD_kPa_int + Solar_rad_Wm2_interpol + SMI +
##   sex_M_F + date
##
```

	Df	Sum of Sq	RSS	AIC
<none>			3774.6	425.83
VPD_kPa_int	1	141.307	3916.0	428.24
Solar_rad_Wm2_interpol	1	51.172	3825.8	425.44
SMI	1	35.942	3810.6	424.97
sex_M_F	1	132.828	3907.5	427.98
date	1	82.198	3856.8	426.41

```
drop SMI:
```

```
hct_mod8 <- lm(data = morpho_blood_SMI,
               # response variable
               hematocrit_percent ~
               # predictor variables
               VPD_kPa_int +
               Solar_rad_Wm2_interpol +
               sex_M_F +
               date)
```

```
summary(hct_mod8)
```

```
##
## Call:
## lm(formula = hematocrit_percent ~ VPD_kPa_int + Solar_rad_Wm2_interpol +
##   sex_M_F + date, data = morpho_blood_SMI)
##
## Residuals:
```

	Min	1Q	Median	3Q	Max
	-17.8461	-3.5790	0.1439	3.0483	18.0026

```
##
## Coefficients:
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	-1.395e+03	1.033e+03	-1.351	0.1794
VPD_kPa_int	3.040e+00	1.485e+00	2.048	0.0428 *
Solar_rad_Wm2_interpol	-3.684e-03	3.506e-03	-1.051	0.2956
sex_M_FM	2.451e+00	1.115e+00	2.197	0.0300 *
date	7.626e-02	5.502e-02	1.386	0.1684

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5.756 on 115 degrees of freedom
## (28 observations deleted due to missingness)
## Multiple R-squared:  0.09408,    Adjusted R-squared:  0.06257
```

```
## F-statistic: 2.986 on 4 and 115 DF, p-value: 0.02185
```

```
drop1(hct_mod8)
```

```
## Single term deletions
```

```
##
```

```
## Model:
```

```
## hematocrit_percent ~ VPD_kPa_int + Solar_rad_Wm2_interpol + sex_M_F +
```

```
## date
```

	Df	Sum of Sq	RSS	AIC
<none>			3810.6	424.97
VPD_kPa_int	1	138.974	3949.6	427.26
Solar_rad_Wm2_interpol	1	36.578	3847.2	424.11
sex_M_F	1	159.995	3970.6	427.90
date	1	63.656	3874.2	424.95

```
drop solar radiation:
```

```
hct_mod9 <- lm(data = morpho_blood_SMI,  
               # response variable  
               hematocrit_percent ~  
               # predictor variables  
               VPD_kPa_int +  
               sex_M_F +  
               date)
```

```
summary(hct_mod9)
```

```
##
```

```
## Call:
```

```
## lm(formula = hematocrit_percent ~ VPD_kPa_int + sex_M_F + date,
```

```
## data = morpho_blood_SMI)
```

```
##
```

```
## Residuals:
```

	Min	1Q	Median	3Q	Max
	-18.2141	-3.6316	0.3251	3.1251	17.3605

```
##
```

```
## Coefficients:
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	-1.686e+03	9.953e+02	-1.694	0.0929 .
VPD_kPa_int	2.757e+00	1.461e+00	1.888	0.0616 .
sex_M_FM	2.415e+00	1.115e+00	2.166	0.0324 *
date	9.161e-02	5.306e-02	1.727	0.0869 .

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
```

```
## Residual standard error: 5.759 on 116 degrees of freedom
```

```
## (28 observations deleted due to missingness)
```

```
## Multiple R-squared:  0.08538, Adjusted R-squared:  0.06173
```

```
## F-statistic: 3.61 on 3 and 116 DF, p-value: 0.01547
```

```
drop1(hct_mod9)
```

```
## Single term deletions
```

```
##
```

```
## Model:
```

```
## hematocrit_percent ~ VPD_kPa_int + sex_M_F + date
```

	Df	Sum of Sq	RSS	AIC
--	----	-----------	-----	-----

```
## <none>                3847.2 424.11
## VPD_kPa_int    1    118.182 3965.4 425.74
## sex_M_F        1    155.542 4002.7 426.87
## date           1     98.863 3946.0 425.16
```

drop date:

```
hct_mod10 <- lm(data = morpho_blood_SMI,
                 # response variable
                 hematocrit_percent ~
                 # predictor variables
                 VPD_kPa_int +
                 sex_M_F)
summary(hct_mod10)
```

```
##
## Call:
## lm(formula = hematocrit_percent ~ VPD_kPa_int + sex_M_F, data = morpho_blood_SMI)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -19.6708  -3.4437   0.3852   2.9727  17.9685
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   32.257      1.322   24.395  <2e-16 ***
## VPD_kPa_int    1.983      1.402    1.415   0.1599
## sex_M_FM       2.312      1.123    2.059   0.0418 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5.807 on 117 degrees of freedom
## (28 observations deleted due to missingness)
## Multiple R-squared:  0.06188,    Adjusted R-squared:  0.04585
## F-statistic: 3.859 on 2 and 117 DF,  p-value: 0.02383
```

```
drop1(hct_mod10)
```

```
## Single term deletions
##
## Model:
## hematocrit_percent ~ VPD_kPa_int + sex_M_F
##              Df Sum of Sq    RSS    AIC
## <none>                3946.0 425.16
## VPD_kPa_int    1     67.486 4013.5 425.19
## sex_M_F        1    142.923 4089.0 427.43
```

drop VPD:

```
hct_mod11 <- lm(data = morpho_blood_SMI,
                 # response variable
                 hematocrit_percent ~
                 # predictor variables
                 sex_M_F)
summary(hct_mod11)
```

```
##
```



```
## Call:
## lm(formula = hematocrit_percent ~ sex_M_F, data = morpho_blood_SMI)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -20.3247  -3.3247   0.6753   3.3409  17.6753
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  33.6591     0.8763  38.410  <2e-16 ***
## sex_M_FM      2.6656     1.0985   2.427  0.0167 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5.813 on 119 degrees of freedom
## (27 observations deleted due to missingness)
## Multiple R-squared:  0.04715,    Adjusted R-squared:  0.03914
## F-statistic: 5.888 on 1 and 119 DF,  p-value: 0.01674
```

```
drop1(hct_mod11)
```

```
## Single term deletions
##
## Model:
## hematocrit_percent ~ sex_M_F
##           Df Sum of Sq  RSS   AIC
## <none>                 4020.8 427.92
## sex_M_F  1       198.95 4219.7 431.76
```

finally, test the null model

```
hct_mod_null <- lm(data = morpho_blood_SMI,
                    # response variable
                    hematocrit_percent ~ 1)
summary(hct_mod_null)
```

```
##
## Call:
## lm(formula = hematocrit_percent ~ 1, data = morpho_blood_SMI)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -19.3554  -2.3554  -0.3554   2.6446  18.6446
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  35.3554     0.5391  65.58  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5.93 on 120 degrees of freedom
## (27 observations deleted due to missingness)
```

```
drop1(hct_mod_null)
```

```
## Single term deletions
##
```

```
## Model:
## hematocrit_percent ~ 1
##           Df Sum of Sq    RSS    AIC
## <none>             4219.7 431.76
```

Selection

models 4-11 and the null model are the ones we should compare. models 1-3 had serious multicollinearity thus are not trustworthy models.

```
hct_models <- list(hct_mod4, hct_mod5, hct_mod6, hct_mod7,
                  hct_mod8, hct_mod9, hct_mod10, hct_mod11,
                  hct_mod_null)
```

#specify model names

```
hct_mod_names <- c('(model 4) ~ ',
                  '(model 5) ~ ',
                  '(model 6) ~ ',
                  '(model 7) ~ ',
                  '(model 8) ~ ',
                  '(model 9) ~ ',
                  '(model 10) ~ ',
                  '(model 11) ~ ',
                  'null model')
```

#calculate AIC of each model

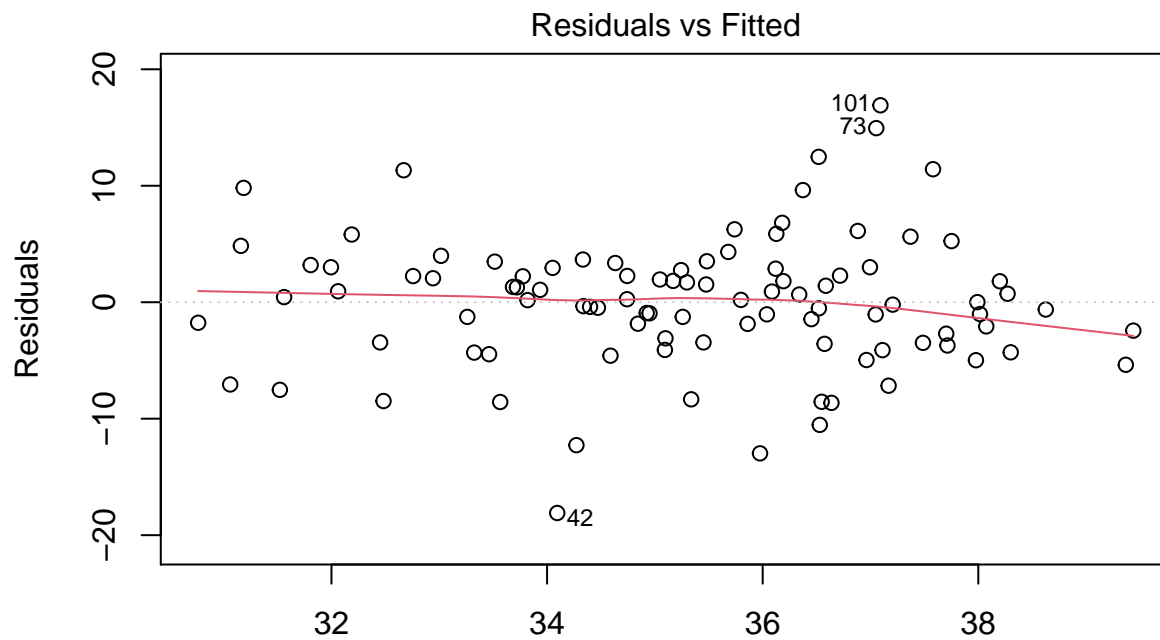
```
hct_AICc <- data.frame(aictab(cand.set = hct_models,
                             modnames = hct_mod_names))
```

```
hct_AICc
```

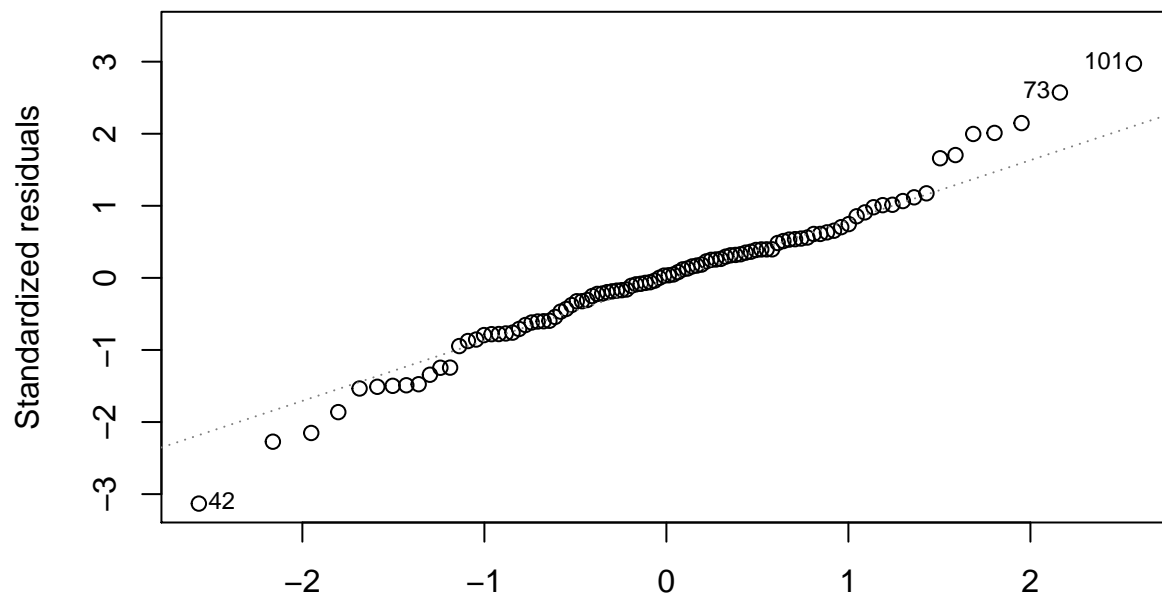
```
##           Modnames  K      AICc Delta_AICc      ModelLik      AICcWt      LL
## 3 (model 6) ~      8 636.0965   0.000000 1.000000e+00 7.142847e-01 -309.2393
## 2 (model 5) ~      9 638.4483   2.351739 3.085505e-01 2.203929e-01 -309.2014
## 1 (model 4) ~     10 640.8804   4.783896 9.145139e-02 6.532233e-02 -309.1758
## 6 (model 9) ~      5 767.1837 131.087158 3.425983e-29 2.447127e-29 -378.3287
## 7 (model 10) ~     4 768.0500 131.953418 2.221668e-29 1.586904e-29 -379.8511
## 5 (model 8) ~      6 768.2543 132.157808 2.005841e-29 1.432742e-29 -377.7555
## 4 (model 7) ~      7 769.3737 133.277207 1.146099e-29 8.186414e-30 -377.1869
## 8 (model 11) ~     3 773.5043 137.407723 1.453088e-30 1.037919e-30 -383.6496
## 9      null model   2 777.2445 141.148014 2.239227e-31 1.599446e-31 -386.5714
##           Cum.Wt
## 3 0.7142847
## 2 0.9346777
## 1 1.0000000
## 6 1.0000000
## 7 1.0000000
## 5 1.0000000
## 4 1.0000000
## 8 1.0000000
## 9 1.0000000
```

Check LM Assumptions

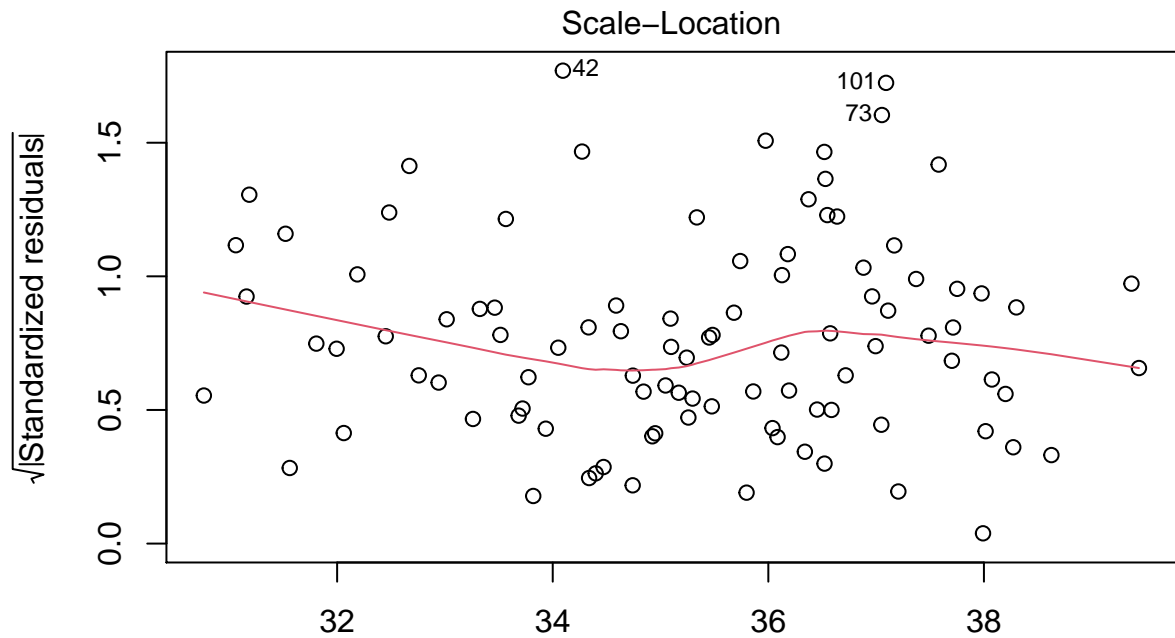
```
plot(hct_mod4)
```



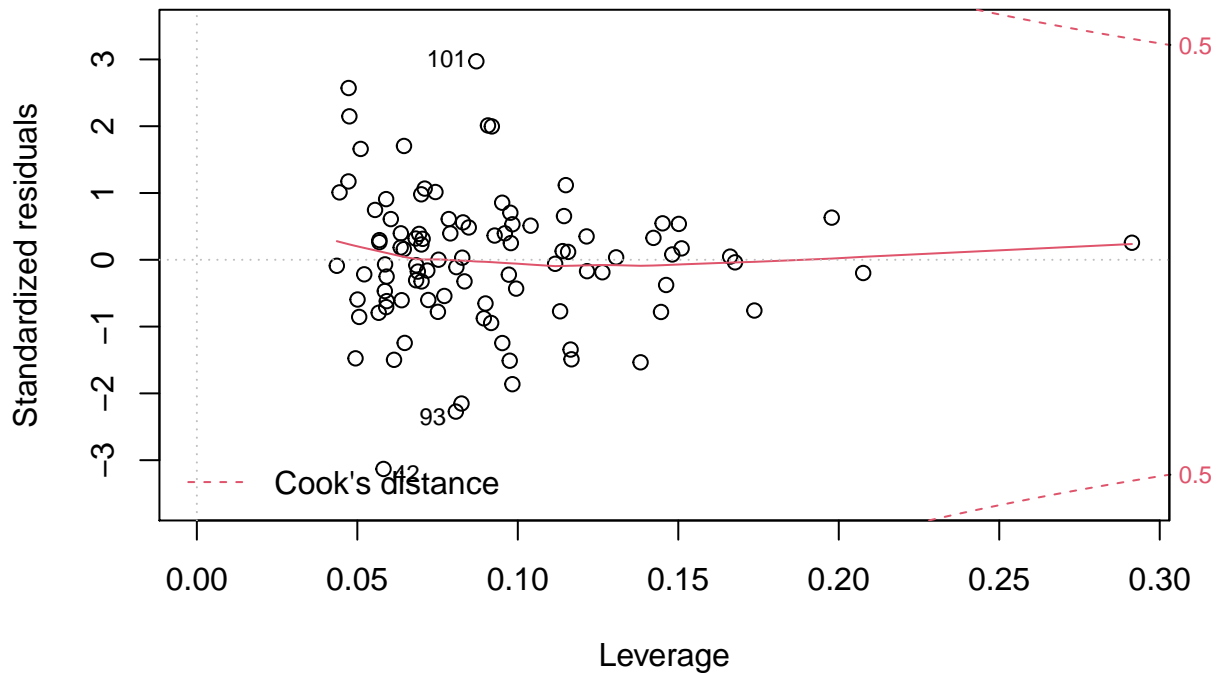
Fitted values
 $\text{lm}(\text{hematocrit_percent} \sim \text{VPD_kPa_int} + \text{Wind_mph_interpol} + \text{Solar_rad_Wm2_int})$
 Normal Q-Q



Theoretical Quantiles
 $\text{lm}(\text{hematocrit_percent} \sim \text{VPD_kPa_int} + \text{Wind_mph_interpol} + \text{Solar_rad_Wm2_int})$

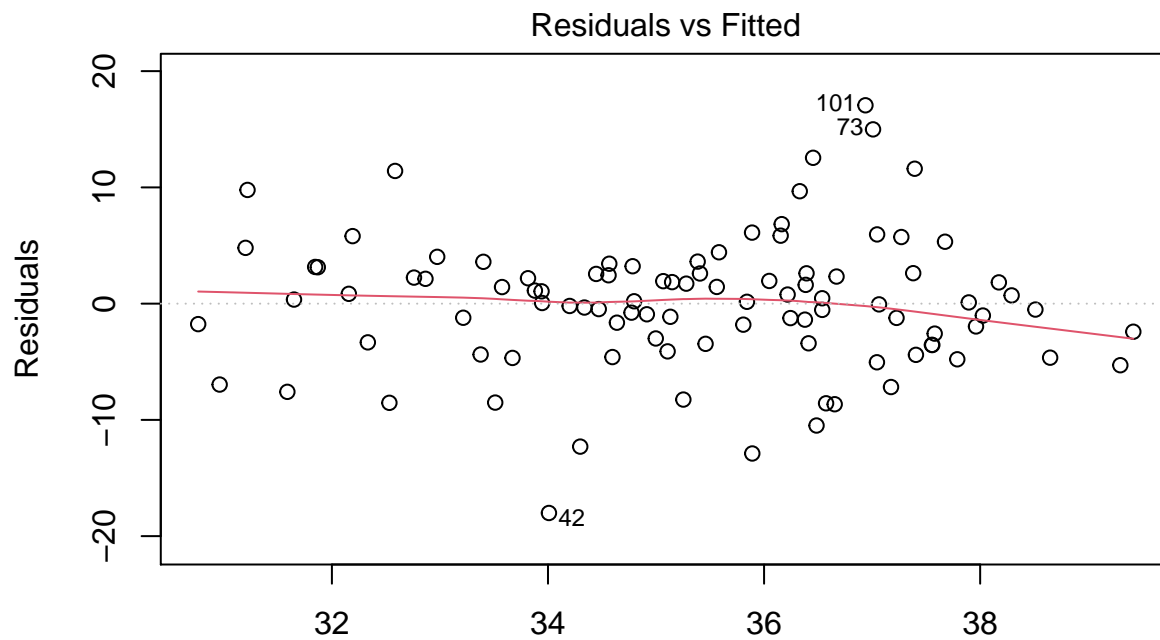


lm(hematocrit_percent ~ VPD_kPa_int + Wind_mph_interpol + Solar_rad_Wm2_int .
Residuals vs Leverage

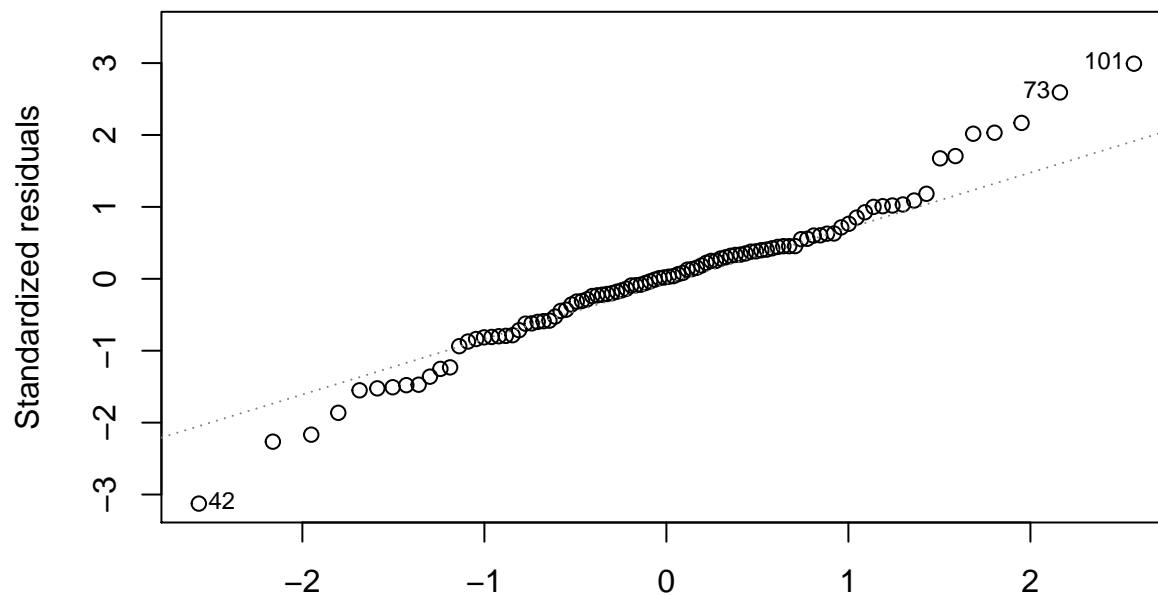


lm(hematocrit_percent ~ VPD_kPa_int + Wind_mph_interpol + Solar_rad_Wm2_int .

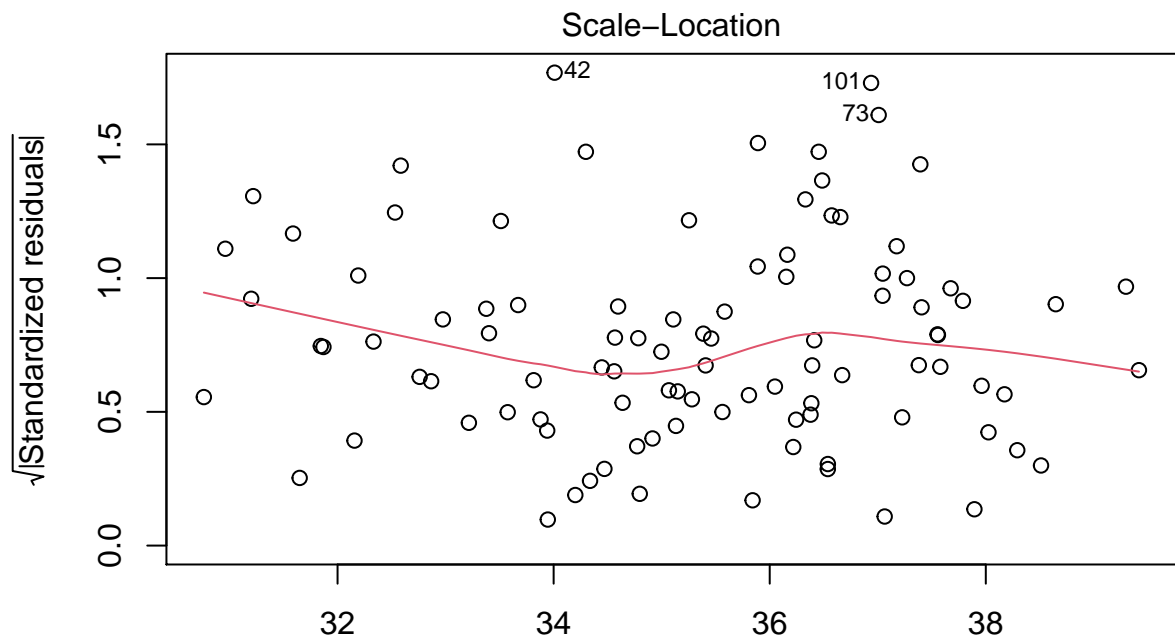
```
plot(hct_mod5)
```



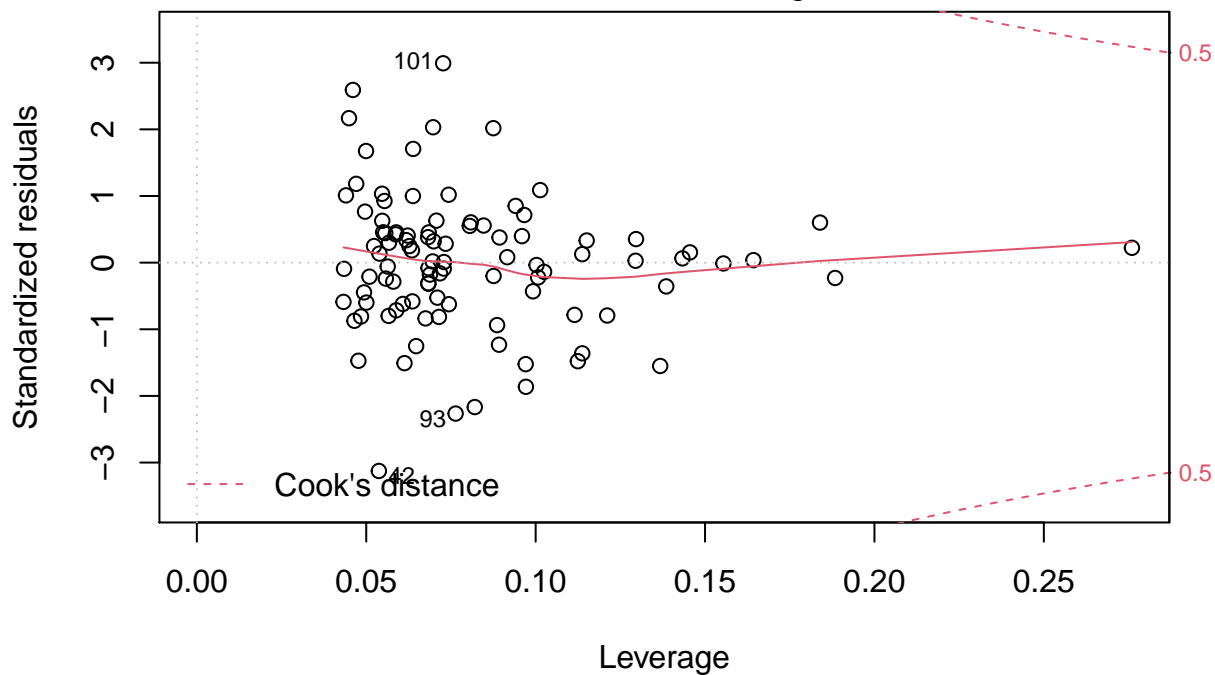
Fitted values
 $\text{lm}(\text{hematocrit_percent} \sim \text{VPD_kPa_int} + \text{Wind_mph_interpol} + \text{Solar_rad_Wm2_int})$
 Normal Q-Q



Theoretical Quantiles
 $\text{lm}(\text{hematocrit_percent} \sim \text{VPD_kPa_int} + \text{Wind_mph_interpol} + \text{Solar_rad_Wm2_int})$

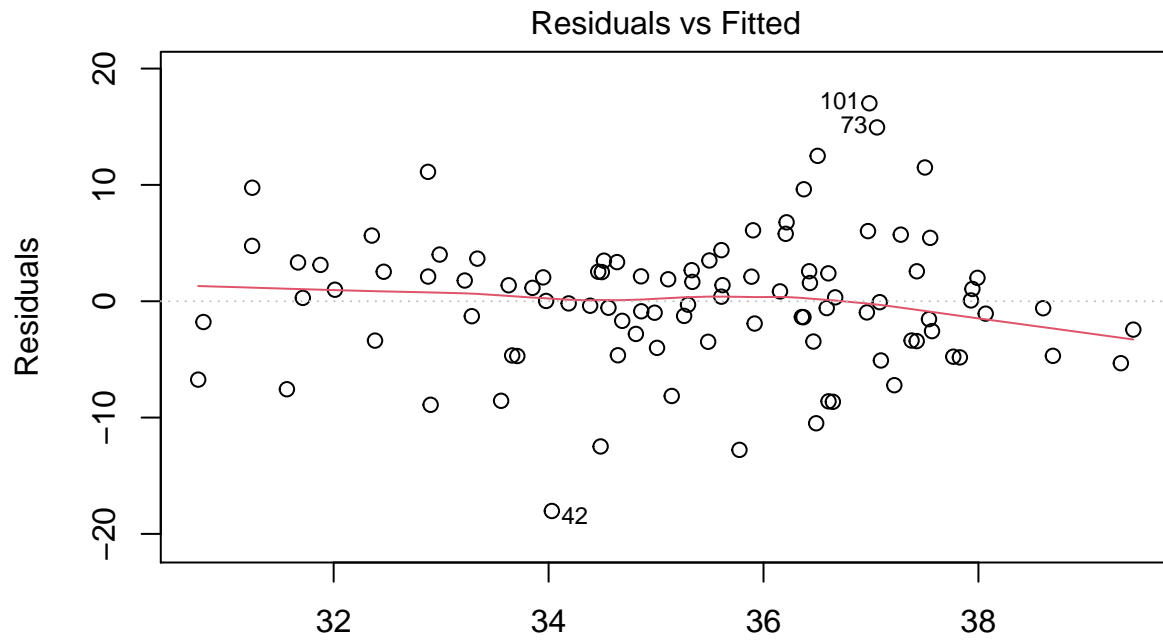


lm(hematocrit_percent ~ VPD_kPa_int + Wind_mph_interpol + Solar_rad_Wm2_int .
Residuals vs Leverage

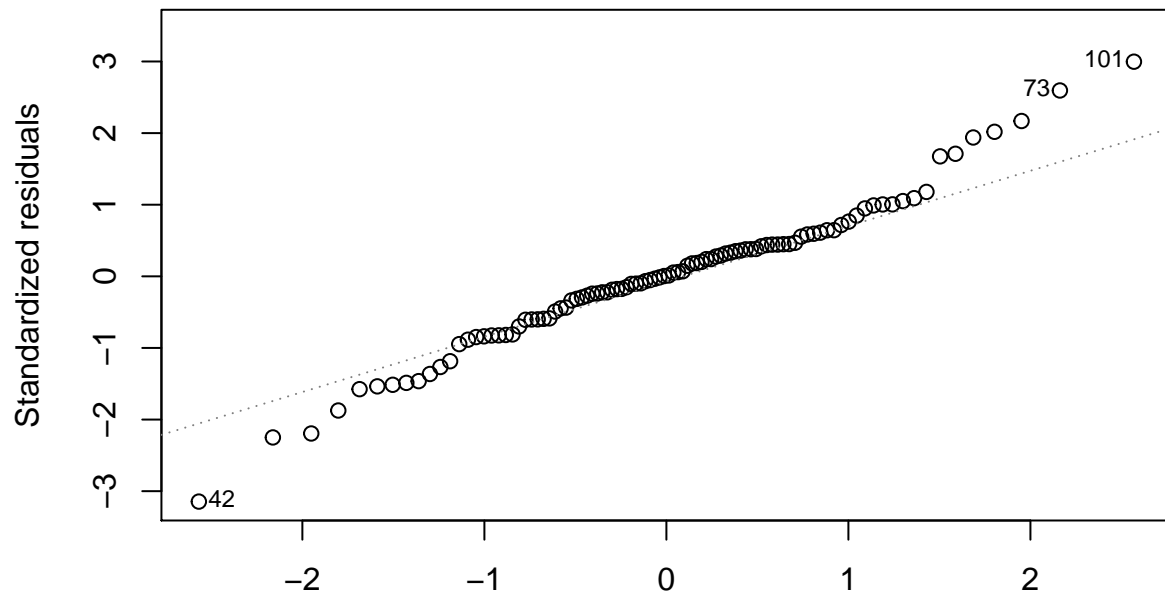


lm(hematocrit_percent ~ VPD_kPa_int + Wind_mph_interpol + Solar_rad_Wm2_int .

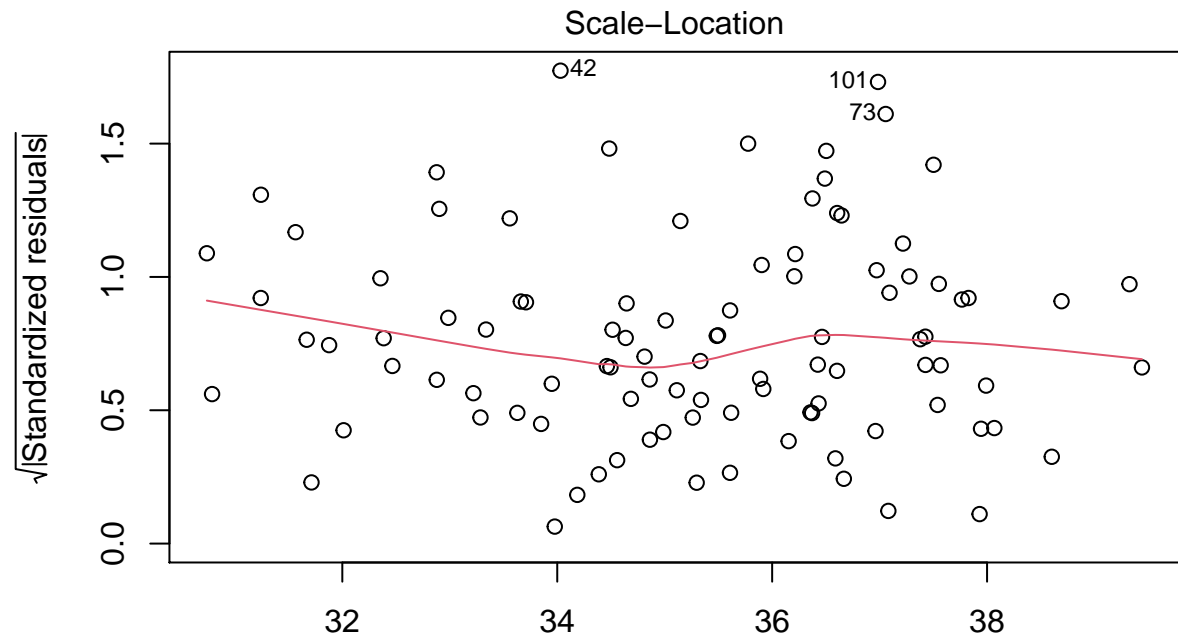
```
plot(hct_mod6)
```



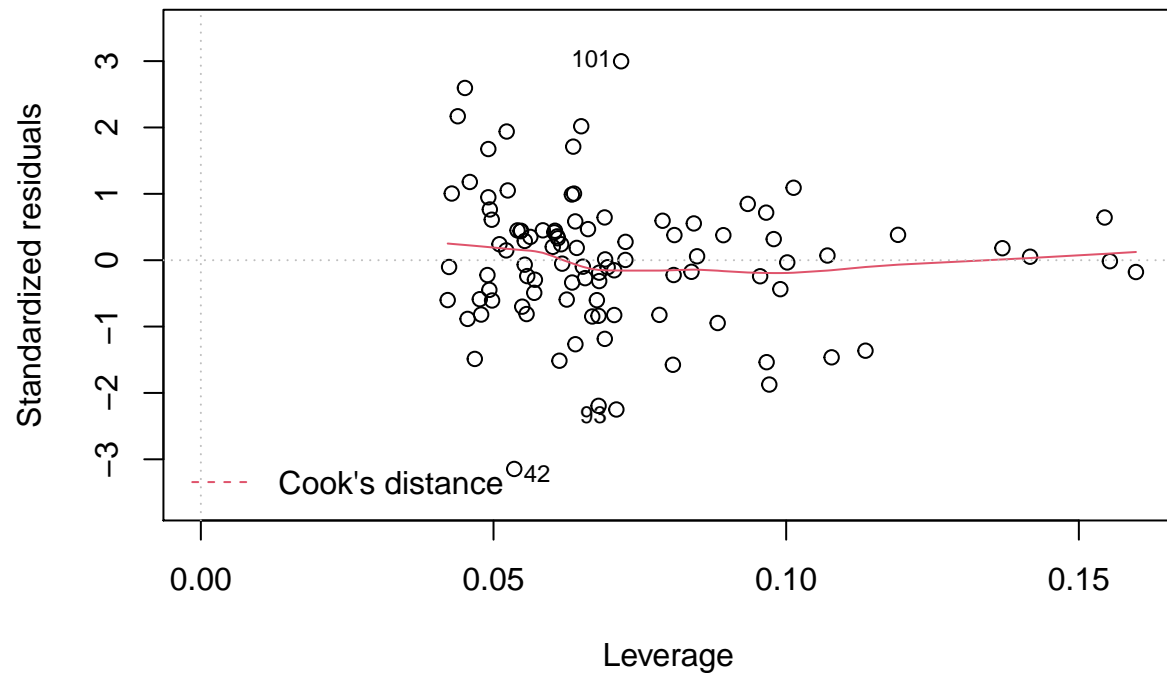
lm(hematocrit_percent ~ VPD_kPa_int + Solar_rad_Wm2_interpol + SMI + sex_M_ .
Normal Q-Q



lm(hematocrit_percent ~ VPD_kPa_int + Solar_rad_Wm2_interpol + SMI + sex_M_ .



lm(hematocrit_percent ~ VPD_kPa_int + Solar_rad_Wm2_interpol + SMI + sex_M_ .
Residuals vs Leverage



lm(hematocrit_percent ~ VPD_kPa_int + Solar_rad_Wm2_interpol + SMI + sex_M_ .

residuals all look fine

Export

We should save the information for the top three models, as well as the table showing the rankings of the different models.


```
write.csv(hct_AICc, "./best_models/hct_mod_rankings.csv")
write.csv(broom.mixed::tidy(hct_mod6),
          "./best_models/hct_best_mod1.csv")
```

```
## Registered S3 method overwritten by 'broom.mixed':
##   method      from
##   tidy.gamlss broom
```

```
write.csv(broom.mixed::tidy(hct_mod5),
          "./best_models/hct_best_mod2.csv")
write.csv(broom.mixed::tidy(hct_mod4),
          "./best_models/hct_best_mod3.csv")
```

Hydration

Models

Start with all the variables that may explain osmolality variation. Female gravidity cannot be included because of the low sample size and number of contrasts.

FULL model:

```
# model 1
hydrat_mod1 <- lme4::lmer(data = morpho_blood_SMI,
                          # response variable
                          osmolality_mmol_kg ~
                          # start with interaction + singular effect
                          VPD_kPa_int*temp_C_interpol +
                          # other potentially important factors
                          Wind_mph_interpol + Solar_rad_Wm2_interpol +
                          SMI + SVL_mm + mass_g + sex_M_F +
                          # random effects
                          (1|date) + (1|hemoalyzed))

summary(hydrat_mod1)

## Linear mixed model fit by REML ['lmerMod']
## Formula:
## osmolality_mmol_kg ~ VPD_kPa_int * temp_C_interpol + Wind_mph_interpol +
##   Solar_rad_Wm2_interpol + SMI + SVL_mm + mass_g + sex_M_F +
##   (1 | date) + (1 | hemoalyzed)
##   Data: morpho_blood_SMI
##
## REML criterion at convergence: 1004.5
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.22241 -0.60921  0.03156  0.61122  2.89018
##
## Random effects:
##   Groups      Name            Variance Std.Dev.
##   date      (Intercept)    873.0      29.546
##   hemoalyzed (Intercept)    12.9       3.591
##   Residual                    279.3     16.712
## Number of obs: 121, groups:  date, 6; hemoalyzed, 2
##
## Fixed effects:
```

```
##               Estimate Std. Error t value
## (Intercept)      80.39452   160.83850   0.500
## VPD_kPa_int       45.56514   252.99508   0.180
## temp_C_interpol    5.54233    8.27609   0.670
## Wind_mph_interpol -12.19637    3.57919  -3.408
## Solar_rad_Wm2_interpol  0.02156    0.04926   0.438
## SMI               7.03145    3.75975   1.870
## SVL_mm           3.76244    1.78472   2.108
## mass_g          -8.36413    3.80569  -2.198
## sex_M_FM        -3.22976    3.65764  -0.883
## VPD_kPa_int:temp_C_interpol -2.59443    9.88785  -0.262
##
## Correlation of Fixed Effects:
##          (Intr) VPD_kP_ tmp_C_ Wnd_m_ S__W2_ SMI      SVL_mm mass_g s_M_FM
## VPD_kPa_int -0.529
## tmp_C_ntrpl -0.631  0.305
## Wnd_mph_ntr -0.024  0.152  0.047
## Slr_rd_Wm2_  0.387 -0.201 -0.669 -0.313
## SMI          -0.550 -0.041 -0.148 -0.095  0.009
## SVL_mm       -0.574 -0.020 -0.132 -0.123 -0.029  0.944
## mass_g       0.576  0.025  0.120  0.091  0.023 -0.944 -0.987
## sex_M_FM     -0.081 -0.043  0.020 -0.016 -0.106  0.108  0.163 -0.190
## VPD_kP_:_C_  0.598 -0.986 -0.448 -0.148  0.291  0.059  0.039 -0.042  0.035
```

use VIF to look for multicollinearity:

```
hydrat_mod1_VIFs <- data.frame(VIF = car::vif(hydrat_mod1)) %>%
  arrange(VIF)
hydrat_mod1_VIFs
```

```
##               VIF
## sex_M_F        1.133868
## Wind_mph_interpol  1.364988
## Solar_rad_Wm2_interpol  2.461837
## SMI            10.381792
## temp_C_interpol  12.176616
## SVL_mm         46.248205
## mass_g         46.660633
## VPD_kPa_int     292.161561
## VPD_kPa_int:temp_C_interpol 331.767379
```

Remove the highest VIF variables one at a time. First, the temp*VPD interaction.

```
# model 2
hydrat_mod2 <- lme4::lmer(data = morpho_blood_SMI,
  # response variable
  osmolality_mmol_kg ~
  VPD_kPa_int + temp_C_interpol +
  Wind_mph_interpol + Solar_rad_Wm2_interpol +
  SMI + SVL_mm + mass_g + sex_M_F +
  # random effects
  (1|date) + (1|hemoalyzed))
hydrat_mod2_VIFs <- data.frame(VIF = car::vif(hydrat_mod2)) %>%
  arrange(VIF)
hydrat_mod2_VIFs
```

```
##                                VIF
## sex_M_F                      1.132554
## Wind_mph_interpol            1.325221
## Solar_rad_Wm2_interpol       2.205583
## VPD_kPa_int                  7.985485
## temp_C_interpol              9.796437
## SMI                          10.318447
## SVL_mm                      46.100677
## mass_g                       46.519718
```

drop mass.

```
# model 3
hydrat_mod3 <- lme4::lmer(data = morpho_blood_SMI,
  # response variable
  osmolality_mmol_kg ~
  VPD_kPa_int + temp_C_interpol +
  Wind_mph_interpol + Solar_rad_Wm2_interpol +
  SMI + SVL_mm + sex_M_F +
  # random effects
  (1|date) + (1|hemoalyzed))
hydrat_mod3_VIFs <- data.frame(VIF = car::vif(hydrat_mod3)) %>%
  arrange(VIF)
hydrat_mod3_VIFs
```

```
##                                VIF
## sex_M_F                      1.092686
## SMI                          1.127133
## SVL_mm                      1.223489
## Wind_mph_interpol            1.307367
## Solar_rad_Wm2_interpol       2.173764
## VPD_kPa_int                  7.990447
## temp_C_interpol              9.741839
```

drop temperature

```
# model 4
hydrat_mod4 <- lme4::lmer(data = morpho_blood_SMI,
  # response variable
  osmolality_mmol_kg ~
  VPD_kPa_int +
  Wind_mph_interpol + Solar_rad_Wm2_interpol +
  SMI + SVL_mm + sex_M_F +
  # random effects
  (1|date) + (1|hemoalyzed))
hydrat_mod4_VIFs <- data.frame(VIF = car::vif(hydrat_mod4)) %>%
  arrange(VIF)
hydrat_mod4_VIFs
```

```
##                                VIF
## VPD_kPa_int                  1.056725
## sex_M_F                      1.088032
## SMI                          1.122785
## SVL_mm                      1.212112
## Wind_mph_interpol            1.323659
## Solar_rad_Wm2_interpol       1.334494
```

Okay, now that all VIFs are reasonable values, we can do the remaining model selection based on AIC and t-value.

```
summary(hydrat_mod4)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula:
## osmolality_mmol_kg ~ VPD_kPa_int + Wind_mph_interpol + Solar_rad_Wm2_interpol +
## SMI + SVL_mm + sex_M_F + (1 | date) + (1 | hemolyzed)
## Data: morpho_blood_SMI
##
## REML criterion at convergence: 1026.9
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.22452 -0.63811  0.06486  0.65425  2.72400
##
## Random effects:
## Groups      Name                Variance Std.Dev.
## date        (Intercept)    930.06     30.497
## hemolyzed    (Intercept)    19.33      4.397
## Residual                    284.66     16.872
## Number of obs: 121, groups:  date, 6; hemolyzed, 2
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)    385.41079   37.34722  10.320
## VPD_kPa_int      4.10087   15.42376   0.266
## Wind_mph_interpol -11.58238   3.56118  -3.252
## Solar_rad_Wm2_interpol  0.05656   0.03674   1.540
## SMI             -0.63969   1.24862  -0.512
## SVL_mm          -0.07346   0.29247  -0.251
## sex_M_FM        -4.92854   3.61752  -1.362
##
## Correlation of Fixed Effects:
##              (Intr) VPD_P_ Wnd_m_ S_W2_ SMI      SVL_mm
## VPD_kPa_int  -0.141
## Wnd_mph_ntr  -0.005  0.039
## Slr_rd_Wm2_  -0.591 -0.135 -0.404
## SMI           -0.420 -0.153 -0.024  0.030
## SVL_mm        -0.335 -0.072 -0.213 -0.133  0.229
## sex_M_FM      0.182 -0.034  0.007 -0.100 -0.216 -0.141
```

```
drop1(hydrat_mod4)
```

```
## Single term deletions
##
## Model:
## osmolality_mmol_kg ~ VPD_kPa_int + Wind_mph_interpol + Solar_rad_Wm2_interpol +
## SMI + SVL_mm + sex_M_F + (1 | date) + (1 | hemolyzed)
##              npar      AIC
## <none>                1066.0
## VPD_kPa_int            1 1064.2
## Wind_mph_interpol      1 1074.2
## Solar_rad_Wm2_interpol  1 1065.9
```

```
## SMI                1 1064.3
## SVL_mm             1 1064.1
## sex_M_F            1 1066.0
```

drop SVL:

```
# model 5
hydrat_mod5 <- lme4::lmer(data = morpho_blood_SMI,
  # response variable
  osmolality_mmol_kg ~
  VPD_kPa_int +
  Wind_mph_interpol + Solar_rad_Wm2_interpol +
  SMI + sex_M_F +
  # random effects
  (1|date) + (1|hemolyzed))
summary(hydrat_mod5)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula:
## osmolality_mmol_kg ~ VPD_kPa_int + Wind_mph_interpol + Solar_rad_Wm2_interpol +
## SMI + sex_M_F + (1 | date) + (1 | hemolyzed)
## Data: morpho_blood_SMI
##
## REML criterion at convergence: 1026.3
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.21547 -0.65331  0.05192  0.63351  2.76644
##
## Random effects:
## Groups      Name      Variance Std.Dev.
## date      (Intercept) 920.9    30.347
## hemolyzed (Intercept)  20.5     4.528
## Residual                282.2    16.800
## Number of obs: 121, groups: date, 6; hemolyzed, 2
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)    382.20594   35.04299   10.907
## VPD_kPa_int      3.82691   15.31564    0.250
## Wind_mph_interpol -11.76568    3.46435   -3.396
## Solar_rad_Wm2_interpol  0.05539    0.03626    1.528
## SMI             -0.57016    1.21036   -0.471
## sex_M_FM        -5.05674    3.56580   -1.418
##
## Correlation of Fixed Effects:
##              (Intr) VPD_P_ Wnd_m_ S__W2_ SMI
## VPD_kPa_int  -0.176
## Wnd_mph_ntr  -0.083  0.024
## Slr_rd_Wm2_  -0.680 -0.146 -0.446
## SMI           -0.374 -0.141  0.027  0.062
## sex_M_FM      0.144 -0.045 -0.024 -0.121 -0.190
```

```
drop1(hydrat_mod5)
```

```
## Single term deletions
```

```
##
## Model:
## osmolality_mmol_kg ~ VPD_kPa_int + Wind_mph_interpol + Solar_rad_Wm2_interpol +
##   SMI + sex_M_F + (1 | date) + (1 | hemolyzed)
##               npar    AIC
## <none>                1064.1
## VPD_kPa_int           1 1062.2
## Wind_mph_interpol     1 1072.9
## Solar_rad_Wm2_interpol 1 1063.9
## SMI                   1 1062.4
## sex_M_F               1 1064.2
```

drop VPD:

```
# model 6
hydrat_mod6 <- lme4::lmer(data = morpho_blood_SMI,
  # response variable
  osmolality_mmol_kg ~
    Wind_mph_interpol + Solar_rad_Wm2_interpol +
    SMI + sex_M_F +
  # random effects
  (1|date) + (1|hemolyzed))
summary(hydrat_mod6)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: osmolality_mmol_kg ~ Wind_mph_interpol + Solar_rad_Wm2_interpol +
##   SMI + sex_M_F + (1 | date) + (1 | hemolyzed)
## Data: morpho_blood_SMI
##
## REML criterion at convergence: 1033.7
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.21786 -0.66082  0.05462  0.63355  2.76432
##
## Random effects:
##   Groups      Name      Variance Std.Dev.
##   date      (Intercept) 933.36   30.551
##   hemolyzed (Intercept)  20.58    4.536
##   Residual                279.66   16.723
## Number of obs: 121, groups: date, 6; hemolyzed, 2
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)   383.46657   34.42551  11.139
## Wind_mph_interpol -11.79963    3.44895  -3.421
## Solar_rad_Wm2_interpol  0.05708    0.03576   1.596
## SMI            -0.52561    1.19286  -0.441
## sex_M_FM       -5.01920    3.54614  -1.415
##
## Correlation of Fixed Effects:
##              (Intr) Wnd_m_ S__W2_ SMI
## Wnd_mph_ntr -0.079
## Slr_rd_Wm2_ -0.724 -0.448
## SMI         -0.409  0.030  0.043
```

```
## sex_M_FM      0.139 -0.022 -0.129 -0.199
```

```
drop1(hydrat_mod6)
```

```
## Single term deletions
```

```
##
```

```
## Model:
```

```
## osmolality_mmol_kg ~ Wind_mph_interpol + Solar_rad_Wm2_interpol +
```

```
##      SMI + sex_M_F + (1 | date) + (1 | hemolyzed)
```

```
##              npar      AIC
```

```
## <none>              1062.2
```

```
## Wind_mph_interpol      1 1071.4
```

```
## Solar_rad_Wm2_interpol  1 1062.5
```

```
## SMI                    1 1060.5
```

```
## sex_M_F                1 1062.3
```

```
drop SMI:
```

```
# model 7
```

```
hydrat_mod7 <- lme4::lmer(data = morpho_blood_SMI,
```

```
      # response variable
```

```
      osmolality_mmol_kg ~
```

```
      Wind_mph_interpol + Solar_rad_Wm2_interpol +
```

```
      sex_M_F +
```

```
      # random effects
```

```
      (1|date) + (1|hemolyzed))
```

```
summary(hydrat_mod7)
```

```
## Linear mixed model fit by REML ['lmerMod']
```

```
## Formula: osmolality_mmol_kg ~ Wind_mph_interpol + Solar_rad_Wm2_interpol +
```

```
##      sex_M_F + (1 | date) + (1 | hemolyzed)
```

```
##      Data: morpho_blood_SMI
```

```
##
```

```
## REML criterion at convergence: 1036.1
```

```
##
```

```
## Scaled residuals:
```

```
##      Min      1Q   Median      3Q      Max
```

```
## -2.17326 -0.70062  0.01535  0.58677  2.78981
```

```
##
```

```
## Random effects:
```

```
## Groups   Name      Variance Std.Dev.
```

```
## date      (Intercept) 949.18   30.809
```

```
## hemolyzed (Intercept)  19.82    4.452
```

```
## Residual                277.51   16.659
```

```
## Number of obs: 121, groups: date, 6; hemolyzed, 2
```

```
##
```

```
## Fixed effects:
```

```
##              Estimate Std. Error t value
```

```
## (Intercept)    377.04913    31.38254   12.015
```

```
## Wind_mph_interpol    -11.77287     3.43552   -3.427
```

```
## Solar_rad_Wm2_interpol  0.05809     0.03566    1.629
```

```
## sex_M_FM          -5.33018     3.46222   -1.540
```

```
##
```

```
## Correlation of Fixed Effects:
```

```
##              (Intr) Wnd_m_ S__W2_
```

```
## Wnd_mph_ntr -0.071
```

```

## Slr_rd_Wm2_ -0.774 -0.451
## sex_M_FM      0.064 -0.017 -0.123
drop1(hydrat_mod7)

## Single term deletions
##
## Model:
## osmolality_mmol_kg ~ Wind_mph_interpol + Solar_rad_Wm2_interpol +
##      sex_M_F + (1 | date) + (1 | hemolyzed)
##               npar      AIC
## <none>                1060.5
## Wind_mph_interpol      1 1069.5
## Solar_rad_Wm2_interpol  1 1060.7
## sex_M_F                1 1060.8

drop sex:
# model 8
hydrat_mod8 <- lme4::lmer(data = morpho_blood_SMI,
                        # response variable
                        osmolality_mmol_kg ~
                        Wind_mph_interpol + Solar_rad_Wm2_interpol +
                        # random effects
                        (1|date) + (1|hemolyzed))
summary(hydrat_mod8)

## Linear mixed model fit by REML ['lmerMod']
## Formula: osmolality_mmol_kg ~ Wind_mph_interpol + Solar_rad_Wm2_interpol +
##      (1 | date) + (1 | hemolyzed)
##      Data: morpho_blood_SMI
##
## REML criterion at convergence: 1042.8
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.19796 -0.70878  0.06156  0.65376  2.60941
##
## Random effects:
##      Groups      Name      Variance Std.Dev.
##      date      (Intercept) 941.54   30.685
##      hemolyzed (Intercept)  19.35    4.399
##      Residual                281.02   16.764
## Number of obs: 121, groups: date, 6; hemolyzed, 2
##
## Fixed effects:
##               Estimate Std. Error t value
## (Intercept)      380.40699    31.42939   12.104
## Wind_mph_interpol    -11.85141     3.45542    -3.430
## Solar_rad_Wm2_interpol  0.05099     0.03555     1.434
##
## Correlation of Fixed Effects:
##              (Intr) Wnd_m_
## Wnd_mph_ntr -0.072
## Slr_rd_Wm2_ -0.775 -0.456

```



```
drop1(hydrat_mod8)
```

```
## Single term deletions
```

```
##
```

```
## Model:
```

```
## osmolality_mmol_kg ~ Wind_mph_interpol + Solar_rad_Wm2_interpol +
```

```
## (1 | date) + (1 | hemolyzed)
```

```
## npar AIC
```

```
## <none> 1060.8
```

```
## Wind_mph_interpol 1 1069.9
```

```
## Solar_rad_Wm2_interpol 1 1060.6
```

```
drop solar radiation:
```

```
# model 9
```

```
hydrat_mod9 <- lme4::lmer(data = morpho_blood_SMI,
```

```
  # response variable
```

```
  osmolality_mmol_kg ~
```

```
  Wind_mph_interpol +
```

```
  # random effects
```

```
  (1|date) + (1|hemolyzed))
```

```
finally, test the null model
```

```
hydrat_mod_null <- lme4::lmer(data = morpho_blood_SMI,
```

```
  osmolality_mmol_kg ~ 1 +
```

```
  (1|date) + (1|hemolyzed))
```

Selection

models 4-9 and the null model are the ones we should compare. models 1-3 had serious multicollinearity thus are not trustworthy models.

```
hydrat_models <- list(hydrat_mod4, hydrat_mod5, hydrat_mod6,
```

```
  hydrat_mod7, hydrat_mod8, hydrat_mod9,
```

```
  hydrat_mod_null)
```

```
#specify model names
```

```
hydrat_mod_names <- c('(model 4) ~ VPD, Wind, Solar, SMI, SVL, sex',
```

```
  '(model 5) ~ VPD, Wind, Solar, SMI, sex',
```

```
  '(model 6) ~ Wind, Solar, SMI, sex',
```

```
  '(model 7) ~ Wind, Solar, sex',
```

```
  '(model 8) ~ Wind, Solar',
```

```
  '(model 9) ~ Wind',
```

```
  'null model')
```

```
#calculate AIC of each model
```

```
hydrat_AICc <- data.frame(aictab(cand.set = hydrat_models,
```

```
  modnames = hydrat_mod_names))
```

```
## Warning in aictab.AIClmerMod(cand.set = hydrat_models, modnames = hydrat_mod_names):
```

```
## Model selection for fixed effects is only appropriate with ML estimation:
```

```
## REML (default) should only be used to select random effects for a constant set of fixed effects
```

```
hydrat_AICc
```

```
## Modnames K AICc Delta_AICc
## 2 (model 5) ~ VPD, Wind, Solar, SMI, sex 9 1045.969 0.000000
```

```
## 1 (model 4) ~ VPD, Wind, Solar, SMI, SVL, sex 10 1048.910 2.941314
## 6 (model 9) ~ Wind 5 1050.348 4.379199
## 3 (model 6) ~ Wind, Solar, SMI, sex 8 1050.986 5.017215
## 4 (model 7) ~ Wind, Solar, sex 7 1051.072 5.103056
## 5 (model 8) ~ Wind, Solar 6 1055.500 9.531431
## 7 null model 4 1078.070 32.101007
##      ModellLik      AICcWt    Res.LL    Cum.Wt
## 2 1.000000e+00 6.624285e-01 -513.1735 0.6624285
## 1 2.297745e-01 1.522092e-01 -513.4550 0.8146376
## 6 1.119616e-01 7.416655e-02 -519.9130 0.8888042
## 3 8.138149e-02 5.390942e-02 -516.8501 0.9427136
## 4 7.796245e-02 5.164455e-02 -518.0403 0.9943582
## 5 8.516791e-03 5.641765e-03 -521.3816 0.9999999
## 7 1.069929e-07 7.087514e-08 -534.8653 1.0000000
```

Re-run top 2 models using lmerTest to get p-values:

```
hydrat_mod5p <- lmerTest::lmer(data = morpho_blood_SMI,
  # response variable
  osmolality_mmol_kg ~
  VPD_kPa_int +
  Wind_mph_interpol + Solar_rad_Wm2_interpol +
  SMI + sex_M_F +
  # random effects
  (1|date) + (1|hemolyzed))
summary(hydrat_mod5p)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula:
## osmolality_mmol_kg ~ VPD_kPa_int + Wind_mph_interpol + Solar_rad_Wm2_interpol +
## SMI + sex_M_F + (1 | date) + (1 | hemolyzed)
## Data: morpho_blood_SMI
##
## REML criterion at convergence: 1026.3
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.21547 -0.65331  0.05192  0.63351  2.76644
##
## Random effects:
## Groups      Name                Variance Std.Dev.
## date      (Intercept)          920.9     30.347
## hemolyzed (Intercept)          20.5      4.528
## Residual                        282.2     16.800
## Number of obs: 121, groups:  date, 6; hemolyzed, 2
##
## Fixed effects:
##              Estimate Std. Error    df t value Pr(>|t|)
## (Intercept)   382.20594   35.04299  59.29144  10.907 8.44e-16 ***
## VPD_kPa_int     3.82691   15.31564  72.68400   0.250 0.803393
## Wind_mph_interpol -11.76568    3.46435 114.19881 -3.396 0.000941 ***
## Solar_rad_Wm2_interpol  0.05539    0.03626  86.94121   1.528 0.130190
## SMI             -0.57016    1.21036 110.48891 -0.471 0.638520
## sex_M_FM       -5.05674    3.56580 109.47729 -1.418 0.158996
```

```

## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##          (Intr) VPD_P_ Wnd_m_ S__W2_ SMI
## VPD_kPa_int -0.176
## Wnd_mph_ntr -0.083  0.024
## Slr_rd_Wm2_ -0.680 -0.146 -0.446
## SMI          -0.374 -0.141  0.027  0.062
## sex_M_FM     0.144 -0.045 -0.024 -0.121 -0.190
hydrat_mod4p <- lmerTest::lmer(data = morpho_blood_SMI,
                              # response variable
                              osmolality_mmol_kg ~
                                VPD_kPa_int +
                                Wind_mph_interpol + Solar_rad_Wm2_interpol +
                                SMI + SVL_mm + sex_M_F +
                              # random effects
                              (1|date) + (1|hemolyzed))
summary(hydrat_mod4p)

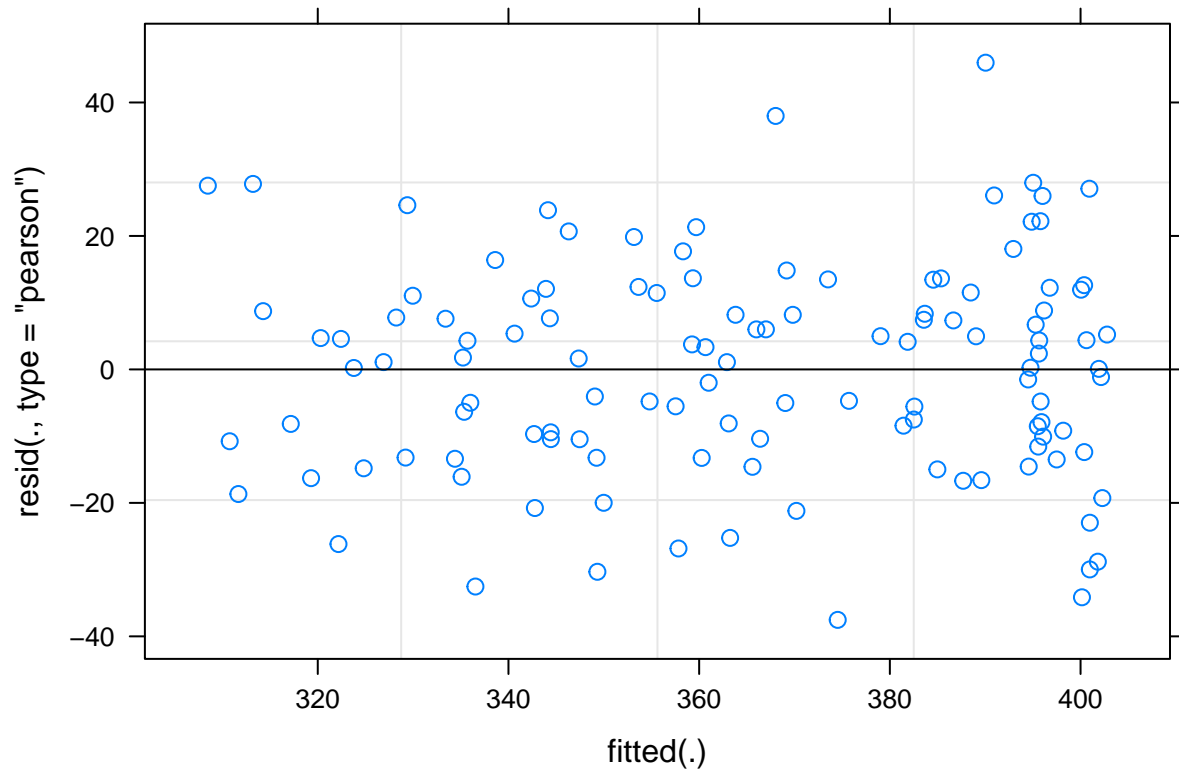
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula:
## osmolality_mmol_kg ~ VPD_kPa_int + Wind_mph_interpol + Solar_rad_Wm2_interpol +
## SMI + SVL_mm + sex_M_F + (1 | date) + (1 | hemolyzed)
## Data: morpho_blood_SMI
##
## REML criterion at convergence: 1026.9
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.22452 -0.63811  0.06486  0.65425  2.72400
##
## Random effects:
## Groups   Name                Variance Std.Dev.
## date      (Intercept)    930.06     30.497
## hemolyzed (Intercept)    19.33       4.397
## Residual                    284.66     16.872
## Number of obs: 121, groups:  date, 6; hemolyzed, 2
##
## Fixed effects:
##              Estimate Std. Error    df t value Pr(>|t|)
## (Intercept)   385.41079   37.34722  71.15211  10.320  8.8e-16 ***
## VPD_kPa_int     4.10087   15.42376  72.07437   0.266  0.79109
## Wind_mph_interpol -11.58238   3.56118 112.70287  -3.252  0.00151 **
## Solar_rad_Wm2_interpol  0.05656   0.03674  85.31715   1.540  0.12737
## SMI            -0.63969   1.24862 109.24695  -0.512  0.60946
## SVL_mm         -0.07346   0.29247 109.90093  -0.251  0.80215
## sex_M_FM       -4.92854   3.61752 108.48257  -1.362  0.17589
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##          (Intr) VPD_P_ Wnd_m_ S__W2_ SMI    SVL_mm

```

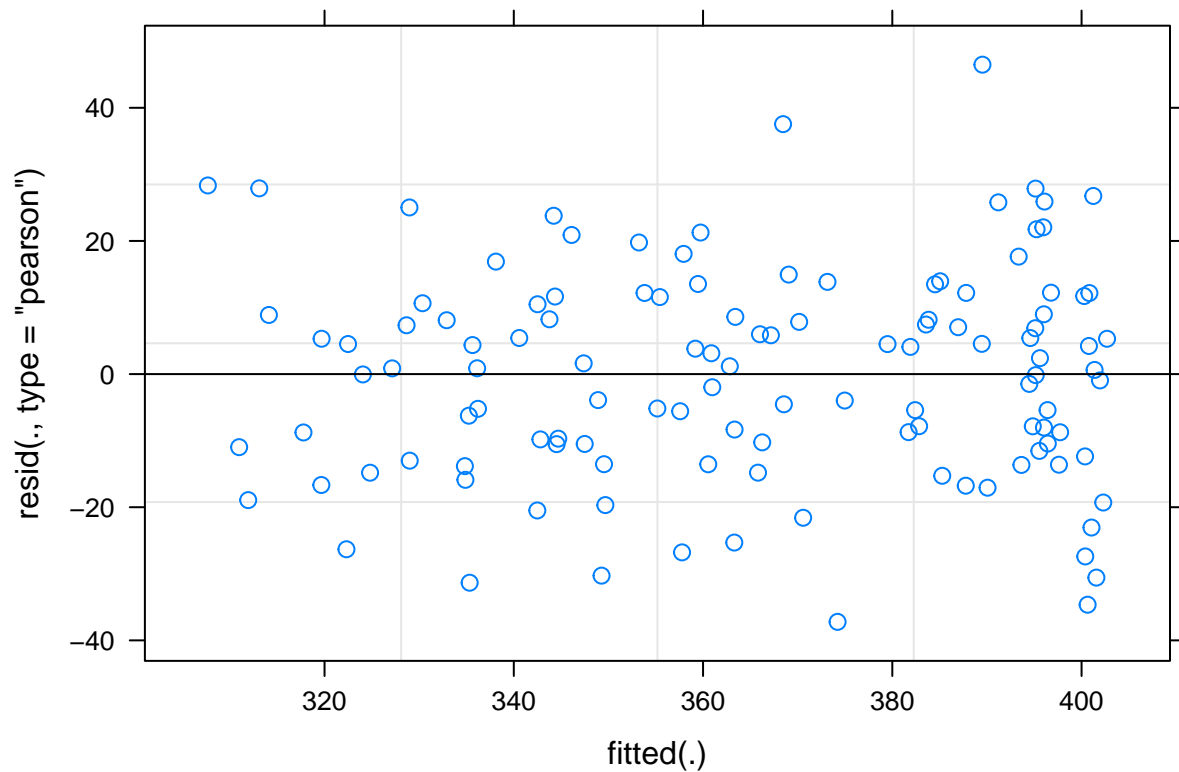
```
## VPD_kPa_int -0.141
## Wnd_mph_ntr -0.005  0.039
## Slr_rd_Wm2_ -0.591 -0.135 -0.404
## SMI         -0.420 -0.153 -0.024  0.030
## SVL_mm      -0.335 -0.072 -0.213 -0.133  0.229
## sex_M_FM    0.182 -0.034  0.007 -0.100 -0.216 -0.141
```

Check LM Assumptions

```
plot(hydrat_mod4)
```



```
plot(hydrat_mod5)
```



residuals look fantastic for both

Export

We should save the information for the top two models, as well as the table showing the rankings of the different models.

```
write.csv(hydrat_AICc, "./best_models/osml_mod_rankings.csv")
write.csv(broom.mixed::tidy(hydrat_mod5p),
          "./best_models/osml_best_mod1.csv")
write.csv(broom.mixed::tidy(hydrat_mod4p),
          "./best_models/osml_best_mod2.csv")
```

CEWL

Models

Start with all the variables that may explain CEWL variation.

FULL model:

```
CEWL_mod1 <- lme4::lmer(data = CEWL_data_full,
                        # response variable
                        TEWL_g_m2h ~
                        # potential predictors
                        region * (ambient_temp_C + VPD_kPa +
                                VPD_kPa_int + temp_C_interpol +
                                Wind_mph_interpol + Solar_rad_Wm2_interpol +
                                SMI + SVL_mm + mass_g + sex_M_F) +
                        hematocrit_percent + osmolality_mmol_kg +
                        cloacal_temp_C + hold_time +
```

```

# random effect
(1|individual_ID))

## Warning: Some predictor variables are on very different scales: consider
## rescaling

use VIF to look for multicollinearity:
CEWL_mod1_VIFs <- data.frame(VIF = car::vif(CEWL_mod1)[,3]) %>%
  arrange(desc(VIF))
CEWL_mod1_VIFs

##               VIF
## region          126.729225
## region:SVL_mm    112.721822
## region:temp_C_interpol  67.633209
## region:ambient_temp_C  59.087411
## region:mass_g      39.233887
## region:SMI         37.409634
## region:VPD_kPa     27.621337
## region:VPD_kPa_int  22.544002
## region:Wind_mph_interpol 16.270053
## VPD_kPa_int       15.833098
## temp_C_interpol   15.170912
## SVL_mm            13.537645
## mass_g            13.330899
## region:Solar_rad_Wm2_interpol 10.039703
## SMI                6.867408
## VPD_kPa            4.504115
## ambient_temp_C     3.104472
## Solar_rad_Wm2_interpol 3.012467
## Wind_mph_interpol  2.172535
## region:sex_M_F      1.845081
## hold_time          1.725647
## sex_M_F            1.717440
## cloacal_temp_C     1.665980
## osmolality_mmol_kg  1.568857
## hematocrit_percent  1.144660

drop region*SVL interaction:
CEWL_mod2 <- lme4::lmer(data = CEWL_data_full,
  # response variable
  TEWL_g_m2h ~
  # potential predictors
  region * (ambient_temp_C + VPD_kPa +
    VPD_kPa_int + temp_C_interpol +
    Wind_mph_interpol + Solar_rad_Wm2_interpol +
    SMI + mass_g + sex_M_F) + SVL_mm +
  hematocrit_percent + osmolality_mmol_kg +
  cloacal_temp_C + hold_time +
  # random effect
  (1|individual_ID))

## Warning: Some predictor variables are on very different scales: consider
## rescaling

```

```
CEWL_mod2_VIFs <- data.frame(VIF = car::vif(CEWL_mod2)[,3]) %>%
  arrange(desc(VIF))
CEWL_mod2_VIFs
```

```
##                                VIF
## region:temp_C_interpol        67.444164
## region:ambient_temp_C        58.627992
## region                      46.900376
## region:VPD_kPa                27.586548
## region:VPD_kPa_int           22.512055
## region:Wind_mph_interpol      16.137303
## VPD_kPa_int                  15.864370
## temp_C_interpol              15.190670
## region:Solar_rad_Wm2_interpol  9.923071
## region:SMI                   8.915999
## mass_g                       8.731814
## SVL_mm                       8.727856
## region:mass_g                4.686016
## SMI                          4.651856
## VPD_kPa                      4.512255
## ambient_temp_C               3.100788
## Solar_rad_Wm2_interpol       2.995616
## Wind_mph_interpol            2.168899
## region:sex_M_F               1.834121
## hold_time                    1.725623
## sex_M_F                     1.720184
## cloacal_temp_C              1.665622
## osmolality_mmol_kg           1.568265
## hematocrit_percent           1.144307
```

drop region*ambient temp interaction:

```
CEWL_mod3 <- lme4::lmer(data = CEWL_data_full,
  # response variable
  TEWL_g_m2h ~
  # potential predictors
  region * (VPD_kPa +
    VPD_kPa_int + temp_C_interpol +
    Wind_mph_interpol + Solar_rad_Wm2_interpol +
    SMI + mass_g + sex_M_F) + SVL_mm +
  hematocrit_percent + osmolality_mmol_kg +
  cloacal_temp_C + hold_time + ambient_temp_C +
  # random effect
  (1|individual_ID))
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
CEWL_mod3_VIFs <- data.frame(VIF = car::vif(CEWL_mod3)[,3]) %>%
  arrange(desc(VIF))
CEWL_mod3_VIFs
```

```
##                                VIF
## region:temp_C_interpol        56.144669
## region                      46.523915
## region:VPD_kPa                20.839190
```

```
## region:VPD_kPa_int          18.650539
## VPD_kPa_int                14.358488
## temp_C_interpol           13.794367
## region:Wind_mph_interpol   13.329957
## region:Solar_rad_Wm2_interpol 9.843737
## region:SMI                 8.869649
## mass_g                    8.726825
## SVL_mm                    8.722792
## region:mass_g              4.656175
## SMI                       4.647370
## VPD_kPa                   3.874445
## Solar_rad_Wm2_interpol     2.978020
## Wind_mph_interpol          1.959622
## ambient_temp_C             1.952667
## region:sex_M_F             1.833502
## hold_time                  1.725459
## sex_M_F                    1.720311
## cloacal_temp_C             1.665393
## osmolality_mmol_kg         1.568109
## hematocrit_percent         1.144282
```

drop other region * temperature interaction:

```
CEWL_mod4 <- lme4::lmer(data = CEWL_data_full,
                        # response variable
                        TEWL_g_m2h ~
                        # potential predictors
                        region * (VPD_kPa + VPD_kPa_int +
                        Wind_mph_interpol + Solar_rad_Wm2_interpol +
                        SMI + mass_g + sex_M_F) + SVL_mm +
                        hematocrit_percent + osmolality_mmol_kg +
                        cloacal_temp_C + hold_time +
                        ambient_temp_C + temp_C_interpol +
                        # random effect
                        (1|individual_ID))
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
CEWL_mod4_VIFs <- data.frame(VIF = car::vif(CEWL_mod4)[,3]) %>%
  arrange(desc(VIF))
CEWL_mod4_VIFs
```

```
##                                VIF
## region                        25.258239
## region:VPD_kPa                19.963109
## region:Wind_mph_interpol      13.124017
## VPD_kPa_int                   10.400445
## temp_C_interpol               9.708892
## region:SMI                    8.806453
## mass_g                        8.729644
## SVL_mm                        8.724491
## region:Solar_rad_Wm2_interpol 8.270208
## region:VPD_kPa_int            4.833504
## region:mass_g                 4.656277
## SMI                           4.647721
```



```
## VPD_kPa 3.779206
## Solar_rad_Wm2_interpol 2.749008
## ambient_temp_C 1.952601
## Wind_mph_interpol 1.948642
## region:sex_M_F 1.833544
## sex_M_F 1.725410
## hold_time 1.725326
## cloacal_temp_C 1.665317
## osmolality_mmol_kg 1.568108
## hematocrit_percent 1.144285
```

remove region interaction with ambient VPD at msmt:

```
CEWL_mod5 <- lme4::lmer(data = CEWL_data_full,
  # response variable
  TEWL_g_m2h ~
  # potential predictors
  region * (VPD_kPa_int +
  Wind_mph_interpol + Solar_rad_Wm2_interpol +
  SMI + mass_g + sex_M_F) + SVL_mm +
  hematocrit_percent + osmolality_mmol_kg +
  cloacal_temp_C + hold_time +
  ambient_temp_C + temp_C_interpol + VPD_kPa +
  # random effect
  (1|individual_ID))
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
CEWL_mod5_VIFs <- data.frame(VIF = car::vif(CEWL_mod5)[,3]) %>%
  arrange(desc(VIF))
CEWL_mod5_VIFs
```

```
## VIF
## region 16.466551
## region:Wind_mph_interpol 12.882602
## VPD_kPa_int 10.138740
## temp_C_interpol 9.706791
## region:SMI 8.787887
## mass_g 8.731534
## SVL_mm 8.724861
## region:Solar_rad_Wm2_interpol 6.138976
## SMI 4.651252
## region:mass_g 4.614621
## VPD_kPa 2.838801
## region:VPD_kPa_int 2.622438
## Solar_rad_Wm2_interpol 2.446258
## ambient_temp_C 1.951671
## Wind_mph_interpol 1.940963
## region:sex_M_F 1.834019
## sex_M_F 1.731281
## hold_time 1.725295
## cloacal_temp_C 1.665036
## osmolality_mmol_kg 1.568036
## hematocrit_percent 1.144262
```

remove region interaction with wind at capture:

```
CEWL_mod6 <- lme4::lmer(data = CEWL_data_full,
  # response variable
  TEWL_g_m2h ~
  # potential predictors
  region * (VPD_kPa_int + Solar_rad_Wm2_interpol +
  SMI + mass_g + sex_M_F) + SVL_mm +
  hematocrit_percent + osmolality_mmol_kg +
  cloacal_temp_C + hold_time +
  ambient_temp_C + temp_C_interpol + VPD_kPa +
  Wind_mph_interpol +
  # random effect
  (1|individual_ID))
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
CEWL_mod6_VIFs <- data.frame(VIF = car::vif(CEWL_mod6)[,3]) %>%
  arrange(desc(VIF))
CEWL_mod6_VIFs
```

##	VIF
## VPD_kPa_int	10.135498
## temp_C_interpol	9.705914
## region	9.072210
## mass_g	8.734035
## region:SMI	8.732760
## SVL_mm	8.726249
## region:Solar_rad_Wm2_interpol	6.131410
## SMI	4.652630
## region:mass_g	4.605420
## VPD_kPa	2.837898
## region:VPD_kPa_int	2.560882
## Solar_rad_Wm2_interpol	2.449554
## ambient_temp_C	1.951377
## region:sex_M_F	1.834689
## sex_M_F	1.736889
## hold_time	1.725299
## cloacal_temp_C	1.665040
## osmolality_mmol_kg	1.568027
## Wind_mph_interpol	1.417380
## hematocrit_percent	1.144269

The predictors in this model are much less collinear. Now we will begin model selection using AIC and t-values.

Need dataset without NAs first.

```
CEWL_dat_sub1 <- CEWL_data_full %>%
  dplyr::filter(complete.cases(region, VPD_kPa_int,
    Solar_rad_Wm2_interpol,
    SMI, SVL_mm, mass_g, sex_M_F,
    hematocrit_percent, osmolality_mmol_kg,
    cloacal_temp_C, hold_time,
    ambient_temp_C, temp_C_interpol,
    Wind_mph_interpol, VPD_kPa))
```

```
CEWL_mod6a <- lme4::lmer(data = CEWL_dat_sub1,
  # response variable
  TEWL_g_m2h ~
  # potential predictors
  region * (VPD_kPa_int + Solar_rad_Wm2_interpol +
  SMI + mass_g + sex_M_F) + SVL_mm +
  hematocrit_percent + osmolality_mmol_kg +
  cloacal_temp_C + hold_time +
  ambient_temp_C + temp_C_interpol + VPD_kPa +
  Wind_mph_interpol +
  # random effect
  (1|individual_ID))
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
summary(CEWL_mod6a)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: TEWL_g_m2h ~ region * (VPD_kPa_int + Solar_rad_Wm2_interpol +
##       SMI + mass_g + sex_M_F) + SVL_mm + hematocrit_percent + osmolality_mmol_kg +
##       cloacal_temp_C + hold_time + ambient_temp_C + temp_C_interpol +
##       VPD_kPa + Wind_mph_interpol + (1 | individual_ID)
## Data: CEWL_dat_sub1
##
## REML criterion at convergence: 4290.1
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.0037 -0.5475 -0.1039  0.4156  5.3855
##
## Random effects:
##   Groups             Name             Variance Std.Dev.
## individual_ID (Intercept) 28.82       5.368
## Residual                99.93       9.996
## Number of obs: 570, groups: individual_ID, 116
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)   -5.050e+01  7.980e+01  -0.633
## regionVentrum  -3.554e+00  1.198e+01  -0.297
## regionHead     -7.150e+00  1.196e+01  -0.598
## regionDewlap   -2.436e+01  1.205e+01  -2.022
## regionMite Patch -9.044e+00  1.204e+01  -0.751
## VPD_kPa_int    -5.157e+01  1.719e+01  -3.000
## Solar_rad_Wm2_interpol 1.337e-02  9.815e-03  1.362
## SMI            5.601e-01  2.303e+00  0.243
## mass_g        -5.258e-01  2.208e+00  -0.238
## sex_M_FM       1.792e+00  2.343e+00  0.765
## SVL_mm         3.885e-01  1.051e+00  0.369
## hematocrit_percent -2.839e-01  1.241e-01  -2.288
## osmolality_mmol_kg -1.076e-02  3.969e-02  -0.271
## cloacal_temp_C  2.313e+00  5.952e-01  3.887
## hold_time      -7.909e-03  1.694e-02  -0.467
```

```

## ambient_temp_C -5.550e+00 1.661e+00 -3.341
## temp_C_interpol 5.925e+00 2.438e+00 2.431
## VPD_kPa 2.766e+01 1.123e+01 2.464
## Wind_mph_interpol 1.632e+00 2.342e+00 0.697
## regionVentrums:VPD_kPa_int 7.429e+00 3.678e+00 2.020
## regionHead:VPD_kPa_int 1.830e+00 3.690e+00 0.496
## regionDewlap:VPD_kPa_int 1.431e+01 3.704e+00 3.863
## regionMite Patch:VPD_kPa_int 1.627e+01 3.686e+00 4.414
## regionVentrums:Solar_rad_Wm2_interpol -3.674e-04 8.894e-03 -0.041
## regionHead:Solar_rad_Wm2_interpol 1.173e-02 8.888e-03 1.320
## regionDewlap:Solar_rad_Wm2_interpol -3.166e-03 8.957e-03 -0.354
## regionMite Patch:Solar_rad_Wm2_interpol -1.293e-02 9.020e-03 -1.434
## regionVentrums:SMI -2.672e-01 1.091e+00 -0.245
## regionHead:SMI 6.388e-01 1.087e+00 0.588
## regionDewlap:SMI 5.436e-01 1.093e+00 0.497
## regionMite Patch:SMI -3.879e-02 1.095e+00 -0.035
## regionVentrums:mass_g 9.784e-01 5.385e-01 1.817
## regionHead:mass_g -3.732e-01 5.357e-01 -0.697
## regionDewlap:mass_g 9.755e-01 5.476e-01 1.781
## regionMite Patch:mass_g 1.046e+00 5.573e-01 1.877
## regionVentrums:sex_M_FM 1.102e+00 2.864e+00 0.385
## regionHead:sex_M_FM -2.433e+00 2.883e+00 -0.844
## regionDewlap:sex_M_FM -1.666e+00 2.897e+00 -0.575
## regionMite Patch:sex_M_FM 2.398e+00 2.877e+00 0.833

##
## Correlation matrix not shown by default, as p = 39 > 12.
## Use print(x, correlation=TRUE) or
## vcov(x) if you need it

## fit warnings:
## Some predictor variables are on very different scales: consider rescaling
drop1(CEWL_mod6a)

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Single term deletions
##
## Model:
## TEWL_g_m2h ~ region * (VPD_kPa_int + Solar_rad_Wm2_interpol +
##   SMI + mass_g + sex_M_F) + SVL_mm + hematocrit_percent + osmolality_mmol_kg +
##   cloacal_temp_C + hold_time + ambient_temp_C + temp_C_interpol +
##   VPD_kPa + Wind_mph_interpol + (1 | individual_ID)
##
##               npar      AIC
## <none>                4385.7
## SVL_mm                1 4383.8
## hematocrit_percent    1 4389.5
## osmolality_mmol_kg    1 4383.7
## cloacal_temp_C        1 4399.9
## hold_time             1 4383.9
## ambient_temp_C        1 4395.8
## temp_C_interpol       1 4390.3
## VPD_kPa               1 4390.4
## Wind_mph_interpol     1 4384.2
## region:VPD_kPa_int    4 4409.0
## region:Solar_rad_Wm2_interpol 4 4385.7
## region:SMI            4 4378.8
## region:mass_g         4 4390.3
## region:sex_M_F        4 4381.6

drop region*SMI interaction:
```

```
CEWL_mod7 <- lme4::lmer(data = CEWL_dat_sub1,
  # response variable
  TEWL_g_m2h ~
  # potential predictors
  region * (VPD_kPa_int + Solar_rad_Wm2_interpol +
  mass_g + sex_M_F) + SVL_mm + SMI +
  hematocrit_percent + osmolality_mmol_kg +
  cloacal_temp_C + hold_time +
  ambient_temp_C + temp_C_interpol + VPD_kPa +
  Wind_mph_interpol +
  # random effect
```

```
(1|individual_ID))
```

```
## Warning: Some predictor variables are on very different scales: consider  
## rescaling
```

```
summary(CEWL_mod7)
```

```
## Linear mixed model fit by REML ['lmerMod']  
## Formula: TEWL_g_m2h ~ region * (VPD_kPa_int + Solar_rad_Wm2_interpol +  
##      mass_g + sex_M_F) + SVL_mm + SMI + hematocrit_percent + osmolality_mmol_kg +  
##      cloacal_temp_C + hold_time + ambient_temp_C + temp_C_interpol +  
##      VPD_kPa + Wind_mph_interpol + (1 | individual_ID)  
##      Data: CEWL_dat_sub1  
##  
## REML criterion at convergence: 4298  
##  
## Scaled residuals:  
##      Min      1Q  Median      3Q      Max  
## -2.0010 -0.5518 -0.1184  0.4093  5.3989  
##  
## Random effects:  
##      Groups      Name      Variance Std.Dev.  
## individual_ID (Intercept) 28.96      5.382  
## Residual                99.25      9.962  
## Number of obs: 570, groups: individual_ID, 116  
##  
## Fixed effects:  
##  
##      Estimate Std. Error t value  
## (Intercept) -5.149e+01  7.962e+01 -0.647  
## regionVentrum -5.594e+00  8.998e+00 -0.622  
## regionHead -2.535e+00  9.020e+00 -0.281  
## regionDewlap -2.051e+01  9.204e+00 -2.229  
## regionMite Patch -9.271e+00  9.287e+00 -0.998  
## VPD_kPa_int -5.157e+01  1.719e+01 -3.000  
## Solar_rad_Wm2_interpol 1.296e-02  9.670e-03  1.340  
## mass_g -5.396e-01  2.205e+00 -0.245  
## sex_M_FM 1.739e+00  2.329e+00  0.747  
## SVL_mm 3.853e-01  1.051e+00  0.367  
## SMI 7.305e-01  2.196e+00  0.333  
## hematocrit_percent -2.837e-01  1.241e-01 -2.287  
## osmolality_mmol_kg -1.080e-02  3.969e-02 -0.272  
## cloacal_temp_C 2.314e+00  5.952e-01  3.888  
## hold_time -7.852e-03  1.694e-02 -0.463  
## ambient_temp_C -5.553e+00  1.661e+00 -3.343  
## temp_C_interpol 5.925e+00  2.438e+00  2.431  
## VPD_kPa 2.766e+01  1.122e+01  2.465  
## Wind_mph_interpol 1.632e+00  2.342e+00  0.697  
## regionVentrum:VPD_kPa_int 7.379e+00  3.665e+00  2.014  
## regionHead:VPD_kPa_int 1.870e+00  3.677e+00  0.509  
## regionDewlap:VPD_kPa_int 1.433e+01  3.691e+00  3.882  
## regionMite Patch:VPD_kPa_int 1.628e+01  3.673e+00  4.431  
## regionVentrum:Solar_rad_Wm2_interpol -9.398e-04  8.519e-03 -0.110  
## regionHead:Solar_rad_Wm2_interpol 1.315e-02  8.520e-03  1.543  
## regionDewlap:Solar_rad_Wm2_interpol -1.927e-03  8.574e-03 -0.225
```

```

## regionMite Patch:Solar_rad_Wm2_interpol -1.304e-02  8.621e-03  -1.513
## regionVentrum:mass_g                    9.639e-01  5.268e-01   1.830
## regionHead:mass_g                      -3.112e-01  5.228e-01  -0.595
## regionDewlap:mass_g                    1.033e+00  5.334e-01   1.937
## regionMite Patch:mass_g                1.039e+00  5.412e-01   1.920
## regionVentrum:sex_M_FM                 9.875e-01  2.831e+00   0.349
## regionHead:sex_M_FM                   -2.227e+00  2.852e+00  -0.781
## regionDewlap:sex_M_FM                 -1.484e+00  2.865e+00  -0.518
## regionMite Patch:sex_M_FM              2.383e+00  2.847e+00   0.837
##
## Correlation matrix not shown by default, as p = 35 > 12.
## Use print(x, correlation=TRUE) or
##     vcov(x)           if you need it
## fit warnings:
## Some predictor variables are on very different scales: consider rescaling
drop1(CEWL_mod7)

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Single term deletions

##
## Model:
## TEWL_g_m2h ~ region * (VPD_kPa_int + Solar_rad_Wm2_interpol +
##   mass_g + sex_M_F) + SVL_mm + SMI + hematocrit_percent + osmolality_mmol_kg +
##   cloacal_temp_C + hold_time + ambient_temp_C + temp_C_interpol +
##   VPD_kPa + Wind_mph_interpol + (1 | individual_ID)
##
##               npar      AIC
## <none>                4378.8
## SVL_mm                1 4376.9
## SMI                   1 4376.9
## hematocrit_percent    1 4382.6
## osmolality_mmol_kg    1 4376.9
## cloacal_temp_C        1 4393.0
## hold_time             1 4377.0
## ambient_temp_C        1 4388.9
## temp_C_interpol       1 4383.4
## VPD_kPa               1 4383.6
## Wind_mph_interpol     1 4377.3
## region:VPD_kPa_int    4 4402.0
## region:Solar_rad_Wm2_interpol 4 4380.5
## region:mass_g         4 4383.3
## region:sex_M_F        4 4374.3
```

drop region*sex interaction:

```
CEWL_mod8 <- lme4::lmer(data = CEWL_dat_sub1,
  # response variable
  TEWL_g_m2h ~
  # potential predictors
  region * (VPD_kPa_int + Solar_rad_Wm2_interpol +
  mass_g) + SVL_mm + SMI + sex_M_F +
  hematocrit_percent + osmolality_mmol_kg +
  cloacal_temp_C + hold_time +
  ambient_temp_C + temp_C_interpol + VPD_kPa +
  Wind_mph_interpol +
  # random effect
  (1|individual_ID))
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
summary(CEWL_mod8)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: TEWL_g_m2h ~ region * (VPD_kPa_int + Solar_rad_Wm2_interpol +
##   mass_g) + SVL_mm + SMI + sex_M_F + hematocrit_percent + osmolality_mmol_kg +
##   cloacal_temp_C + hold_time + ambient_temp_C + temp_C_interpol +
##   VPD_kPa + Wind_mph_interpol + (1 | individual_ID)
## Data: CEWL_dat_sub1
##
## REML criterion at convergence: 4315.9
##
```



```

## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.9570 -0.5539 -0.1066  0.4054  5.2381
##
## Random effects:
##      Groups             Name             Variance Std.Dev.
## individual_ID (Intercept) 29.08         5.393
## Residual                  99.06         9.953
## Number of obs: 570, groups: individual_ID, 116
##
## Fixed effects:
##
##              Estimate Std. Error t value
## (Intercept)      -5.068e+01  7.966e+01  -0.636
## regionVentrum      -5.585e+00  8.987e+00  -0.621
## regionHead         -2.329e+00  9.008e+00  -0.259
## regionDewlap       -2.037e+01  9.193e+00  -2.216
## regionMite Patch   -9.422e+00  9.276e+00  -1.016
## VPD_kPa_int        -5.145e+01  1.720e+01  -2.992
## Solar_rad_Wm2_interpol  1.290e-02  9.670e-03   1.334
## mass_g             -5.332e-01  2.206e+00  -0.242
## SVL_mm             3.852e-01  1.051e+00   0.366
## SMI                7.293e-01  2.197e+00   0.332
## sex_M_FM           1.696e+00  1.495e+00   1.134
## hematocrit_percent -2.858e-01  1.242e-01  -2.301
## osmolality_mmol_kg -1.015e-02  3.972e-02  -0.255
## cloacal_temp_C      2.316e+00  5.957e-01   3.889
## hold_time          -8.048e-03  1.696e-02  -0.475
## ambient_temp_C      -5.601e+00  1.662e+00  -3.370
## temp_C_interpol      5.924e+00  2.440e+00   2.428
## VPD_kPa            2.743e+01  1.123e+01   2.443
## Wind_mph_interpol    1.725e+00  2.343e+00   0.736
## regionVentrum:VPD_kPa_int  7.597e+00  3.610e+00   2.105
## regionHead:VPD_kPa_int  1.278e+00  3.608e+00   0.354
## regionDewlap:VPD_kPa_int  1.394e+01  3.623e+00   3.848
## regionMite Patch:VPD_kPa_int  1.678e+01  3.618e+00   4.637
## regionVentrum:Solar_rad_Wm2_interpol -8.488e-04  8.503e-03  -0.100
## regionHead:Solar_rad_Wm2_interpol  1.284e-02  8.502e-03   1.511
## regionDewlap:Solar_rad_Wm2_interpol -2.171e-03  8.556e-03  -0.254
## regionMite Patch:Solar_rad_Wm2_interpol -1.262e-02  8.601e-03  -1.468
## regionVentrum:mass_g  9.970e-01  5.155e-01   1.934
## regionHead:mass_g    -3.925e-01  5.114e-01  -0.767
## regionDewlap:mass_g  9.816e-01  5.232e-01   1.876
## regionMite Patch:mass_g  1.119e+00  5.311e-01   2.107
##
## Correlation matrix not shown by default, as p = 31 > 12.
## Use print(x, correlation=TRUE) or
##      vcov(x)          if you need it
##
## fit warnings:
## Some predictor variables are on very different scales: consider rescaling
drop1(CEWL_mod8)

## Warning: Some predictor variables are on very different scales: consider
## rescaling

```

```

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
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## Warning: Some predictor variables are on very different scales: consider
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## Warning: Some predictor variables are on very different scales: consider
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## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Single term deletions
##
## Model:
## TEWL_g_m2h ~ region * (VPD_kPa_int + Solar_rad_Wm2_interpol +
##   mass_g) + SVL_mm + SMI + sex_M_F + hematocrit_percent + osmolality_mmol_kg +
##   cloacal_temp_C + hold_time + ambient_temp_C + temp_C_interpol +
##   VPD_kPa + Wind_mph_interpol + (1 | individual_ID)
##
##               npar      AIC
## <none>                4374.3
## SVL_mm                1 4372.4
## SMI                   1 4372.4
## sex_M_F              1 4373.7
## hematocrit_percent   1 4378.2
## osmolality_mmol_kg   1 4372.4
## cloacal_temp_C       1 4388.5
## hold_time            1 4372.5
## ambient_temp_C       1 4384.6

```

```
## temp_C_interpol          1 4378.9
## VPD_kPa                  1 4379.0
## Wind_mph_interpol        1 4372.9
## region:VPD_kPa_int       4 4400.0
## region:Solar_rad_Wm2_interpol 4 4375.4
## region:mass_g            4 4380.8
```

drop SMI:

```
CEWL_mod9 <- lme4::lmer(data = CEWL_dat_sub1,
  # response variable
  TEWL_g_m2h ~
  # potential predictors
  region * (VPD_kPa_int + Solar_rad_Wm2_interpol +
  mass_g) + SVL_mm + sex_M_F +
  hematocrit_percent + osmolality_mmol_kg +
  cloacal_temp_C + hold_time +
  ambient_temp_C + temp_C_interpol + VPD_kPa +
  Wind_mph_interpol +
  # random effect
  (1|individual_ID))
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
summary(CEWL_mod9)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: TEWL_g_m2h ~ region * (VPD_kPa_int + Solar_rad_Wm2_interpol +
##      mass_g) + SVL_mm + sex_M_F + hematocrit_percent + osmolality_mmol_kg +
##      cloacal_temp_C + hold_time + ambient_temp_C + temp_C_interpol +
##      VPD_kPa + Wind_mph_interpol + (1 | individual_ID)
## Data: CEWL_dat_sub1
##
## REML criterion at convergence: 4319.5
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.9571 -0.5505 -0.1005  0.4076  5.2459
##
## Random effects:
##      Groups      Name      Variance Std.Dev.
## individual_ID (Intercept) 28.69    5.356
## Residual                99.04    9.952
## Number of obs: 570, groups: individual_ID, 116
##
## Fixed effects:
##
##              Estimate Std. Error t value
## (Intercept)    -2.667e+01  3.293e+01  -0.810
## regionVentrum    -5.620e+00  8.986e+00  -0.625
## regionHead       -2.368e+00  9.006e+00  -0.263
## regionDewlap     -2.031e+01  9.191e+00  -2.209
## regionMite Patch  -9.307e+00  9.269e+00  -1.004
## VPD_kPa_int      -5.114e+01  1.710e+01  -2.990
## Solar_rad_Wm2_interpol  1.336e-02  9.548e-03   1.399
## mass_g           1.636e-01  6.771e-01   0.242
```

```

## SVL_mm                4.859e-02  2.747e-01  0.177
## sex_M_FM              1.693e+00  1.489e+00  1.137
## hematocrit_percent    -2.910e-01  1.226e-01 -2.373
## osmolality_mmol_kg     -9.581e-03  3.952e-02 -0.242
## cloacal_temp_C         2.292e+00  5.891e-01  3.891
## hold_time              -8.151e-03  1.689e-02 -0.483
## ambient_temp_C         -5.636e+00  1.652e+00 -3.412
## temp_C_interpol        5.866e+00  2.423e+00  2.421
## VPD_kPa                2.730e+01  1.118e+01  2.442
## Wind_mph_interpol      1.788e+00  2.325e+00  0.769
## regionVentrum:VPD_kPa_int  7.596e+00  3.610e+00  2.104
## regionHead:VPD_kPa_int  1.274e+00  3.608e+00  0.353
## regionDewlap:VPD_kPa_int  1.395e+01  3.622e+00  3.850
## regionMite Patch:VPD_kPa_int  1.679e+01  3.618e+00  4.643
## regionVentrum:Solar_rad_Wm2_interpol -8.269e-04  8.502e-03 -0.097
## regionHead:Solar_rad_Wm2_interpol  1.286e-02  8.501e-03  1.513
## regionDewlap:Solar_rad_Wm2_interpol -2.181e-03  8.555e-03 -0.255
## regionMite Patch:Solar_rad_Wm2_interpol -1.266e-02  8.600e-03 -1.472
## regionVentrum:mass_g    9.985e-01  5.154e-01  1.937
## regionHead:mass_g      -3.905e-01  5.113e-01 -0.764
## regionDewlap:mass_g     9.767e-01  5.230e-01  1.868
## regionMite Patch:mass_g  1.110e+00  5.304e-01  2.093

##
## Correlation matrix not shown by default, as p = 30 > 12.
## Use print(x, correlation=TRUE) or
##     vcov(x)         if you need it

## fit warnings:
## Some predictor variables are on very different scales: consider rescaling
drop1(CEWL_mod9)

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Single term deletions

##
## Model:
## TEWL_g_m2h ~ region * (VPD_kPa_int + Solar_rad_Wm2_interpol +
##   mass_g) + SVL_mm + sex_M_F + hematocrit_percent + osmolality_mmol_kg +
##   cloacal_temp_C + hold_time + ambient_temp_C + temp_C_interpol +
##   VPD_kPa + Wind_mph_interpol + (1 | individual_ID)
##
##               npar      AIC
## <none>                4372.4
## SVL_mm                1 4370.4
## sex_M_F               1 4371.9
## hematocrit_percent    1 4376.6
## osmolality_mmol_kg    1 4370.5
## cloacal_temp_C       1 4386.5
## hold_time            1 4370.7
## ambient_temp_C       1 4382.9
## temp_C_interpol      1 4376.9
## VPD_kPa              1 4377.0
## Wind_mph_interpol    1 4371.1
## region:VPD_kPa_int    4 4398.2
## region:Solar_rad_Wm2_interpol 4 4373.6
## region:mass_g        4 4378.8
```

drop SVL:

```
CEWL_mod10 <- lme4::lmer(data = CEWL_dat_sub1,
  # response variable
  TEWL_g_m2h ~
  # potential predictors
  region * (VPD_kPa_int + Solar_rad_Wm2_interpol +
  mass_g) + sex_M_F +
  hematocrit_percent + osmolality_mmol_kg +
  cloacal_temp_C + hold_time +
  ambient_temp_C + temp_C_interpol + VPD_kPa +
  Wind_mph_interpol +
  # random effect
  (1|individual_ID))
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
summary(CEWL_mod10)
```

```

## Linear mixed model fit by REML ['lmerMod']
## Formula: TEWL_g_m2h ~ region * (VPD_kPa_int + Solar_rad_Wm2_interpol +
##      mass_g) + sex_M_F + hematocrit_percent + osmolality_mmol_kg +
##      cloacal_temp_C + hold_time + ambient_temp_C + temp_C_interpol +
##      VPD_kPa + Wind_mph_interpol + (1 | individual_ID)
## Data: CEWL_dat_sub1
##
## REML criterion at convergence: 4318.7
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.9630 -0.5493 -0.1038  0.4004  5.2504
##
## Random effects:
##      Groups             Name             Variance Std.Dev.
## individual_ID (Intercept) 28.24         5.314
## Residual                  99.04         9.952
## Number of obs: 570, groups: individual_ID, 116
##
## Fixed effects:
##
##              Estimate Std. Error t value
## (Intercept)      -2.543e+01  3.198e+01  -0.795
## regionVentrum      -5.630e+00  8.985e+00  -0.627
## regionHead         -2.378e+00  9.006e+00  -0.264
## regionDewlap       -2.029e+01  9.190e+00  -2.208
## regionMite Patch   -9.277e+00  9.267e+00  -1.001
## VPD_kPa_int        -5.129e+01  1.701e+01  -3.015
## Solar_rad_Wm2_interpol  1.322e-02  9.481e-03   1.394
## mass_g             2.572e-01  4.237e-01   0.607
## sex_M_FM           1.674e+00  1.479e+00   1.132
## hematocrit_percent -2.952e-01  1.197e-01  -2.465
## osmolality_mmol_kg -8.372e-03  3.874e-02  -0.216
## cloacal_temp_C     2.302e+00  5.833e-01   3.948
## hold_time          -8.444e-03  1.673e-02  -0.505
## ambient_temp_C     -5.627e+00  1.644e+00  -3.423
## temp_C_interpol     5.876e+00  2.412e+00   2.437
## VPD_kPa            2.731e+01  1.113e+01   2.455
## Wind_mph_interpol   1.844e+00  2.292e+00   0.804
## regionVentrum:VPD_kPa_int  7.593e+00  3.609e+00   2.104
## regionHead:VPD_kPa_int  1.273e+00  3.608e+00   0.353
## regionDewlap:VPD_kPa_int  1.395e+01  3.622e+00   3.851
## regionMite Patch:VPD_kPa_int  1.680e+01  3.617e+00   4.644
## regionVentrum:Solar_rad_Wm2_interpol -8.249e-04  8.502e-03  -0.097
## regionHead:Solar_rad_Wm2_interpol  1.287e-02  8.501e-03   1.514
## regionDewlap:Solar_rad_Wm2_interpol -2.184e-03  8.554e-03  -0.255
## regionMite Patch:Solar_rad_Wm2_interpol -1.267e-02  8.599e-03  -1.473
## regionVentrum:mass_g  9.994e-01  5.153e-01   1.939
## regionHead:mass_g    -3.898e-01  5.113e-01  -0.762
## regionDewlap:mass_g  9.757e-01  5.229e-01   1.866
## regionMite Patch:mass_g  1.108e+00  5.303e-01   2.090
##
## Correlation matrix not shown by default, as p = 29 > 12.
## Use print(x, correlation=TRUE) or

```

```

##      vcov(x)          if you need it
## fit warnings:
## Some predictor variables are on very different scales: consider rescaling
drop1(CEWL_mod10)

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Single term deletions
##
## Model:
## TEWL_g_m2h ~ region * (VPD_kPa_int + Solar_rad_Wm2_interpol +
##      mass_g) + sex_M_F + hematocrit_percent + osmolality_mmol_kg +
##      cloacal_temp_C + hold_time + ambient_temp_C + temp_C_interpol +
##      VPD_kPa + Wind_mph_interpol + (1 | individual_ID)
##              npar      AIC
## <none>                4370.4
## sex_M_F                1 4369.9
## hematocrit_percent     1 4375.1
## osmolality_mmol_kg     1 4368.5
## cloacal_temp_C         1 4384.8
## hold_time              1 4368.7
## ambient_temp_C         1 4381.0
## temp_C_interpol        1 4374.9

```

```
## VPD_kPa                1 4375.1
## Wind_mph_interpol      1 4369.2
## region:VPD_kPa_int     4 4396.2
## region:Solar_rad_Wm2_interpol 4 4371.7
## region:mass_g          4 4376.8
```

drop osmolality:

```
CEWL_mod11 <- lme4::lmer(data = CEWL_dat_sub1,
  # response variable
  TEWL_g_m2h ~
  # potential predictors
  region * (VPD_kPa_int + Solar_rad_Wm2_interpol +
  mass_g) + sex_M_F +
  hematocrit_percent +
  cloacal_temp_C + hold_time +
  ambient_temp_C + temp_C_interpol + VPD_kPa +
  Wind_mph_interpol +
  # random effect
  (1|individual_ID))
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
summary(CEWL_mod11)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: TEWL_g_m2h ~ region * (VPD_kPa_int + Solar_rad_Wm2_interpol +
##      mass_g) + sex_M_F + hematocrit_percent + cloacal_temp_C +
##      hold_time + ambient_temp_C + temp_C_interpol + VPD_kPa +
##      Wind_mph_interpol + (1 | individual_ID)
## Data: CEWL_dat_sub1
##
## REML criterion at convergence: 4314.1
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.9682 -0.5511 -0.1043  0.4021  5.2537
##
## Random effects:
##      Groups       Name             Variance Std.Dev.
## individual_ID (Intercept) 27.80      5.272
## Residual                99.04      9.952
## Number of obs: 570, groups: individual_ID, 116
##
## Fixed effects:
##
##              Estimate Std. Error t value
## (Intercept)    -2.803e+01  2.959e+01  -0.947
## regionVentrums  -5.615e+00  8.984e+00  -0.625
## regionHead      -2.361e+00  9.005e+00  -0.262
## regionDewlap    -2.029e+01  9.189e+00  -2.208
## regionMite Patch -9.299e+00  9.266e+00  -1.004
## VPD_kPa_int     -5.125e+01  1.693e+01  -3.027
## Solar_rad_Wm2_interpol  1.390e-02  8.933e-03   1.556
## mass_g          2.622e-01  4.224e-01   0.621
## sex_M_FM        1.747e+00  1.431e+00   1.221
```



```

## hematocrit_percent          -3.000e-01  1.170e-01 -2.564
## cloacal_temp_C              2.278e+00  5.700e-01  3.996
## hold_time                   -9.884e-03  1.530e-02 -0.646
## ambient_temp_C              -5.619e+00  1.636e+00 -3.434
## temp_C_interpol              5.816e+00  2.384e+00  2.439
## VPD_kPa                     2.734e+01  1.108e+01  2.467
## Wind_mph_interpol           1.972e+00  2.202e+00  0.895
## regionVentrum:VPD_kPa_int    7.595e+00  3.609e+00  2.104
## regionHead:VPD_kPa_int       1.274e+00  3.608e+00  0.353
## regionDewlap:VPD_kPa_int     1.395e+01  3.622e+00  3.850
## regionMite Patch:VPD_kPa_int 1.679e+01  3.617e+00  4.643
## regionVentrum:Solar_rad_Wm2_interpol -8.316e-04  8.502e-03 -0.098
## regionHead:Solar_rad_Wm2_interpol  1.286e-02  8.501e-03  1.513
## regionDewlap:Solar_rad_Wm2_interpol -2.185e-03  8.554e-03 -0.255
## regionMite Patch:Solar_rad_Wm2_interpol -1.266e-02  8.599e-03 -1.472
## regionVentrum:mass_g         9.985e-01  5.153e-01  1.938
## regionHead:mass_g            -3.907e-01  5.113e-01 -0.764
## regionDewlap:mass_g          9.757e-01  5.229e-01  1.866
## regionMite Patch:mass_g      1.110e+00  5.303e-01  2.093

##
## Correlation matrix not shown by default, as p = 28 > 12.
## Use print(x, correlation=TRUE) or
##     vcov(x)         if you need it

## fit warnings:
## Some predictor variables are on very different scales: consider rescaling
drop1(CEWL_mod11)

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## Single term deletions
```

```
##
```

```
## Model:
```

```
## TEWL_g_m2h ~ region * (VPD_kPa_int + Solar_rad_Wm2_interpol +
##   mass_g) + sex_M_F + hematocrit_percent + cloacal_temp_C +
##   hold_time + ambient_temp_C + temp_C_interpol + VPD_kPa +
##   Wind_mph_interpol + (1 | individual_ID)
```

	npar	AIC
<none>		4368.5
sex_M_F	1	4368.1
hematocrit_percent	1	4373.6
cloacal_temp_C	1	4383.1
hold_time	1	4367.0
ambient_temp_C	1	4379.0
temp_C_interpol	1	4373.0
VPD_kPa	1	4373.1
Wind_mph_interpol	1	4367.4
region:VPD_kPa_int	4	4394.3
region:Solar_rad_Wm2_interpol	4	4369.7
region:mass_g	4	4374.9

```
drop hold time:
```

```
CEWL_mod12 <- lme4::lmer(data = CEWL_dat_sub1,
  # response variable
  TEWL_g_m2h ~
  # potential predictors
  region * (VPD_kPa_int + Solar_rad_Wm2_interpol +
  mass_g) + sex_M_F +
  hematocrit_percent +
  cloacal_temp_C +
  ambient_temp_C + temp_C_interpol + VPD_kPa +
  Wind_mph_interpol +
  # random effect
  (1|individual_ID))
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
summary(CEWL_mod12)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: TEWL_g_m2h ~ region * (VPD_kPa_int + Solar_rad_Wm2_interpol +
##   mass_g) + sex_M_F + hematocrit_percent + cloacal_temp_C +
##   ambient_temp_C + temp_C_interpol + VPD_kPa + Wind_mph_interpol +
##   (1 | individual_ID)
## Data: CEWL_dat_sub1
##
## REML criterion at convergence: 4308
##
## Scaled residuals:
##   Min       1Q   Median       3Q      Max
```

```

## -1.9776 -0.5654 -0.1071  0.4025  5.2559
##
## Random effects:
##   Groups      Name      Variance Std.Dev.
## individual_ID (Intercept) 27.58    5.252
## Residual                99.01    9.951
## Number of obs: 570, groups: individual_ID, 116
##
## Fixed effects:
##                                     Estimate Std. Error t value
## (Intercept)                       -2.819e+01  2.952e+01  -0.955
## regionVentrum                     -5.645e+00  8.983e+00  -0.628
## regionHead                        -2.415e+00  9.004e+00  -0.268
## regionDewlap                     -2.033e+01  9.188e+00  -2.212
## regionMite Patch                  -9.308e+00  9.265e+00  -1.005
## VPD_kPa_int                      -4.766e+01  1.596e+01  -2.987
## Solar_rad_Wm2_interpol            1.393e-02  8.919e-03   1.561
## mass_g                           2.821e-01  4.208e-01   0.670
## sex_M_FM                         1.621e+00  1.415e+00   1.146
## hematocrit_percent               -2.990e-01  1.168e-01  -2.561
## cloacal_temp_C                   2.543e+00  3.939e-01   6.456
## ambient_temp_C                   -5.485e+00  1.620e+00  -3.387
## temp_C_interpol                   5.350e+00  2.267e+00   2.360
## VPD_kPa                          2.500e+01  1.045e+01   2.393
## Wind_mph_interpol                 1.767e+00  2.174e+00   0.813
## regionVentrum:VPD_kPa_int          7.596e+00  3.609e+00   2.105
## regionHead:VPD_kPa_int             1.276e+00  3.607e+00   0.354
## regionDewlap:VPD_kPa_int           1.395e+01  3.622e+00   3.853
## regionMite Patch:VPD_kPa_int        1.681e+01  3.617e+00   4.647
## regionVentrum:Solar_rad_Wm2_interpol -7.923e-04  8.501e-03  -0.093
## regionHead:Solar_rad_Wm2_interpol    1.291e-02  8.499e-03   1.519
## regionDewlap:Solar_rad_Wm2_interpol -2.153e-03  8.553e-03  -0.252
## regionMite Patch:Solar_rad_Wm2_interpol -1.263e-02  8.598e-03  -1.469
## regionVentrum:mass_g               9.989e-01  5.152e-01   1.939
## regionHead:mass_g                  -3.892e-01  5.112e-01  -0.761
## regionDewlap:mass_g                9.772e-01  5.228e-01   1.869
## regionMite Patch:mass_g            1.109e+00  5.302e-01   2.092
##
## Correlation matrix not shown by default, as p = 27 > 12.
## Use print(x, correlation=TRUE) or
##   vcov(x)           if you need it
##
## fit warnings:
## Some predictor variables are on very different scales: consider rescaling
drop1(CEWL_mod12)

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## Single term deletions
```

```
##
```

```
## Model:
```

```
## TEWL_g_m2h ~ region * (VPD_kPa_int + Solar_rad_Wm2_interpol +
##      mass_g) + sex_M_F + hematocrit_percent + cloacal_temp_C +
##      ambient_temp_C + temp_C_interpol + VPD_kPa + Wind_mph_interpol +
##      (1 | individual_ID)
```

	npars	AIC
## <none>		4367.0
## sex_M_F	1	4366.4
## hematocrit_percent	1	4372.0
## cloacal_temp_C	1	4403.9
## ambient_temp_C	1	4377.0
## temp_C_interpol	1	4371.0
## VPD_kPa	1	4371.1
## Wind_mph_interpol	1	4365.7
## region:VPD_kPa_int	4	4392.8
## region:Solar_rad_Wm2_interpol	4	4368.2
## region:mass_g	4	4373.4

```
drop wind:
```

```
CEWL_mod13 <- lme4::lmer(data = CEWL_dat_sub1,
  # response variable
  TEWL_g_m2h ~
  # potential predictors
  region * (VPD_kPa_int + Solar_rad_Wm2_interpol +
  mass_g) + sex_M_F +
  hematocrit_percent +
  cloacal_temp_C +
  ambient_temp_C + temp_C_interpol + VPD_kPa +
  # random effect
  (1|individual_ID))
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
summary(CEWL_mod13)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: TEWL_g_m2h ~ region * (VPD_kPa_int + Solar_rad_Wm2_interpol +
##      mass_g) + sex_M_F + hematocrit_percent + cloacal_temp_C +
##      ambient_temp_C + temp_C_interpol + VPD_kPa + (1 | individual_ID)
##      Data: CEWL_dat_sub1
##
## REML criterion at convergence: 4312.1
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.9675 -0.5520 -0.1066  0.4046  5.2659
##
## Random effects:
##      Groups             Name             Variance Std.Dev.
## individual_ID (Intercept) 27.35          5.230
## Residual                  99.05          9.952
## Number of obs: 570, groups: individual_ID, 116
##
## Fixed effects:
##
##              Estimate Std. Error t value
## (Intercept)      -2.789e+01  2.945e+01  -0.947
## regionVentrum      -5.577e+00  8.984e+00  -0.621
## regionHead         -2.397e+00  9.005e+00  -0.266
## regionDewlap       -2.037e+01  9.189e+00  -2.217
## regionMite Patch   -9.365e+00  9.266e+00  -1.011
## VPD_kPa_int        -4.567e+01  1.573e+01  -2.904
## Solar_rad_Wm2_interpol  1.375e-02  8.903e-03   1.544
## mass_g             2.888e-01  4.204e-01   0.687
## sex_M_FM           1.597e+00  1.411e+00   1.131
## hematocrit_percent  -2.880e-01  1.157e-01  -2.489
## cloacal_temp_C      2.467e+00  3.817e-01   6.463
## ambient_temp_C     -4.707e+00  1.303e+00  -3.611
## temp_C_interpol     4.994e+00  2.219e+00   2.251
## VPD_kPa            2.304e+01  1.014e+01   2.273
## regionVentrum:VPD_kPa_int  7.597e+00  3.610e+00   2.105
## regionHead:VPD_kPa_int  1.283e+00  3.608e+00   0.356
## regionDewlap:VPD_kPa_int  1.396e+01  3.622e+00   3.853
## regionMite Patch:VPD_kPa_int  1.678e+01  3.617e+00   4.638
## regionVentrum:Solar_rad_Wm2_interpol -8.341e-04  8.502e-03  -0.098
## regionHead:Solar_rad_Wm2_interpol  1.288e-02  8.501e-03   1.515
## regionDewlap:Solar_rad_Wm2_interpol -2.131e-03  8.554e-03  -0.249
## regionMite Patch:Solar_rad_Wm2_interpol -1.264e-02  8.599e-03  -1.470
## regionVentrum:mass_g  9.961e-01  5.153e-01   1.933
## regionHead:mass_g    -3.879e-01  5.113e-01  -0.759
## regionDewlap:mass_g  9.790e-01  5.229e-01   1.872
## regionMite Patch:mass_g  1.117e+00  5.302e-01   2.106
##
## Correlation matrix not shown by default, as p = 26 > 12.
## Use print(x, correlation=TRUE) or
##      vcov(x)          if you need it
## fit warnings:
```

```
## Some predictor variables are on very different scales: consider rescaling
drop1(CEWL_mod13)
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## Single term deletions
##
```

```
## Model:
```

```
## TEWL_g_m2h ~ region * (VPD_kPa_int + Solar_rad_Wm2_interpol +
##   mass_g) + sex_M_F + hematocrit_percent + cloacal_temp_C +
##   ambient_temp_C + temp_C_interpol + VPD_kPa + (1 | individual_ID)
##               npar    AIC
## <none>                4365.7
## sex_M_F                1 4365.1
## hematocrit_percent      1 4370.3
## cloacal_temp_C          1 4402.3
## ambient_temp_C          1 4377.2
## temp_C_interpol         1 4369.1
## VPD_kPa                 1 4369.2
## region:VPD_kPa_int       4 4391.4
## region:Solar_rad_Wm2_interpol 4 4366.9
## region:mass_g           4 4372.1
```

```
drop sex:
```

```
CEWL_mod14 <- lme4::lmer(data = CEWL_dat_sub1,
  # response variable
  TEWL_g_m2h ~
  # potential predictors
  region * (VPD_kPa_int + Solar_rad_Wm2_interpol +
  mass_g) +
  hematocrit_percent +
  cloacal_temp_C +
```

```

ambient_temp_C + temp_C_interpol + VPD_kPa +
# random effect
(1|individual_ID))

```

```

## Warning: Some predictor variables are on very different scales: consider
## rescaling

```

```
summary(CEWL_mod14)
```

```

## Linear mixed model fit by REML ['lmerMod']
## Formula: TEWL_g_m2h ~ region * (VPD_kPa_int + Solar_rad_Wm2_interpol +
##      mass_g) + hematocrit_percent + cloacal_temp_C + ambient_temp_C +
##      temp_C_interpol + VPD_kPa + (1 | individual_ID)
##      Data: CEWL_dat_sub1
##
## REML criterion at convergence: 4315.9
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.9876 -0.5559 -0.1019  0.3960  5.2201
##
## Random effects:
##      Groups             Name             Variance Std.Dev.
## individual_ID (Intercept) 27.39          5.233
## Residual                 99.09          9.955
## Number of obs: 570, groups: individual_ID, 116
##
## Fixed effects:
##
##              Estimate Std. Error t value
## (Intercept)    -2.845e+01  2.946e+01  -0.966
## regionVentrum   -5.527e+00  8.986e+00  -0.615
## regionHead      -2.383e+00  9.007e+00  -0.265
## regionDewlap    -2.032e+01  9.191e+00  -2.211
## regionMite Patch -9.317e+00  9.268e+00  -1.005
## VPD_kPa_int     -4.566e+01  1.574e+01  -2.902
## Solar_rad_Wm2_interpol 1.430e-02  8.893e-03  1.608
## mass_g          3.394e-01  4.182e-01  0.812
## hematocrit_percent -2.620e-01  1.135e-01  -2.310
## cloacal_temp_C    2.462e+00  3.818e-01  6.449
## ambient_temp_C   -4.772e+00  1.303e+00  -3.663
## temp_C_interpol   5.016e+00  2.220e+00  2.259
## VPD_kPa          2.354e+01  1.013e+01  2.323
## regionVentrum:VPD_kPa_int 7.595e+00  3.610e+00  2.104
## regionHead:VPD_kPa_int 1.318e+00  3.609e+00  0.365
## regionDewlap:VPD_kPa_int 1.399e+01  3.623e+00  3.862
## regionMite Patch:VPD_kPa_int 1.678e+01  3.618e+00  4.637
## regionVentrum:Solar_rad_Wm2_interpol -8.686e-04  8.504e-03  -0.102
## regionHead:Solar_rad_Wm2_interpol 1.287e-02  8.503e-03  1.513
## regionDewlap:Solar_rad_Wm2_interpol -2.145e-03  8.556e-03  -0.251
## regionMite Patch:Solar_rad_Wm2_interpol -1.264e-02  8.601e-03  -1.470
## regionVentrum:mass_g 9.944e-01  5.154e-01  1.929
## regionHead:mass_g -3.901e-01  5.114e-01  -0.763
## regionDewlap:mass_g 9.735e-01  5.230e-01  1.862
## regionMite Patch:mass_g 1.112e+00  5.303e-01  2.097

```

```
##
## Correlation matrix not shown by default, as p = 25 > 12.
## Use print(x, correlation=TRUE) or
##      vcov(x)          if you need it

## fit warnings:
## Some predictor variables are on very different scales: consider rescaling
drop1(CEWL_mod14)

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Single term deletions
##
## Model:
## TEWL_g_m2h ~ region * (VPD_kPa_int + Solar_rad_Wm2_interpol +
##      mass_g) + hematocrit_percent + cloacal_temp_C + ambient_temp_C +
##      temp_C_interpol + VPD_kPa + (1 | individual_ID)
##              npar      AIC
## <none>                4365.1
## hematocrit_percent    1 4368.7
## cloacal_temp_C        1 4401.3
## ambient_temp_C        1 4376.8
## temp_C_interpol       1 4368.5
## VPD_kPa               1 4368.8
## region:VPD_kPa_int     4 4390.8
## region:Solar_rad_Wm2_interpol 4 4366.3
## region:mass_g         4 4371.4

drop hematocrit:
CEWL_mod15 <- lme4::lmer(data = CEWL_dat_sub1,
  # response variable
  TEWL_g_m2h ~
  # potential predictors
  region * (VPD_kPa_int + Solar_rad_Wm2_interpol +
  mass_g) +
  cloacal_temp_C +
```



```

    ambient_temp_C + temp_C_interpol + VPD_kPa +
    # random effect
    (1|individual_ID))

```

```

## Warning: Some predictor variables are on very different scales: consider
## rescaling

```

```
summary(CEWL_mod15)
```

```

## Linear mixed model fit by REML ['lmerMod']
## Formula: TEWL_g_m2h ~ region * (VPD_kPa_int + Solar_rad_Wm2_interpol +
##      mass_g) + cloacal_temp_C + ambient_temp_C + temp_C_interpol +
##      VPD_kPa + (1 | individual_ID)
##      Data: CEWL_dat_sub1
##
## REML criterion at convergence: 4318.6
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.9727 -0.5678 -0.1167  0.3925  5.2412
##
## Random effects:
##      Groups             Name             Variance Std.Dev.
## individual_ID (Intercept) 29.27          5.410
## Residual                 99.10          9.955
## Number of obs: 570, groups: individual_ID, 116
##
## Fixed effects:
##
##              Estimate Std. Error t value
## (Intercept)    -3.296e+01  2.994e+01  -1.101
## regionVentrum   -5.605e+00  8.987e+00  -0.624
## regionHead      -2.427e+00  9.008e+00  -0.269
## regionDewlap    -2.044e+01  9.193e+00  -2.224
## regionMite Patch -9.316e+00  9.269e+00  -1.005
## VPD_kPa_int     -4.300e+01  1.600e+01  -2.688
## Solar_rad_Wm2_interpol 1.788e-02  8.862e-03   2.017
## mass_g          2.651e-01  4.201e-01   0.631
## cloacal_temp_C   2.305e+00  3.830e-01   6.017
## ambient_temp_C  -4.598e+00  1.326e+00  -3.468
## temp_C_interpol  4.384e+00  2.247e+00   1.951
## VPD_kPa         2.498e+01  1.030e+01   2.424
## regionVentrum:VPD_kPa_int 7.574e+00  3.611e+00   2.098
## regionHead:VPD_kPa_int  1.283e+00  3.609e+00   0.355
## regionDewlap:VPD_kPa_int 1.394e+01  3.623e+00   3.848
## regionMite Patch:VPD_kPa_int 1.677e+01  3.618e+00   4.633
## regionVentrum:Solar_rad_Wm2_interpol -8.689e-04  8.504e-03  -0.102
## regionHead:Solar_rad_Wm2_interpol  1.285e-02  8.503e-03   1.511
## regionDewlap:Solar_rad_Wm2_interpol -2.101e-03  8.557e-03  -0.246
## regionMite Patch:Solar_rad_Wm2_interpol -1.270e-02  8.602e-03  -1.477
## regionVentrum:mass_g  1.002e+00  5.155e-01   1.943
## regionHead:mass_g    -3.836e-01  5.115e-01  -0.750
## regionDewlap:mass_g   9.819e-01  5.231e-01   1.877
## regionMite Patch:mass_g  1.116e+00  5.304e-01   2.105
##

```

```

## Correlation matrix not shown by default, as p = 24 > 12.
## Use print(x, correlation=TRUE) or
##      vcov(x)          if you need it

## fit warnings:
## Some predictor variables are on very different scales: consider rescaling
drop1(CEWL_mod15)

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Single term deletions
##
## Model:
## TEWL_g_m2h ~ region * (VPD_kPa_int + Solar_rad_Wm2_interpol +
##      mass_g) + cloacal_temp_C + ambient_temp_C + temp_C_interpol +
##      VPD_kPa + (1 | individual_ID)
##
##               npar      AIC
## <none>                4368.7
## cloacal_temp_C        1 4400.3
## ambient_temp_C        1 4379.0
## temp_C_interpol       1 4370.7
## VPD_kPa               1 4372.8
## region:VPD_kPa_int     4 4394.4
## region:Solar_rad_Wm2_interpol 4 4369.9
## region:mass_g         4 4375.1

drop region*sorad interaction:
CEWL_mod16 <- lme4::lmer(data = CEWL_dat_sub1,
  # response variable
  TEWL_g_m2h ~
  # potential predictors
  region * (VPD_kPa_int + mass_g) +
  Solar_rad_Wm2_interpol +
  cloacal_temp_C +
  ambient_temp_C + temp_C_interpol + VPD_kPa +
  # random effect
  (1|individual_ID))
summary(CEWL_mod16)

```

```

## Linear mixed model fit by REML ['lmerMod']
## Formula:
## TEWL_g_m2h ~ region * (VPD_kPa_int + mass_g) + Solar_rad_Wm2_interpol +
##   cloacal_temp_C + ambient_temp_C + temp_C_interpol + VPD_kPa +
##   (1 | individual_ID)
## Data: CEWL_dat_sub1
##
## REML criterion at convergence: 4295.7
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.0352 -0.5858 -0.1210  0.3869  5.4385
##
## Random effects:
## Groups      Name      Variance Std.Dev.
## individual_ID (Intercept) 29.06    5.391
## Residual              100.21   10.011
## Number of obs: 570, groups: individual_ID, 116
##
## Fixed effects:
##
##              Estimate Std. Error t value
## (Intercept)    -32.909846   29.607707  -1.112
## regionVentrum    -6.228368    6.247217  -0.997
## regionHead       7.364134    6.247501   1.179
## regionDewlap    -22.083459    6.358260  -3.473
## regionMite Patch -19.373854    6.413066  -3.021
## VPD_kPa_int    -42.543813   15.976119  -2.663
## mass_g           0.268075    0.421516   0.636
## Solar_rad_Wm2_interpol  0.017407    0.006995   2.488
## cloacal_temp_C    2.296740    0.383048   5.996
## ambient_temp_C   -4.526612    1.325540  -3.415
## temp_C_interpol    4.329559    2.246854   1.927
## VPD_kPa          24.691304   10.305080   2.396
## regionVentrum:VPD_kPa_int  7.467234    3.453473   2.162
## regionHead:VPD_kPa_int    2.943301    3.450477   0.853
## regionDewlap:VPD_kPa_int  13.663075    3.456064   3.953
## regionMite Patch:VPD_kPa_int 14.968835    3.438133   4.354
## regionVentrum:mass_g    0.996443    0.518135   1.923
## regionHead:mass_g    -0.359870    0.514148  -0.700
## regionDewlap:mass_g    0.981930    0.525960   1.867
## regionMite Patch:mass_g  1.131285    0.533287   2.121
##
## Correlation matrix not shown by default, as p = 20 > 12.
## Use print(x, correlation=TRUE) or
##   vcov(x) if you need it
drop1(CEWL_mod16)

## Single term deletions
##
## Model:
## TEWL_g_m2h ~ region * (VPD_kPa_int + mass_g) + Solar_rad_Wm2_interpol +
##   cloacal_temp_C + ambient_temp_C + temp_C_interpol + VPD_kPa +
##   (1 | individual_ID)

```

```
##               npar    AIC
## <none>                4369.9
## Solar_rad_Wm2_interpol    1 4374.4
## cloacal_temp_C            1 4401.3
## ambient_temp_C            1 4379.8
## temp_C_interpol           1 4371.8
## VPD_kPa                   1 4373.9
## region:VPD_kPa_int        4 4390.4
## region:mass_g             4 4375.8
```

drop temp at capture:

```
CEWL_mod17 <- lme4::lmer(data = CEWL_dat_sub1,
  # response variable
  TEWL_g_m2h ~
  # potential predictors
  region * (VPD_kPa_int + mass_g) +
  Solar_rad_Wm2_interpol +
  cloacal_temp_C +
  ambient_temp_C + VPD_kPa +
  # random effect
  (1|individual_ID))
summary(CEWL_mod17)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula:
## TEWL_g_m2h ~ region * (VPD_kPa_int + mass_g) + Solar_rad_Wm2_interpol +
##   cloacal_temp_C + ambient_temp_C + VPD_kPa + (1 | individual_ID)
##   Data: CEWL_dat_sub1
##
## REML criterion at convergence: 4302.8
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.0661 -0.5956 -0.1231  0.3725  5.4784
##
## Random effects:
##   Groups             Name             Variance Std.Dev.
## individual_ID (Intercept)  30.39         5.512
## Residual                  100.17        10.009
## Number of obs: 570, groups: individual_ID, 116
##
## Fixed effects:
##               Estimate Std. Error t value
## (Intercept)      4.097965  22.870441   0.179
## regionVentrum     -6.107394   6.245885  -0.978
## regionHead         7.471656   6.246290   1.196
## regionDewlap     -22.025097   6.357613  -3.464
## regionMite Patch  -19.424710   6.412131  -3.029
## VPD_kPa_int      -12.733030   4.057068  -3.138
## mass_g             0.291158   0.423411   0.688
## Solar_rad_Wm2_interpol  0.022793   0.006491   3.511
## cloacal_temp_C     2.343638   0.387322   6.051
## ambient_temp_C    -3.147068   1.129079  -2.787
## VPD_kPa           14.409836   8.940416   1.612
```

```

## regionVentrum:VPD_kPa_int      7.476906   3.452851   2.165
## regionHead:VPD_kPa_int        2.939064   3.449868   0.852
## regionDewlap:VPD_kPa_int     13.660303   3.455489   3.953
## regionMite Patch:VPD_kPa_int  14.966590   3.437480   4.354
## regionVentrum:mass_g          0.987961   0.518046   1.907
## regionHead:mass_g            -0.365361   0.514064  -0.711
## regionDewlap:mass_g          0.980463   0.525926   1.864
## regionMite Patch:mass_g       1.139601   0.533206   2.137

##
## Correlation matrix not shown by default, as p = 19 > 12.
## Use print(x, correlation=TRUE) or
##      vcov(x)          if you need it

drop1(CEWL_mod17)

## Single term deletions
##
## Model:
## TEWL_g_m2h ~ region * (VPD_kPa_int + mass_g) + Solar_rad_Wm2_interpol +
##      cloacal_temp_C + ambient_temp_C + VPD_kPa + (1 | individual_ID)
##               npar      AIC
## <none>                4371.8
## Solar_rad_Wm2_interpol  1 4382.2
## cloacal_temp_C          1 4403.5
## ambient_temp_C          1 4377.9
## VPD_kPa                 1 4372.6
## region:VPD_kPa_int       4 4392.3
## region:mass_g            4 4377.8

drop ambient VPD at msmt:
CEWL_mod18 <- lme4::lmer(data = CEWL_dat_sub1,
                        # response variable
                        TEWL_g_m2h ~
                        # potential predictors
                        region * (VPD_kPa_int + mass_g) +
                        Solar_rad_Wm2_interpol +
                        cloacal_temp_C +
                        ambient_temp_C +
                        # random effect
                        (1|individual_ID))

summary(CEWL_mod18)

## Linear mixed model fit by REML ['lmerMod']
## Formula:
## TEWL_g_m2h ~ region * (VPD_kPa_int + mass_g) + Solar_rad_Wm2_interpol +
##      cloacal_temp_C + ambient_temp_C + (1 | individual_ID)
##      Data: CEWL_dat_sub1
##
## REML criterion at convergence: 4311.6
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.1109 -0.5796 -0.1096  0.3721  5.5173
##

```

```

## Random effects:
##   Groups      Name      Variance Std.Dev.
## individual_ID (Intercept) 31.36    5.6
## Residual              100.07   10.0
## Number of obs: 570, groups: individual_ID, 116
##
## Fixed effects:
##               Estimate Std. Error t value
## (Intercept)      8.787318  22.888471   0.384
## regionVentrum    -5.968820   6.242171  -0.956
## regionHead       7.613204   6.242608   1.220
## regionDewlap    -21.887146   6.354175  -3.445
## regionMite Patch -19.374143   6.409004  -3.023
## VPD_kPa_int     -8.185200   2.928817  -2.795
## mass_g           0.355432   0.422858   0.841
## Solar_rad_Wm2_interpol 0.014955   0.004342   3.444
## cloacal_temp_C    2.320429   0.390650   5.940
## ambient_temp_C   -2.191820   0.968373  -2.263
## regionVentrum:VPD_kPa_int 7.513621   3.451025   2.177
## regionHead:VPD_kPa_int 2.957280   3.448109   0.858
## regionDewlap:VPD_kPa_int 13.677128   3.453759   3.960
## regionMite Patch:VPD_kPa_int 15.031802   3.435475   4.375
## regionVentrum:mass_g 0.978204   0.517761   1.889
## regionHead:mass_g -0.373426   0.513790  -0.727
## regionDewlap:mass_g 0.974520   0.525688   1.854
## regionMite Patch:mass_g 1.138635   0.532959   2.136
##
## Correlation matrix not shown by default, as p = 18 > 12.
## Use print(x, correlation=TRUE) or
##   vcov(x)      if you need it

```

```

drop1(CEWL_mod18)

```

```

## Single term deletions
##
## Model:
## TEWL_g_m2h ~ region * (VPD_kPa_int + mass_g) + Solar_rad_Wm2_interpol +
##   cloacal_temp_C + ambient_temp_C + (1 | individual_ID)
##               npar      AIC
## <none>                4372.6
## Solar_rad_Wm2_interpol 1 4382.4
## cloacal_temp_C         1 4402.9
## ambient_temp_C         1 4375.9
## region:VPD_kPa_int     4 4393.3
## region:mass_g          4 4378.6

```

drop ambient temp at msmt:

```

CEWL_mod19 <- lme4::lmer(data = CEWL_dat_sub1,
  # response variable
  TEWL_g_m2h ~
  # potential predictors
  region * (VPD_kPa_int + mass_g) +
  Solar_rad_Wm2_interpol +
  cloacal_temp_C +

```

```

# random effect
(1|individual_ID))
summary(CEWL_mod19)

## Linear mixed model fit by REML ['lmerMod']
## Formula:
## TEWL_g_m2h ~ region * (VPD_kPa_int + mass_g) + Solar_rad_Wm2_interpol +
##   cloacal_temp_C + (1 | individual_ID)
##   Data: CEWL_dat_sub1
##
## REML criterion at convergence: 4318.4
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.0534 -0.5793 -0.1149  0.3663  5.5727
##
## Random effects:
##   Groups             Name             Variance Std.Dev.
## individual_ID (Intercept)  32.83         5.73
## Residual                  100.27        10.01
## Number of obs: 570, groups:  individual_ID, 116
##
## Fixed effects:
##
##              Estimate Std. Error t value
## (Intercept)    -36.517535   11.228115  -3.252
## regionVentrum    -5.871231    6.248478  -0.940
## regionHead       7.616510    6.249127   1.219
## regionDewlap   -22.077391    6.360725  -3.471
## regionMite Patch -19.711866    6.414020  -3.073
## VPD_kPa_int     -9.530937    2.887205  -3.301
## mass_g           0.324757    0.425310   0.764
## Solar_rad_Wm2_interpol  0.014247    0.004394   3.242
## cloacal_temp_C   2.145770    0.388516   5.523
## regionVentrum:VPD_kPa_int  7.472441    3.454491   2.163
## regionHead:VPD_kPa_int   2.936226    3.451612   0.851
## regionDewlap:VPD_kPa_int 13.655712    3.457297   3.950
## regionMite Patch:VPD_kPa_int 14.870102    3.438166   4.325
## regionVentrum:mass_g    0.970339    0.518299   1.872
## regionHead:mass_g     -0.372651    0.514330  -0.725
## regionDewlap:mass_g    0.987712    0.526257   1.877
## regionMite Patch:mass_g  1.172912    0.533314   2.199
##
## Correlation matrix not shown by default, as p = 17 > 12.
## Use print(x, correlation=TRUE) or
##   vcov(x)           if you need it
drop1(CEWL_mod19)

## Single term deletions
##
## Model:
## TEWL_g_m2h ~ region * (VPD_kPa_int + mass_g) + Solar_rad_Wm2_interpol +
##   cloacal_temp_C + (1 | individual_ID)
##
##               npar      AIC

```

```
## <none> 4375.9
## Solar_rad_Wm2_interpol 1 4384.3
## cloacal_temp_C 1 4402.0
## region:VPD_kPa_int 4 4396.1
## region:mass_g 4 4382.2
```

finally, test the null model

```
CEWL_mod_null <- lme4::lmer(data = CEWL_dat_sub1,
                           TEWL_g_m2h ~ 1 + (1|individual_ID))
```

Selection

Models 6a to 19 and the null model are the ones we should compare.

```
CEWL_models <- list(CEWL_mod6a, CEWL_mod7, CEWL_mod8, CEWL_mod9,
                   CEWL_mod10, CEWL_mod11, CEWL_mod12, CEWL_mod13,
                   CEWL_mod14, CEWL_mod15, CEWL_mod16, CEWL_mod17,
                   CEWL_mod18, CEWL_mod19, CEWL_mod_null)
```

#specify model names

```
CEWL_mod_names <- c('(model 6a) ~ ',
                    '(model 7) ~ ',
                    '(model 8) ~ ',
                    '(model 9) ~ ',
                    '(model 10) ~ ',
                    '(model 11) ~ ',
                    '(model 12) ~ ',
                    '(model 13) ~ ',
                    '(model 14) ~ ',
                    '(model 15) ~ ',
                    '(model 16) ~ ',
                    '(model 17) ~ ',
                    '(model 18) ~ ',
                    '(model 19) ~ ',
                    'null model')
```

#calculate AIC of each model

```
CEWL_AICc <- data.frame(aictab(cand.set = CEWL_models,
                              modnames = CEWL_mod_names))
```

```
## Warning in aictab.AIClmerMod(cand.set = CEWL_models, modnames = CEWL_mod_names):
```

```
## Model selection for fixed effects is only appropriate with ML estimation:
```

```
## REML (default) should only be used to select random effects for a constant set of fixed effects
```

```
CEWL_AICc
```

##	Modnames	K	AICc	Delta_AICc	ModelLik	AICcWt	Res.LL
## 11	(model 16) ~	22	4341.508	0.000000	1.000000e+00	9.202316e-01	-2147.829
## 12	(model 17) ~	21	4346.476	4.968639	8.338226e-02	7.673099e-02	-2151.395
## 13	(model 18) ~	20	4353.118	11.610312	3.011985e-03	2.771724e-03	-2155.794
## 14	(model 19) ~	19	4357.820	16.311809	2.870356e-04	2.641392e-04	-2159.219
## 7	(model 12) ~	29	4369.240	27.731954	9.507859e-07	8.749432e-07	-2154.009
## 8	(model 13) ~	28	4371.070	29.562367	3.807269e-07	3.503569e-07	-2156.034
## 9	(model 14) ~	27	4372.665	31.156848	1.715443e-07	1.578605e-07	-2157.937
## 10	(model 15) ~	26	4373.198	31.690000	1.314026e-07	1.209208e-07	-2159.306
## 2	(model 7) ~	37	4377.297	35.789635	1.691919e-08	1.556957e-08	-2149.006
## 6	(model 11) ~	30	4377.574	36.065982	1.473573e-08	1.356028e-08	-2157.061


```
## 1 (model 6a) ~ 41 4378.606 37.098343 8.794219e-09 8.092718e-09 -2145.042
## 5 (model 10) ~ 31 4384.432 42.924320 4.776418e-10 4.395411e-10 -2159.372
## 3 (model 8) ~ 33 4386.132 44.623845 2.041997e-10 1.879110e-10 -2157.973
## 4 (model 9) ~ 32 4387.397 45.889237 1.084623e-10 9.981041e-11 -2159.732
## 15 null model 3 4509.547 168.039322 3.241341e-37 2.982785e-37 -2251.752
## Cum.Wt
## 11 0.9202316
## 12 0.9969626
## 13 0.9997343
## 14 0.9999985
## 7 0.9999993
## 8 0.9999997
## 9 0.9999998
## 10 1.0000000
## 2 1.0000000
## 6 1.0000000
## 1 1.0000000
## 5 1.0000000
## 3 1.0000000
## 4 1.0000000
## 15 1.0000000
```

Re-run top 2 models using lmerTest to get p-values:

```
CEWL_mod16p <- lmerTest::lmer(data = CEWL_dat_sub1,
                             # response variable
                             TEWL_g_m2h ~
                             # potential predictors
                             region * (VPD_kPa_int + mass_g) +
                             Solar_rad_Wm2_interpol +
                             cloacal_temp_C +
                             ambient_temp_C + temp_C_interpol + VPD_kPa +
                             # random effect
                             (1|individual_ID))
summary(CEWL_mod16p)

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula:
## TEWL_g_m2h ~ region * (VPD_kPa_int + mass_g) + Solar_rad_Wm2_interpol +
## cloacal_temp_C + ambient_temp_C + temp_C_interpol + VPD_kPa +
## (1 | individual_ID)
## Data: CEWL_dat_sub1
##
## REML criterion at convergence: 4295.7
##
## Scaled residuals:
## Min 1Q Median 3Q Max
## -2.0352 -0.5858 -0.1210 0.3869 5.4385
##
## Random effects:
## Groups Name Variance Std.Dev.
## individual_ID (Intercept) 29.06 5.391
## Residual 100.21 10.011
## Number of obs: 570, groups: individual_ID, 116
```

```

##
## Fixed effects:
##
##           Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)    -32.909846   29.607707  114.999468  -1.112  0.268659
## regionVentrum    -6.228368    6.247217  444.802904  -0.997  0.319315
## regionHead       7.364134    6.247501  444.836608    1.179  0.239135
## regionDewlap   -22.083459    6.358260  449.172834  -3.473  0.000564
## regionMite Patch -19.373854    6.413066  445.592471  -3.021  0.002664
## VPD_kPa_int    -42.543813   15.976119  112.305198  -2.663  0.008884
## mass_g          0.268075    0.421516  450.541075    0.636  0.525113
## Solar_rad_Wm2_interpol  0.017407    0.006995  107.447880    2.488  0.014364
## cloacal_temp_C   2.296740    0.383048  107.357738    5.996  2.76e-08
## ambient_temp_C  -4.526612    1.325540  111.836286  -3.415  0.000890
## temp_C_interpol   4.329559    2.246854  107.335445    1.927  0.056631
## VPD_kPa         24.691304   10.305080  114.154457    2.396  0.018199
## regionVentrum:VPD_kPa_int  7.467234    3.453473  442.945754    2.162  0.031134
## regionHead:VPD_kPa_int   2.943301    3.450477  443.066029    0.853  0.394113
## regionDewlap:VPD_kPa_int 13.663075    3.456064  443.729837    3.953  8.97e-05
## regionMite Patch:VPD_kPa_int 14.968835    3.438133  442.150933    4.354  1.66e-05
## regionVentrum:mass_g    0.996443    0.518135  446.636242    1.923  0.055099
## regionHead:mass_g     -0.359870    0.514148  445.253712   -0.700  0.484333
## regionDewlap:mass_g    0.981930    0.525960  450.744396    1.867  0.062561
## regionMite Patch:mass_g  1.131285    0.533287  446.743940    2.121  0.034443
##
## (Intercept)
## regionVentrum
## regionHead
## regionDewlap      ***
## regionMite Patch  **
## VPD_kPa_int        **
## mass_g
## Solar_rad_Wm2_interpol  *
## cloacal_temp_C      ***
## ambient_temp_C      ***
## temp_C_interpol     .
## VPD_kPa              *
## regionVentrum:VPD_kPa_int  *
## regionHead:VPD_kPa_int
## regionDewlap:VPD_kPa_int  ***
## regionMite Patch:VPD_kPa_int ***
## regionVentrum:mass_g  .
## regionHead:mass_g
## regionDewlap:mass_g  .
## regionMite Patch:mass_g  *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## Correlation matrix not shown by default, as p = 20 > 12.
## Use print(x, correlation=TRUE) or
##       vcov(x)           if you need it
CEWL_mod17p <- lmerTest::lmer(data = CEWL_dat_sub1,
                              # response variable
                              TEWL_g_m2h ~

```

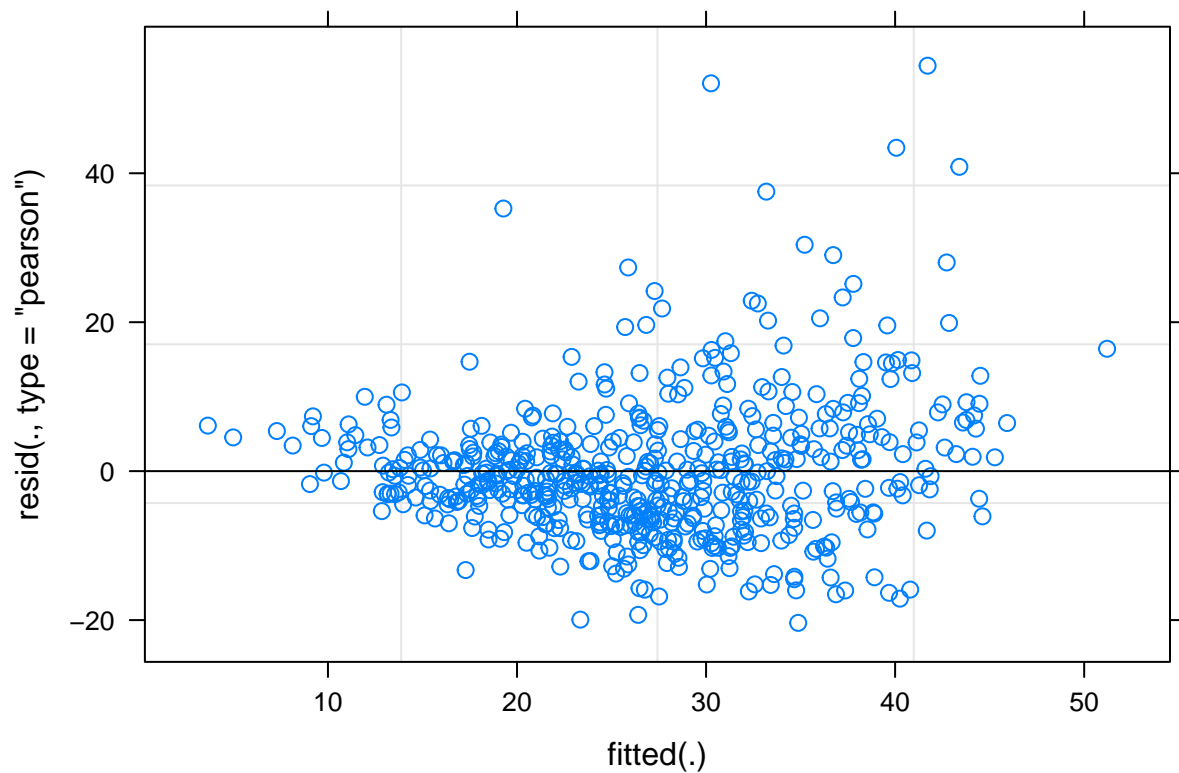


```
## regionMite Patch          **
## VPD_kPa_int              **
## mass_g                   ***
## Solar_rad_Wm2_interpol   ***
## cloacal_temp_C           ***
## ambient_temp_C           **
## VPD_kPa                   *
## regionVentrum:VPD_kPa_int *
## regionHead:VPD_kPa_int
## regionDewlap:VPD_kPa_int ***
## regionMite Patch:VPD_kPa_int ***
## regionVentrum:mass_g      .
## regionHead:mass_g         .
## regionDewlap:mass_g       .
## regionMite Patch:mass_g   *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

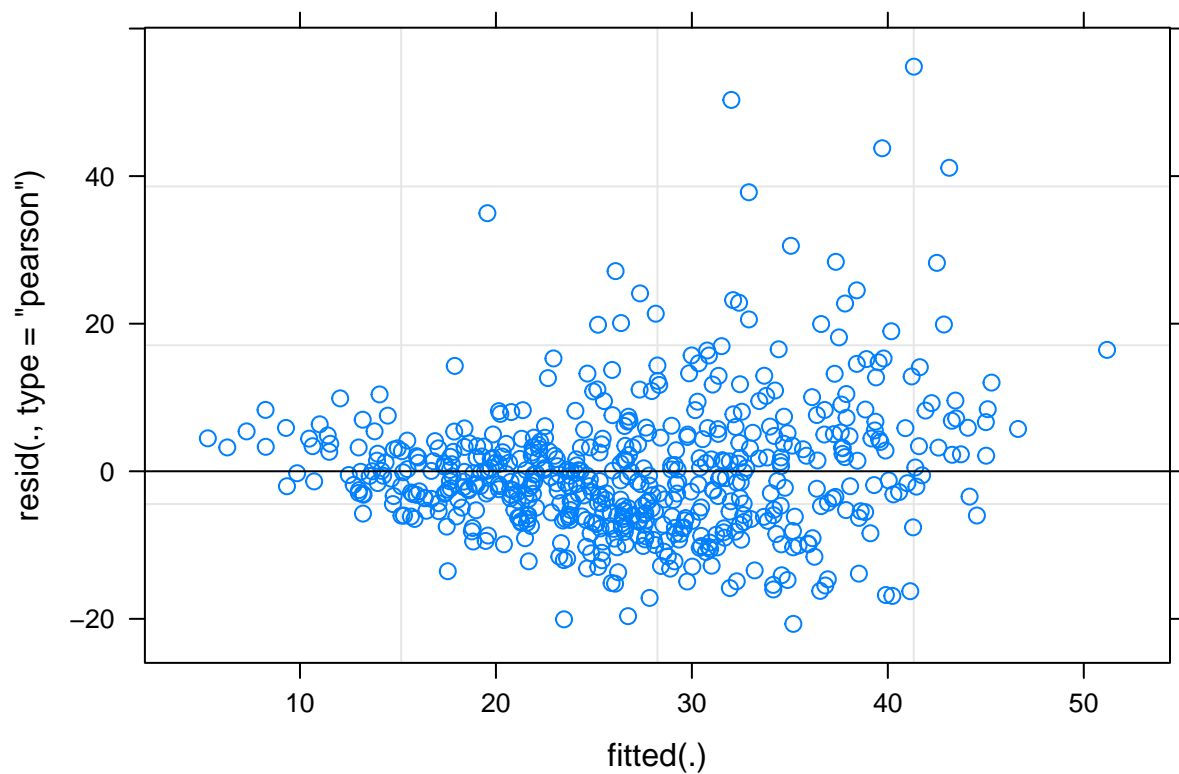
##
## Correlation matrix not shown by default, as p = 19 > 12.
## Use print(x, correlation=TRUE) or
##     vcov(x)           if you need it
```

Check LM Assumptions

```
plot(CEWL_mod16)
```



```
plot(CEWL_mod17)
```

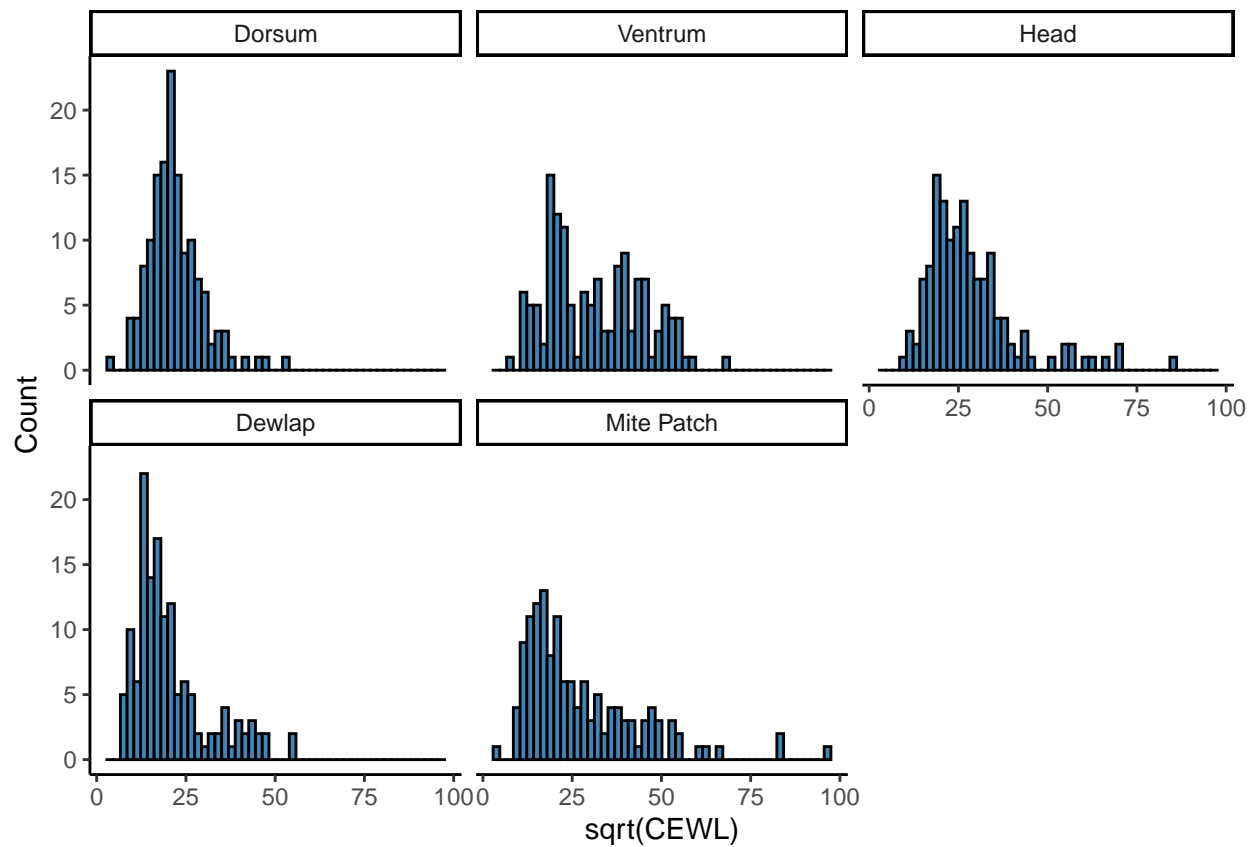


Both have fanning, which indicates that linearity and equal error variance are not satisfied.

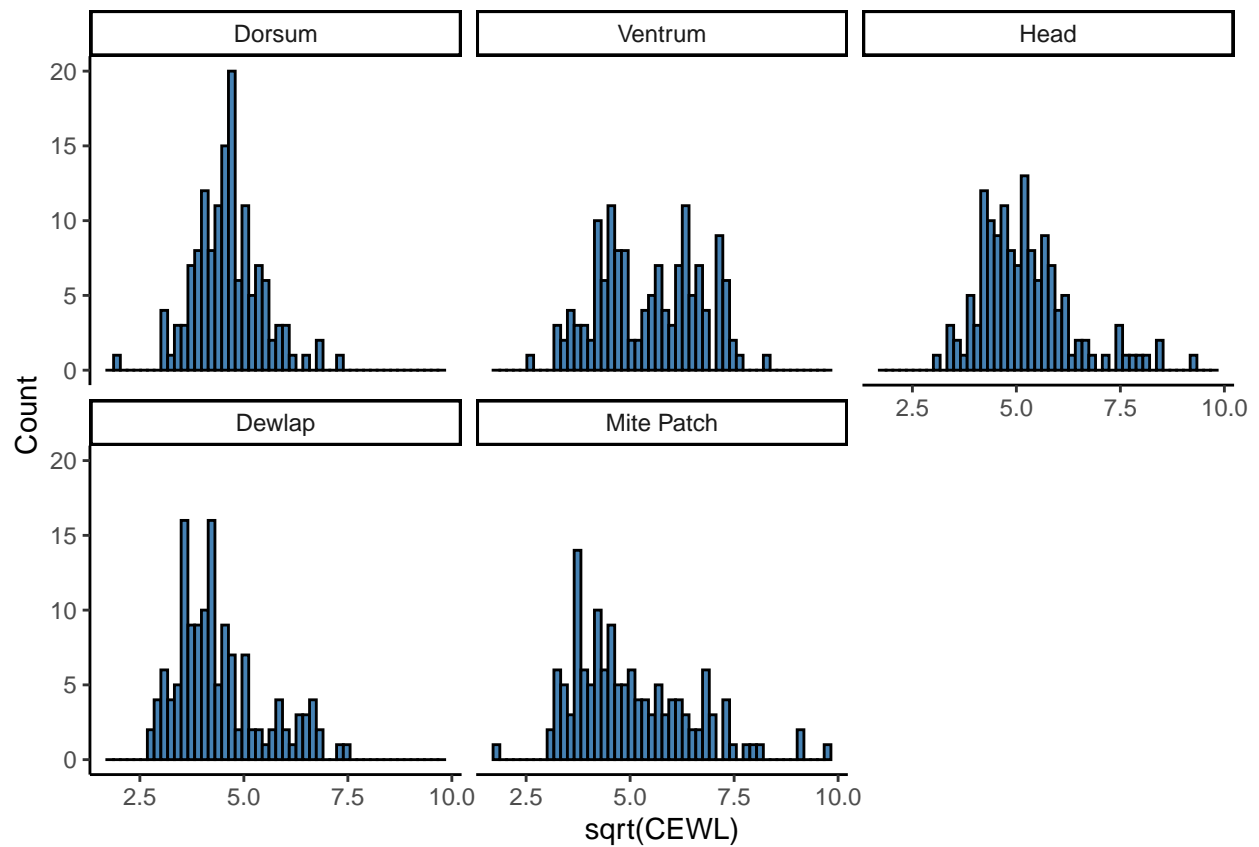
Test Transformations

Can I improve satisfaction of LM assumptions by transforming the dependent variable? In particular, conditions of linearity and normality are not met.

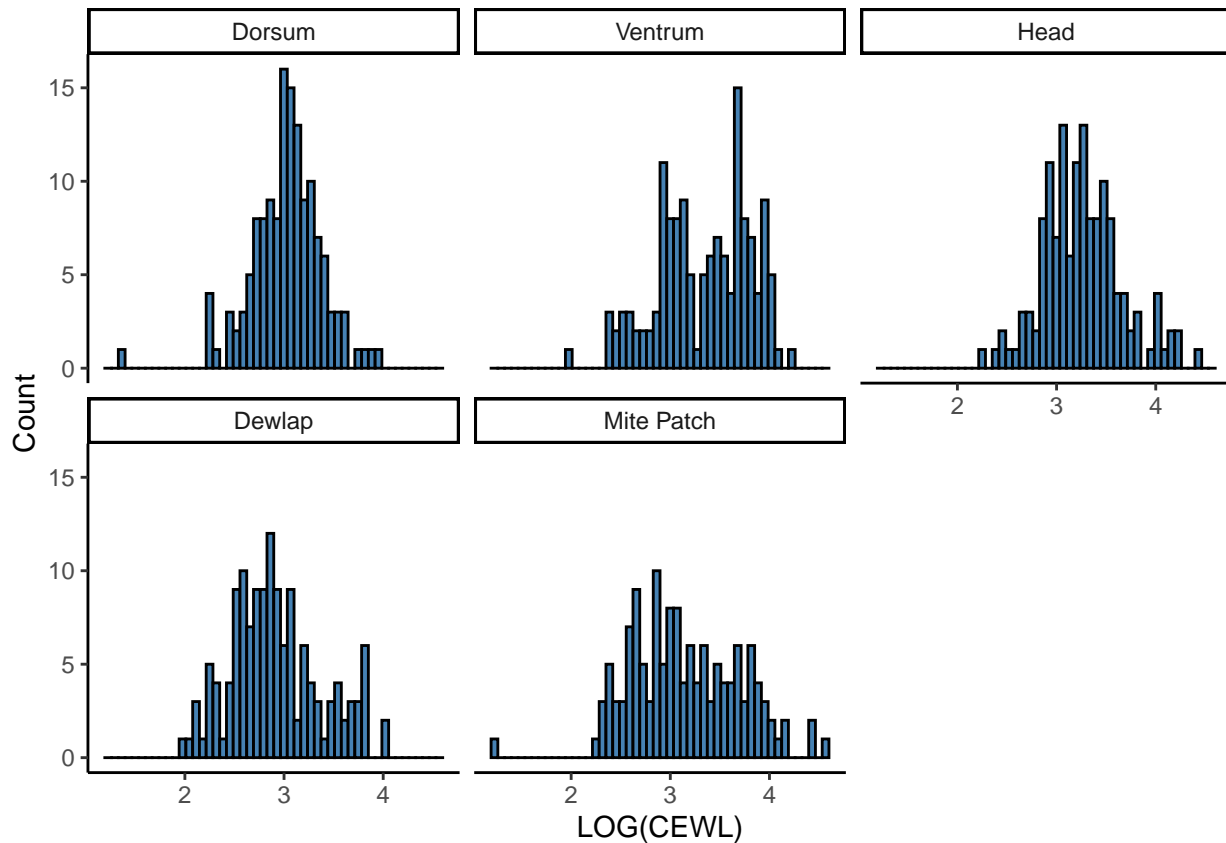
```
# normal TEWL
CEWL_data_full %>%
  ggplot(., aes(x = (TEWL_g_m2h))) +
  geom_histogram(color = "black", fill="steelblue", bins=50) +
  theme_classic() +
  xlab("sqrt(CEWL)") +
  ylab("Count") +
  facet_wrap(~region)
```



```
# sqrt(TEWL)
CEWL_data_full %>%
  ggplot(., aes(x = sqrt(TEWL_g_m2h))) +
  geom_histogram(color = "black", fill="steelblue", bins=50) +
  theme_classic() +
  xlab("sqrt(CEWL)") +
  ylab("Count") +
  facet_wrap(~region)
```



```
# log(TEWL)
CEWL_data_full %>%
  ggplot(., aes(x = log(TEWL_g_m2h))) +
  geom_histogram(color = "black", fill="steelblue", bins=50) +
  theme_classic() +
  xlab("LOG(CEWL)") +
  ylab("Count") +
  facet_wrap(~region)
```



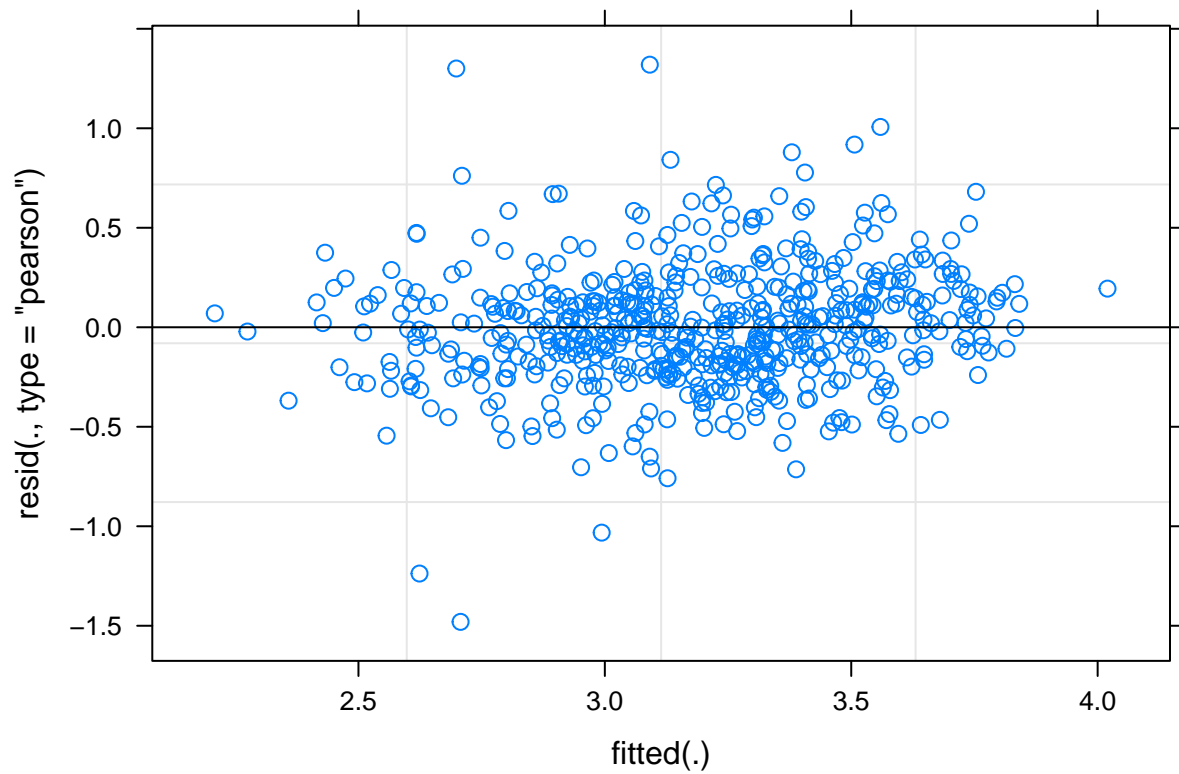
Log transforming seems to be pretty effective across body regions.

Transform & Re-Model

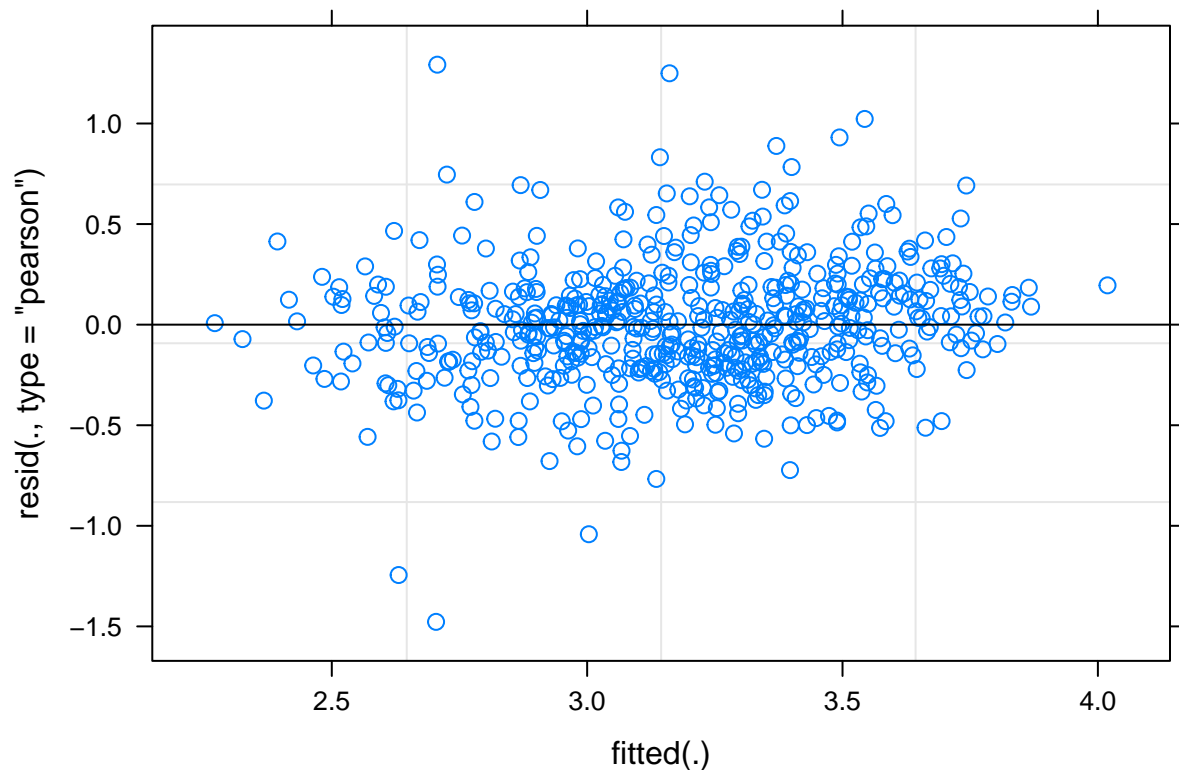
I will log-transform CEWL and see whether it makes the models satisfy LMM assumptions better.

Run top 2 CEWL models with log-transformed CEWL:

```
CEWL_mod16t <- lme4::lmer(data = CEWL_dat_sub1,
  # response variable
  log(TEWL_g_m2h) ~
  # potential predictors
  region * (VPD_kPa_int + mass_g) +
  Solar_rad_Wm2_interpol +
  cloacal_temp_C +
  ambient_temp_C + temp_C_interpol + VPD_kPa +
  # random effect
  (1|individual_ID))
plot(CEWL_mod16t)
```

```
CEWL_mod17t <- lme4::lmer(data = CEWL_dat_sub1,
  # response variable
  log(TEWL_g_m2h) ~
  # potential predictors
  region * (VPD_kPa_int + mass_g) +
  Solar_rad_Wm2_interpol +
  cloacal_temp_C +
  ambient_temp_C + VPD_kPa +
  # random effect
  (1|individual_ID))
plot(CEWL_mod17t)
```



MUCH better! These models are good.

Re-select model data for only the variables included in the final models:

```
CEWL_dat_sub2 <- CEWL_data_full %>%
  dplyr::filter(complete.cases(region,
                                VPD_kPa_int,
                                Solar_rad_Wm2_interpol,
                                mass_g,
                                cloacal_temp_C,
                                ambient_temp_C, temp_C_interpol,
                                VPD_kPa))

CEWL_mod16tp <- lmerTest::lmer(data = CEWL_dat_sub2,
  # response variable
  log(TEWL_g_m2h) ~
  # potential predictors
  region * (VPD_kPa_int + mass_g) +
  Solar_rad_Wm2_interpol +
  cloacal_temp_C +
  ambient_temp_C + temp_C_interpol + VPD_kPa +
  # random effect
  (1|individual_ID))

summary(CEWL_mod16tp)

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula:
## log(TEWL_g_m2h) ~ region * (VPD_kPa_int + mass_g) + Solar_rad_Wm2_interpol +
##   cloacal_temp_C + ambient_temp_C + temp_C_interpol + VPD_kPa +
##   (1 | individual_ID)
```

```

## Data: CEWL_dat_sub2
##
## REML criterion at convergence: 629.4
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -4.4784 -0.5927 -0.0390  0.4821  3.9107
##
## Random effects:
##   Groups             Name             Variance Std.Dev.
## individual_ID (Intercept) 0.03659  0.1913
## Residual                  0.11350  0.3369
## Number of obs: 635, groups: individual_ID, 129
##
## Fixed effects:
##
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)    -4.043e-02  8.840e-01  1.357e+02  -0.046  0.963592
## regionVentrum    -2.050e-01  2.016e-01  4.969e+02  -1.017  0.309689
## regionHead       2.341e-01  2.018e-01  4.970e+02   1.160  0.246528
## regionDewlap    -1.018e+00  2.049e-01  5.011e+02  -4.965  9.42e-07
## regionMite Patch -8.023e-01  2.064e-01  4.976e+02  -3.888  0.000115
## VPD_kPa_int     -1.866e+00  4.352e-01  1.310e+02  -4.287  3.48e-05
## mass_g          1.819e-02  1.363e-02  4.918e+02   1.335  0.182545
## Solar_rad_Wm2_interpol  5.754e-04  2.041e-04  1.214e+02   2.819  0.005630
## cloacal_temp_C   8.684e-02  1.297e-02  1.209e+02   6.695  7.16e-10
## ambient_temp_C  -1.374e-01  4.475e-02  1.257e+02  -3.070  0.002622
## temp_C_interpol  1.914e-01  5.585e-02  1.222e+02   3.426  0.000834
## VPD_kPa         8.543e-01  3.541e-01  1.294e+02   2.413  0.017234
## regionVentrum:VPD_kPa_int  3.393e-01  1.153e-01  4.954e+02   2.943  0.003398
## regionHead:VPD_kPa_int   1.835e-01  1.152e-01  4.956e+02   1.593  0.111751
## regionDewlap:VPD_kPa_int  6.200e-01  1.154e-01  4.964e+02   5.372  1.20e-07
## regionMite Patch:VPD_kPa_int  5.235e-01  1.148e-01  4.946e+02   4.561  6.44e-06
## regionVentrum:mass_g    2.600e-02  1.658e-02  4.988e+02   1.568  0.117450
## regionHead:mass_g     -1.596e-02  1.646e-02  4.975e+02  -0.969  0.332780
## regionDewlap:mass_g    4.070e-02  1.681e-02  5.028e+02   2.421  0.015829
## regionMite Patch:mass_g  4.826e-02  1.702e-02  4.988e+02   2.836  0.004758
##
## (Intercept)
## regionVentrum
## regionHead
## regionDewlap      ***
## regionMite Patch  ***
## VPD_kPa_int       ***
## mass_g
## Solar_rad_Wm2_interpol  **
## cloacal_temp_C     ***
## ambient_temp_C     **
## temp_C_interpol    ***
## VPD_kPa            *
## regionVentrum:VPD_kPa_int  **
## regionHead:VPD_kPa_int
## regionDewlap:VPD_kPa_int  ***
## regionMite Patch:VPD_kPa_int ***
## regionVentrum:mass_g

```

```

## regionHead:mass_g
## regionDewlap:mass_g      *
## regionMite Patch:mass_g  **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## Correlation matrix not shown by default, as p = 20 > 12.
## Use print(x, correlation=TRUE) or
##     vcov(x)           if you need it
CEWL_mod17tp <- lmerTest::lmer(data = CEWL_dat_sub2,
  # response variable
  log(TEWL_g_m2h) ~
  # potential predictors
  region * (VPD_kPa_int + mass_g) +
  Solar_rad_Wm2_interpol +
  cloacal_temp_C +
  ambient_temp_C + VPD_kPa +
  # random effect
  (1|individual_ID))
summary(CEWL_mod17p)

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula:
## TEWL_g_m2h ~ region * (VPD_kPa_int + mass_g) + Solar_rad_Wm2_interpol +
##     cloacal_temp_C + ambient_temp_C + VPD_kPa + (1 | individual_ID)
## Data: CEWL_dat_sub1
##
## REML criterion at convergence: 4302.8
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.0661 -0.5956 -0.1231  0.3725  5.4784
##
## Random effects:
## Groups           Name      Variance Std.Dev.
## individual_ID (Intercept) 30.39    5.512
## Residual                100.17   10.009
## Number of obs: 570, groups: individual_ID, 116
##
## Fixed effects:
##              Estimate Std. Error    df t value Pr(>|t|)
## (Intercept)    4.097965  22.870441 123.456940   0.179  0.858089
## regionVentrum  -6.107394   6.245885 444.635136  -0.978  0.328692
## regionHead      7.471656   6.246290 444.668104   1.196  0.232266
## regionDewlap   -22.025097   6.357613 448.920268  -3.464  0.000583
## regionMite Patch -19.424710   6.412131 445.398476  -3.029  0.002593
## VPD_kPa_int    -12.733030   4.057068 211.322355  -3.138  0.001941
## mass_g          0.291158   0.423411 447.687594   0.688  0.492030
## Solar_rad_Wm2_interpol 0.022793   0.006491 109.611562   3.511  0.000648
## cloacal_temp_C   2.343638   0.387322 108.290774   6.051  2.10e-08
## ambient_temp_C  -3.147068   1.129079 111.835533  -2.787  0.006247
## VPD_kPa         14.409836   8.940416 114.195750   1.612  0.109774

```

```

## regionVentrurn:VPD_kPa_int      7.476906    3.452851 442.783297    2.165 0.030888
## regionHead:VPD_kPa_int          2.939064    3.449868 442.902557    0.852 0.394710
## regionDewlap:VPD_kPa_int       13.660303    3.455489 443.552232    3.953 8.97e-05
## regionMite Patch:VPD_kPa_int   14.966590    3.437480 442.010751    4.354 1.66e-05
## regionVentrurn:mass_g           0.987961    0.518046 446.468204    1.907 0.057150
## regionHead:mass_g              -0.365361    0.514064 445.096592   -0.711 0.477623
## regionDewlap:mass_g            0.980463    0.525926 450.477002    1.864 0.062935
## regionMite Patch:mass_g        1.139601    0.533206 446.519281    2.137 0.033119
##
## (Intercept)
## regionVentrurn
## regionHead
## regionDewlap                    ***
## regionMite Patch                **
## VPD_kPa_int                     **
## mass_g
## Solar_rad_Wm2_interpol          ***
## cloacal_temp_C                  ***
## ambient_temp_C                  **
## VPD_kPa
## regionVentrurn:VPD_kPa_int      *
## regionHead:VPD_kPa_int
## regionDewlap:VPD_kPa_int        ***
## regionMite Patch:VPD_kPa_int    ***
## regionVentrurn:mass_g           .
## regionHead:mass_g
## regionDewlap:mass_g             .
## regionMite Patch:mass_g         *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## Correlation matrix not shown by default, as p = 19 > 12.
## Use print(x, correlation=TRUE) or
##     vcov(x)           if you need it

```

Export

We should save the information for the top two models, as well as the table showing the rankings of the different models.

```

write.csv(CEWL_AICc, "./best_models/CEWL_mod_rankings.csv")
write.csv(broom.mixed::tidy(CEWL_mod16tp),
          "./best_models/CEWL_best_mod1.csv")
write.csv(broom.mixed::tidy(CEWL_mod17tp),
          "./best_models/CEWL_best_mod2.csv")

```