# Cal Poly Herpetology CURE - Capture Data Analyses

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## Contents

## 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

```r
# 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
```

```r
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"
```

```r
# 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
```

```r
# 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.

```r
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)

```r
# 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")) %>%
```

```r
  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"),
```

```r
                      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.

```r
# 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.

```r
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
)
```
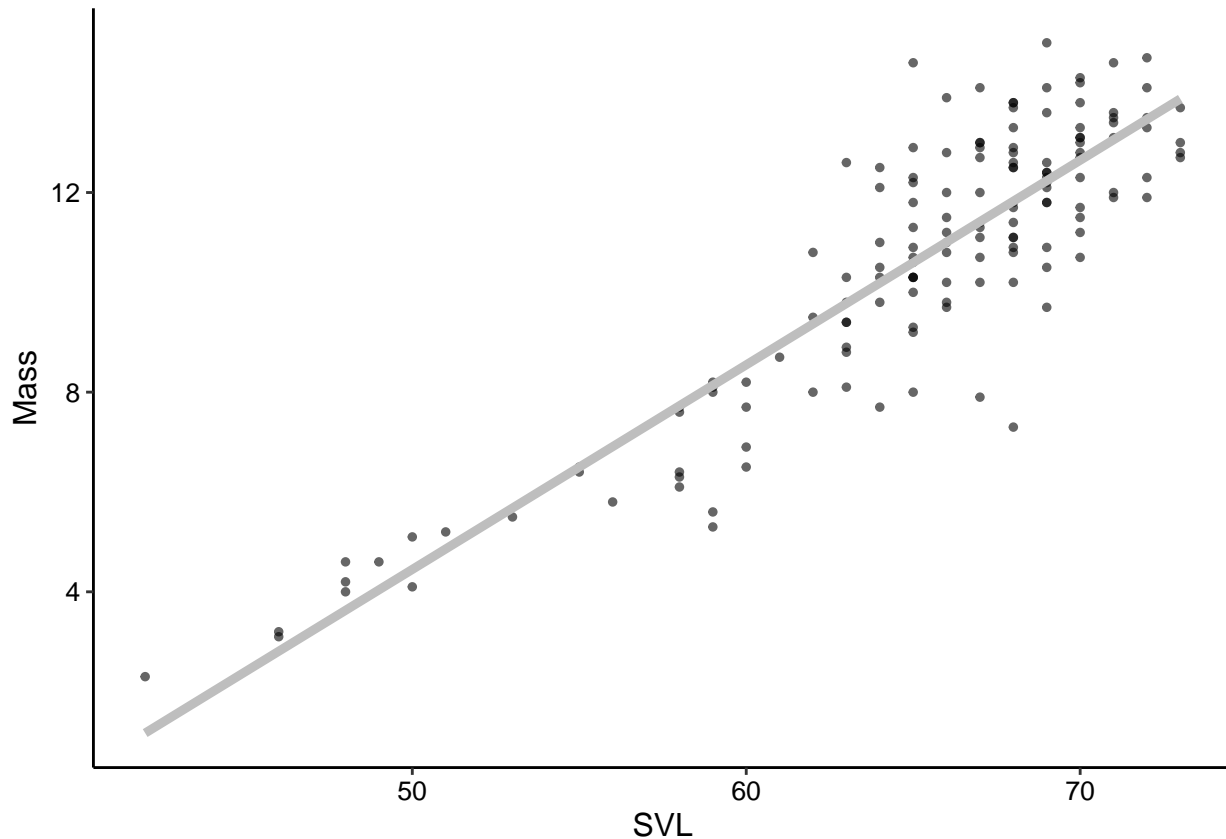
create a simple linear regression

```
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)
```
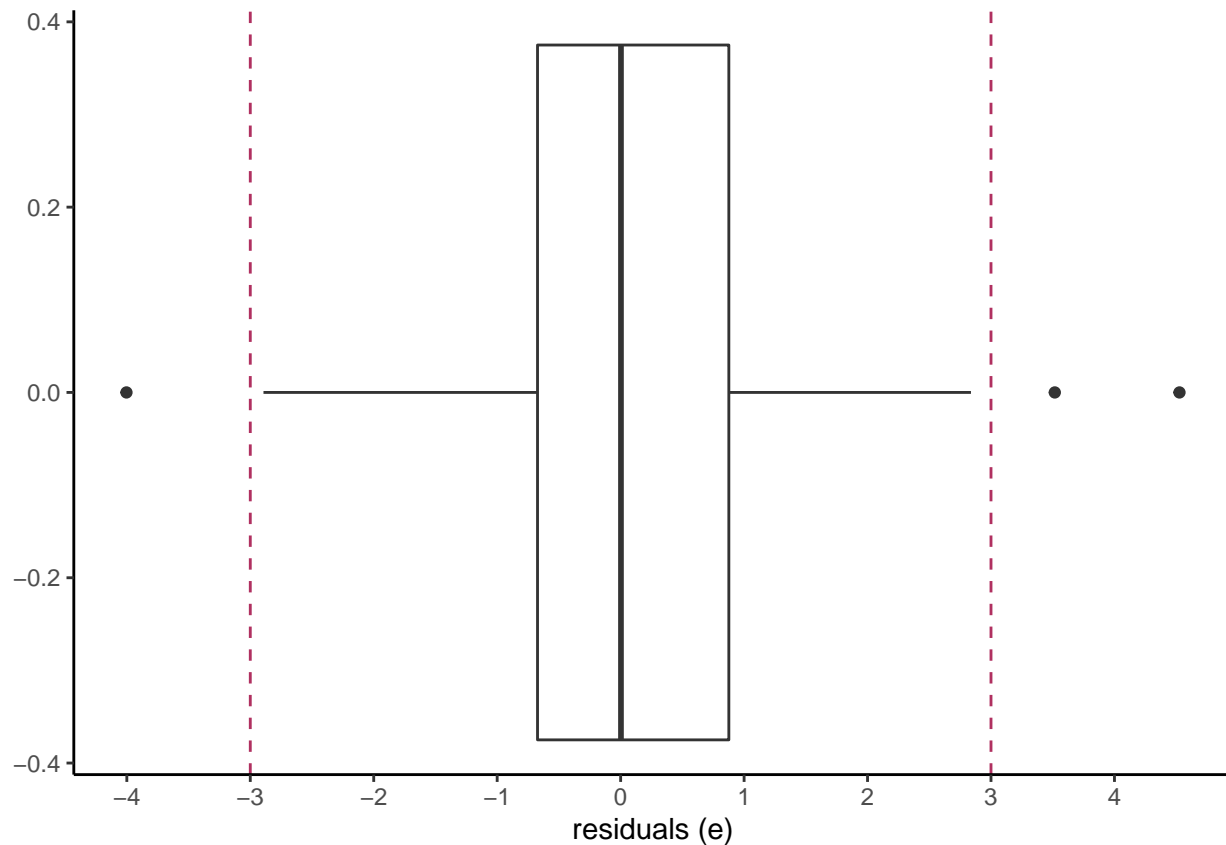
plot residuals

```
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`.
```
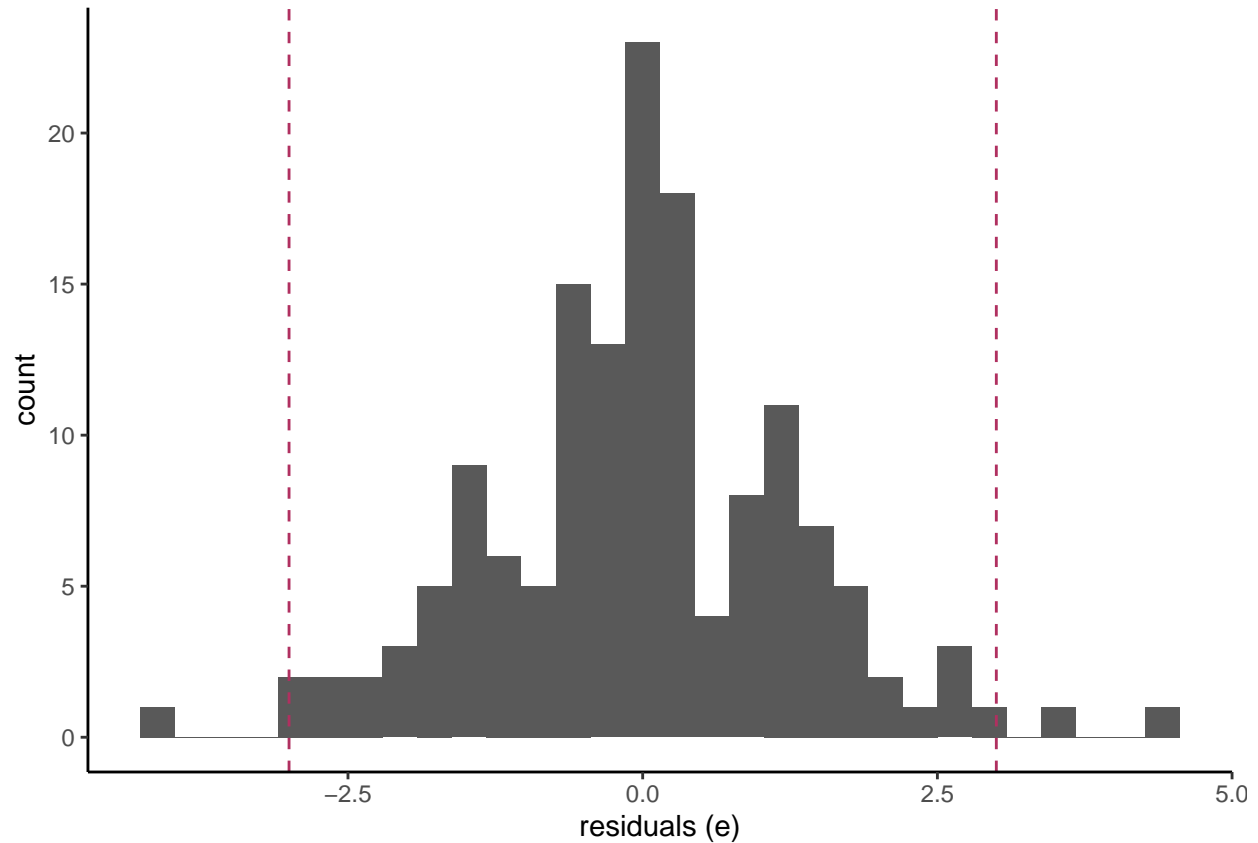


```
ggplot(data = mass_SVL_SLR_residuals,
       aes(x = e)) +
  geom_boxplot() +
  theme_classic() +
  scale_x_continuous(breaks = c(seq(-5, 5, 1))) +
  xlab("residuals (e)") +
  geom_vline(xintercept = -3, linetype = "dashed", color = "maroon") +
  geom_vline(xintercept = 3, linetype = "dashed", color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

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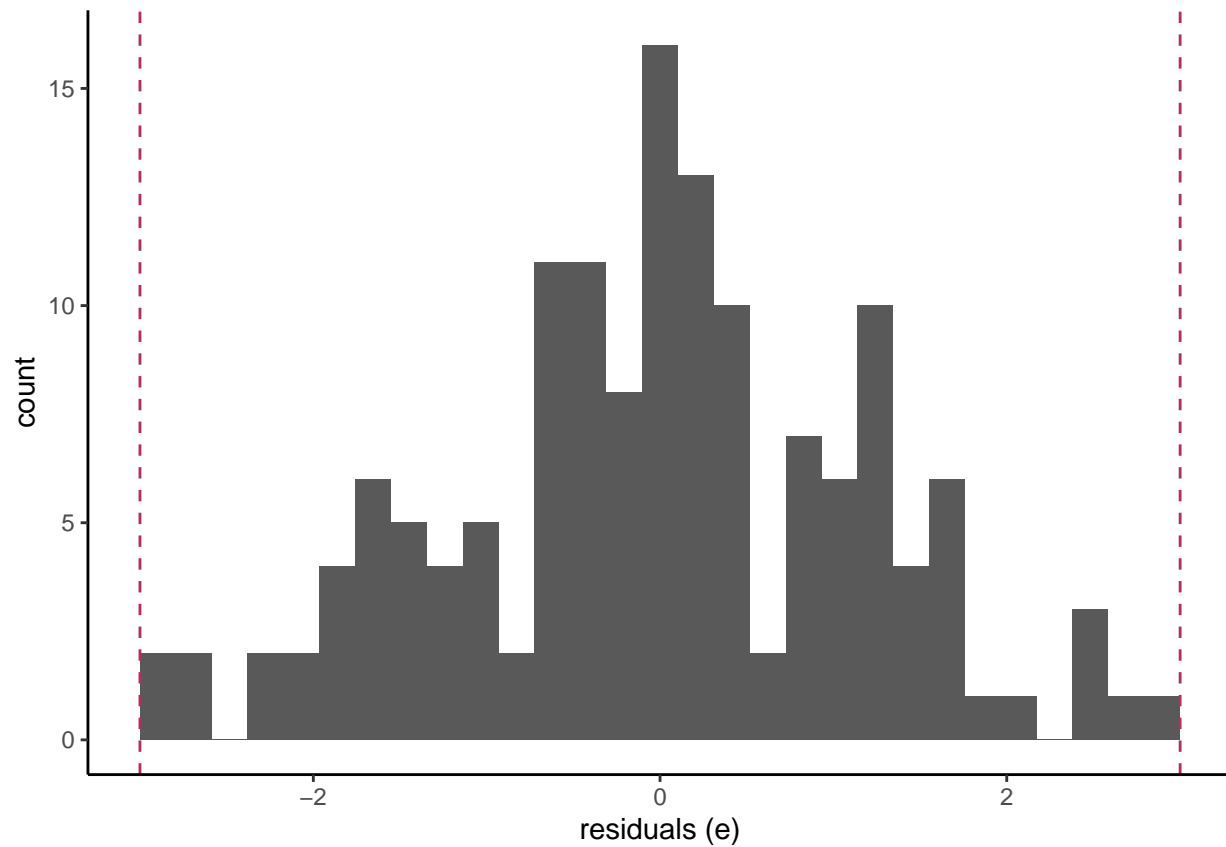
```
ggplot(data = mass_SVL_SLR_residuals2,
       aes(x = e)) +
  geom_boxplot() +
  theme_classic() +
  scale_x_continuous(breaks = c(seq(-5, 5, 1))) +
  xlab("residuals (e)") +
  geom_vline(xintercept = -3, linetype = "dashed", color = "maroon") +
  geom_vline(xintercept = 3, linetype = "dashed", color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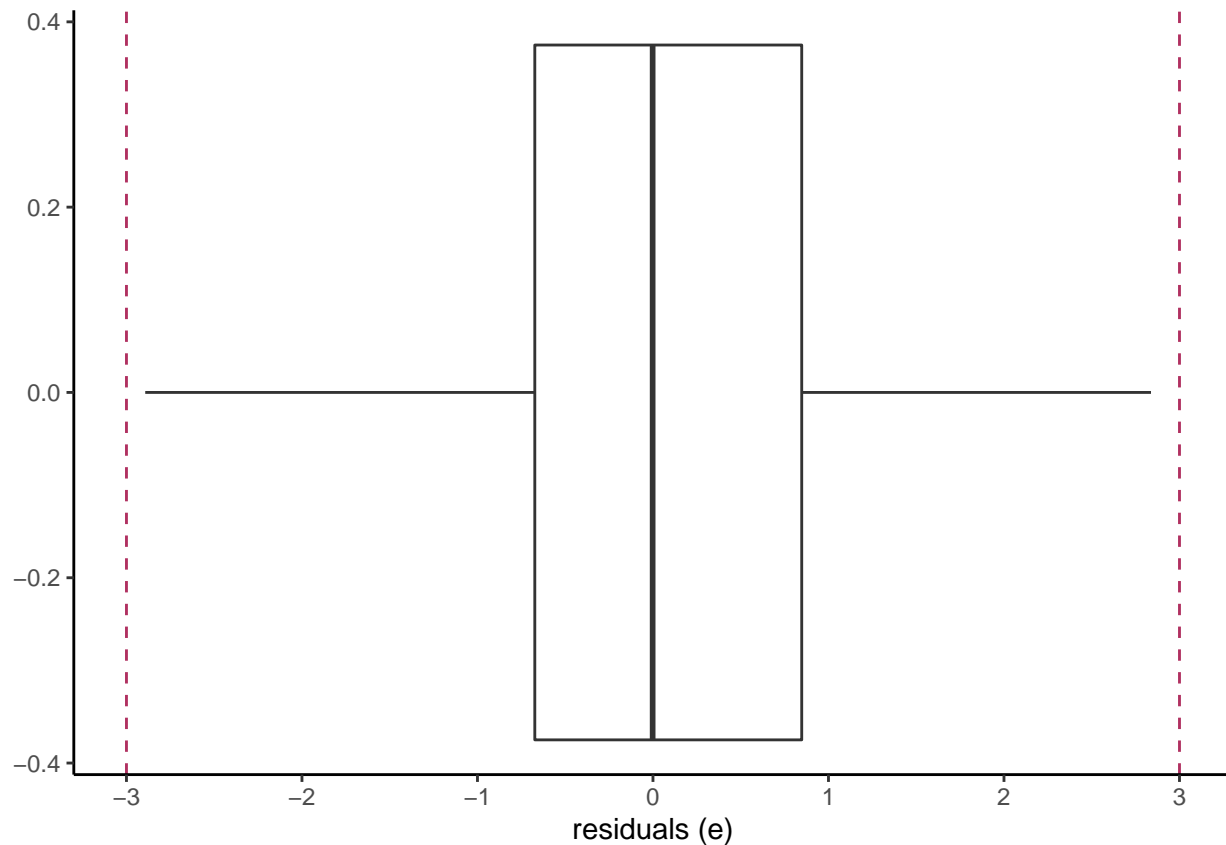
And, check mean residual value:

```
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(.)) %>%
```

```r
  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-infuential 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:

```r
# 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
```

```r
# 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
)
```
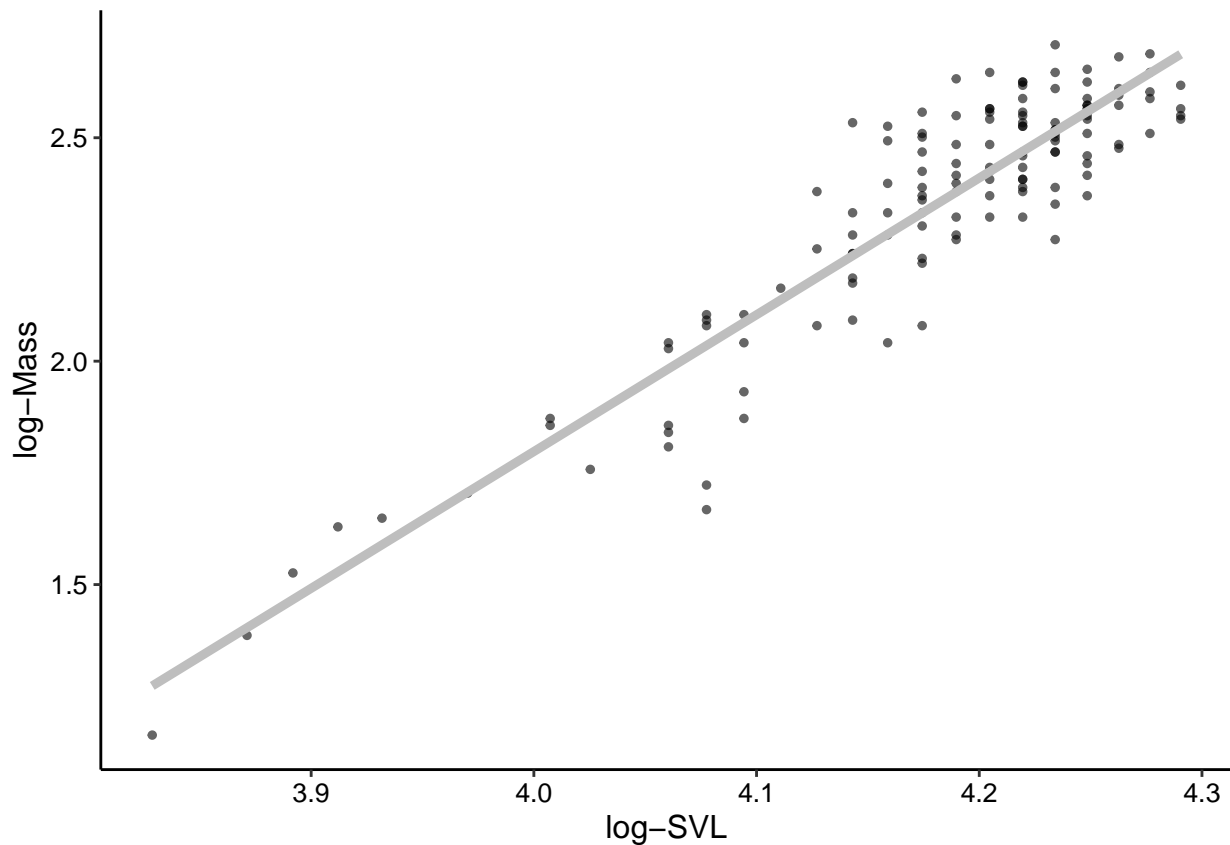
SLR

```
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
```

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

also get a value for L0:

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

**Step 3: calculate scaled mass index**

(And join weather data.)

```r
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:

```r
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
)
```
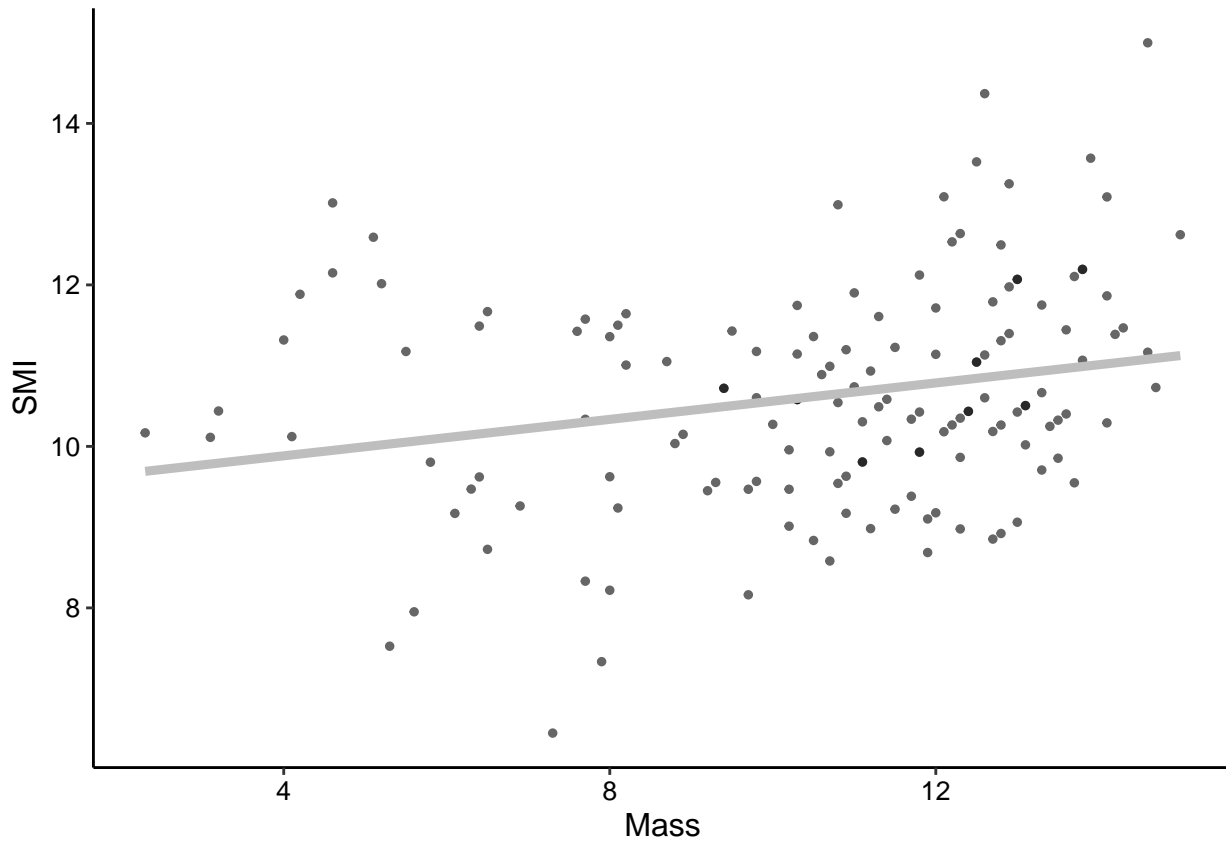
**Join Data**

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    Ventrum    Dewlap    Head       Mite Patch
## Levels: Dorsum Ventrum Head Dewlap Mite Patch
```

NOTE: running this more than once overrides things, so be careful
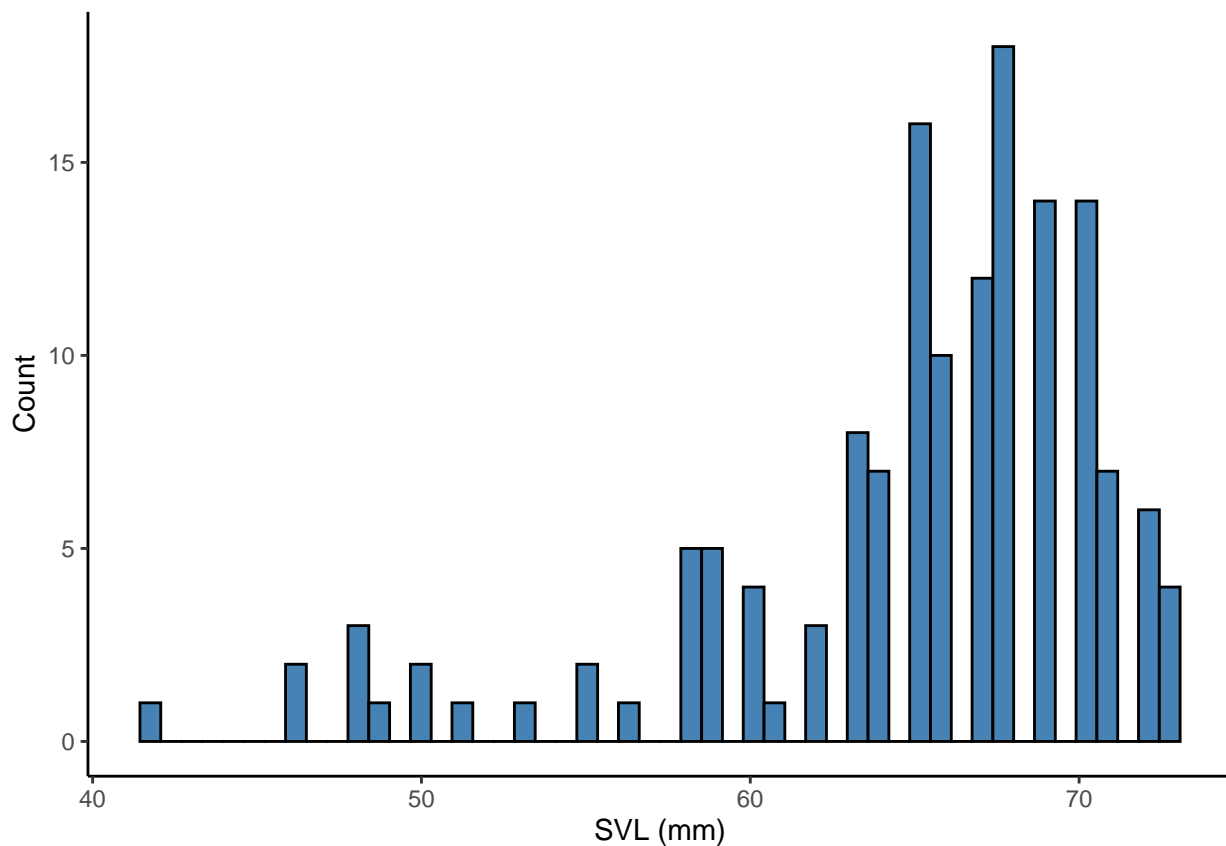
## Check Data Distributions
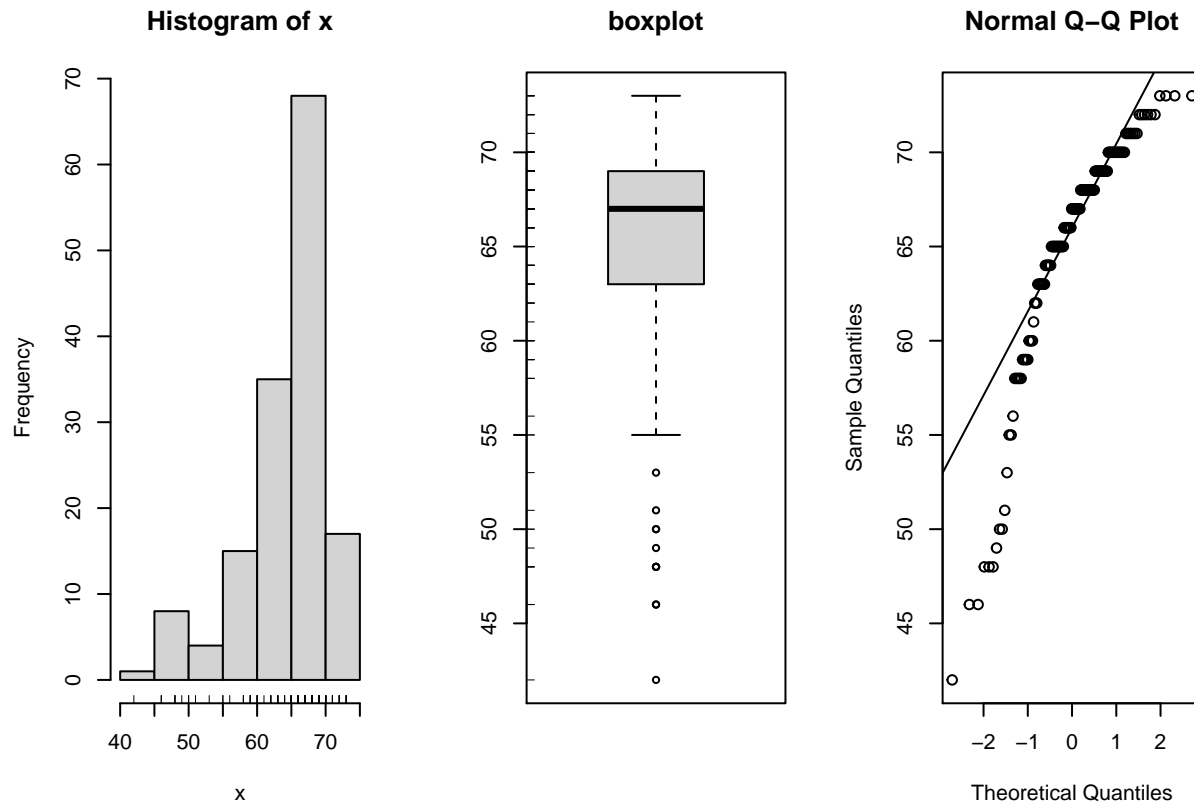
### Histograms & Q-Q Plots

**SVL**

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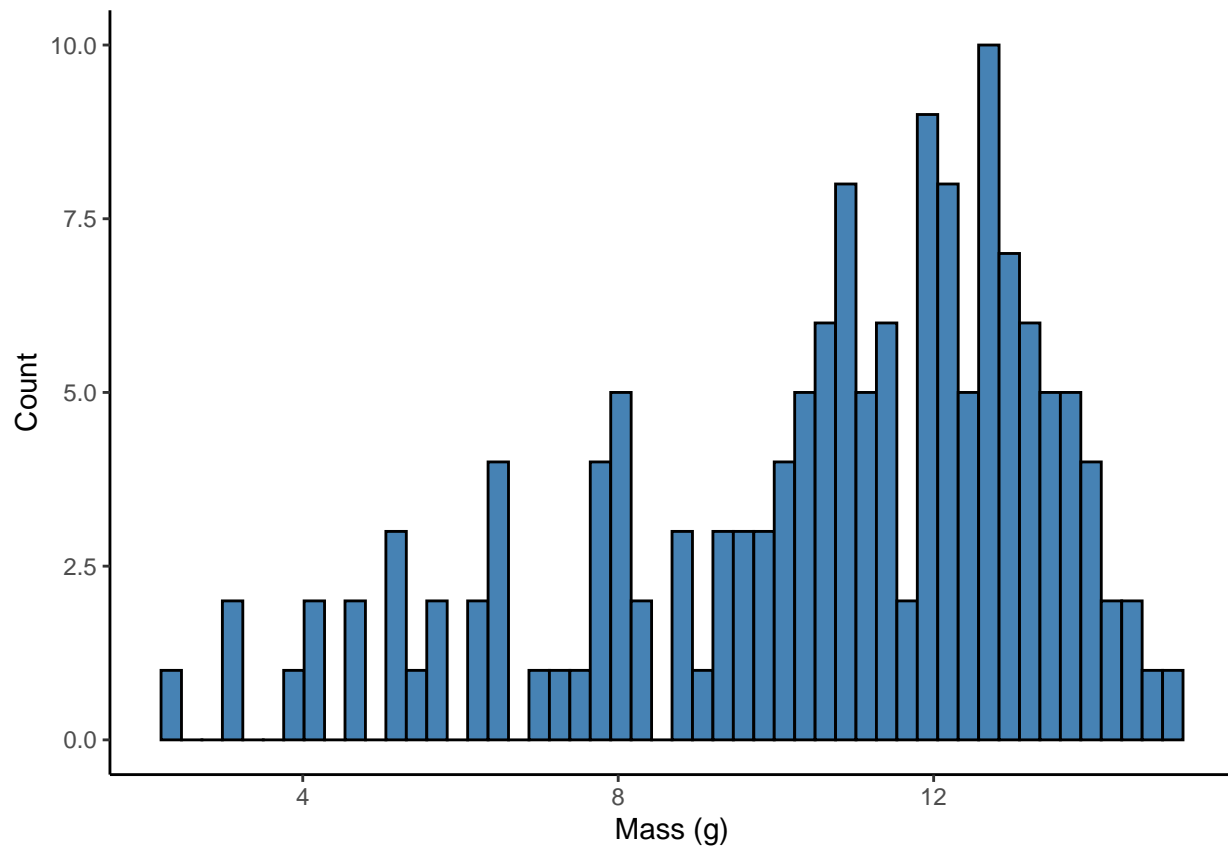
```
simple.eda(morpho_blood_SMI$SVL_mm)
```



**Histogram of x**      **boxplot**      **Normal Q–Q Plot**

```
# Normality test if p > .05, data is normal. Data is not normal.
shapiro.test(morpho_blood_SMI$SVL_mm)
```
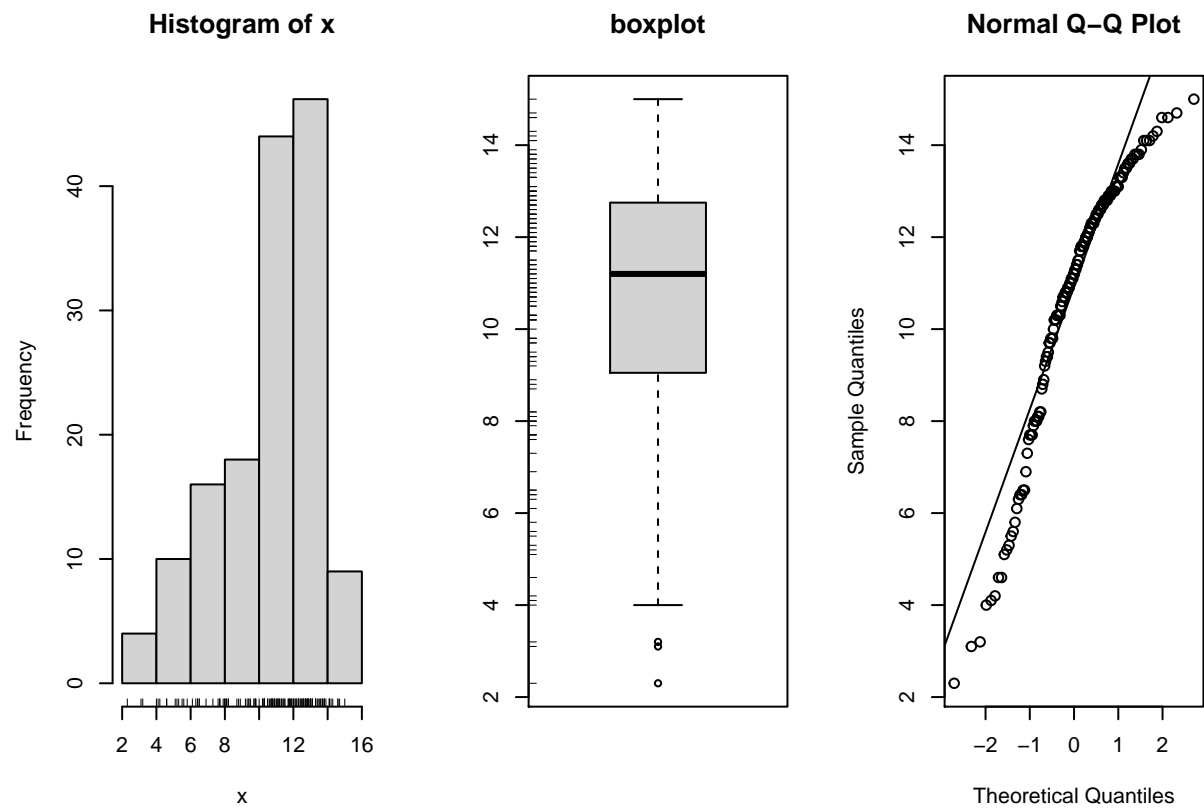
```
##
##   Shapiro-Wilk normality test
##
## data:  morpho_blood_SMI$SVL_mm
## W = 0.85469, p-value = 8.85e-11
```

**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)
```

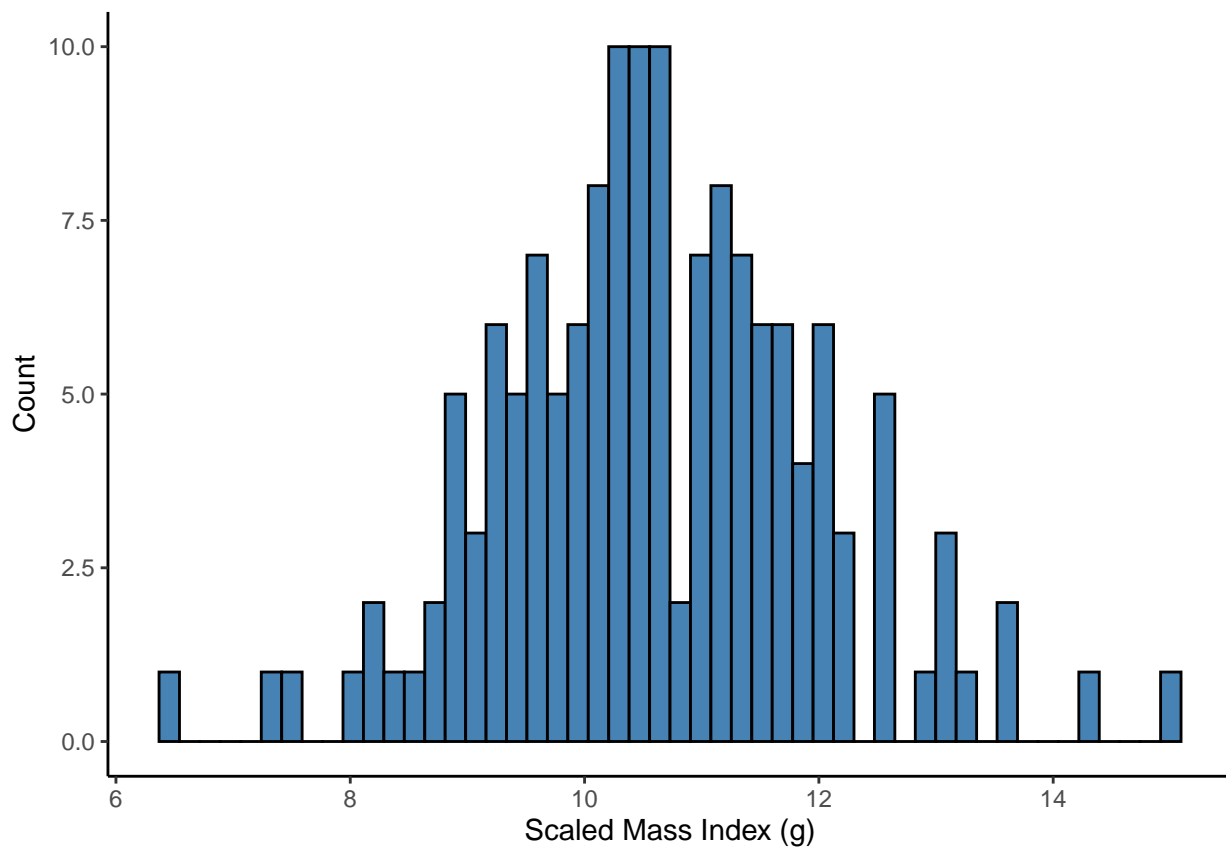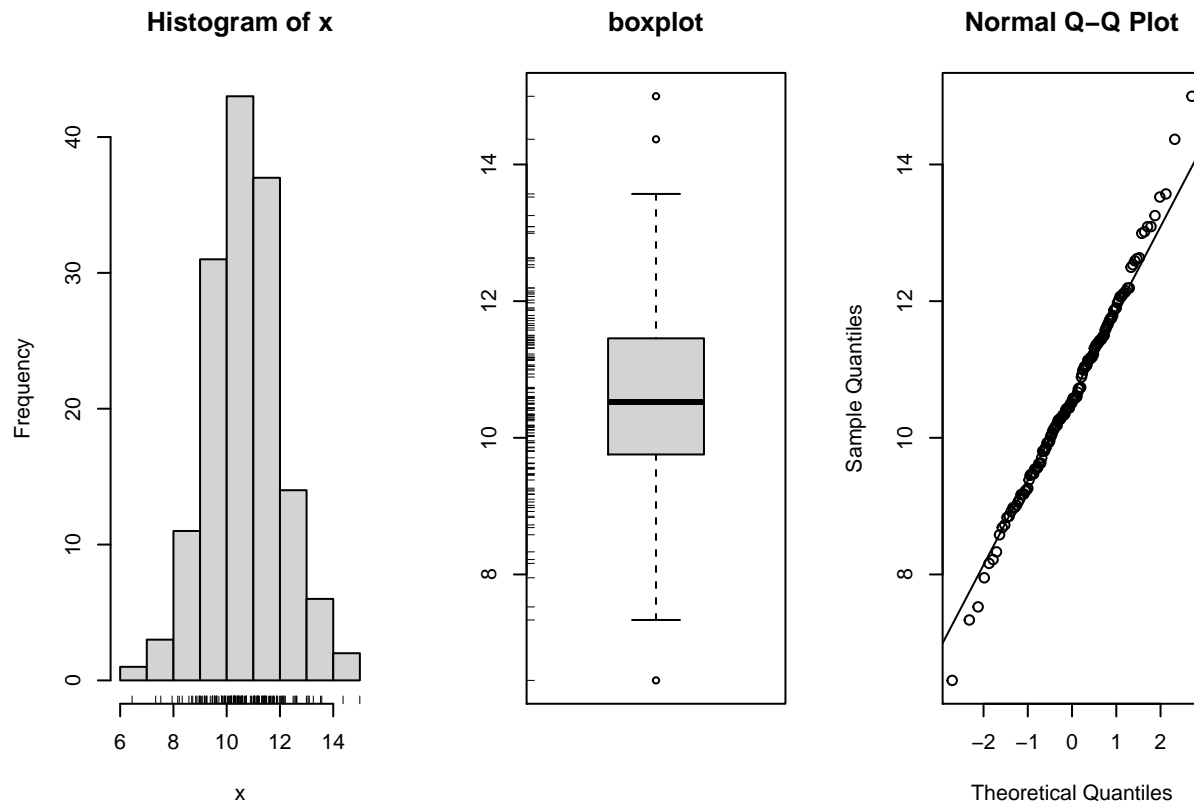| Histogram of x | boxplot | Normal Q–Q Plot |

```r
# 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

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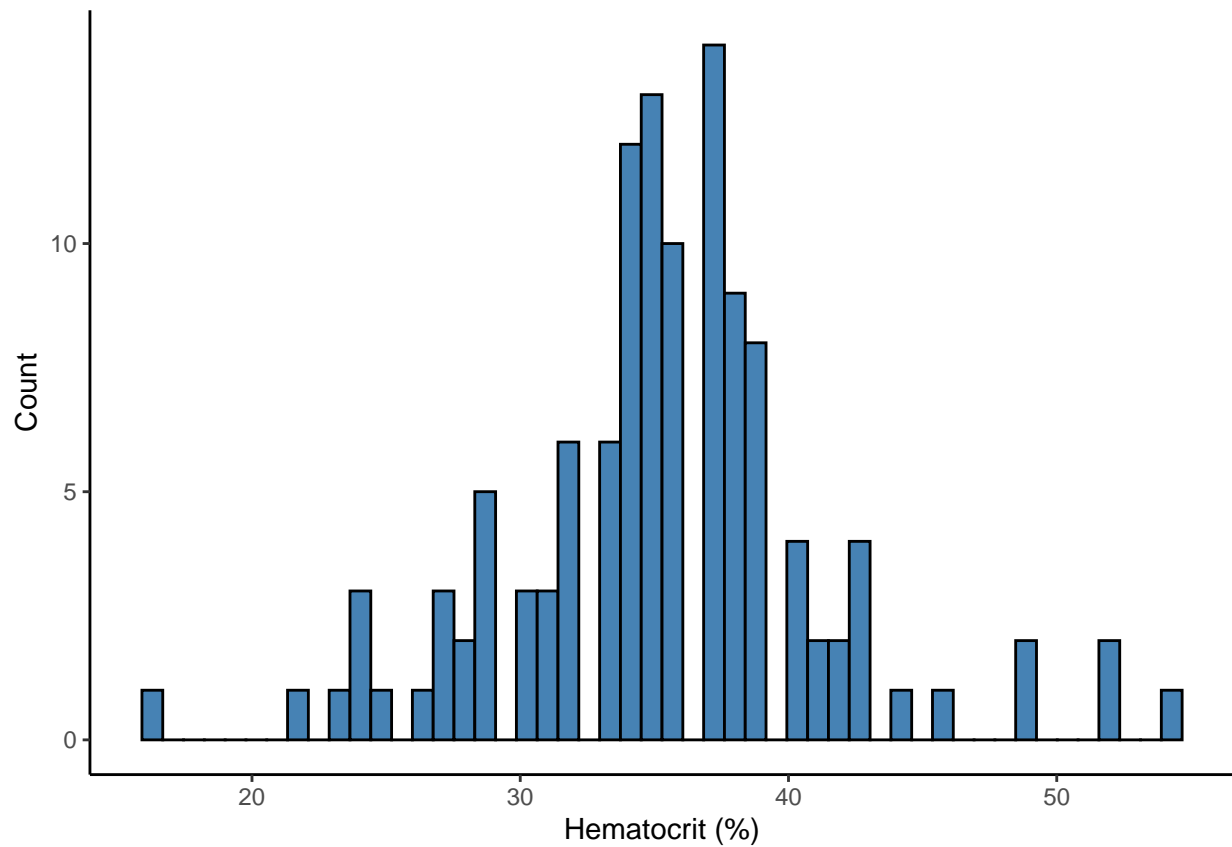
```
simple.eda(morpho_blood_SMI$hematocrit_percent)
```
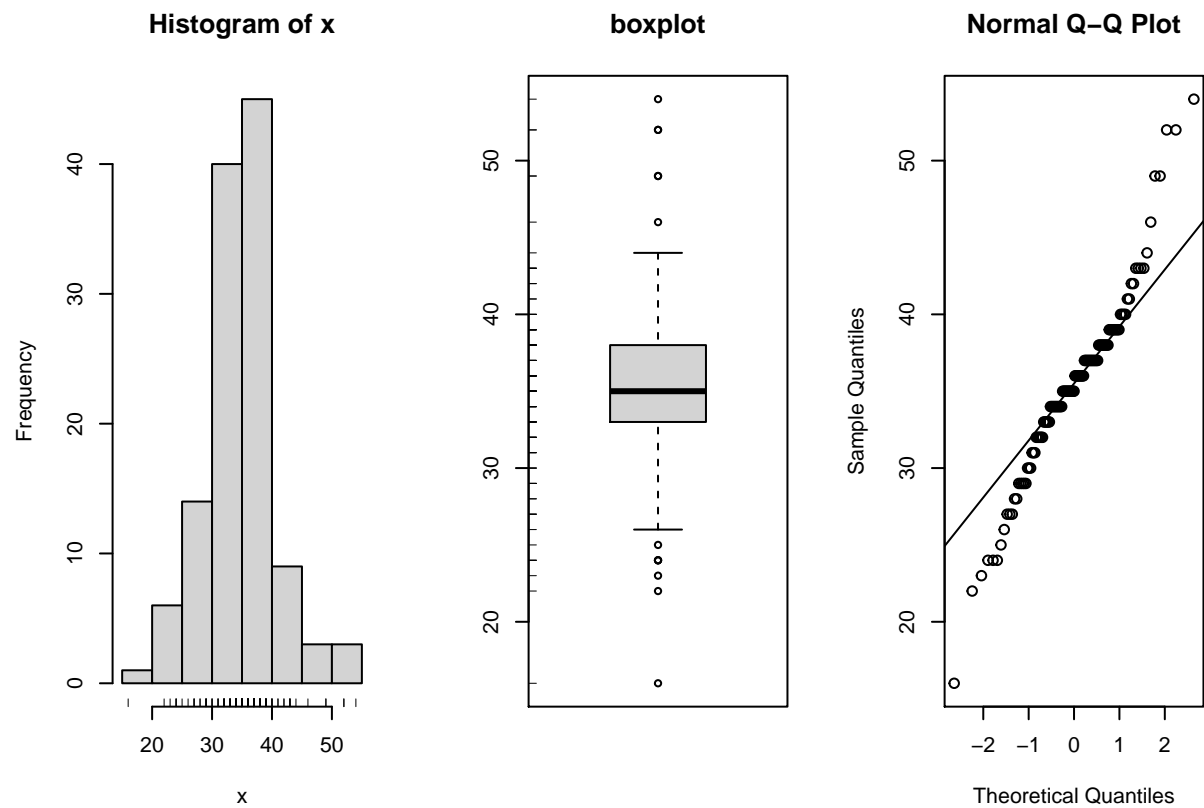
```
# Normality test if p > .05, data is normal. Data is not normal
shapiro.test(morpho_blood_SMI$hematocrit_percent)
```

```
##
##  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).
```
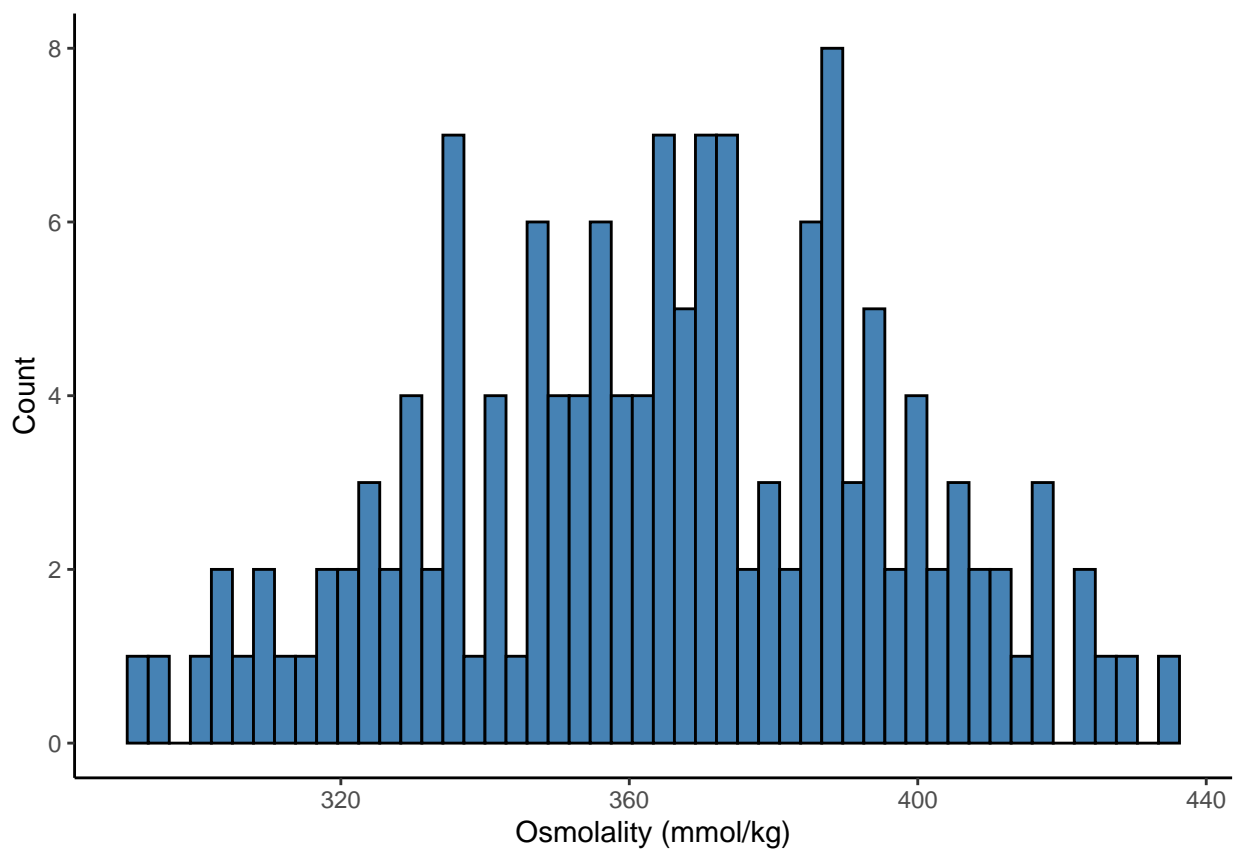


```
simple.eda(morpho_blood_SMI$osmolality_mmol_kg)
```
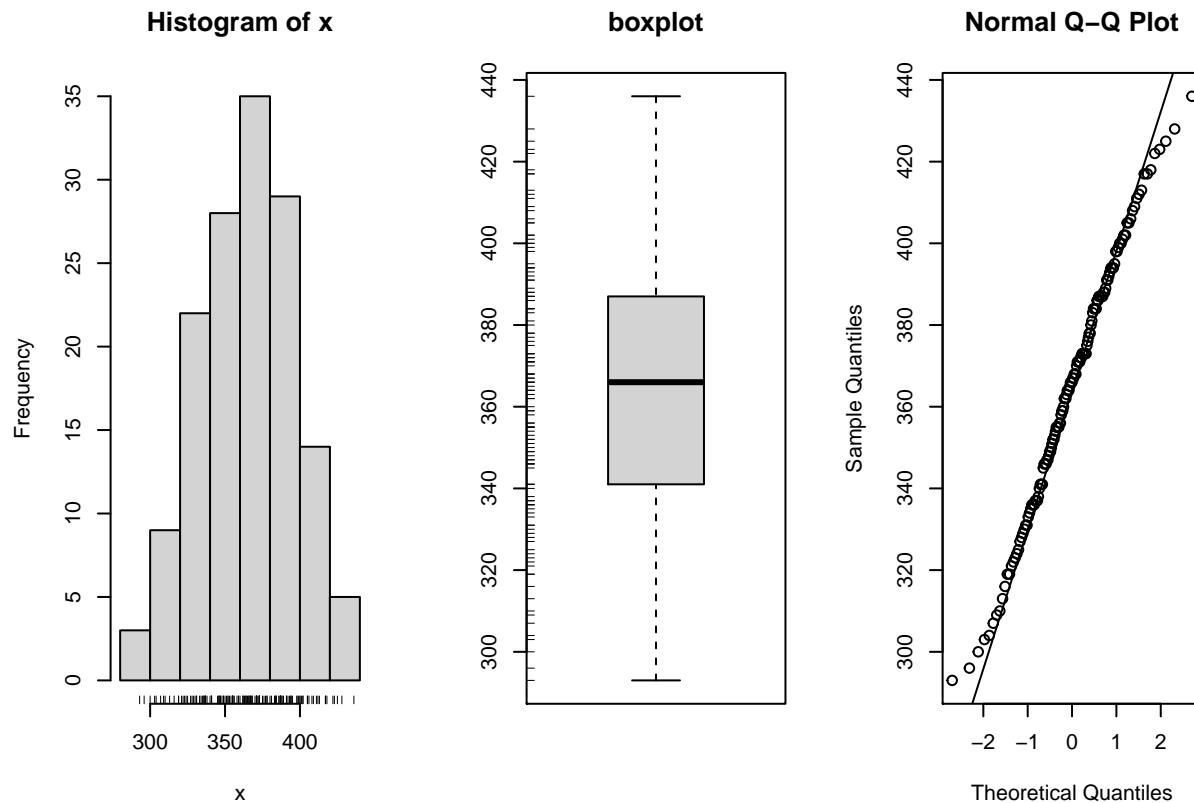
```r
# Normality test if p > .05, data is normal. Data is normal
shapiro.test(morpho_blood_SMI$osmolality_mmol_kg)
```

```
##
##  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

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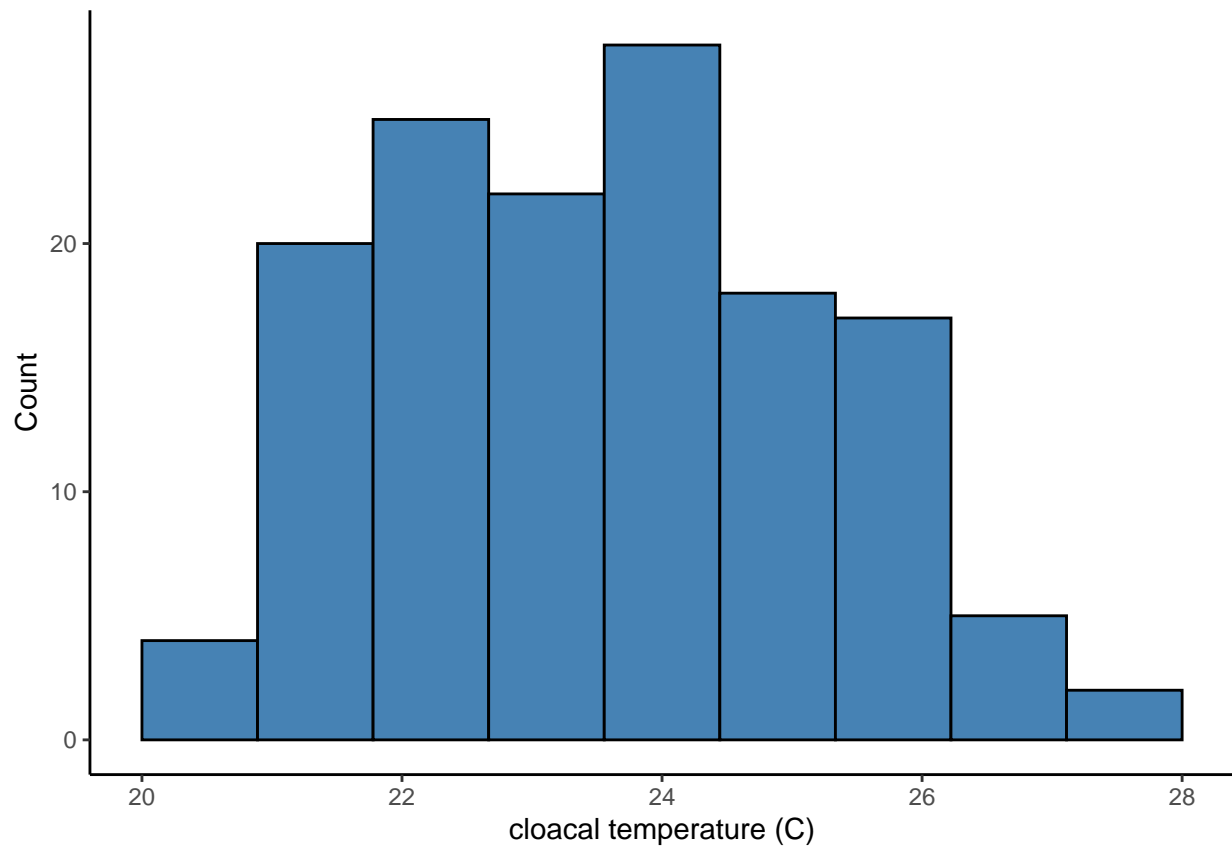
```
simple.eda(morpho_blood_SMI$cloacal_temp_C)
```
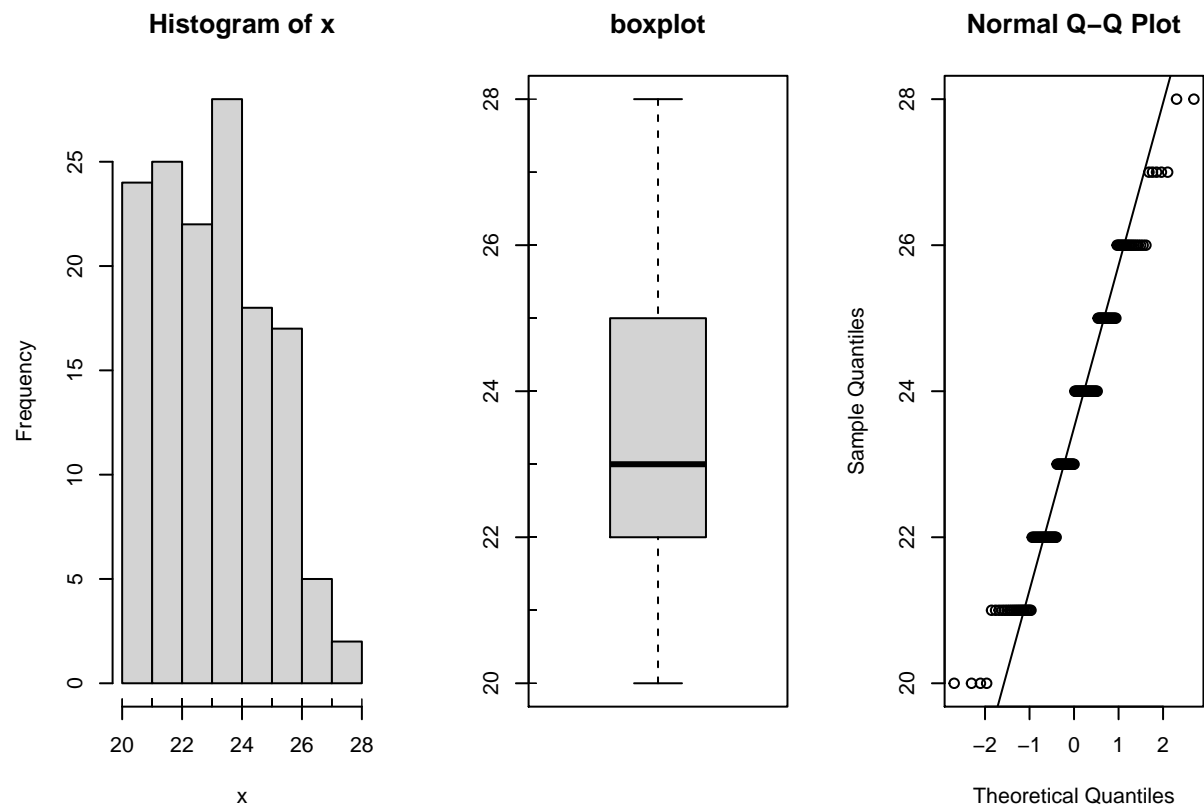
```
# Normality test if p > .05, data is normal. Data is not normal
shapiro.test(morpho_blood_SMI$cloacal_temp_C)
```

```
##
##  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")
```
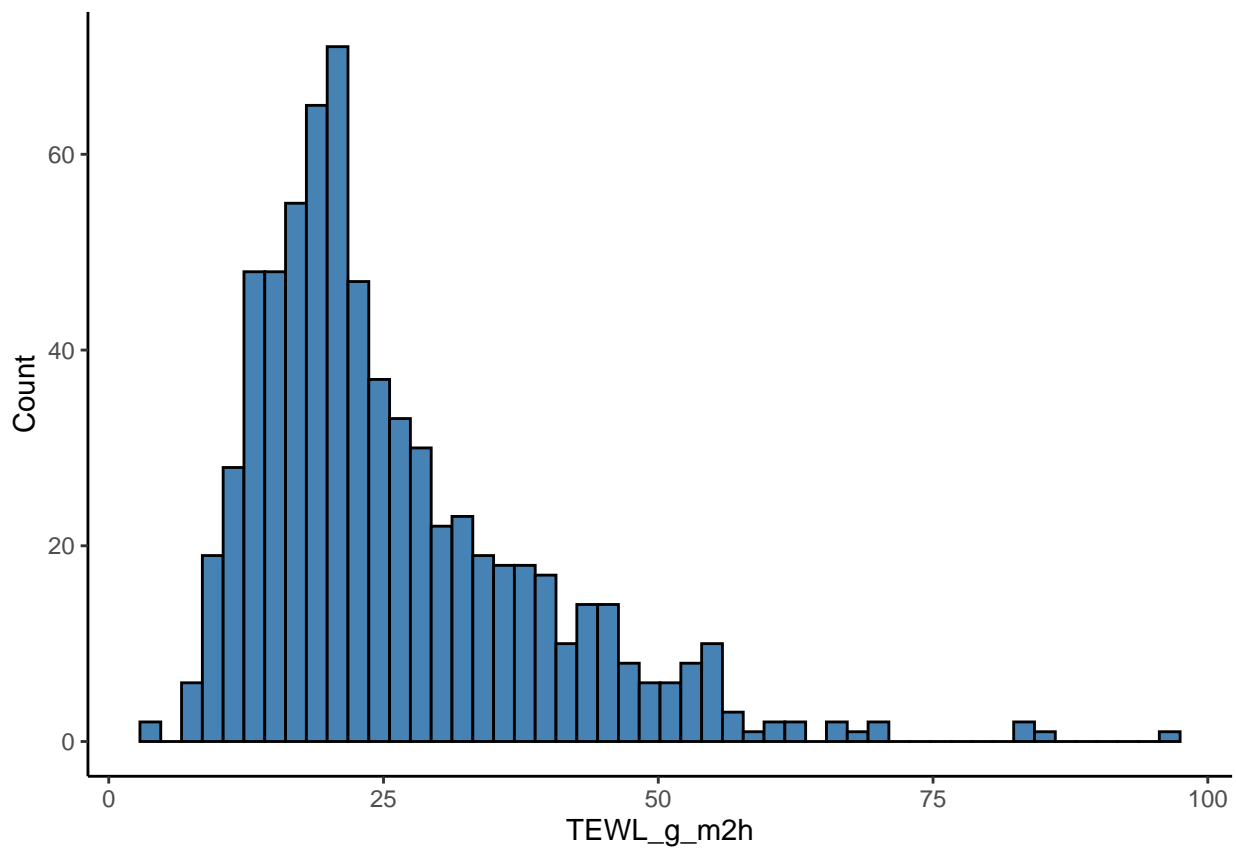


```
simple.eda(CEWL_data_full$TEWL_g_m2h)
```
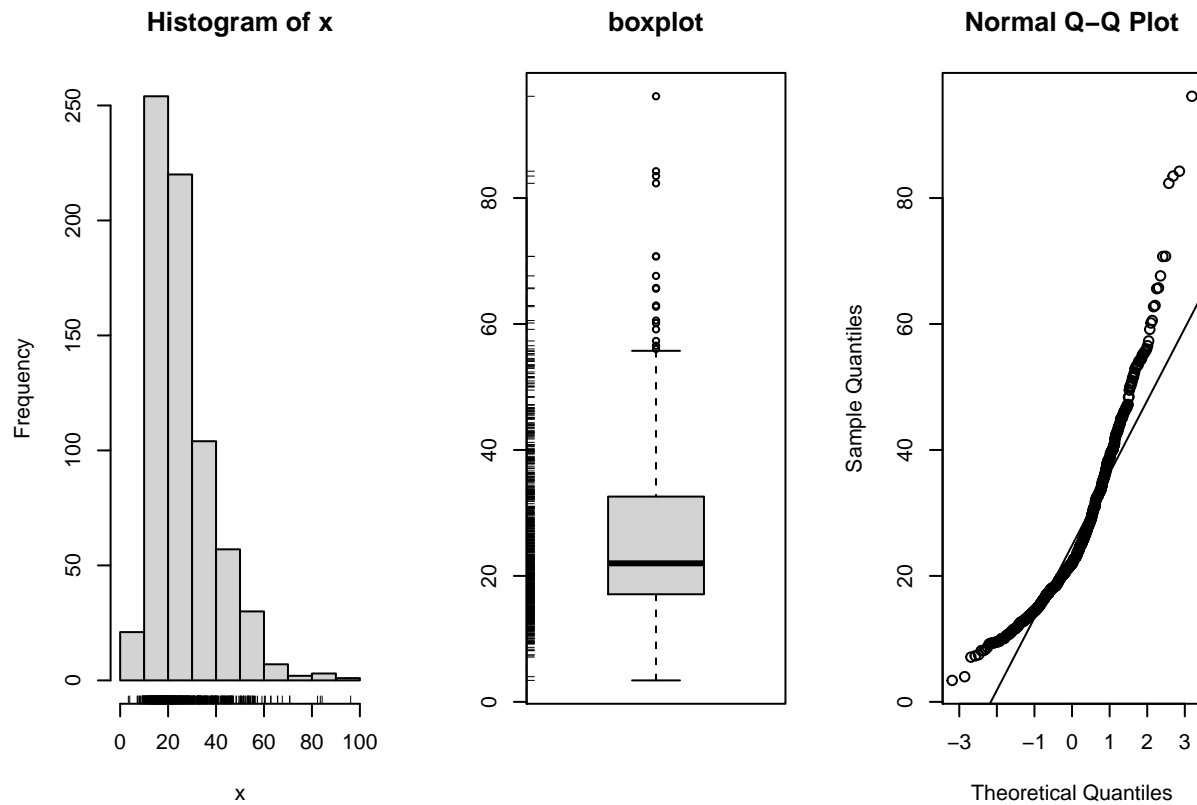
**Histogram of x**   **boxplot**   **Normal Q–Q Plot**



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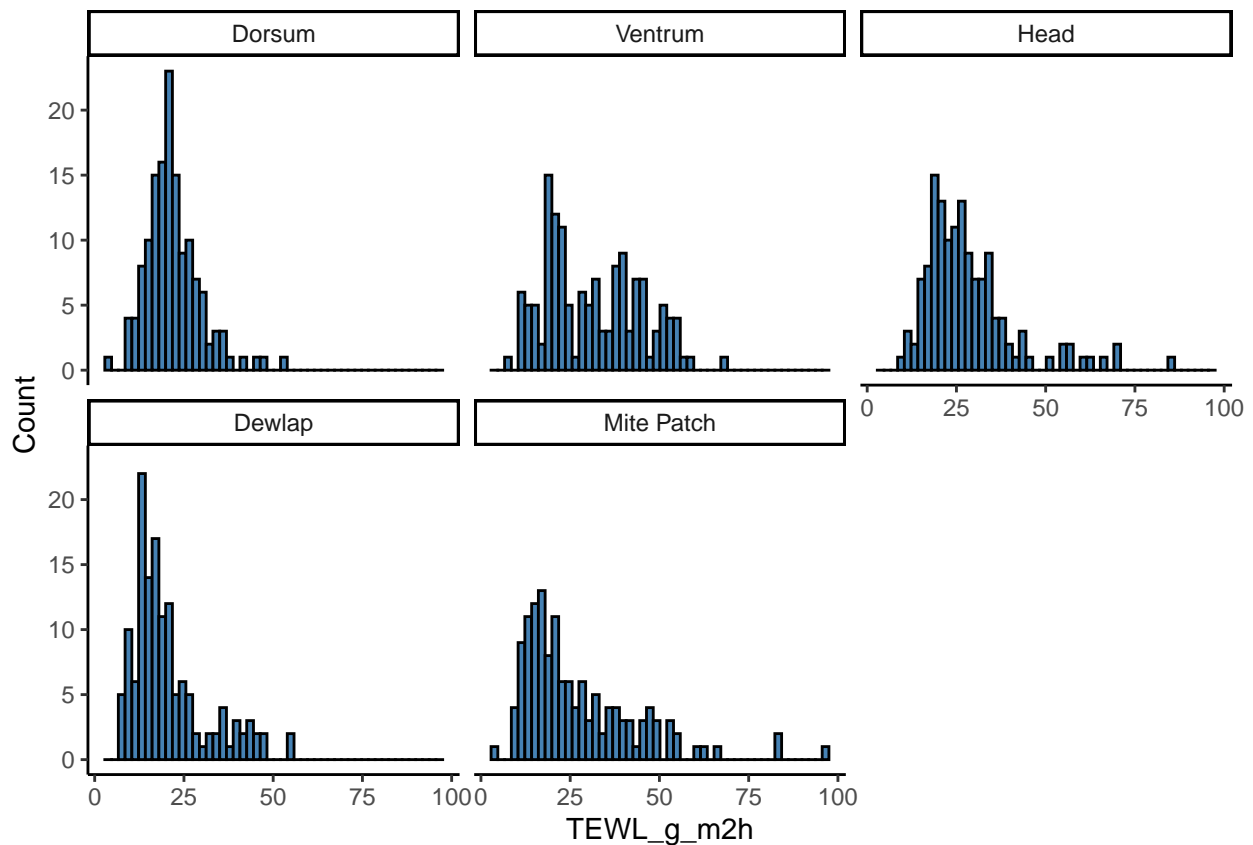
```
# Normality test if p > .05, data is normal. Data is not normal
shapiro.test(CEWL_data_full$TEWL_g_m2h)
```

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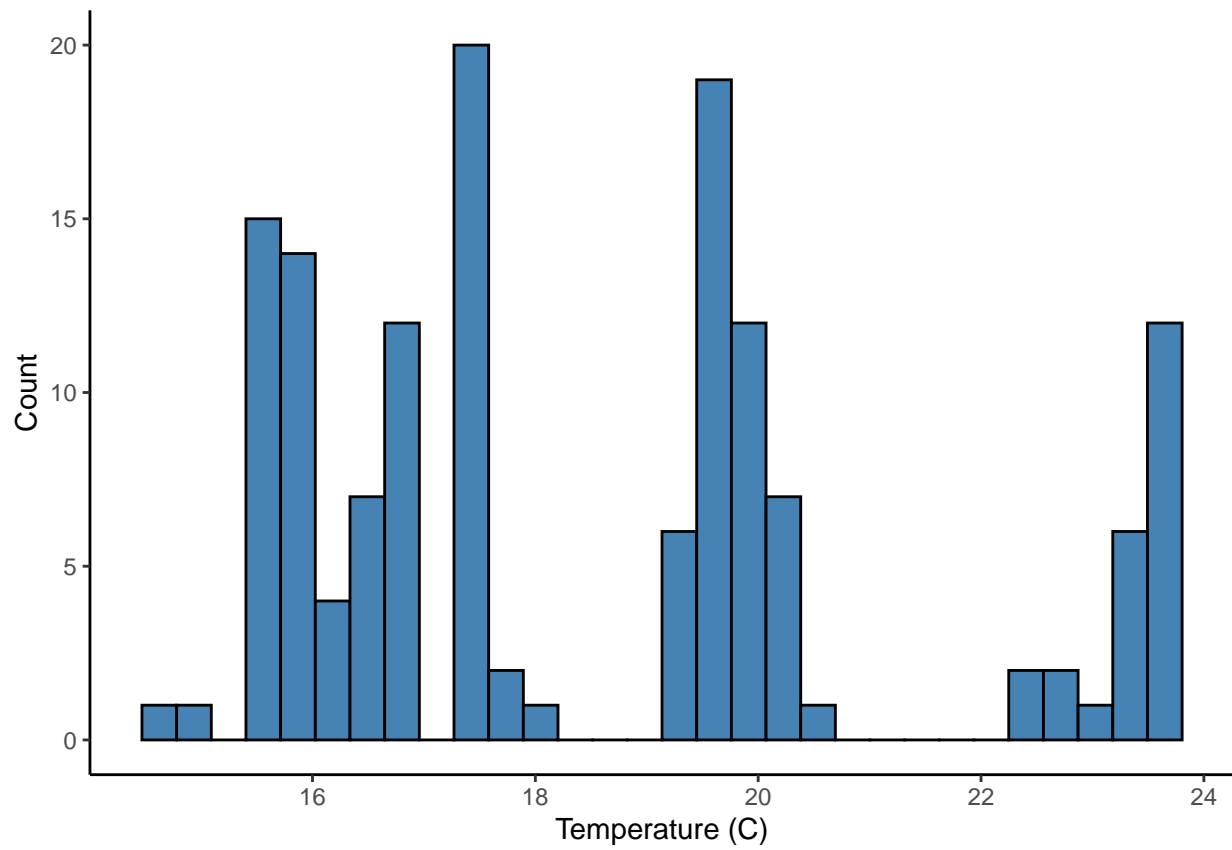
## Warning: Removed 3 rows containing non-finite values (stat_bin).



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

**Histogram of x**     **boxplot**     **Normal Q–Q Plot**

```r
# 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
```

```r
# 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**

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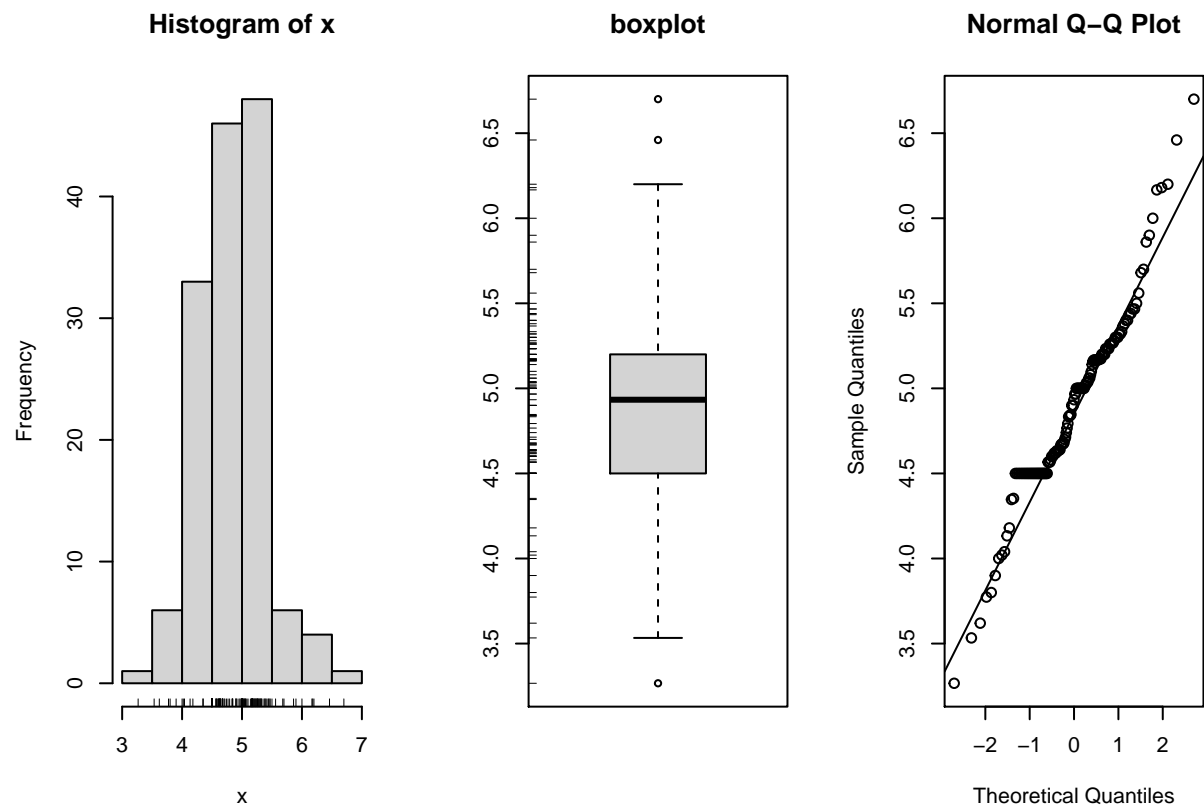
```r
# Normality test if p > .05, data is normal. Data is not normal
shapiro.test(morpho_blood_SMI$Wind_mph_interpol)
```

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

```r
# 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

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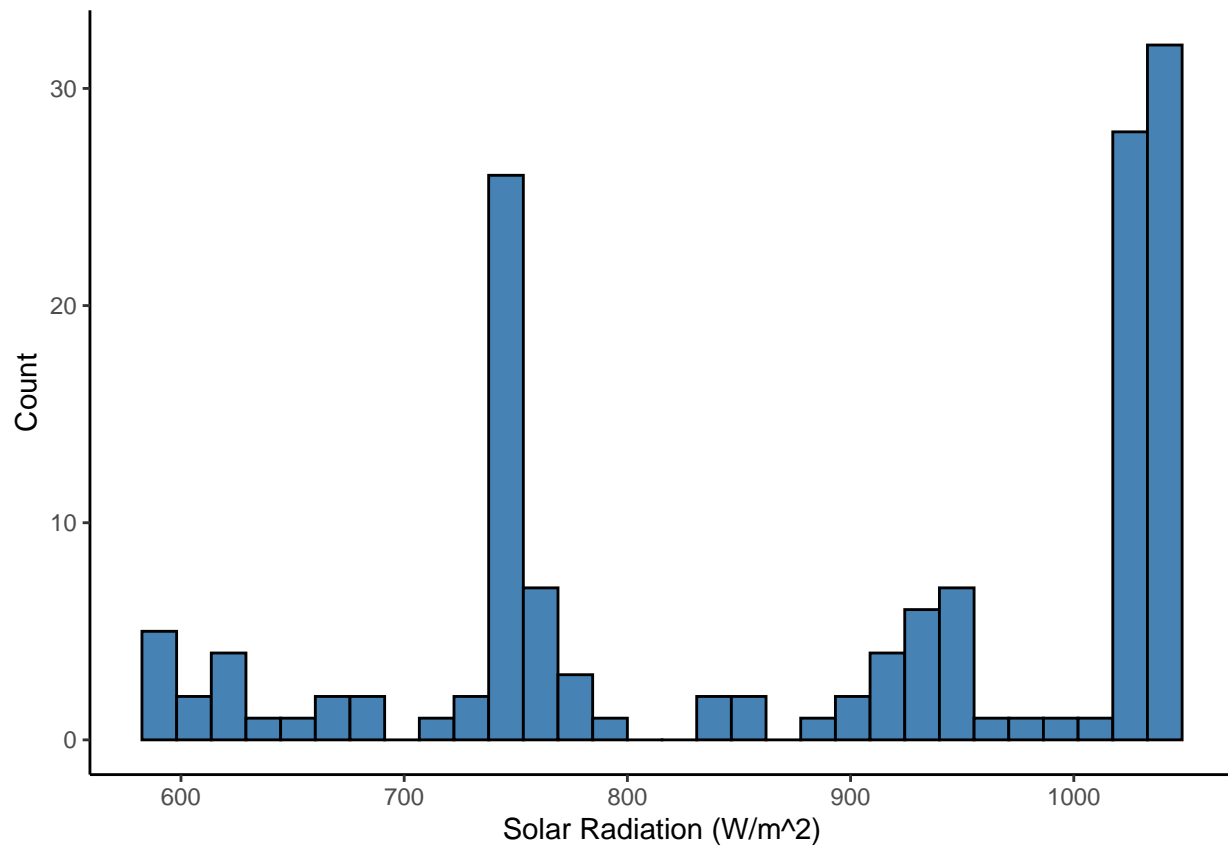
```r
simple.eda(morpho_blood_SMI$Solar_rad_Wm2_interpol)
```

```r
# Normality test if p > .05, data is normal. Data is not normal
shapiro.test(morpho_blood_SMI$Solar_rad_Wm2_interpol)
```
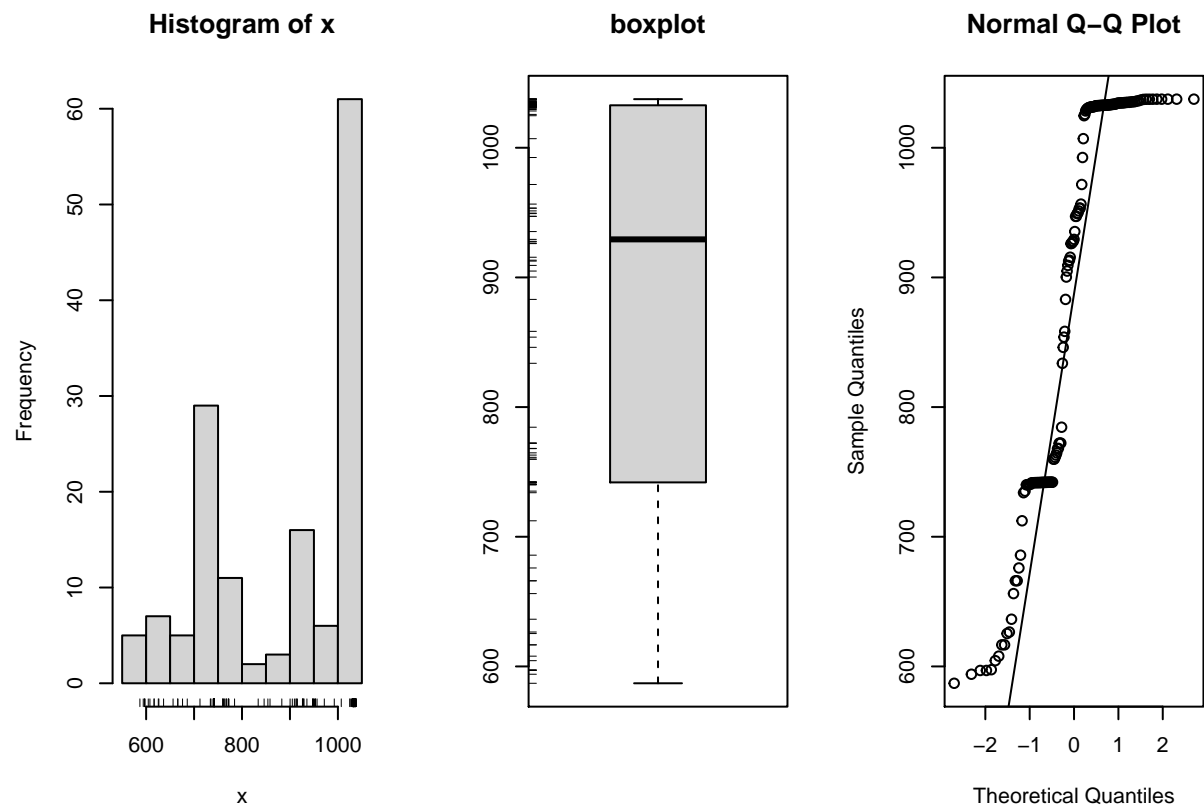
```
##
##  Shapiro-Wilk normality test
##
## data:  morpho_blood_SMI$Solar_rad_Wm2_interpol
## W = 0.82946, p-value = 1.072e-11
```
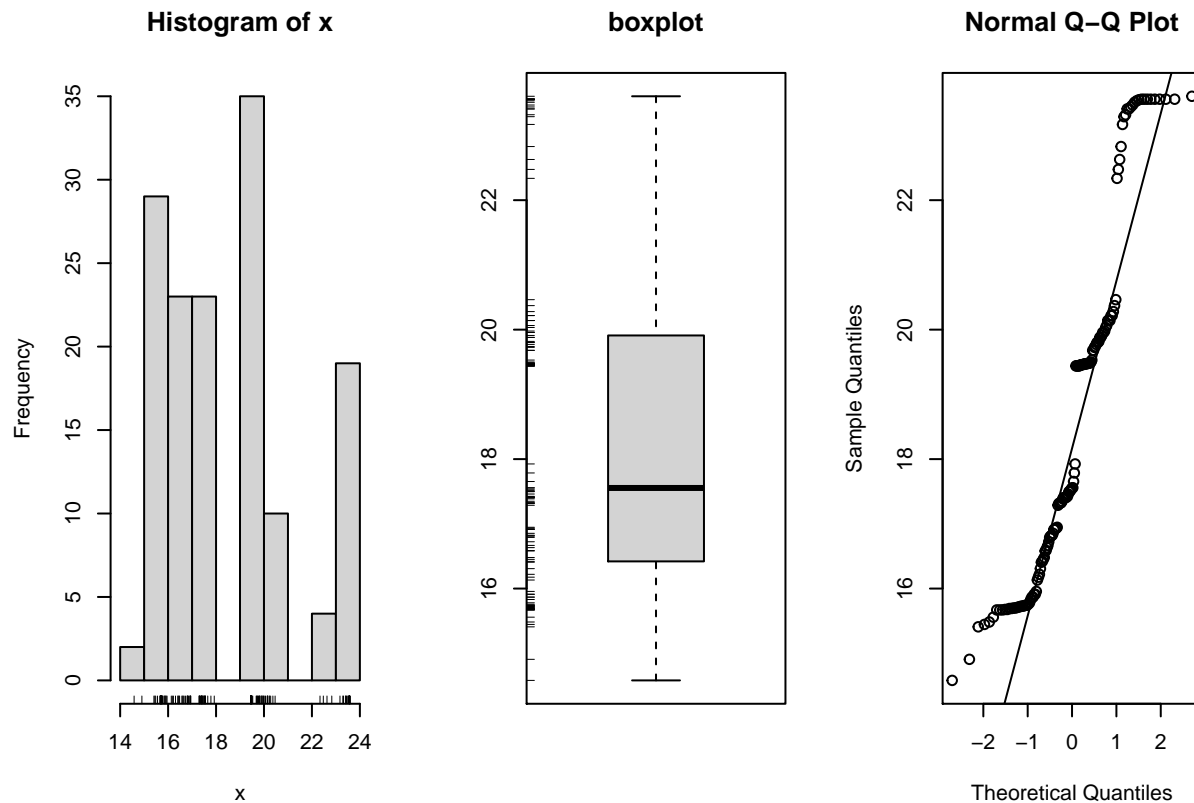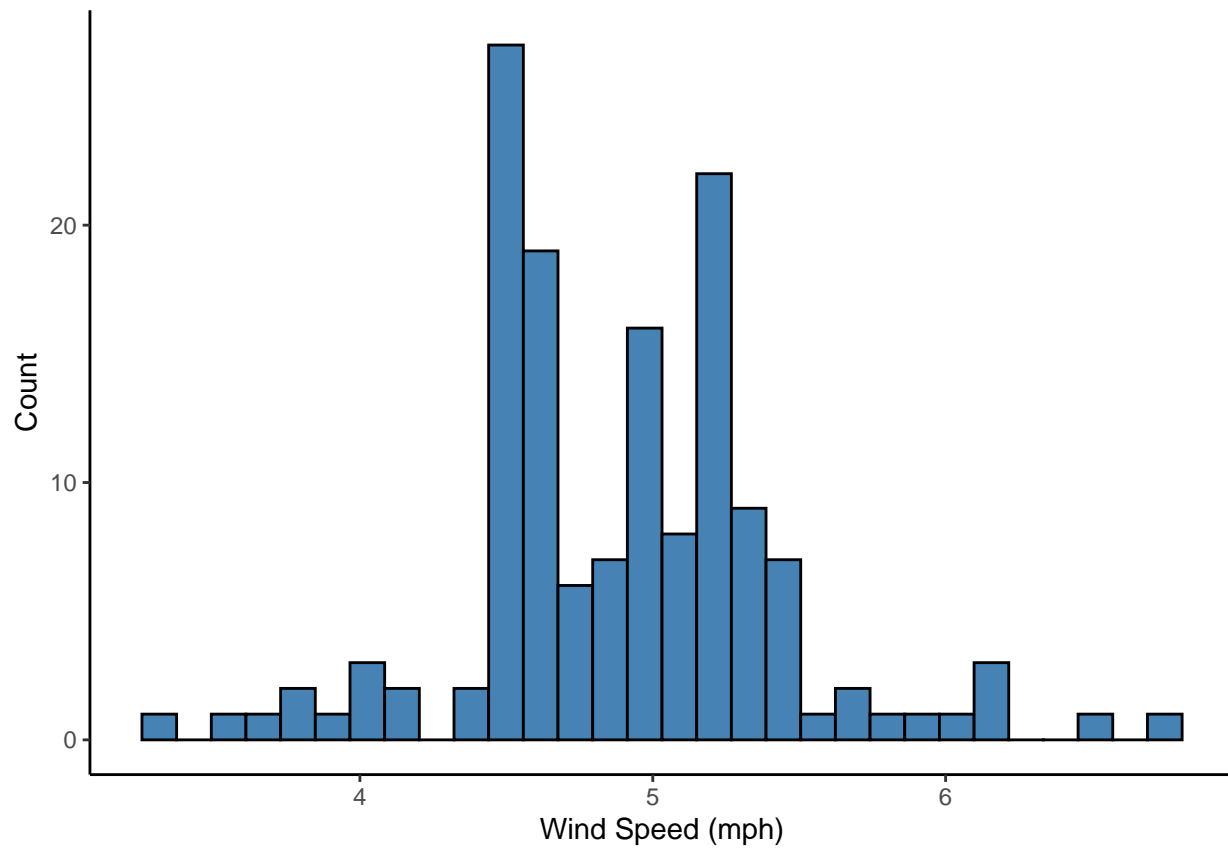
```r
# Doesn't fix non normality
shapiro.test(log(morpho_blood_SMI$Solar_rad_Wm2_interpol))
```

```
##
##  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**

```r
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).
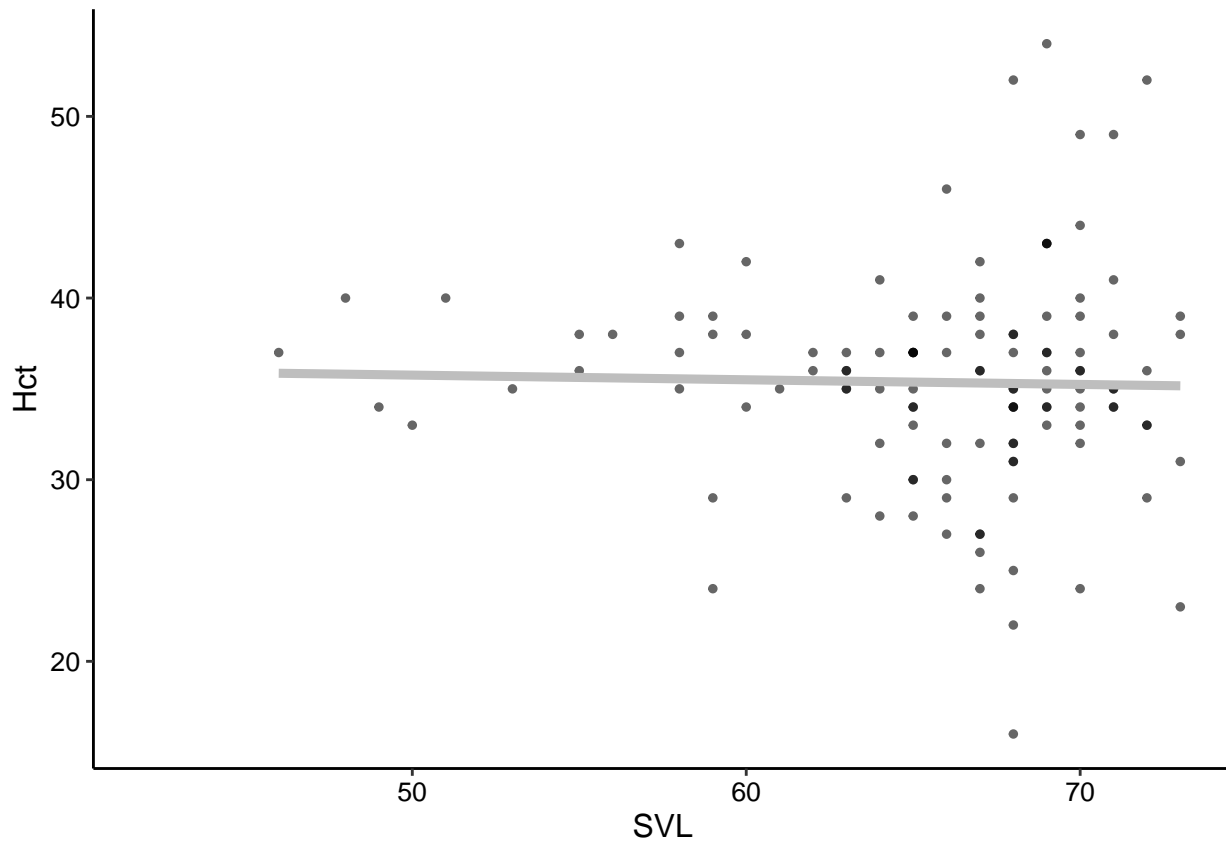


**Osml ~ SVL**

```
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).
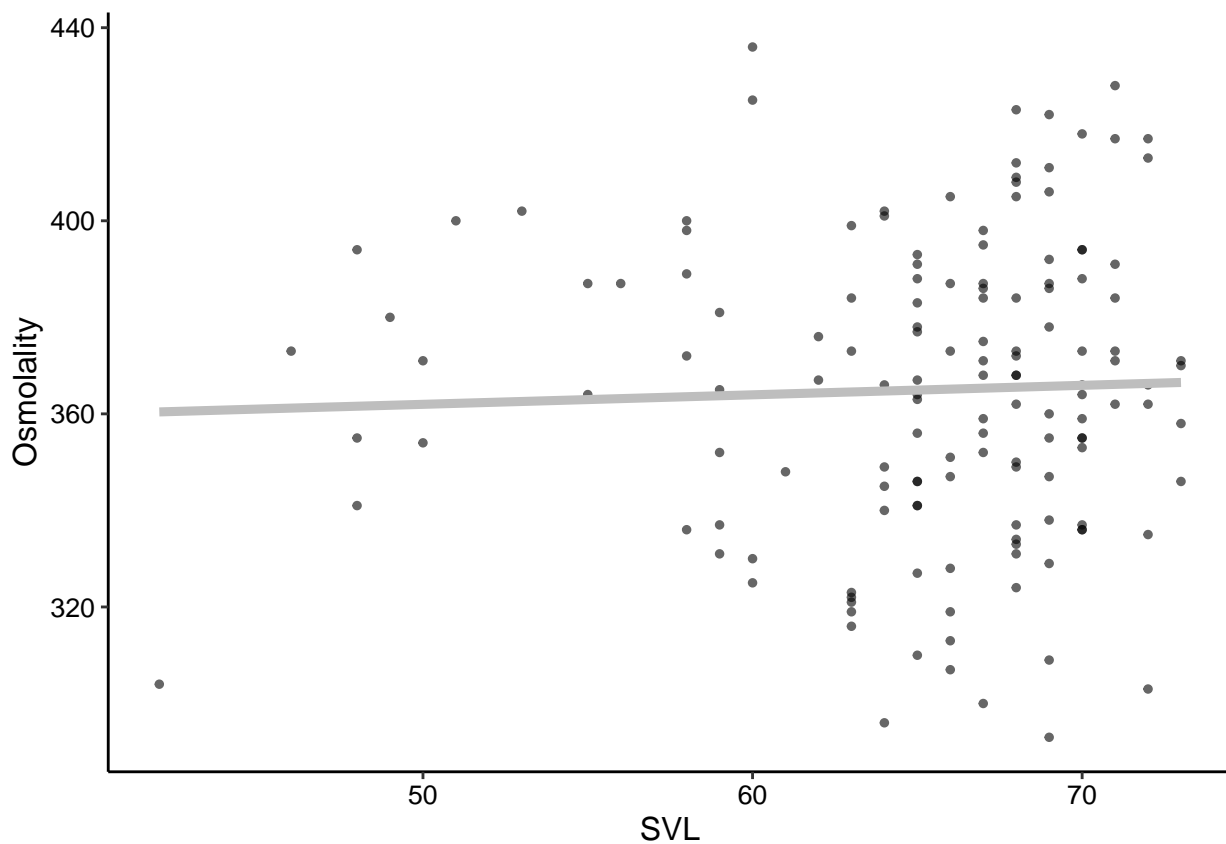


**Hct ~ SMI**

```
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).
```
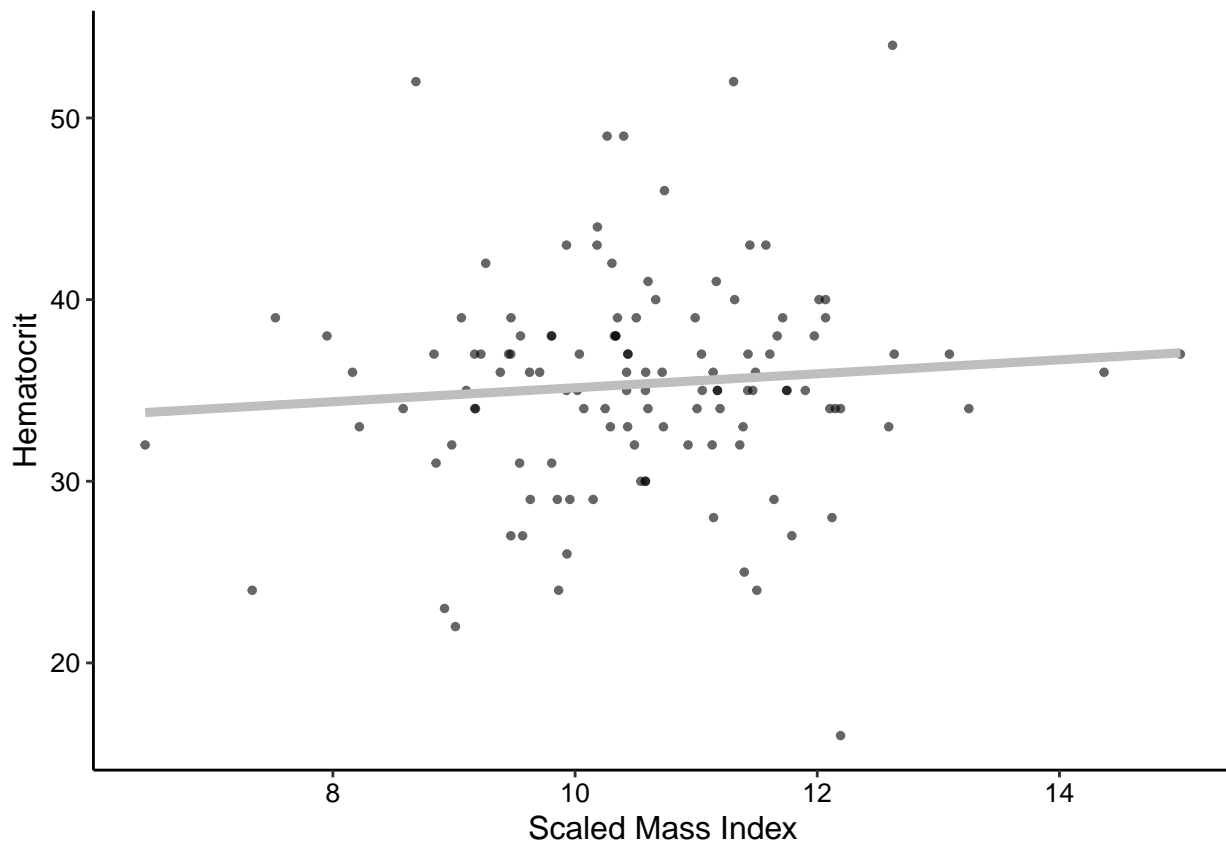


**Osml ~ SMI**

```
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).
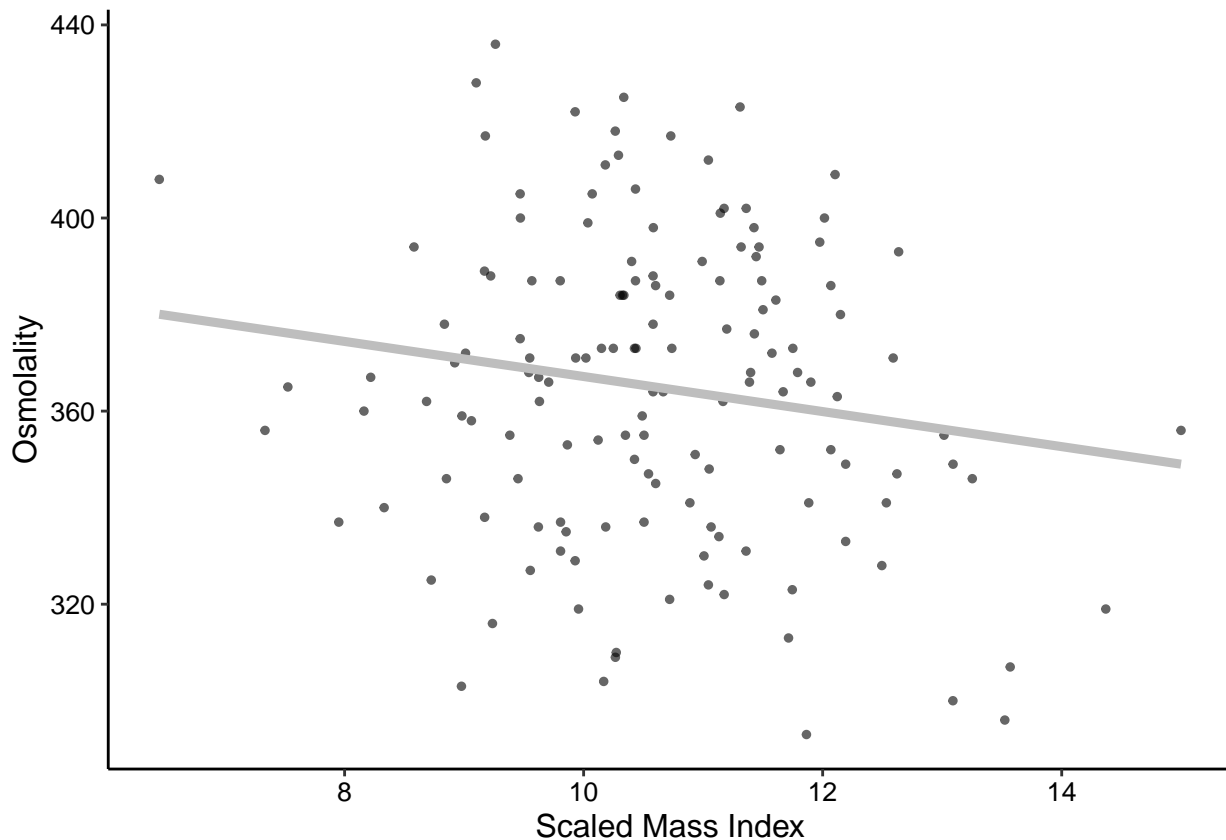
**Hct ~ Sex**

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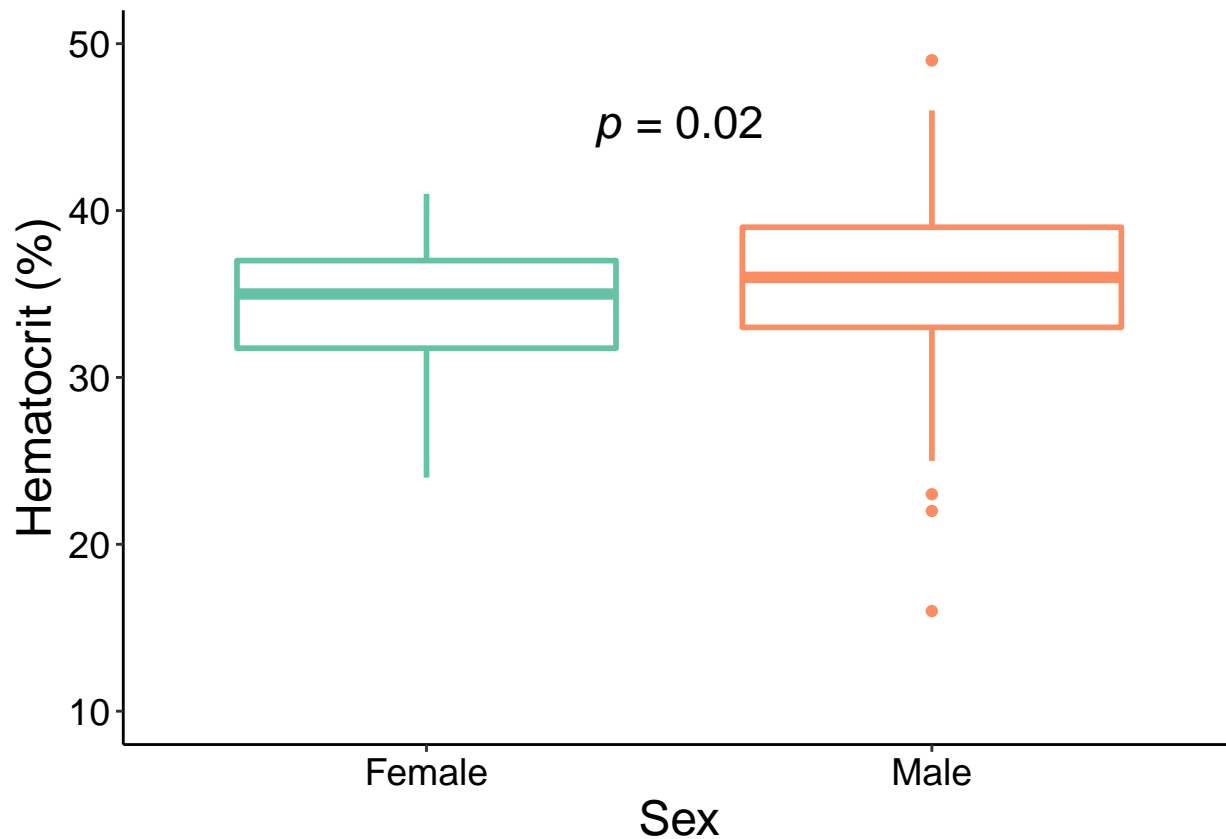
```
# export figure
#ggsave(filename = "hct_sex_fig.jpeg",
 #     plot = hct_sex_fig,
  #    path = "./final_figures",
   #   device = "jpeg",
    #  dpi = 1200,
     #  width = 6, height = 4)


# 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
```

```r
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**

```r
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).
```
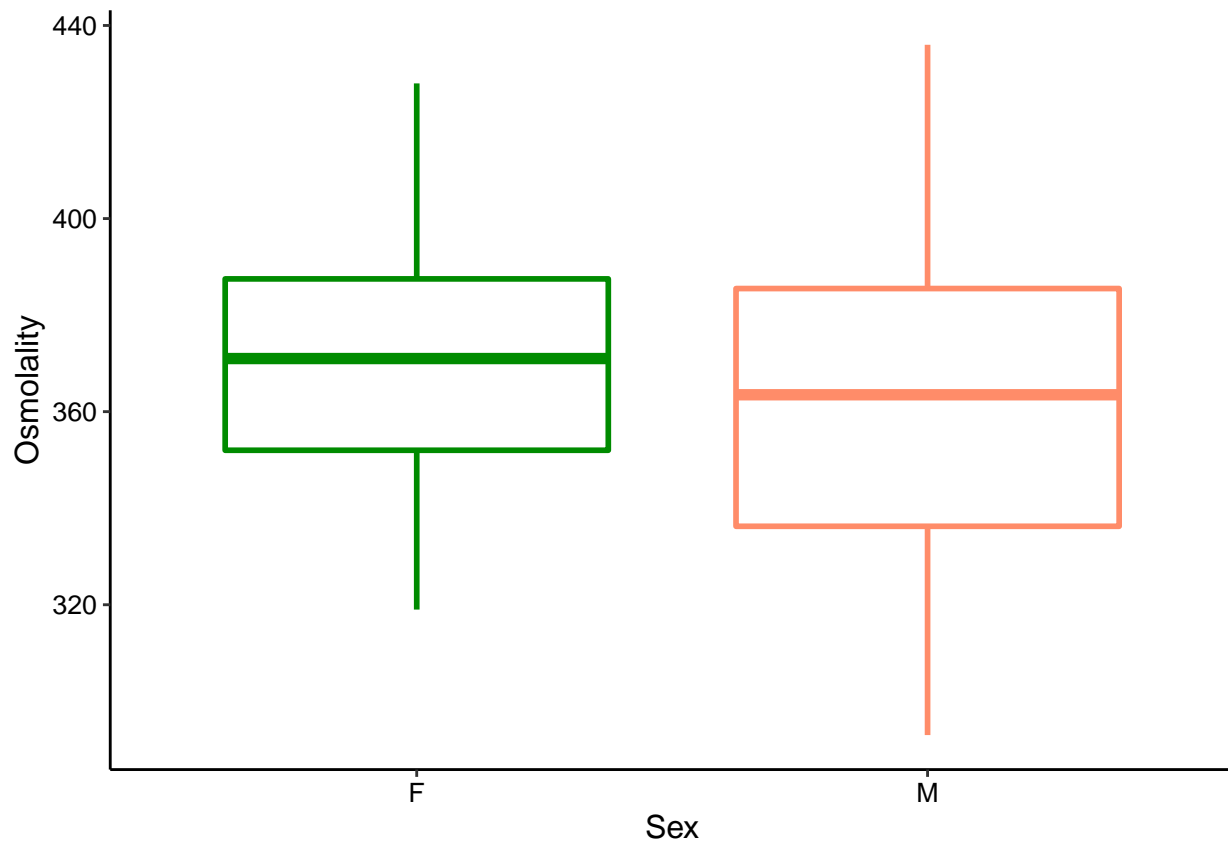
## Hct ~ Gravidity

```r
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).
```
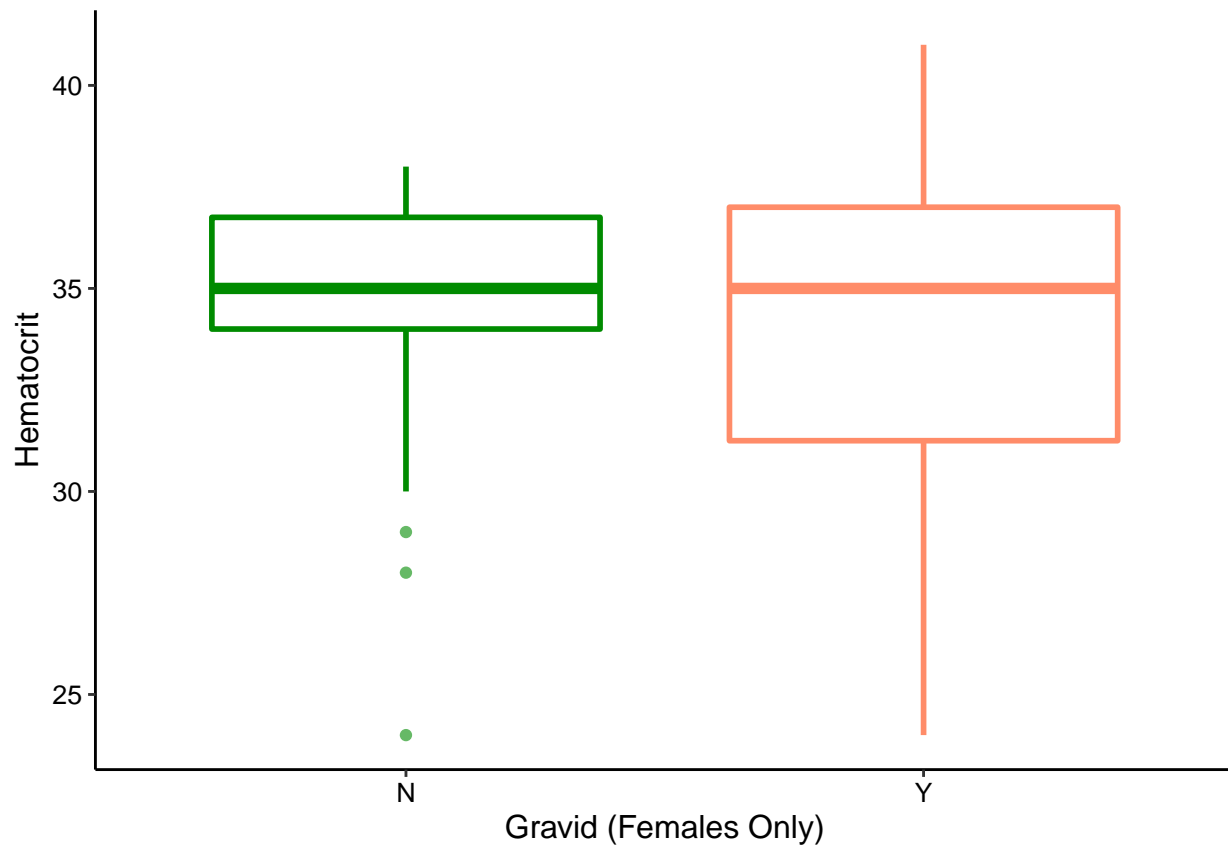
**Osml ~ Gravidity**

```r
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).
```
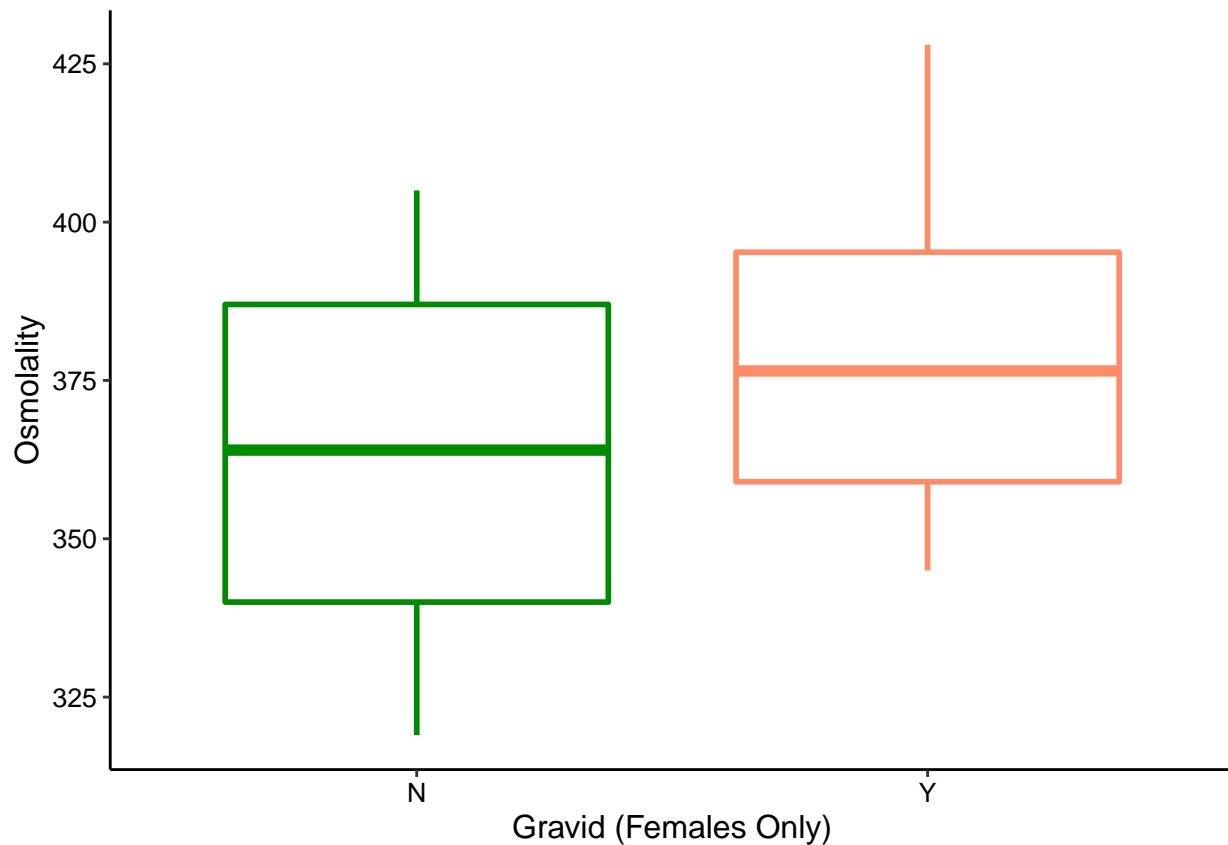
### Hct ~ Sample Eye

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.

```r
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).
```
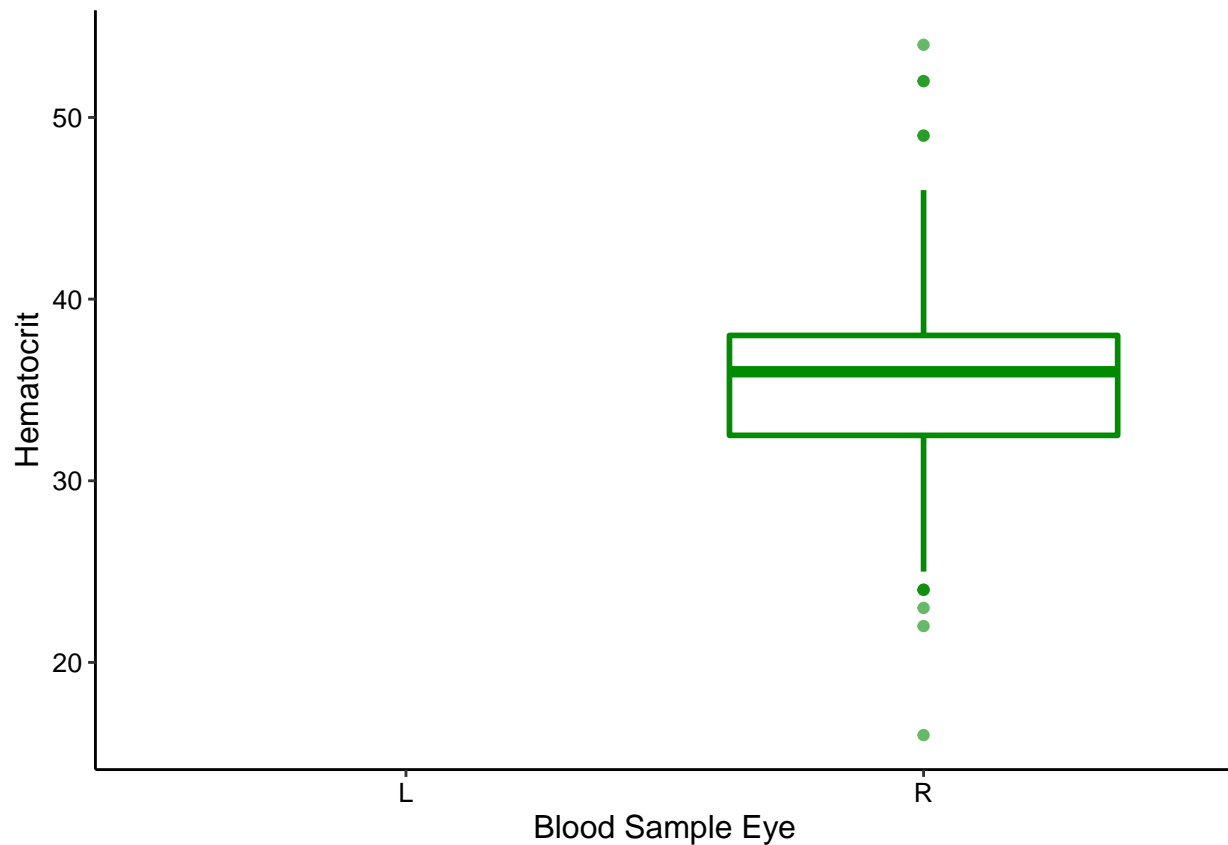
## Osml ~ Sample Eye

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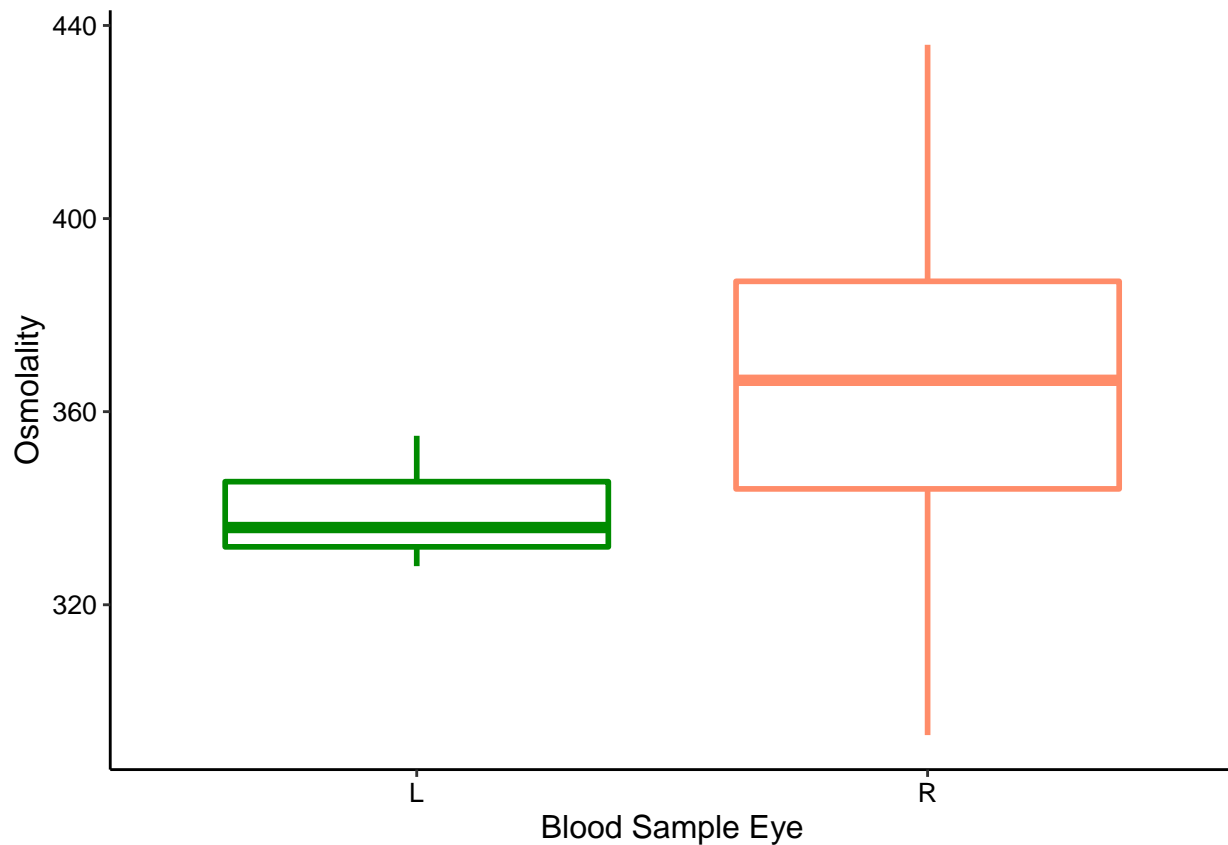
There IS a significant difference, but upon further inspection, the number of blood draws taken from the right postorbital sinus vs left or both is so uneven, this would be unhelpful in the actual model.

**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).
```
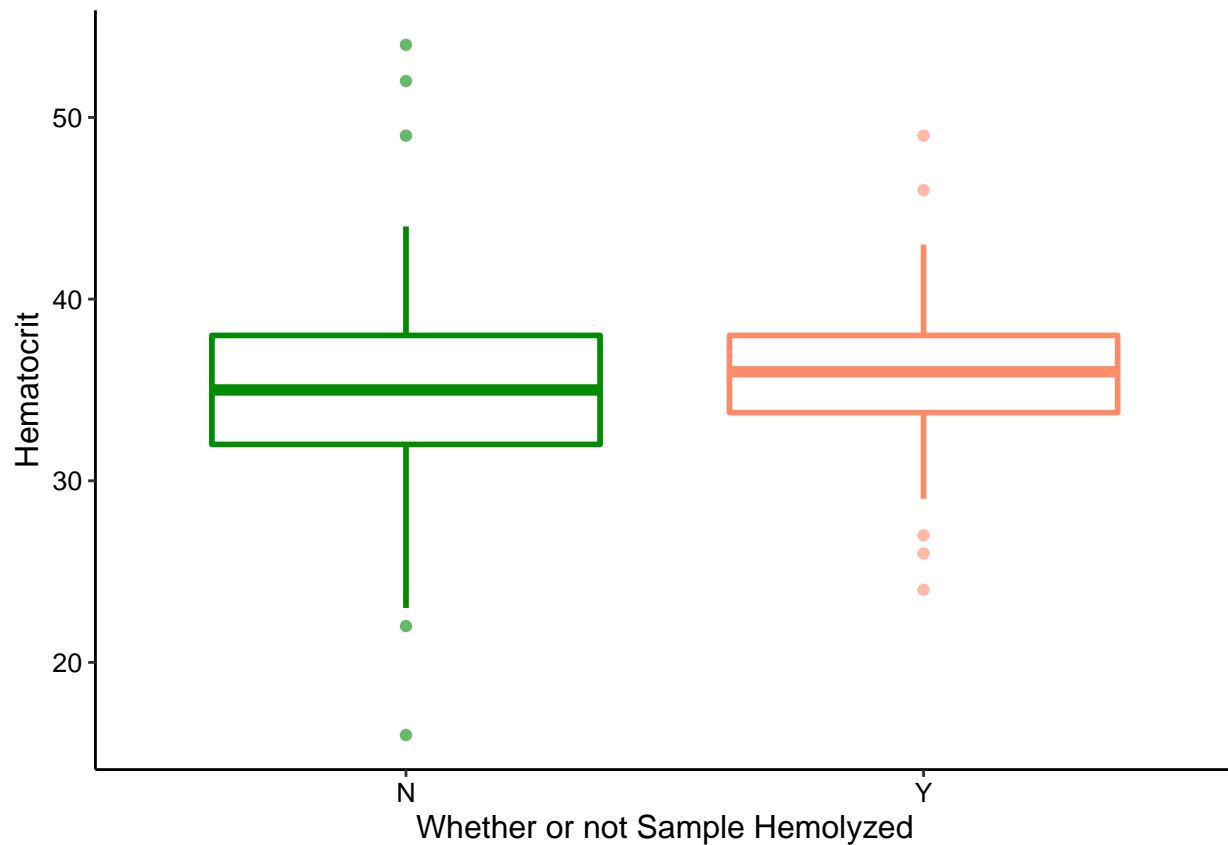
**Osml ~ Hemolyzed/Not**

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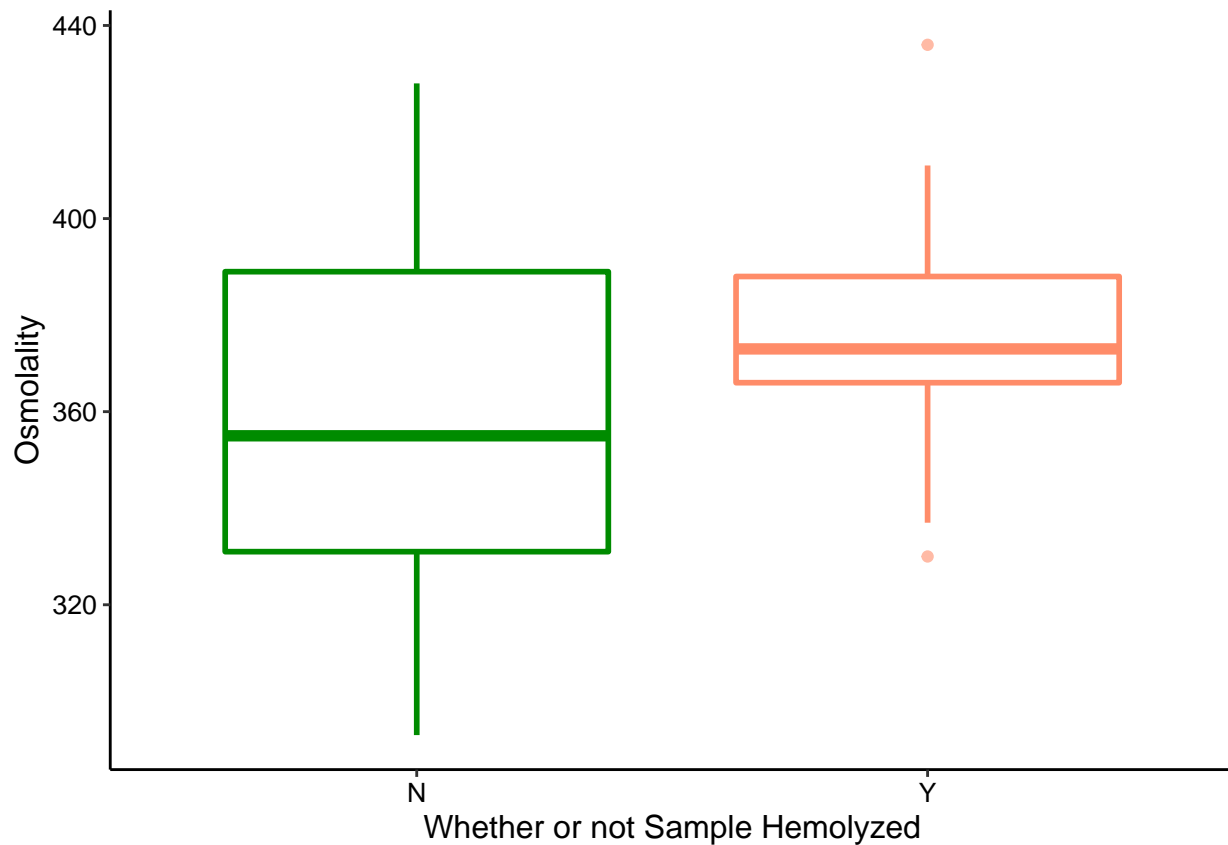
Osmolality in hemolyzed samples versus not are significantly different! This is an unfortunate trait of the dataset, and not something we are specifically interested in testing, so we will include it as a random factor in the LMM.

**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).
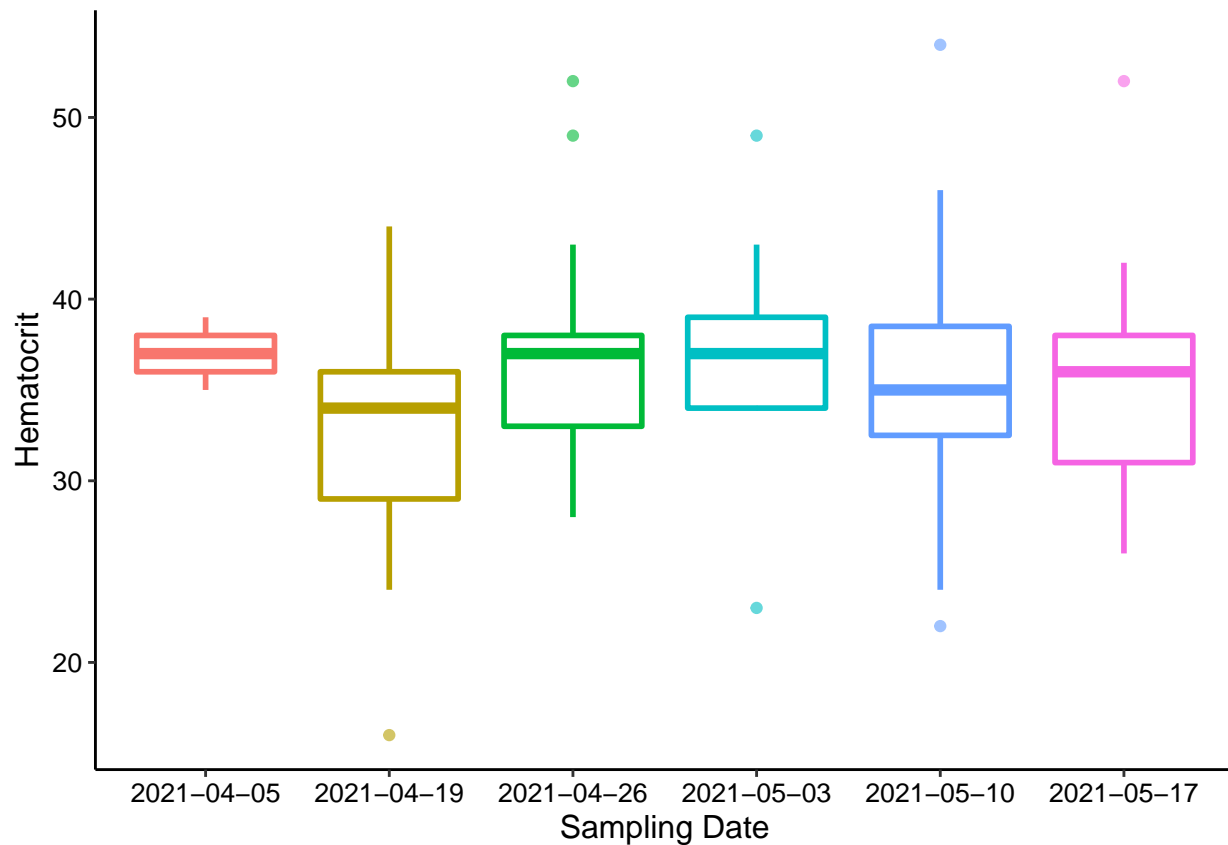
**Osml ~ Week**

```
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).
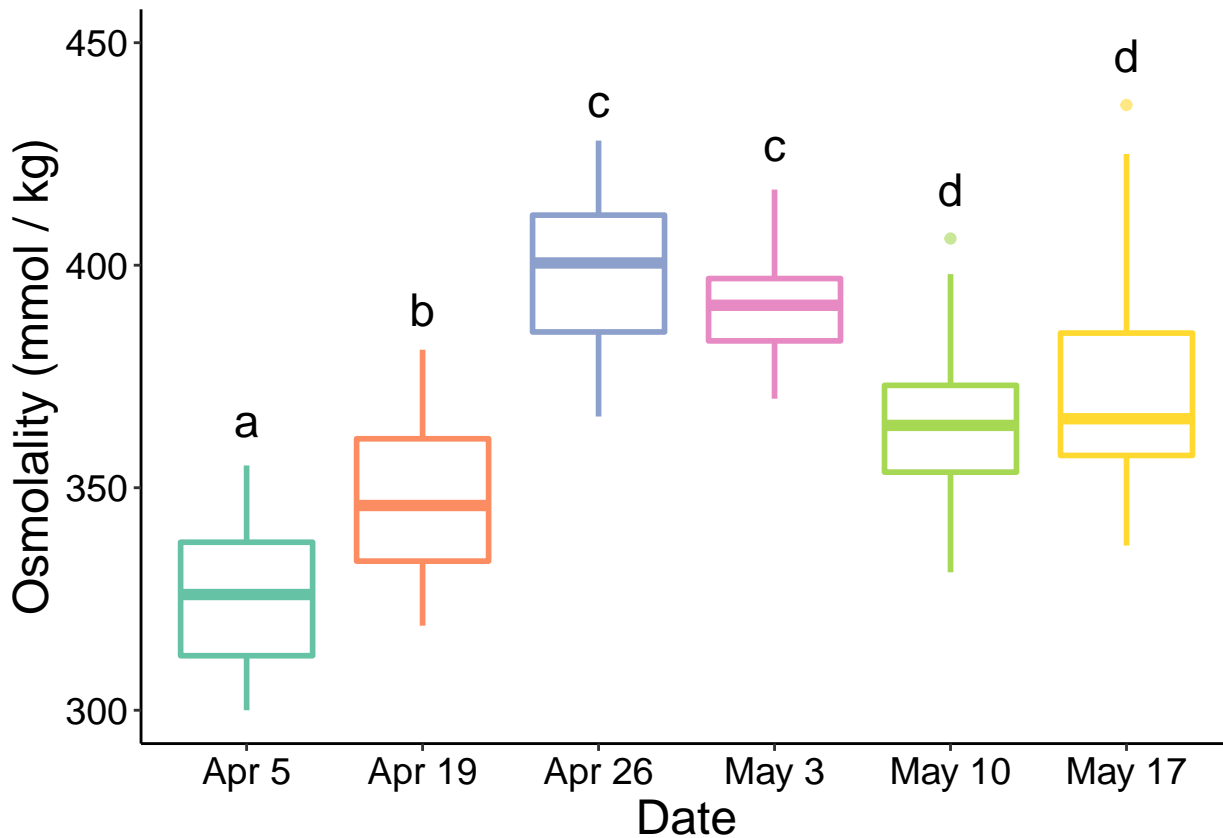


```
# export figure
#ggsave(filename = "osml_date_fig.tiff",
 #      plot = osml_date_fig,
  #     path = "./final_figures",
   #    device = "tiff",
    #   dpi = 1200,
     #  width = 6, height = 4)

# 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
```

**Osml ~ 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).

$R^2 = 0.23$

$p < 0.0001$

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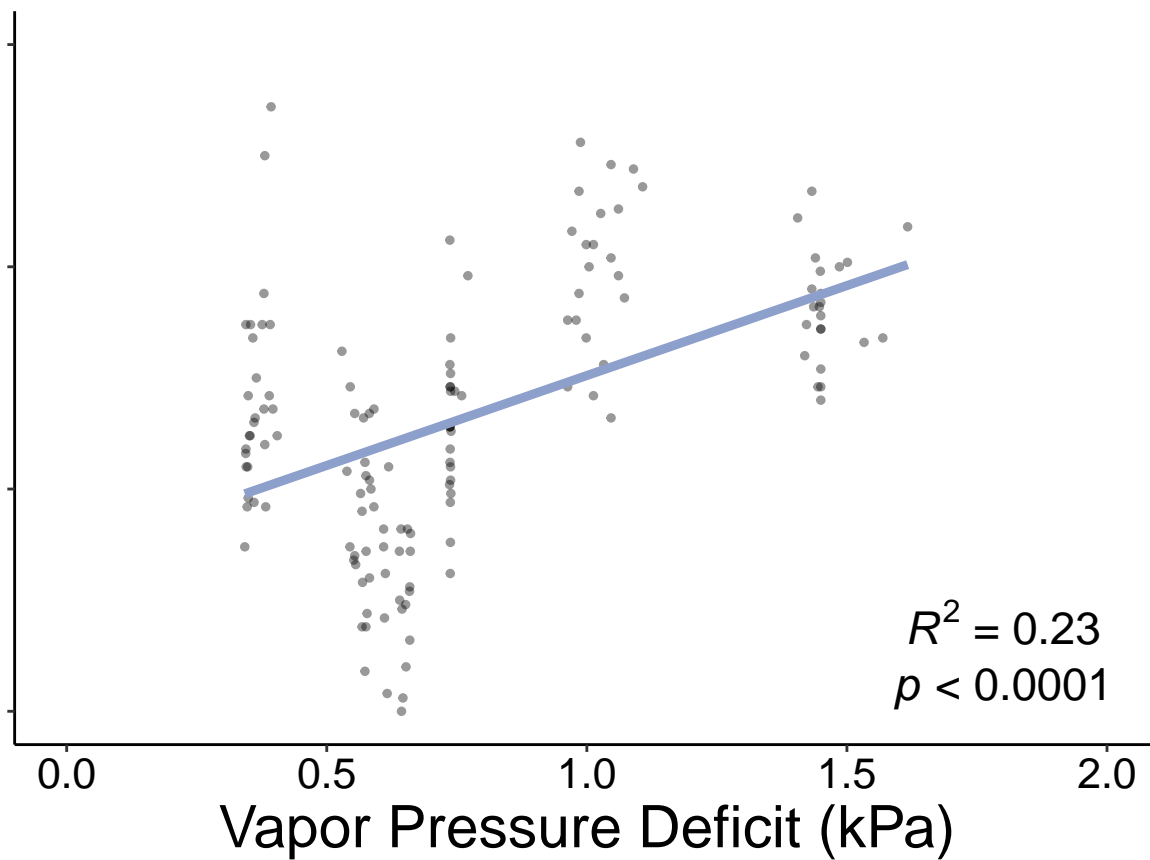
```
# export figure
#ggsave(filename = "osml_abhum_fig.jpeg",
 #      plot = osml_abhum_fig,
  #     path = "./final_figures",
   #    device = "jpeg",
    #   dpi = 1200,
     #  width = 6, height = 4)
```

**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).
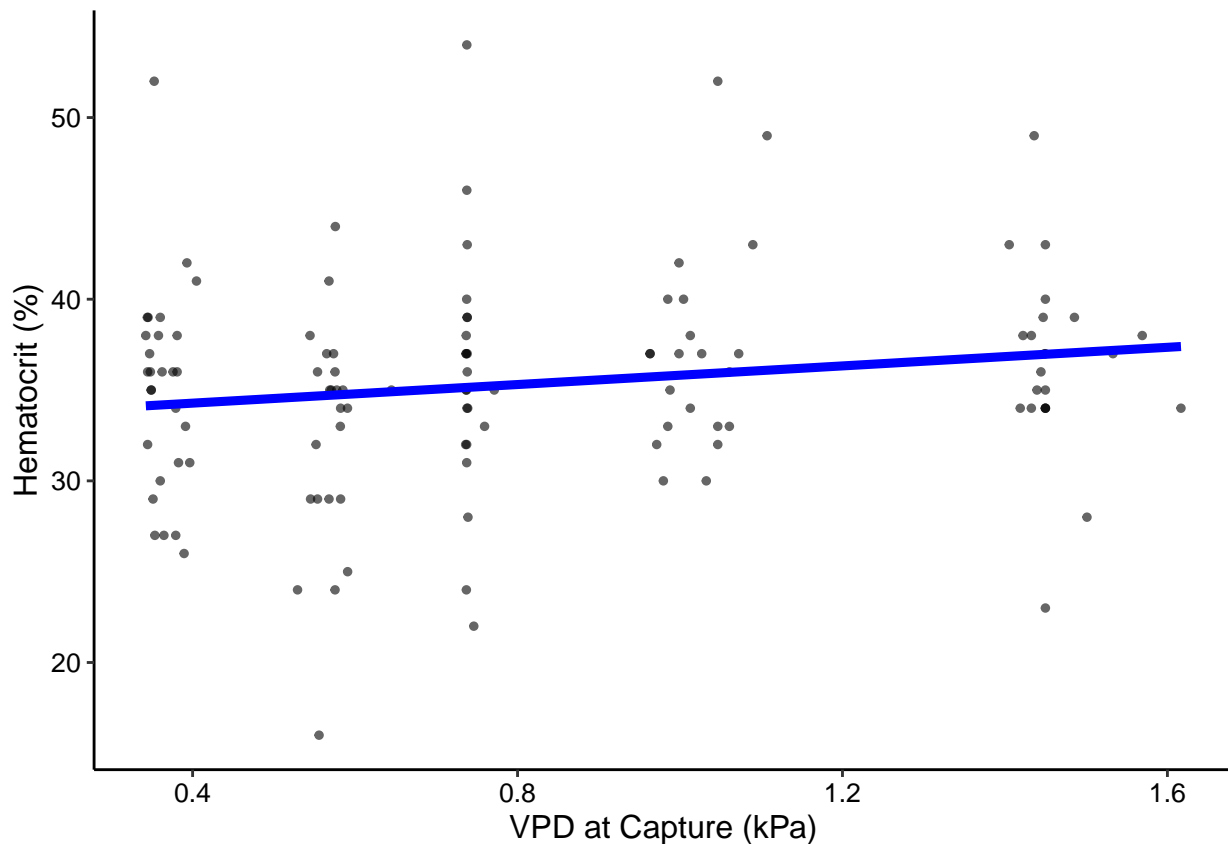


**Hct ~ Temperature**

```
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).
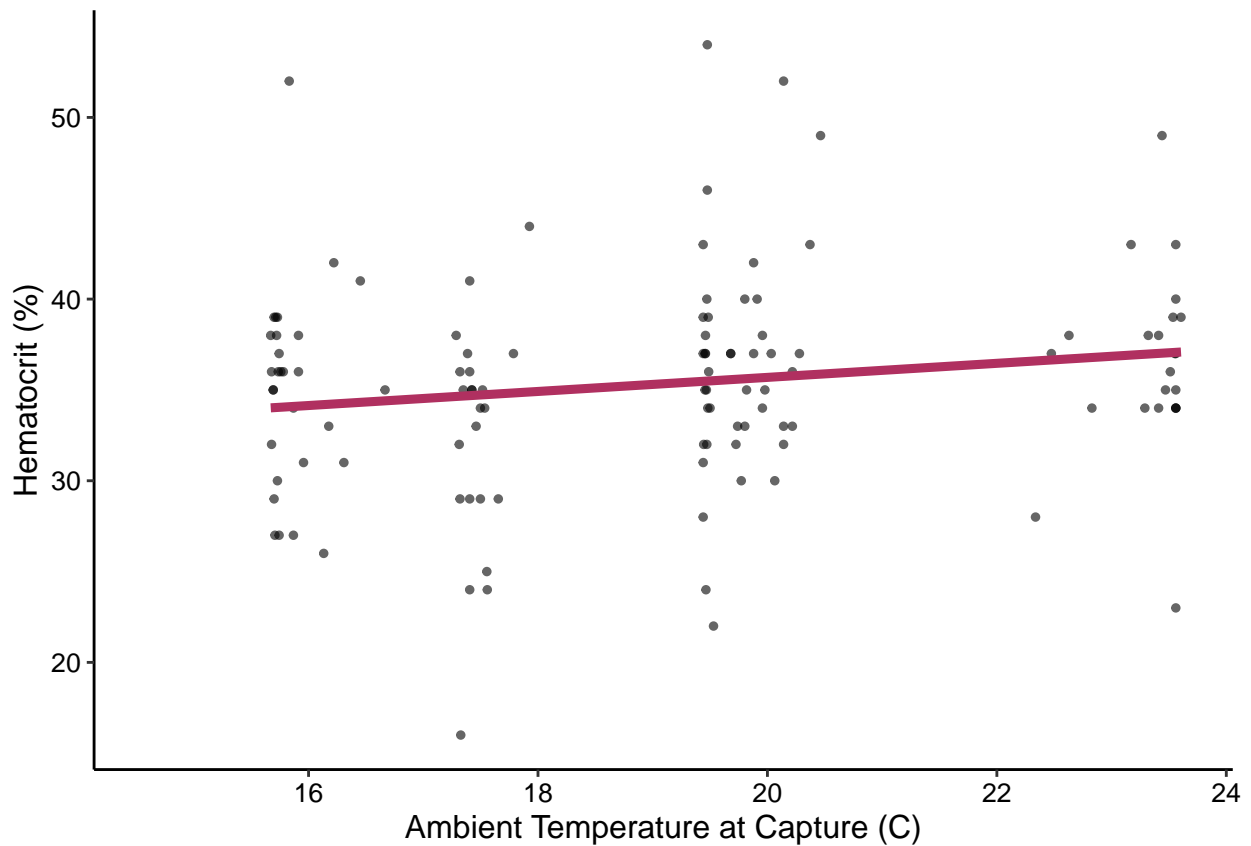


### Osml ~ Temperature

```
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).

$R^2 = 0.29$
$p < 0.0001$
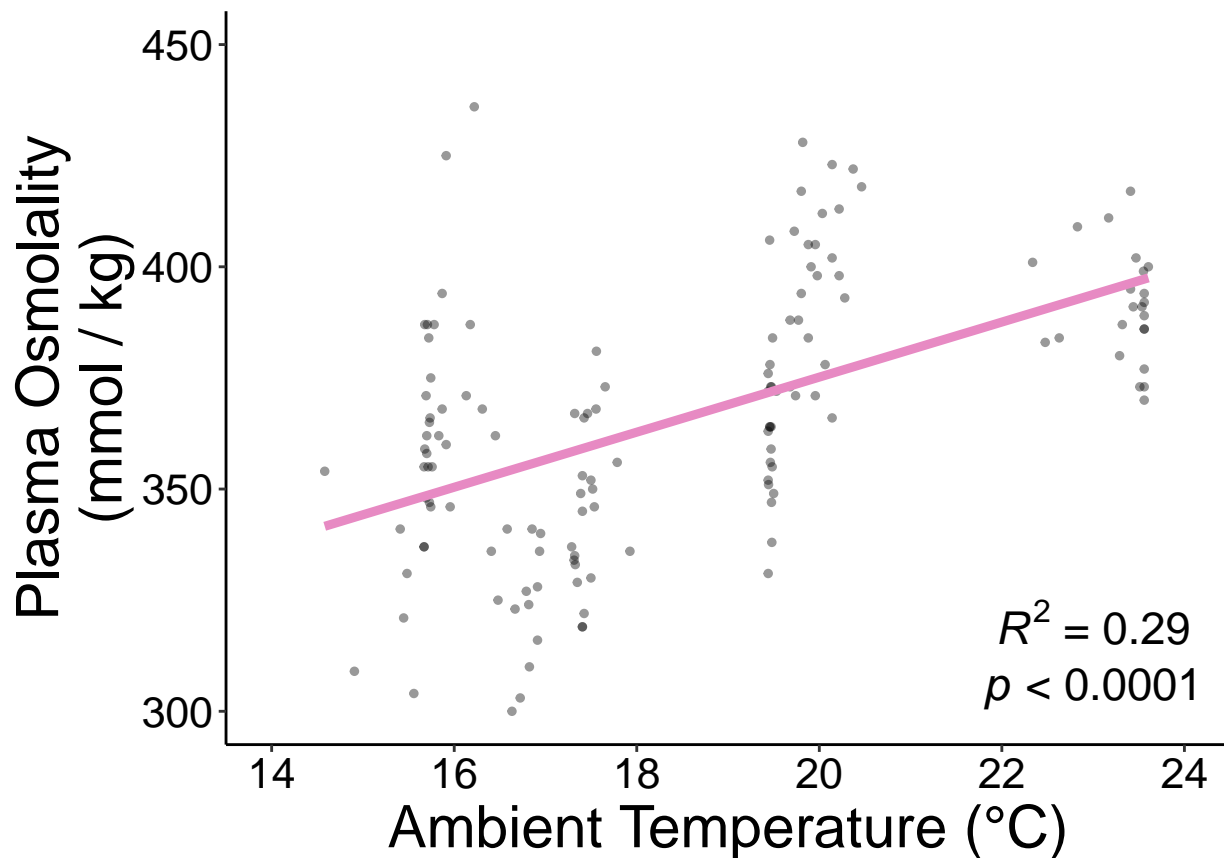
```r
# export figure
#ggsave(filename = "osml_temp_fig.jpeg",
 #      plot = osml_temp_fig,
  #     path = "./final_figures",
   #    device = "jpeg",
    #   dpi = 1200,
     #  width = 6, height = 4)
```

**Hct ~ Individual**

```r
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).
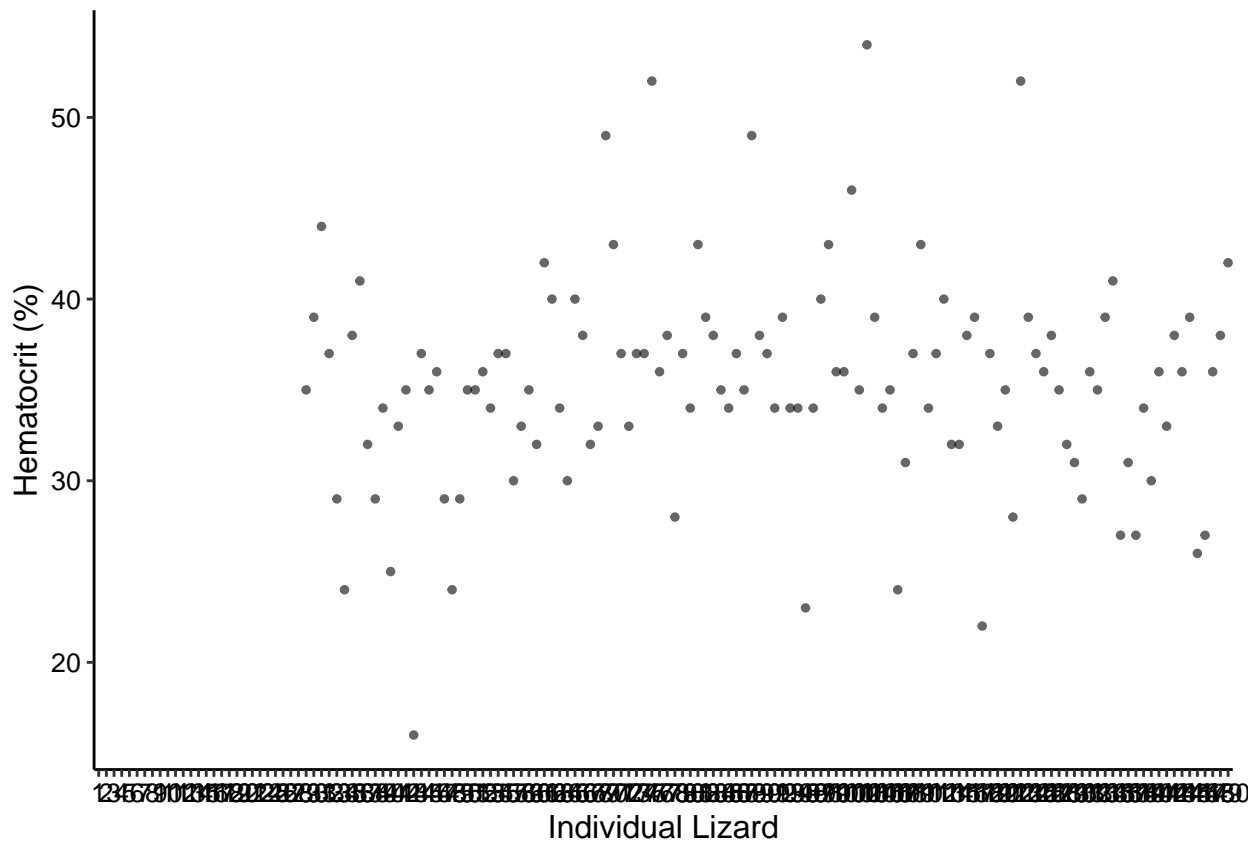


**Osml ~ Individual**

```
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).
```
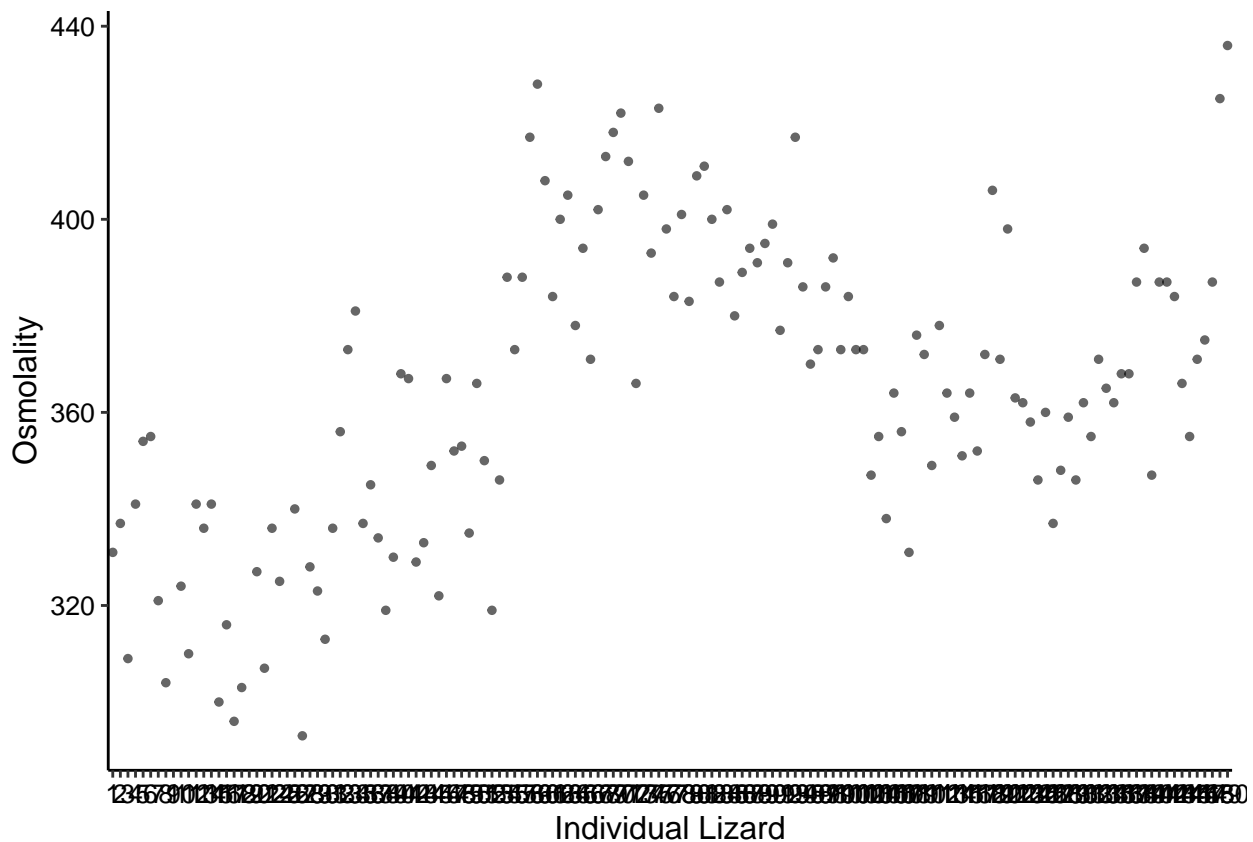


## Osmolality Multi-Figure

```
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
```
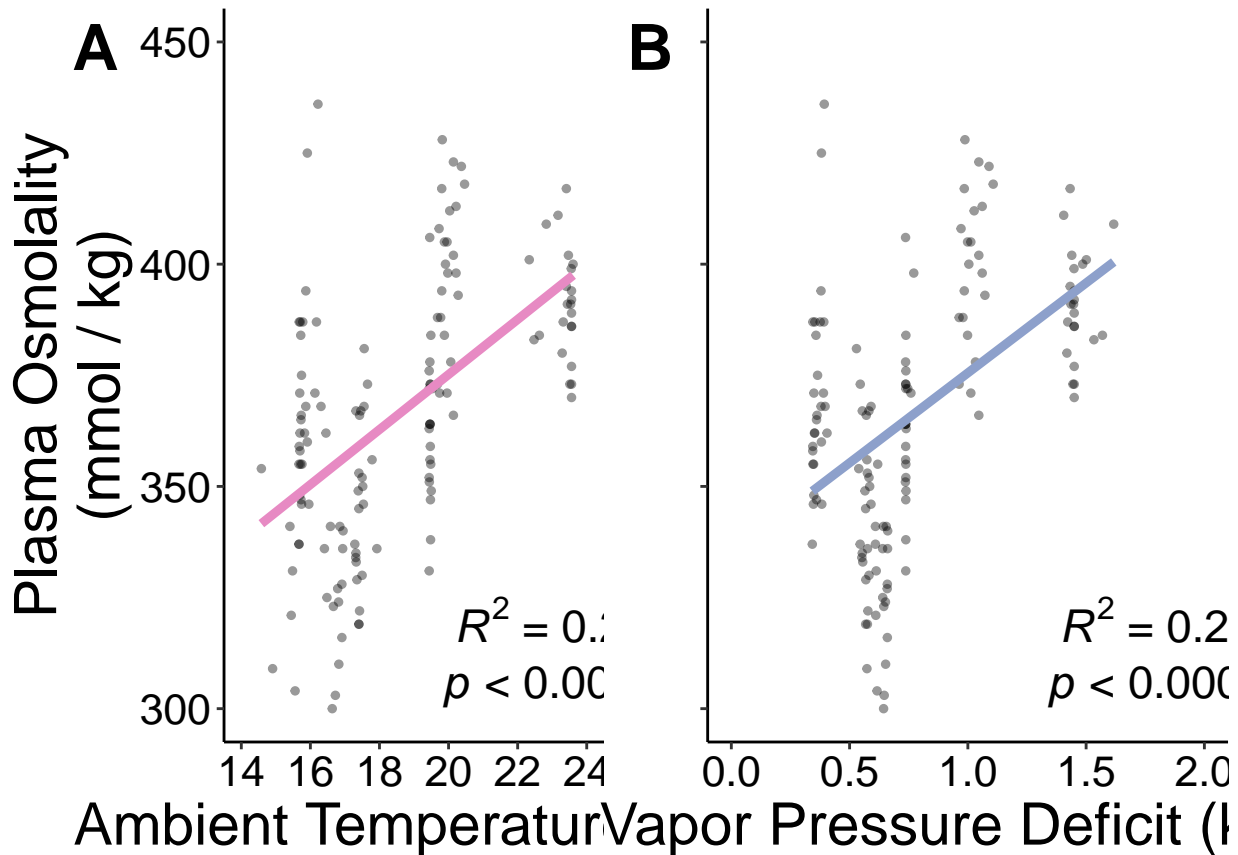


```
# export figure
ggsave(filename = "osml_multi_fig.jpeg",
       plot = osml_multi_fig,
       path = "./final_figures",
       device = "jpeg",
       dpi = 1200,
       width = 12, height = 4)
```

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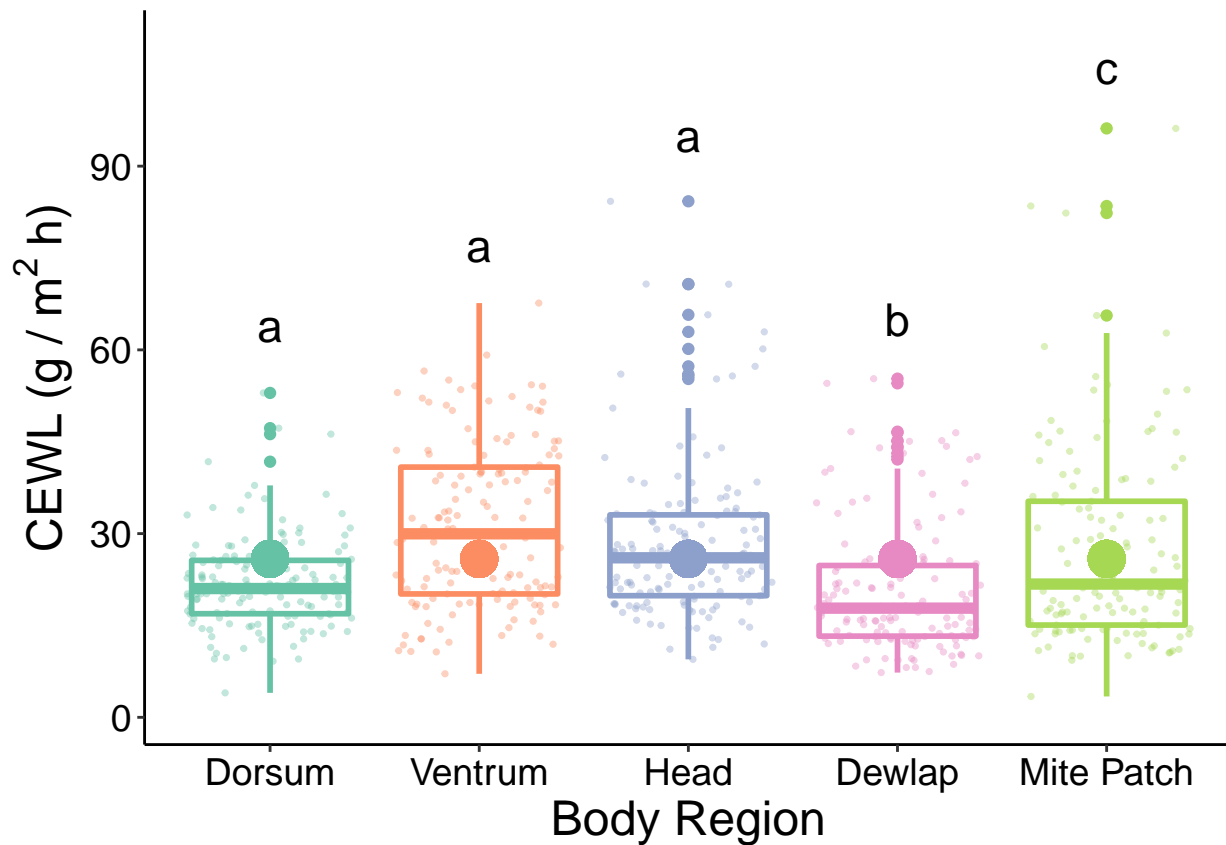
```r
# export figure
ggsave(filename = "CEWL_region_fig.jpeg",
       plot = CEWL_region_fig,
       path = "./final_figures",
       device = "jpeg",
       dpi = 1200,
       width = 6, height = 4)
```

**Body Region Ratios**

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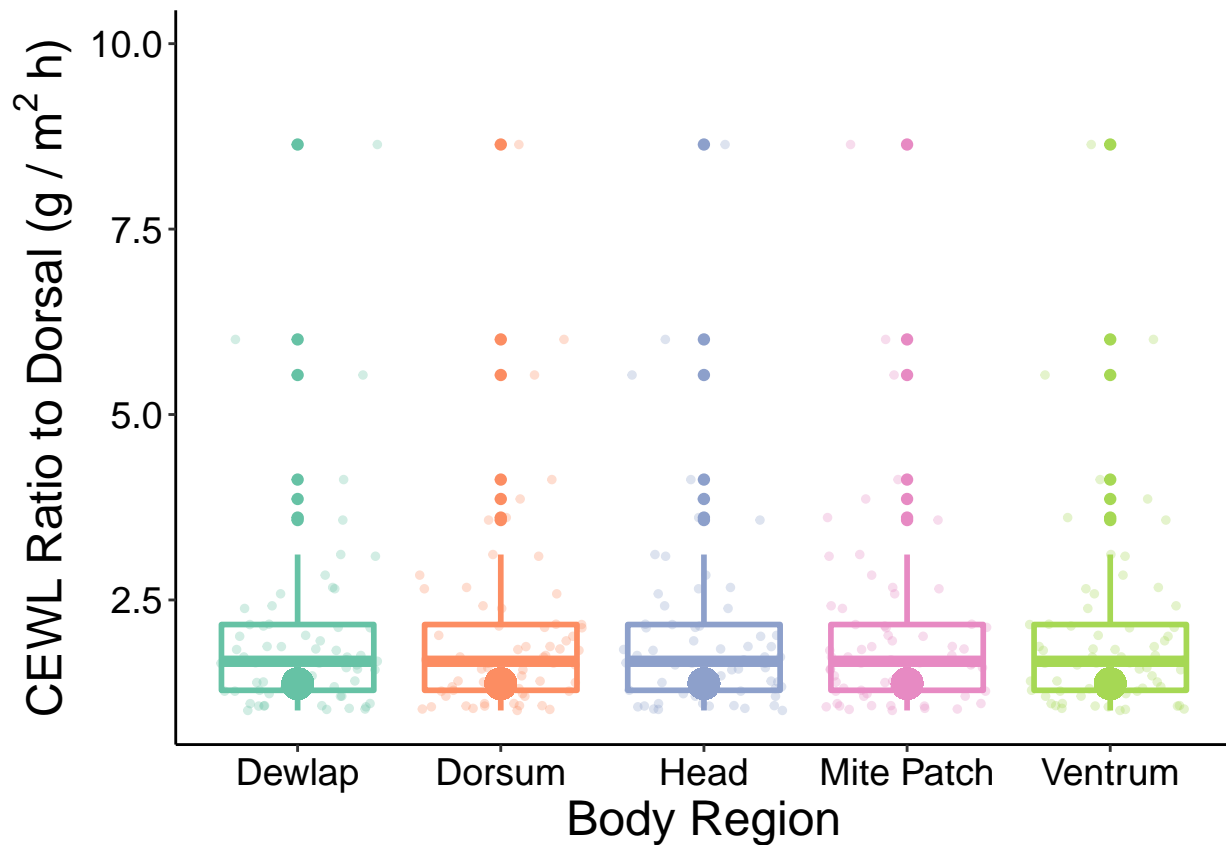
```
# export figure
ggsave(filename = "CEWL_region_fig3.jpeg",
       plot = CEWL_region_fig3,
       path = "./final_figures",
       device = "jpeg",
       dpi = 1200,
       width = 6, height = 4)
```

## 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).
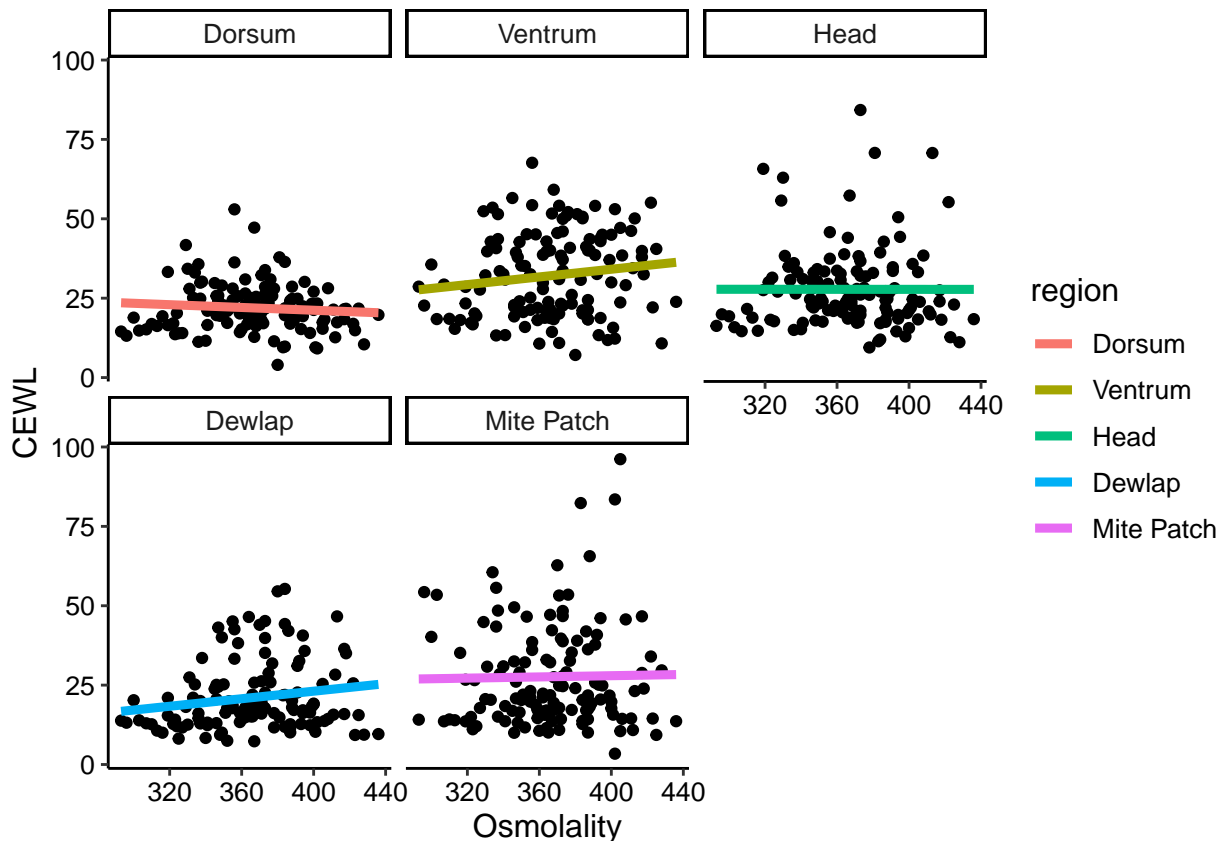
**CEWL ~ Hematocrit**

```
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).
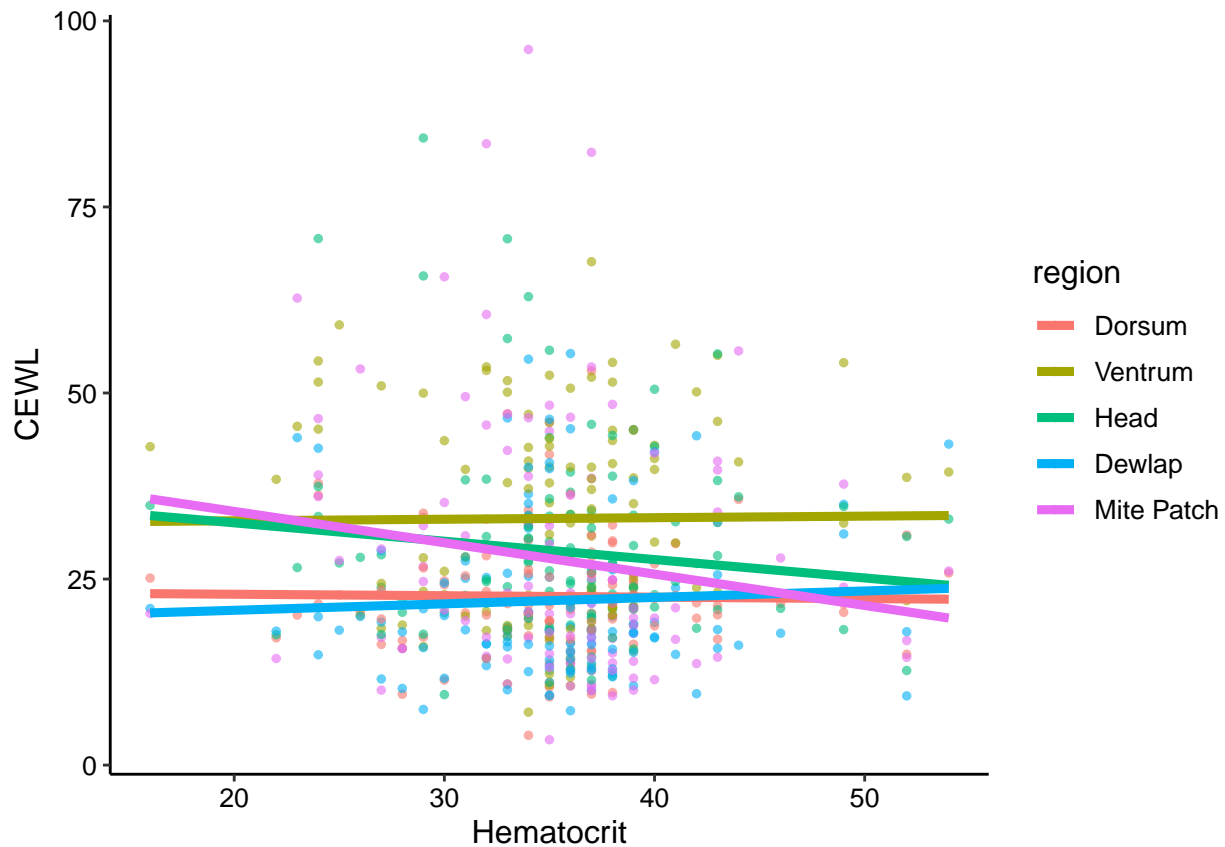
**CEWL ~ Cloacal Temperature**

```
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**

```r
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/'*m^2*'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).
```
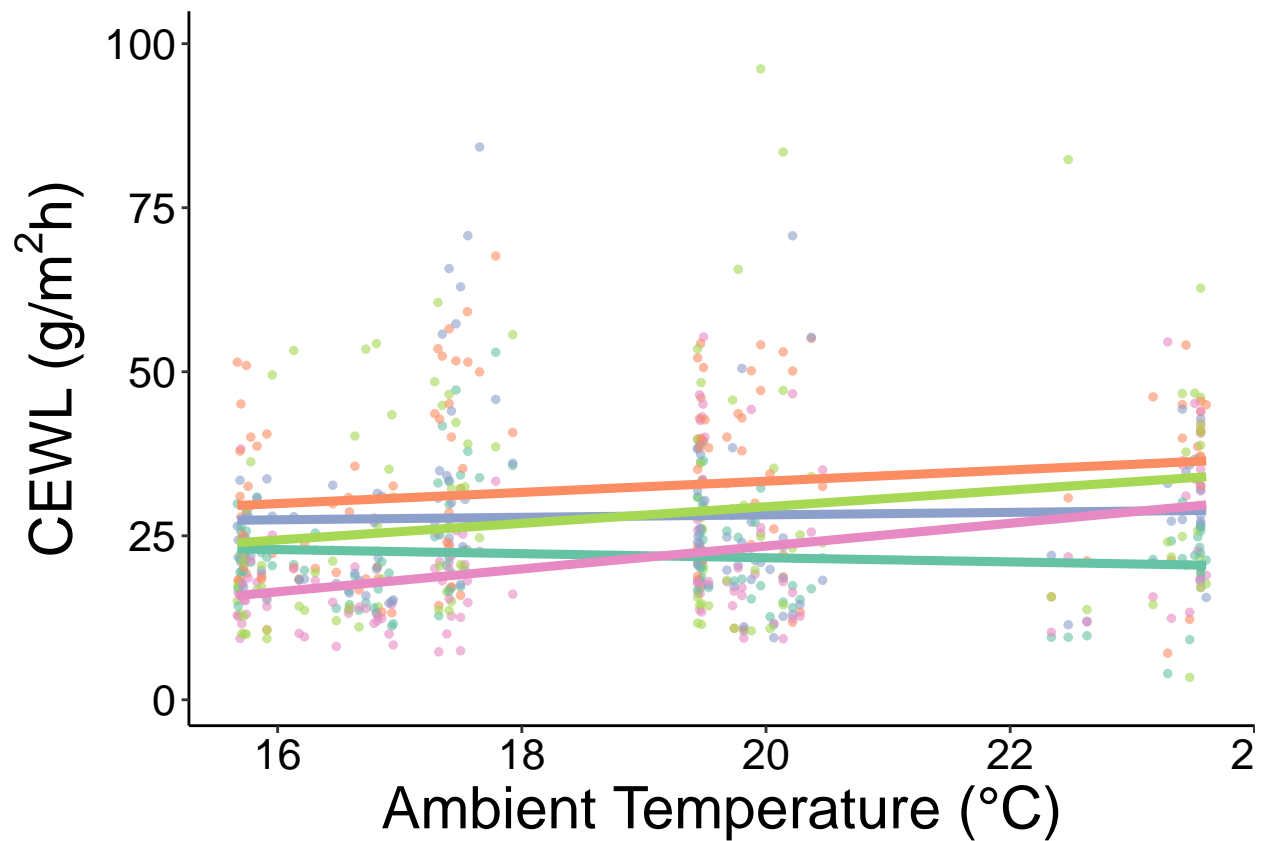
**CEWL ~ Capture VPD**

```r
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).
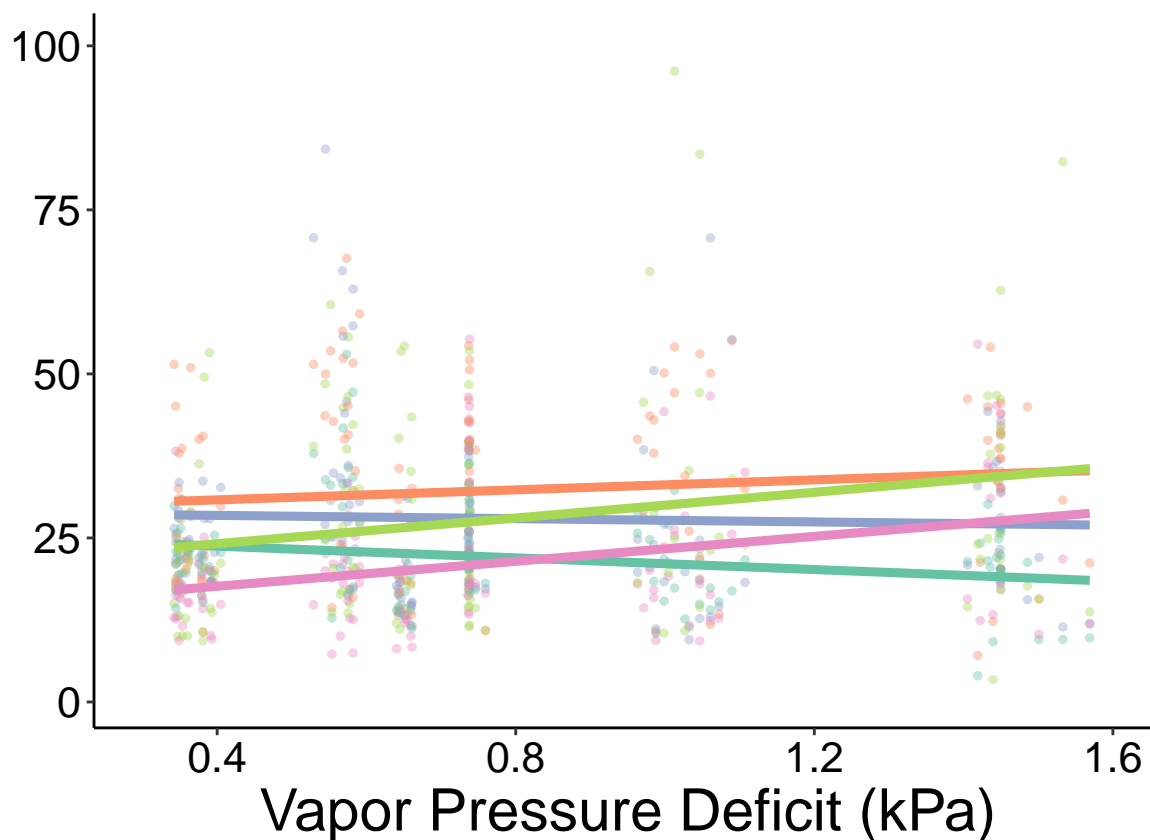


```
# export figure
#ggsave(filename = "CEWL_vpd_fig.tiff",
 #       plot = CEWL_vpd_fig,
  #      path = "./final_figures",
   #     device = "tiff",
    #    dpi = 1200,
```

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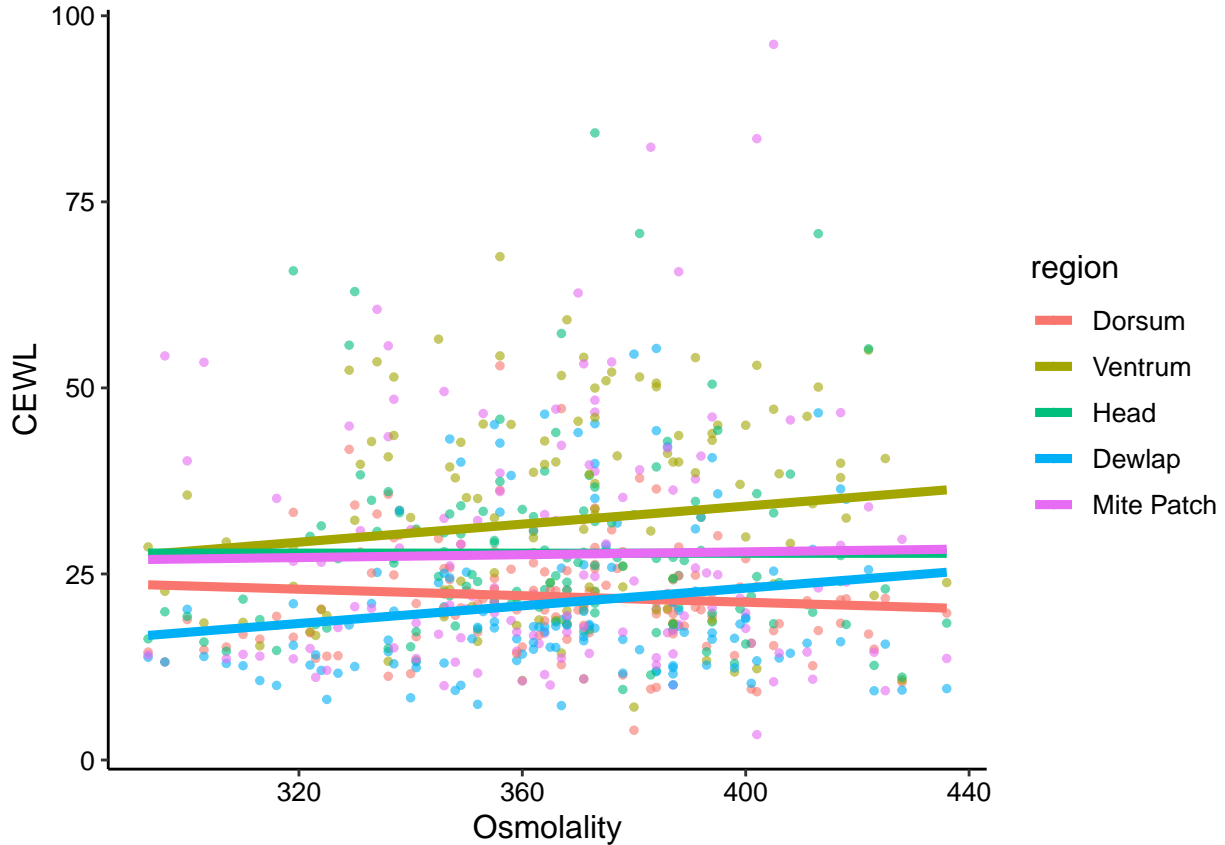
## Warning: Removed 59 rows containing non-finite values (stat_smooth).

## Warning: Removed 59 rows containing missing values (geom_point).
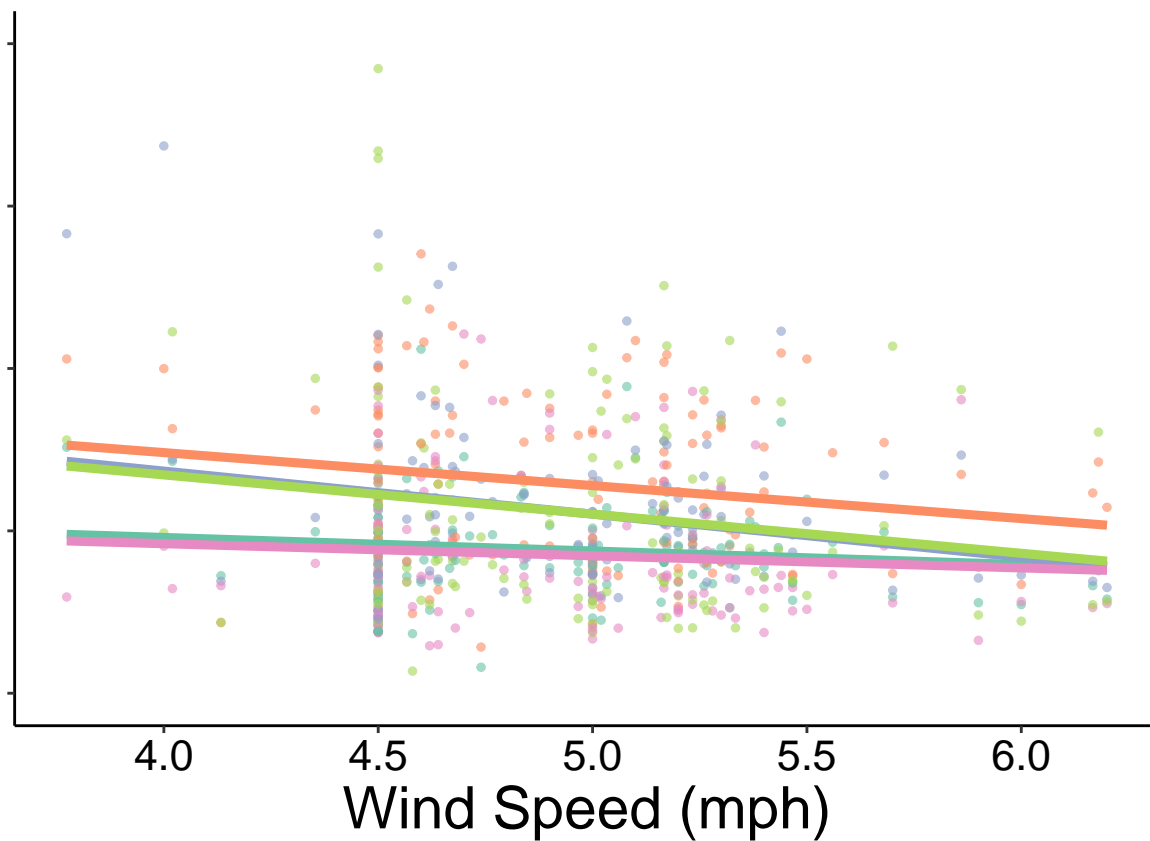
**CEWL ~ Solar Rad**

```r
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).
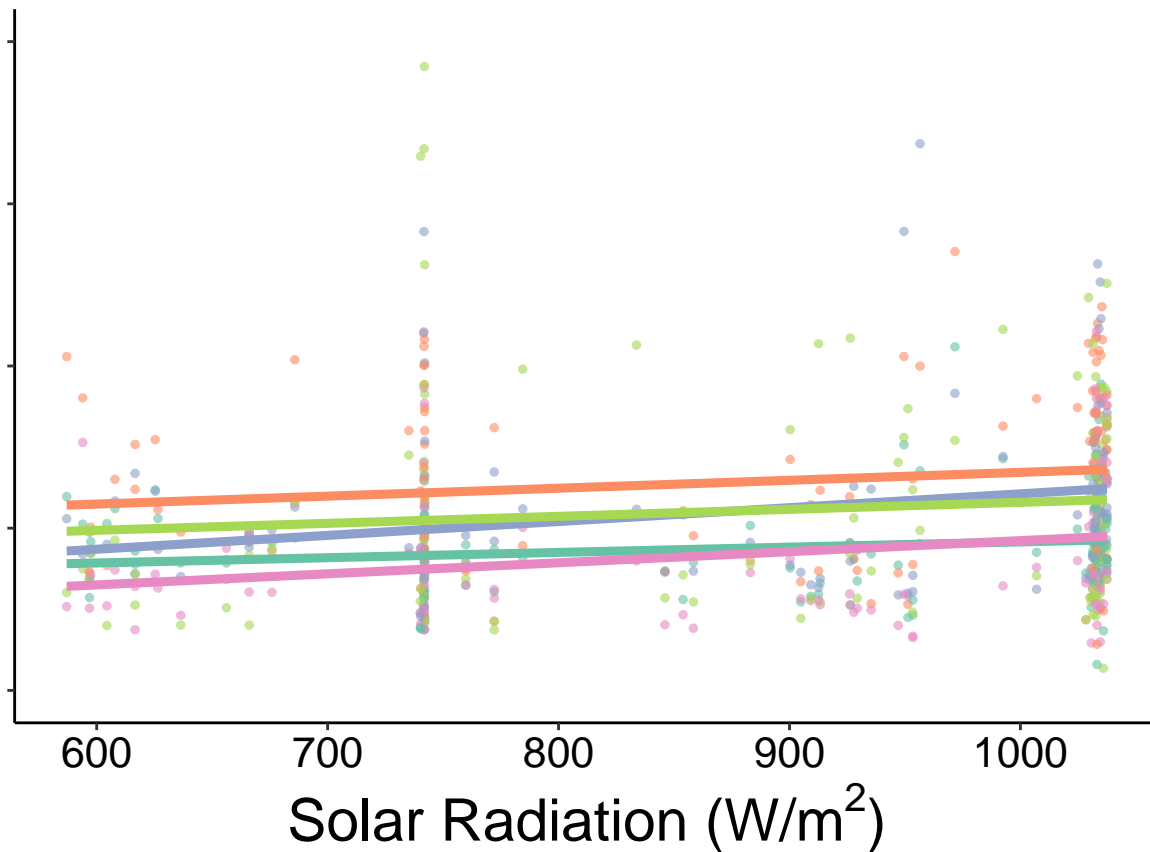


**CEWL ~ Measurement Temperature**

```
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"
)
```
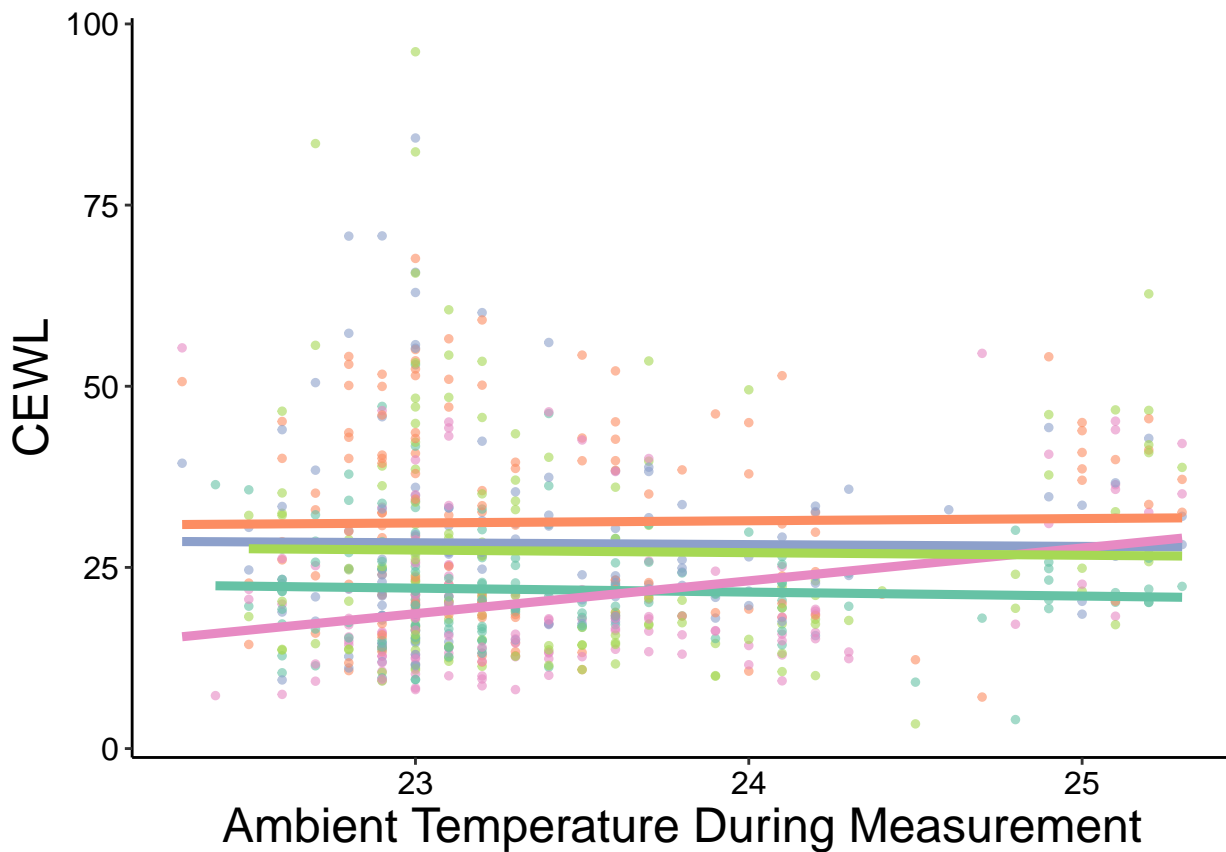
### CEWL ~ Measurement VPD

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.

```r
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)
```
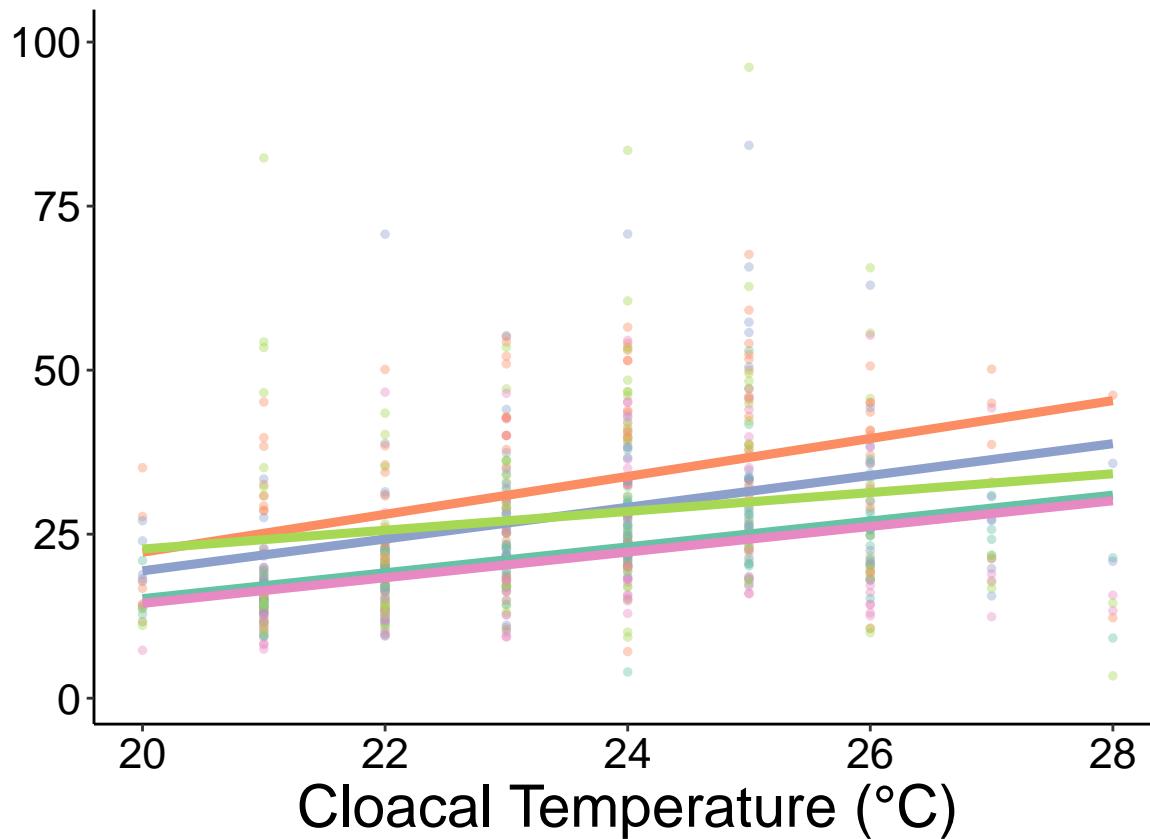
**CEWL ~ Individual**

```r
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)
```
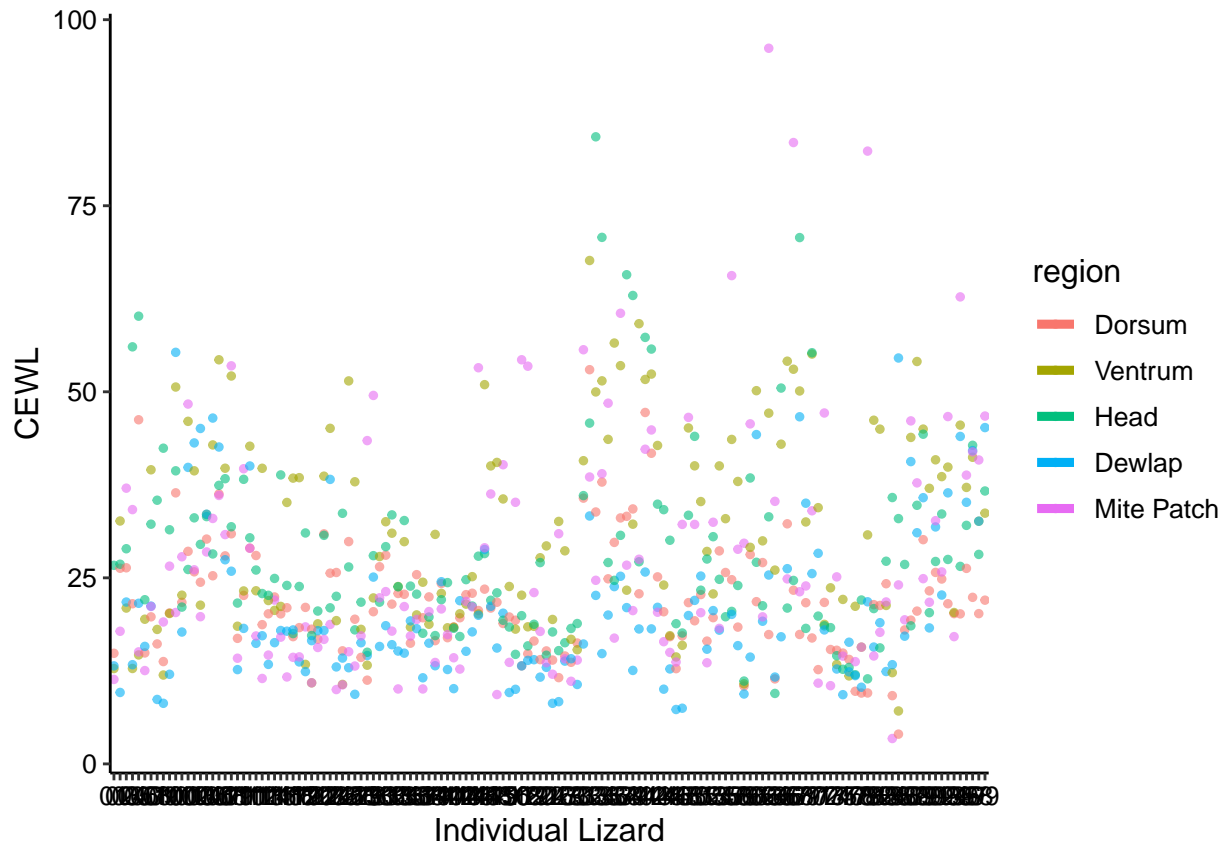


## CEWL ~ SVL

```
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).
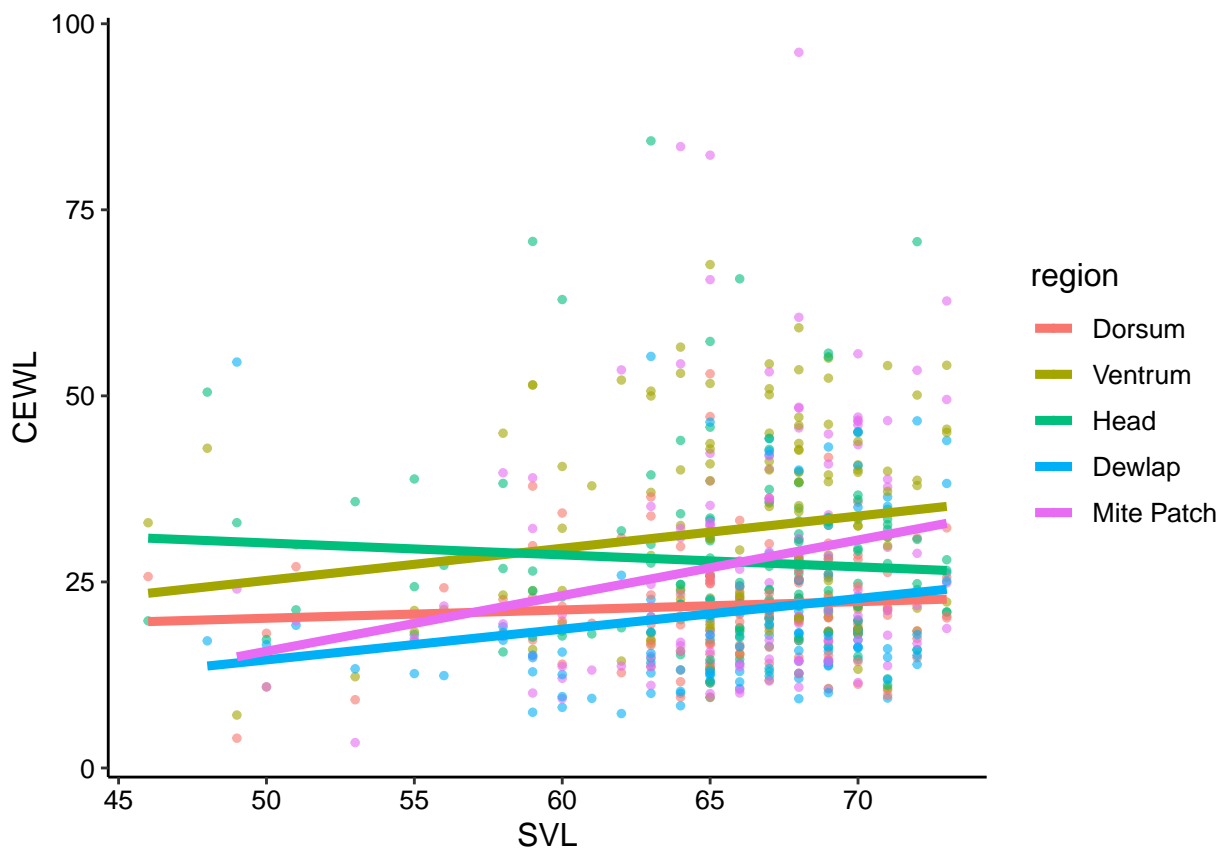


**CEWL ~ SMI**

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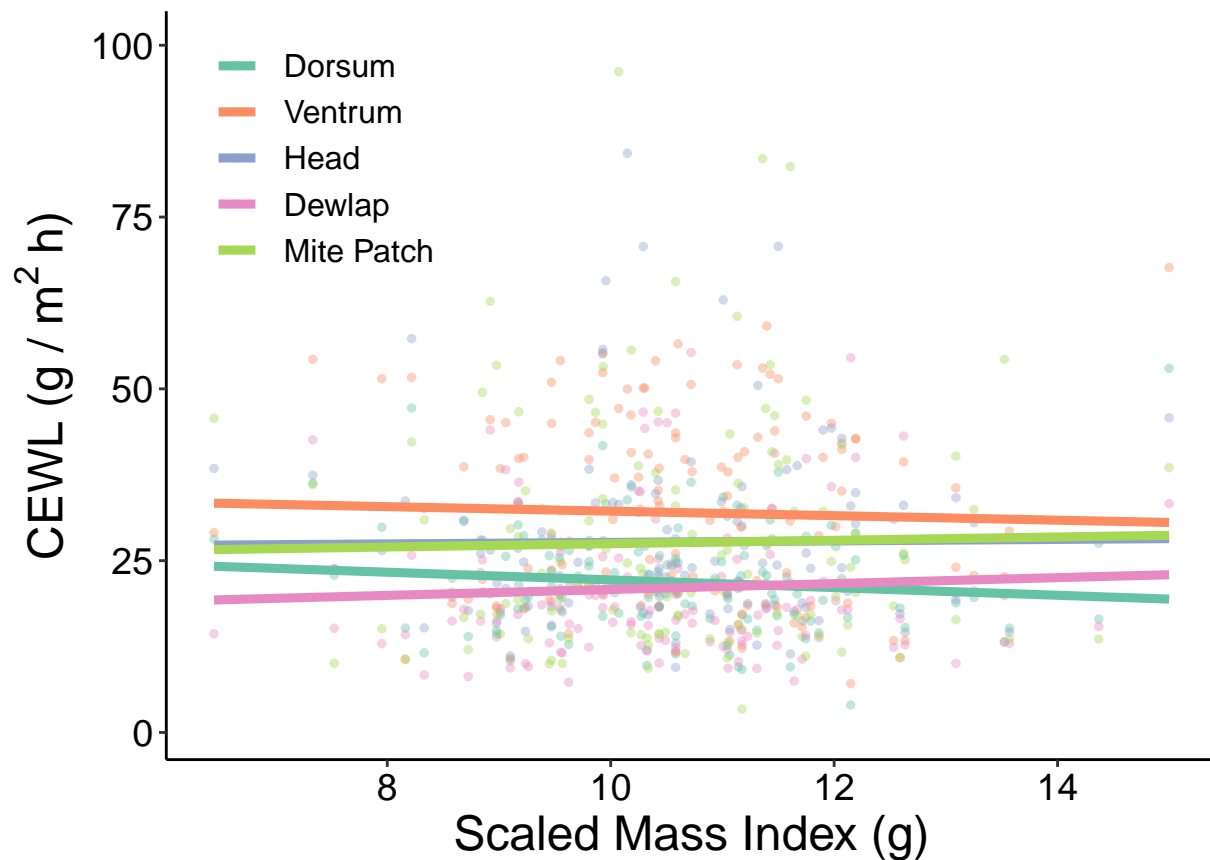
```
# export figure
#ggsave(filename = "CEWL_mass_fig.tiff",
 #       plot = CEWL_mass_fig,
  #      path = "./final_figures",
   #     device = "tiff",
    #    dpi = 1200,
     #  width = 6, height = 4)
```

**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).
```

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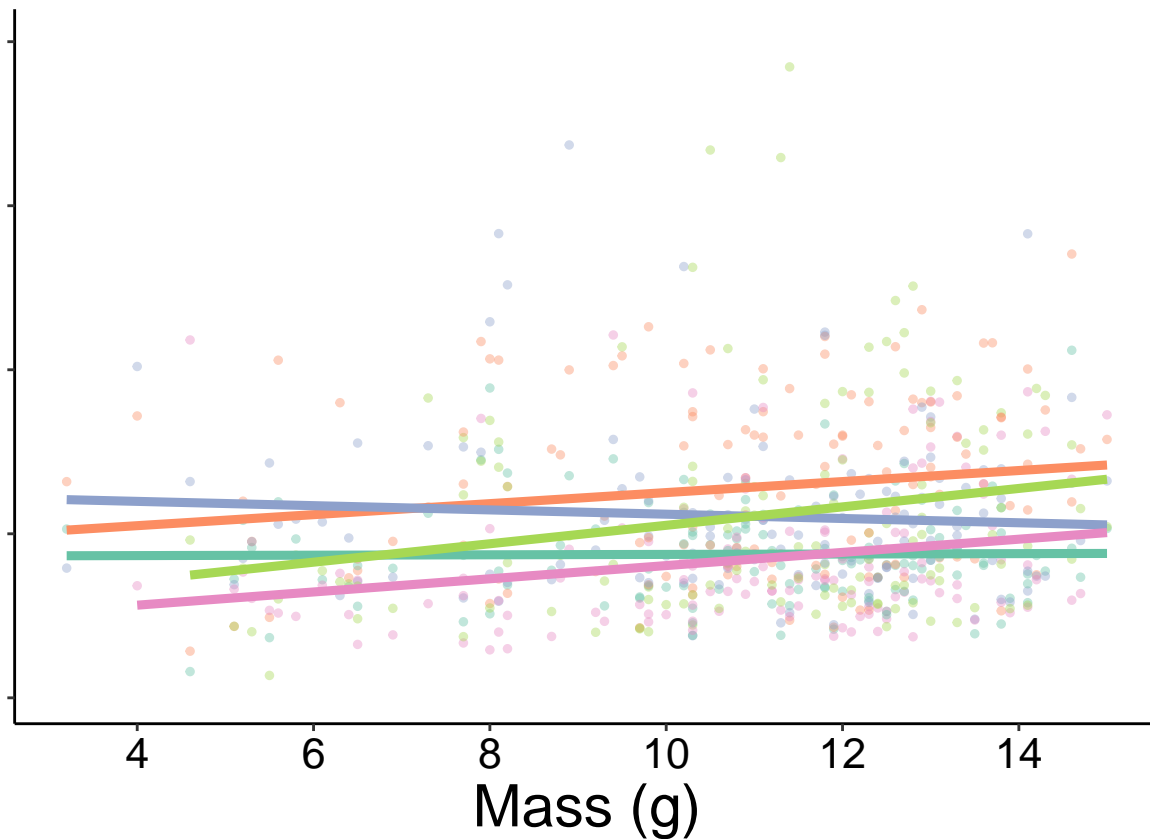
```
# MUST CHANGE COMMENTS ABOVE to produce this
CEWL_legend <- as_ggplot(get_legend(CEWL_mass_fig))
```

## 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")
```
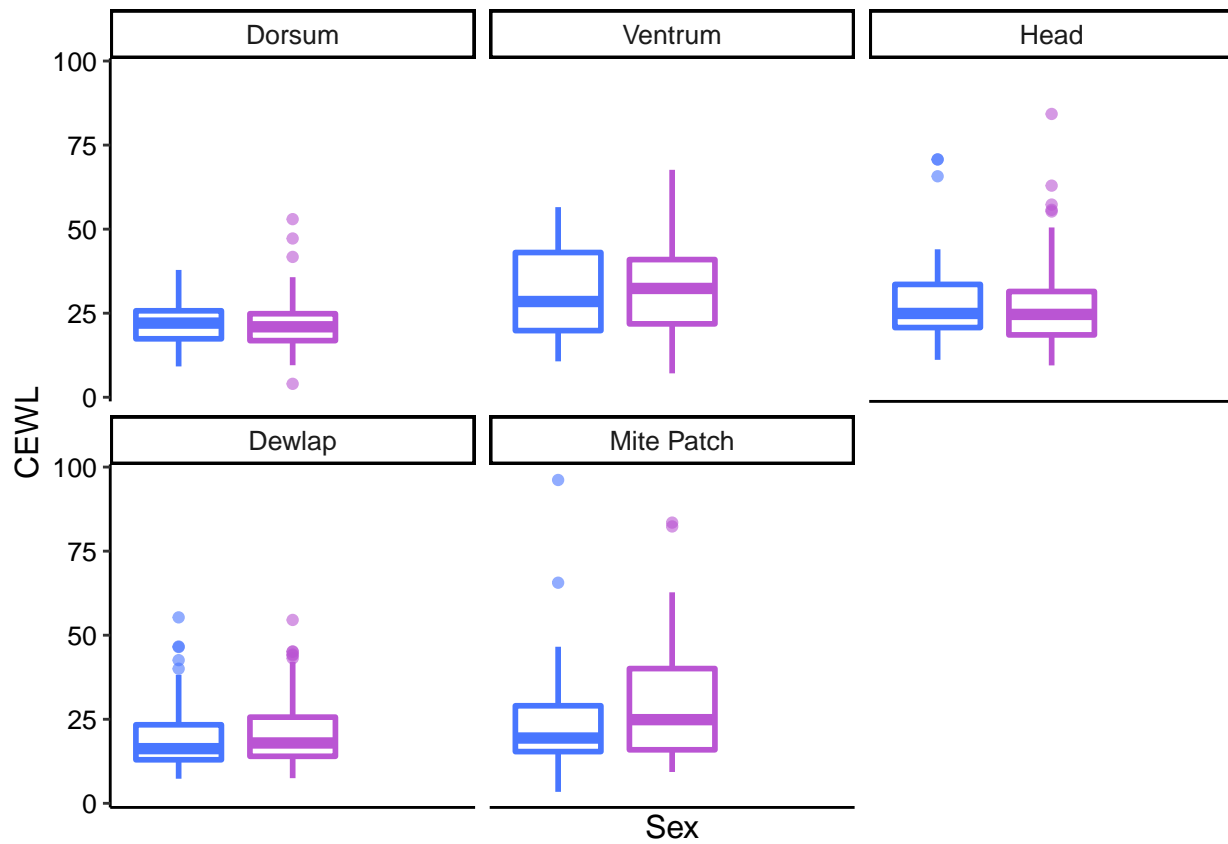


## CEWL ~ Gravidity

```
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")
```
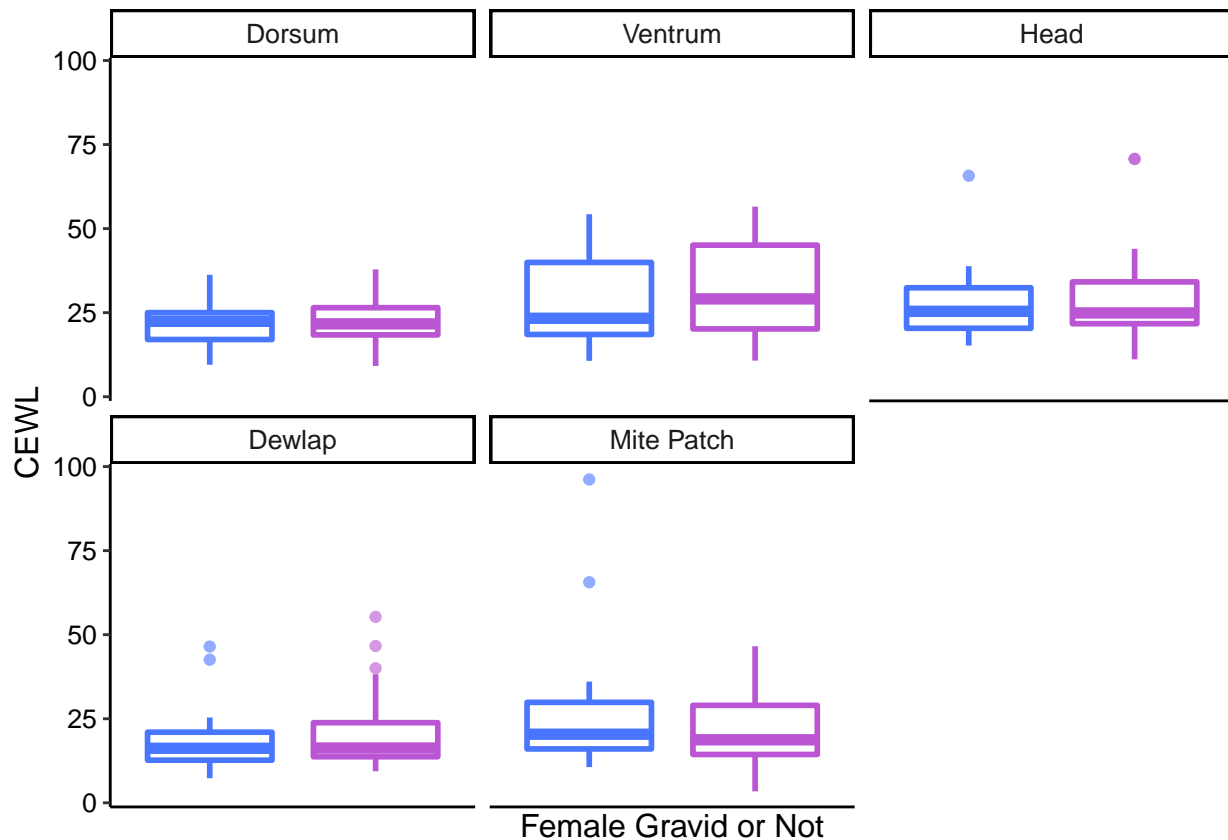


### CEWL ~ Week

```
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")
```
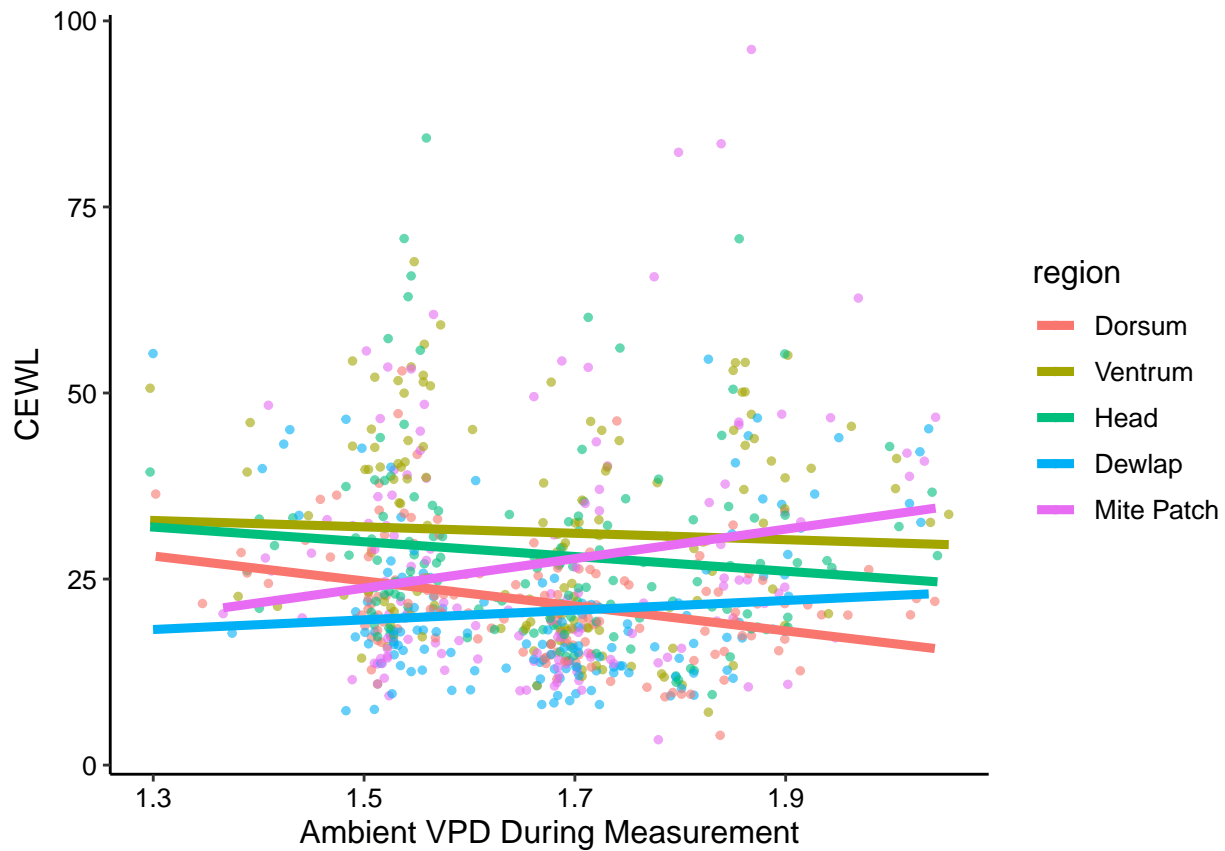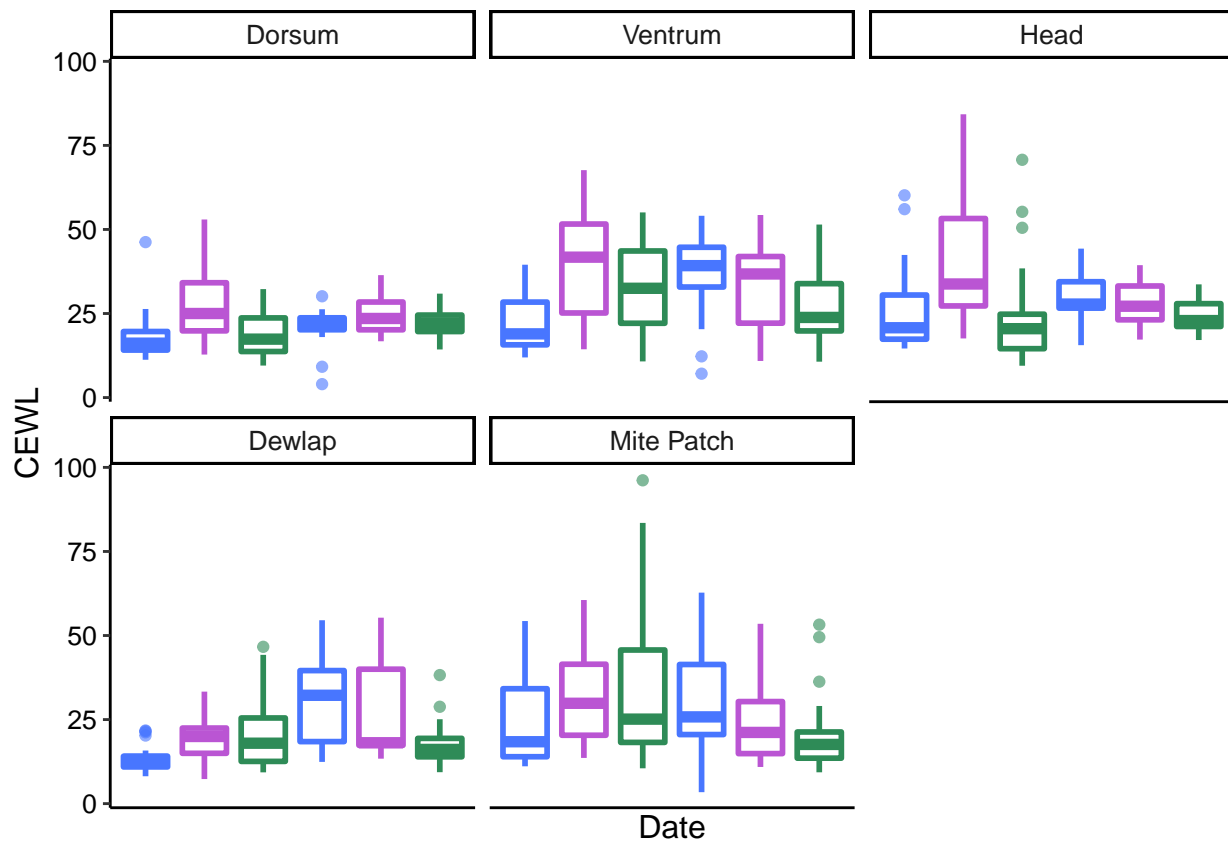
**CEWL ~ holding time**

```
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/m^2/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).
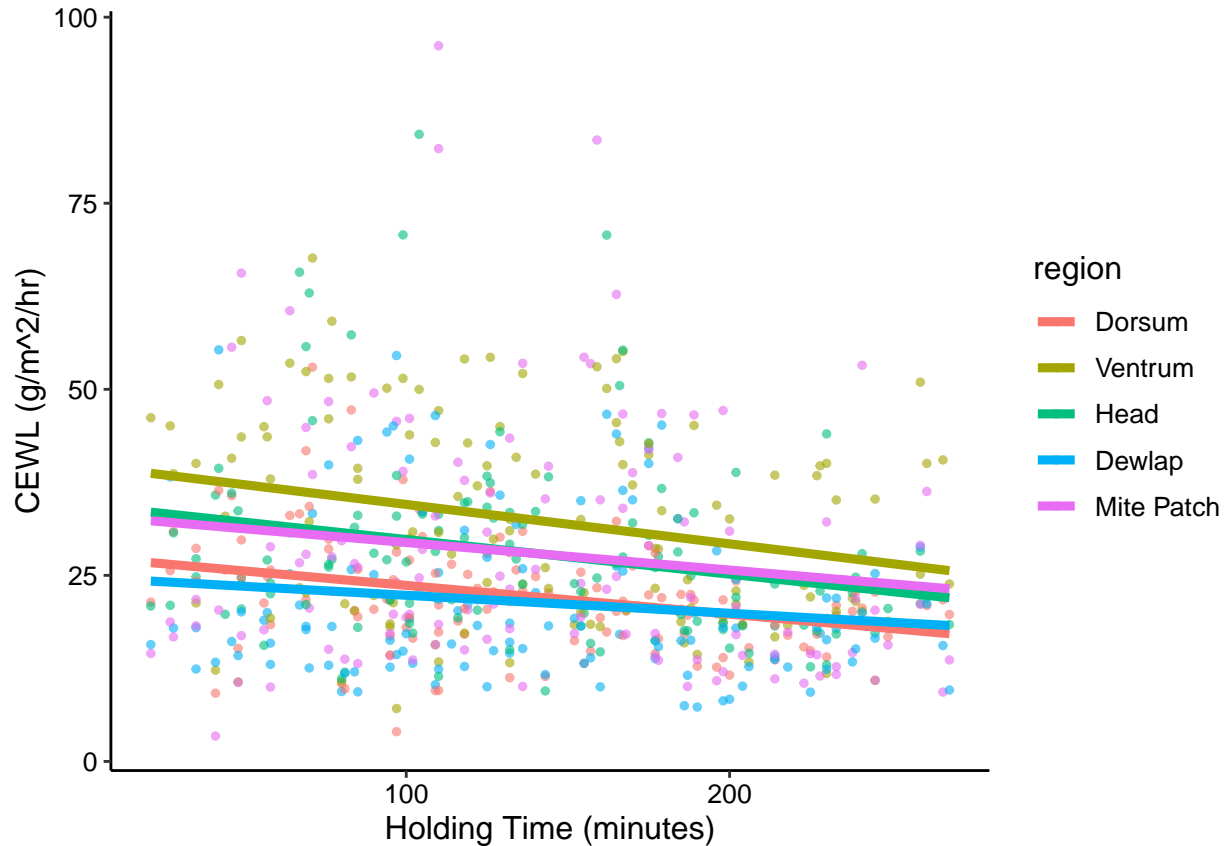


### CEWL Multi-Figure

```
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`



```
# 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)
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, data = morpho_blood_SMI)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -18.6836  -3.4985   0.4699   2.6001  16.1581
##
## Coefficients:
##                            Estimate Std. Error t value Pr(>|t|)
## (Intercept)               76.985812  54.888253   1.403   0.1636
## VPD_kPa_int               -9.279867  18.736603  -0.495   0.6214
## temp_C_interpol            2.962843   1.436544   2.062   0.0415 *
## Wind_mph_interpol          0.884343   1.551037   0.570   0.5697
## Solar_rad_Wm2_interpol    -0.012497   0.005259  -2.376   0.0192 *
## SMI                       -2.220837   1.635150  -1.358   0.1772
## SVL_mm                    -1.317991   0.784328  -1.680   0.0957 .
## mass_g                     2.719505   1.629946   1.668   0.0981 .
## sex_M_FM                   2.139580   1.145642   1.868   0.0645 .
## VPD_kPa_int:temp_C_interpol -0.279123   0.697548  -0.400   0.6898
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5.72 on 110 degrees of freedom
##   (28 observations deleted due to missingness)
## Multiple R-squared:  0.1444, Adjusted R-squared:  0.07437
## F-statistic: 2.062 on 9 and 110 DF,  p-value: 0.039
```

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                  191.916540
## VPD_kPa_int:temp_C_interpol 176.044041
## SVL_mm                        68.150731
## mass_g                        66.507541
## temp_C_interpol               50.517315
## SMI                           17.244577
## Solar_rad_Wm2_interpol         2.658067
## Wind_mph_interpol              1.423097
## sex_M_F                        1.117867
```

drop VPD*temp interaction:

```r
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)
hct_mod2_VIFs <- data.frame(VIF = car::vif(hct_mod2)) %>%
  arrange(desc(VIF))
hct_mod2_VIFs
```

```
##                              VIF
## SVL_mm                 67.781909
## mass_g                 66.200497
## temp_C_interpol        49.046183
## VPD_kPa_int            43.910922
## SMI                    17.059528
## Solar_rad_Wm2_interpol  2.657878
## sex_M_F                 1.117866
## Wind_mph_interpol       1.093684
```

drop SVL:

```r
hct_mod3 <- 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 + mass_g + sex_M_F)
hct_mod3_VIFs <- data.frame(VIF = car::vif(hct_mod3)) %>%
  arrange(desc(VIF))
hct_mod3_VIFs
```

```
##                              VIF
## temp_C_interpol        48.706647
## VPD_kPa_int            43.832686
## Solar_rad_Wm2_interpol  2.577581
## SMI                     1.204359
## sex_M_F                 1.108879
## mass_g                  1.103149
## Wind_mph_interpol       1.090474
```

drop temperature:

```
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)
hct_mod4_VIFs <- data.frame(VIF = car::vif(hct_mod4)) %>%
  arrange(desc(VIF))
hct_mod4_VIFs
```

```
##                            VIF
## SMI                   1.190679
## VPD_kPa_int           1.180363
## Solar_rad_Wm2_interpol 1.167199
## sex_M_F               1.108541
## mass_g                1.095451
## Wind_mph_interpol     1.083849
```

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, data = morpho_blood_SMI)
##
## Residuals:
##      Min      1Q  Median      3Q     Max
## -19.0026  -3.1290  0.0745  3.1393  18.2512
##
## Coefficients:
##                        Estimate Std. Error t value Pr(>|t|)
## (Intercept)           30.182937   8.717611   3.462 0.000757 ***
## VPD_kPa_int            2.669707   1.499055   1.781 0.077611 .
## Wind_mph_interpol      0.693339   1.380907   0.502 0.616582
## Solar_rad_Wm2_interpol -0.005719   0.003555  -1.609 0.110477
## SMI                    0.342622   0.438333   0.782 0.436056
## mass_g                -0.032392   0.213407  -0.152 0.879628
## sex_M_FM               2.266760   1.163872   1.948 0.053943 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5.835 on 113 degrees of freedom
##   (28 observations deleted due to missingness)
## Multiple R-squared:  0.08521,    Adjusted R-squared:  0.03664
## F-statistic: 1.754 on 6 and 113 DF,  p-value: 0.1149
```

```
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
```

```
##                         Df Sum of Sq    RSS    AIC
## <none>                              3847.9 430.13
## VPD_kPa_int             1    108.003 3955.9 431.46
## Wind_mph_interpol       1      8.584 3856.5 428.40
## Solar_rad_Wm2_interpol  1     88.122 3936.0 430.85
## SMI                     1     20.805 3868.7 428.78
## mass_g                  1      0.784 3848.7 428.16
## sex_M_F                 1    129.165 3977.1 432.10
```

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)
summary(hct_mod5)
```

```
##
## Call:
## lm(formula = hematocrit_percent ~ VPD_kPa_int + Wind_mph_interpol +
##     Solar_rad_Wm2_interpol + SMI + sex_M_F, data = morpho_blood_SMI)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -19.074  -3.142   0.119   3.143  18.152
##
## Coefficients:
##                         Estimate Std. Error t value Pr(>|t|)
## (Intercept)            30.073181   8.650263   3.477  0.00072 ***
## VPD_kPa_int             2.667572   1.492553   1.787  0.07655 .
## Wind_mph_interpol       0.673711   1.368935   0.492  0.62356
## Solar_rad_Wm2_interpol -0.005701   0.003538  -1.612  0.10983
## SMI                     0.329499   0.427876   0.770  0.44285
## sex_M_FM                2.235515   1.140603   1.960  0.05244 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5.81 on 114 degrees of freedom
##   (28 observations deleted due to missingness)
## Multiple R-squared:  0.08503,    Adjusted R-squared:  0.0449
## F-statistic: 2.119 on 5 and 114 DF,  p-value: 0.06815
```

```
drop1(hct_mod5)
```

```
## Single term deletions
##
## Model:
## hematocrit_percent ~ VPD_kPa_int + Wind_mph_interpol + Solar_rad_Wm2_interpol +
##     SMI + sex_M_F
##                         Df Sum of Sq    RSS    AIC
## <none>                              3848.7 428.16
## VPD_kPa_int             1    107.840 3956.5 429.48
## Wind_mph_interpol       1      8.177 3856.8 426.41
```

```
## Solar_rad_Wm2_interpol  1    87.677 3936.3 428.86
## SMI                     1    20.021 3868.7 426.78
## sex_M_F                 1   129.686 3978.4 430.14
```

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)
summary(hct_mod6)
```

```
##
## Call:
## lm(formula = hematocrit_percent ~ VPD_kPa_int + Solar_rad_Wm2_interpol +
##     SMI + sex_M_F, data = morpho_blood_SMI)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -19.2152 -3.1252  0.0611  3.0814 18.2033
##
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)            33.677969   4.586562   7.343 3.24e-11 ***
## VPD_kPa_int             2.502902   1.449764   1.726   0.0870 .
## Solar_rad_Wm2_interpol -0.005641   0.003524  -1.601   0.1122
## SMI                     0.305110   0.423594   0.720   0.4728
## sex_M_FM                2.247314   1.136588   1.977   0.0504 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5.791 on 115 degrees of freedom
##   (28 observations deleted due to missingness)
## Multiple R-squared:  0.08308,    Adjusted R-squared:  0.05119
## F-statistic: 2.605 on 4 and 115 DF,  p-value: 0.03942
```

```
drop1(hct_mod6)
```

```
## Single term deletions
##
## Model:
## hematocrit_percent ~ VPD_kPa_int + Solar_rad_Wm2_interpol + SMI +
##     sex_M_F
##                        Df Sum of Sq    RSS    AIC
## <none>                              3856.8 426.41
## VPD_kPa_int             1    99.960 3956.8 427.48
## Solar_rad_Wm2_interpol  1    85.933 3942.8 427.06
## SMI                     1    17.400 3874.2 424.95
## sex_M_F                 1   131.116 3988.0 428.43
```

drop SMI:

```
hct_mod7 <- lm(data = morpho_blood_SMI,
                         # response variable
                         hematocrit_percent ~
```

```
                                # predictor variables
                                VPD_kPa_int + Solar_rad_Wm2_interpol + sex_M_F)
summary(hct_mod7)
```

```
## 
## Call:
## lm(formula = hematocrit_percent ~ VPD_kPa_int + Solar_rad_Wm2_interpol +
##     sex_M_F, data = morpho_blood_SMI)
## 
## Residuals:
##      Min       1Q   Median       3Q      Max
## -18.8440  -3.0879   0.0155   2.9196  18.6980
## 
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)             36.183219   2.983645  12.127   <2e-16 ***
## VPD_kPa_int              2.540607   1.445810   1.757   0.0815 .
## Solar_rad_Wm2_interpol  -0.004975   0.003394  -1.466   0.1453
## sex_M_FM                 2.382976   1.118547   2.130   0.0352 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 5.779 on 116 degrees of freedom
##   (28 observations deleted due to missingness)
## Multiple R-squared:  0.07895,    Adjusted R-squared:  0.05513
## F-statistic: 3.314 on 3 and 116 DF,  p-value: 0.02249
```

```
drop1(hct_mod7)
```

```
## Single term deletions
## 
## Model:
## hematocrit_percent ~ VPD_kPa_int + Solar_rad_Wm2_interpol + sex_M_F
##                        Df Sum of Sq    RSS    AIC
## <none>                              3874.2 424.95
## VPD_kPa_int             1    103.129 3977.4 426.11
## Solar_rad_Wm2_interpol  1     71.785 3946.0 425.16
## sex_M_F                 1    151.586 4025.8 427.56
```

drop solar:

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

```
## 
## 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_mod8)

```
## 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_mod9 <- lm(data = morpho_blood_SMI,
                      # response variable
                      hematocrit_percent ~
                      # predictor variables
                      sex_M_F)
```

**summary**(hct_mod9)

```
##
## 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
```

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)
```

**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_mod_null)

#specify model names
hct_mod_names <- c('(model 4) ~ sex, VPD at capture, solar radiation at capture, SMI, wind speed at cap
                   '(model 5) ~ sex, VPD at capture, solar radiation at capture, SMI, wind speed at
                   '(model 6) ~ sex, VPD at capture, solar radiation at capture, SMI',
                   '(model 7) ~ sex, VPD at capture, solar radiation at capture',
                   '(model 8) ~ sex, VPD at capture',
                   '(model 9) ~ sex',
                   'null model')
#calculate AIC of each model
hct_AICc <- data.frame(aictab(cand.set = hct_models,
                              modnames = hct_mod_names))
hct_AICc

##                                                                       Modnames
## 4                    (model 7) ~ sex, VPD at capture, solar radiation at capture
## 5                                                (model 8) ~ sex, VPD at capture
## 3               (model 6) ~ sex, VPD at capture, solar radiation at capture, SMI
## 2     (model 5) ~ sex, VPD at capture, solar radiation at capture, SMI, wind speed at capture
## 6                                                                (model 9) ~ sex
## 1 (model 4) ~ sex, VPD at capture, solar radiation at capture, SMI, wind speed at capture, mass
## 7                                                                      null model
##   K     AICc  Delta_AICc    ModelLik      AICcWt        LL    Cum.Wt
## 4 5 768.0253 0.00000000 1.000000000 0.369737267 -378.7495 0.3697373
## 5 4 768.0500 0.02461668 0.987767098 0.365214308 -379.8511 0.7349516
## 3 6 769.7022 1.67689258 0.432381797 0.159867664 -378.4794 0.8948192
## 2 7 771.7042 3.67884825 0.158908911 0.058754547 -378.3521 0.9535738
## 6 3 773.5043 5.47892148 0.064605177 0.023886941 -383.6496 0.9774607
```

```
## 1 8 773.9770 5.95168270 0.051004503 0.018858266 -378.3399 0.9963190
## 7 2 777.2445 9.21921256 0.009955737 0.003681007 -386.5714 1.0000000
```

**Check LM Assumptions**

```
plot(hct_mod7)
```

Residuals vs Fitted

Fitted values
lm(hematocrit_percent ~ VPD_kPa_int + Solar_rad_Wm2_interpol + sex_M_F)

Normal Q–Q

Theoretical Quantiles
lm(hematocrit_percent ~ VPD_kPa_int + Solar_rad_Wm2_interpol + sex_M_F)

## Scale–Location



Fitted values
lm(hematocrit_percent ~ VPD_kPa_int + Solar_rad_Wm2_interpol + sex_M_F)

## Residuals vs Leverage



Leverage
lm(hematocrit_percent ~ VPD_kPa_int + Solar_rad_Wm2_interpol + sex_M_F)

```
plot(hct_mod8)
```

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# Residuals vs Fitted



Fitted values
lm(hematocrit_percent ~ VPD_kPa_int + sex_M_F)

# Normal Q–Q



Theoretical Quantiles
lm(hematocrit_percent ~ VPD_kPa_int + sex_M_F)

## Scale-Location



Fitted values
lm(hematocrit_percent ~ VPD_kPa_int + sex_M_F)

## Residuals vs Leverage



Leverage
lm(hematocrit_percent ~ VPD_kPa_int + sex_M_F)

```
plot(hct_mod6)
```

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Residuals vs Fitted

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

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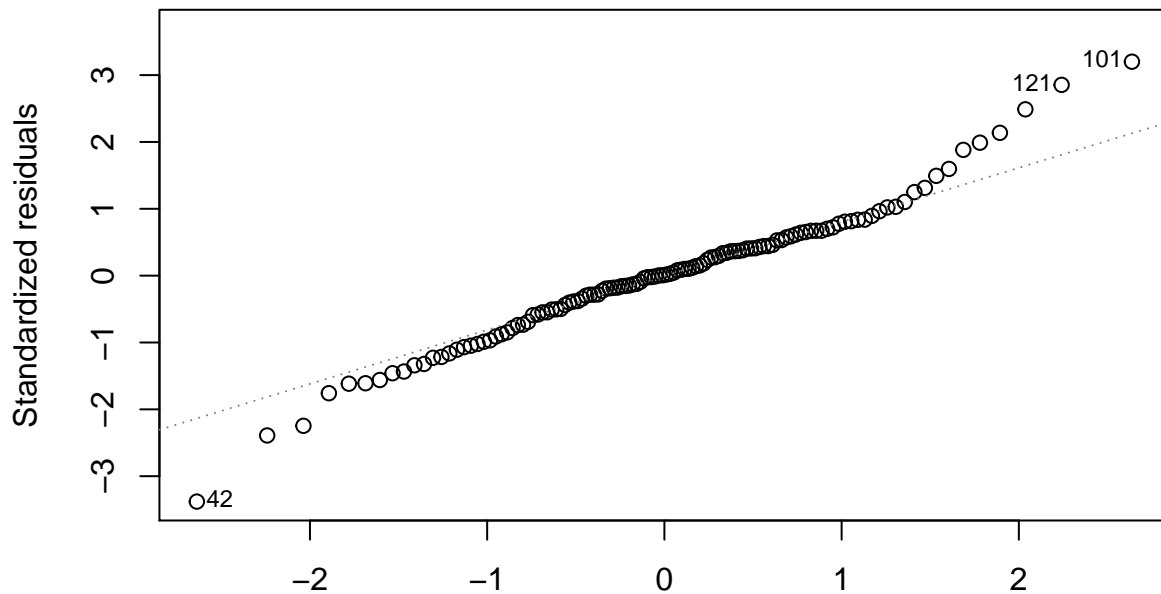
lm(hematocrit_percent ~ VPD_kPa_int + Solar_rad_Wm2_interpol + SMI + sex_M_ .

Scale–Location

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_ .
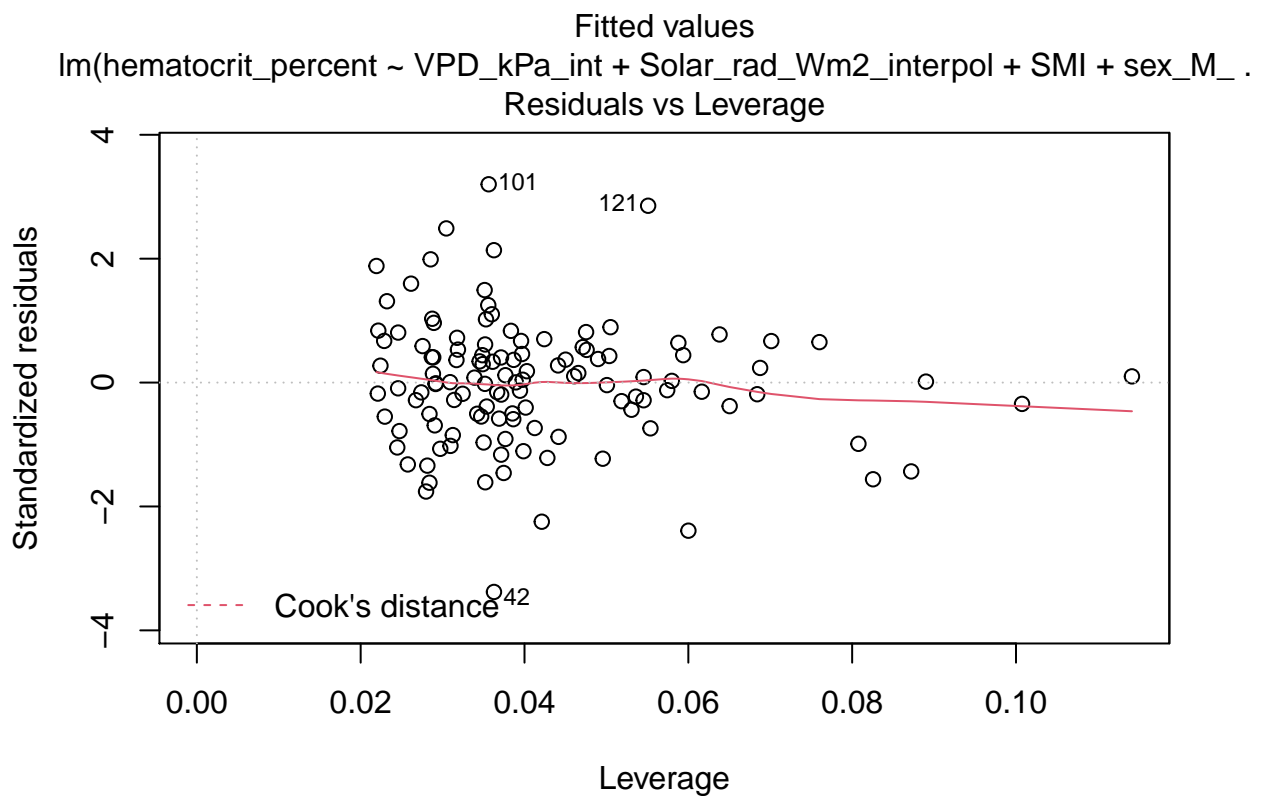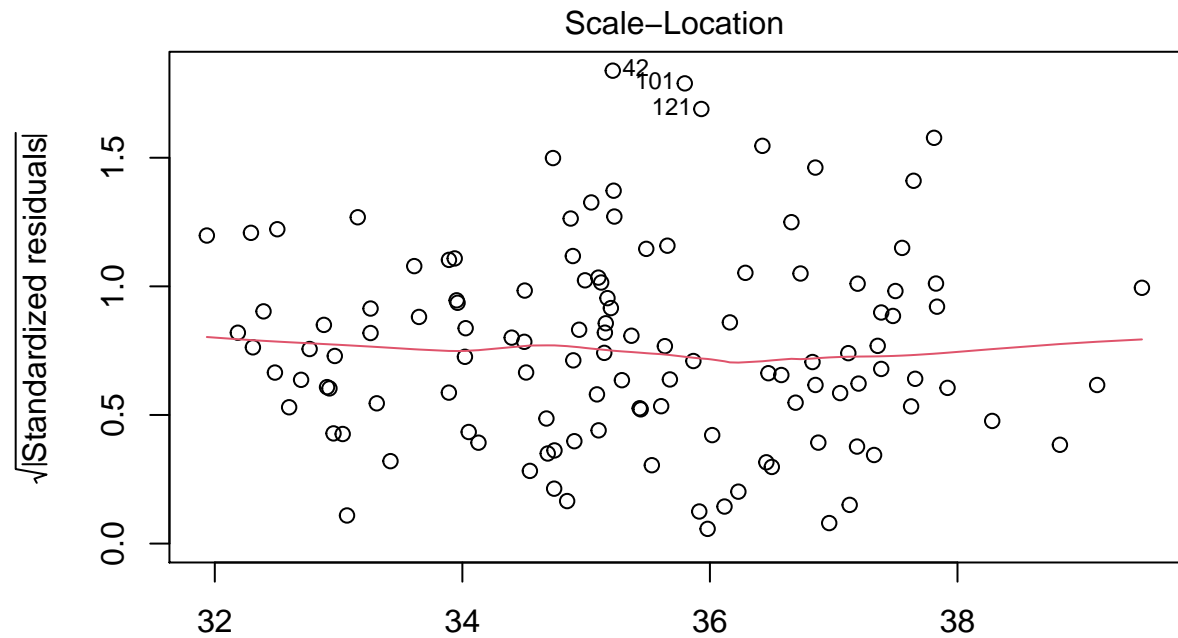
residuals all look fine

**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_mod7),
          "./best_models/hct_best_mod1.csv")
```

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

```
write.csv(broom.mixed::tidy(hct_mod8),
          "./best_models/hct_best_mod2.csv")
write.csv(broom.mixed::tidy(hct_mod6),
          "./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|hemolyzed))
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 | hemolyzed)
##    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
##  hemolyzed (Intercept)  12.9     3.591
##  Residual              279.3    16.712
## Number of obs: 121, groups:  date, 6; hemolyzed, 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|hemolyzed))
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|hemolyzed))
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|hemolyzed))
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
```

```r
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:

```r
# 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
```

```r
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:

```r
# 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

```r
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.

```r
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
```

```r
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
##       ModelLik      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:

```r
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
```

```r
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)
```
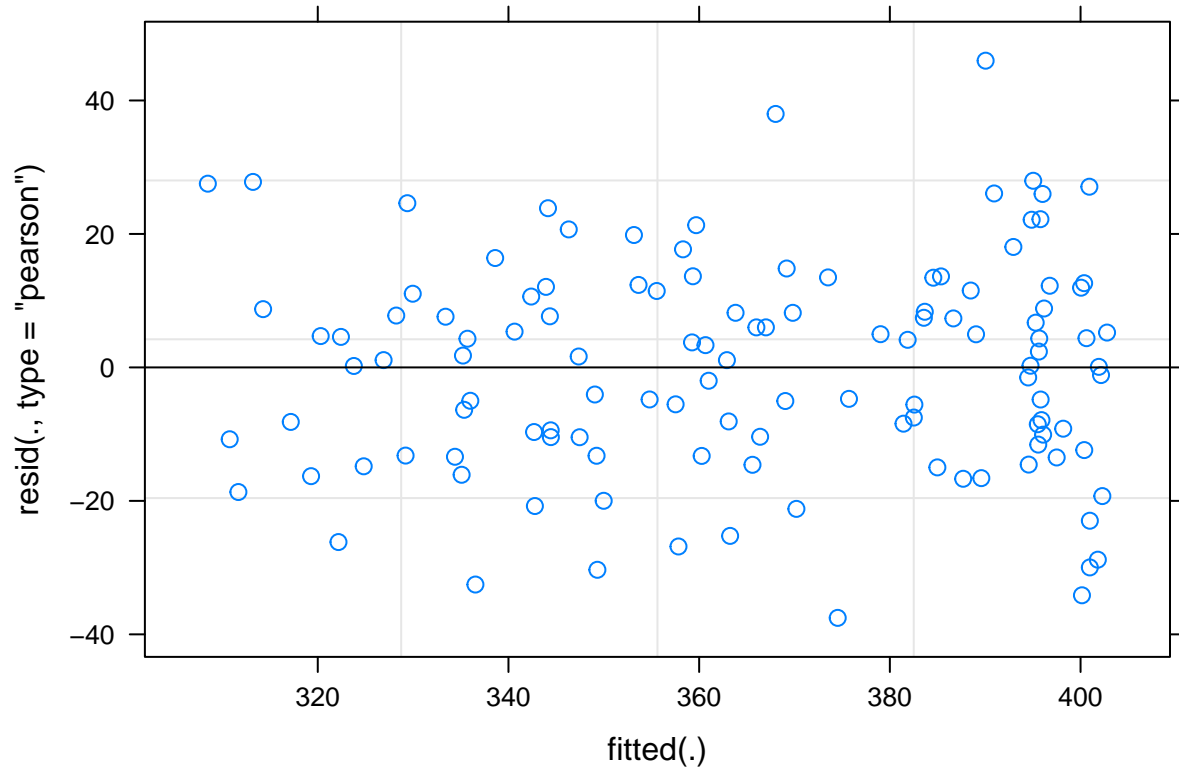


```
plot(hydrat_mod5)
```
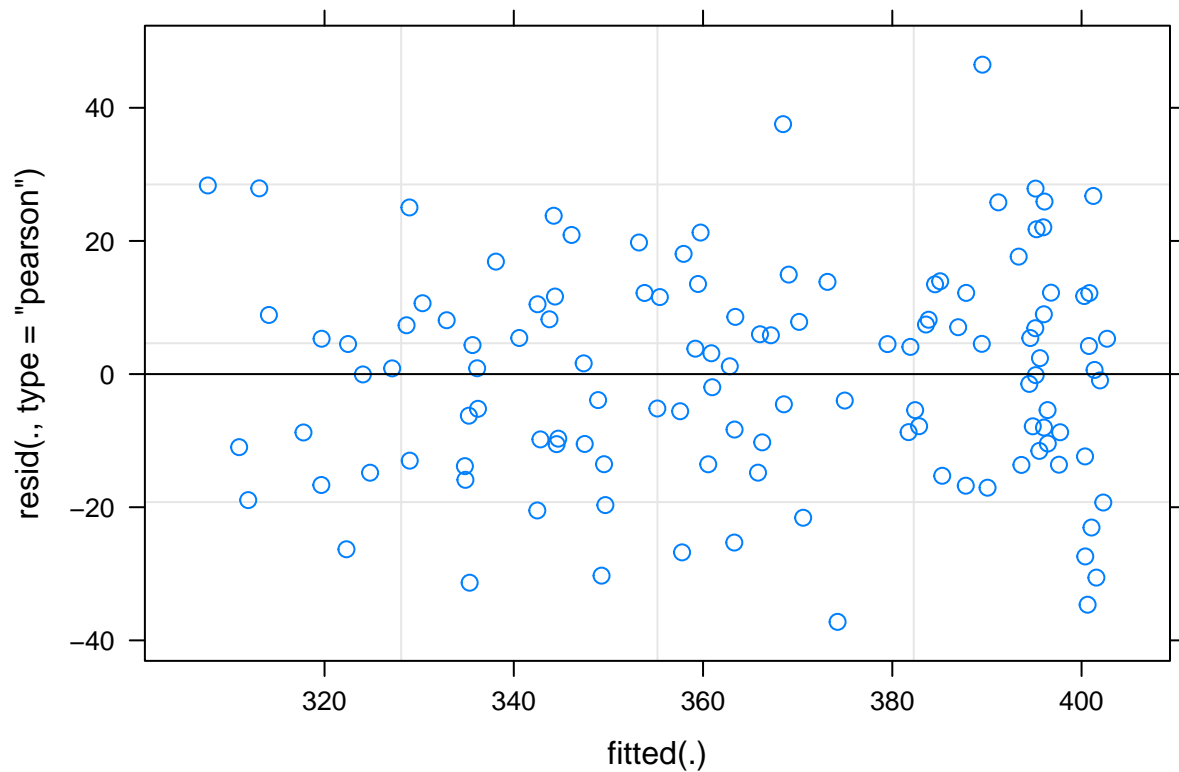
residuals look fantastic for both

**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
## regionVentrum: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
## regionVentrum: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
## regionVentrum: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
## regionVentrum: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
## regionVentrum: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

## 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
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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

## 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
## 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 + 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

## 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
```

```
## 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
## regionVentrum                  -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
```

```r
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)
##                               npar    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

## 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
```

```r
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

## 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:

```r
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
```

```r
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:

```r
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) ~ region*VPD_kPa_int + region*Solar_rad_Wm2_interpol + region*SMI + reg
                    '(model 7) ~ region*VPD_kPa_int + region*Solar_rad_Wm2_interpol + SMI + region*ma
                    '(model 8) ~ region*VPD_kPa_int + region*Solar_rad_Wm2_interpol + SMI + region*ma
                    '(model 9) ~ region*VPD_kPa_int + region*Solar_rad_Wm2_interpol + region*mass_g
                    '(model 10) ~ region*VPD_kPa_int + region*Solar_rad_Wm2_interpol + region*mass_g
                    '(model 11) ~ region*VPD_kPa_int + region*Solar_rad_Wm2_interpol + region*mass_g
                    '(model 12) ~ region*VPD_kPa_int + region*Solar_rad_Wm2_interpol + region*mass_g
                    '(model 13) ~ region*VPD_kPa_int + region*Solar_rad_Wm2_interpol + region*mass_g
                    '(model 14) ~ region*VPD_kPa_int + region*Solar_rad_Wm2_interpol + region*mass_g
                    '(model 15) ~ region*VPD_kPa_int + region*Solar_rad_Wm2_interpol + region*mass_g
                    '(model 16) ~ region*VPD_kPa_int + Solar_rad_Wm2_interpol + region*mass_g + cloaca
                    '(model 17) ~ region*VPD_kPa_int + Solar_rad_Wm2_interpol + region*mass_g + cloaca
                    '(model 18) ~ region*VPD_kPa_int + Solar_rad_Wm2_interpol + region*mass_g + cloaca
                    '(model 19) ~ region*VPD_kPa_int + Solar_rad_Wm2_interpol + region*mass_g + cloaca
                    '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
```

```
##
## 11
## 12
## 13
## 14
## 7                                                      (model 12) ~ region*VPD_kPa_int + re
## 8                                                          (model 13) ~ reg
## 9                                                               (model
## 10
## 2          (model 7) ~ region*VPD_kPa_int + region*Solar_rad_Wm2_interpol + SMI + region*mass_g + reg
## 6                                            (model 11) ~ region*VPD_kPa_int + region*Solar_i
```

```
## 1   (model 6a) ~ region*VPD_kPa_int + region*Solar_rad_Wm2_interpol + region*SMI + region*mass_g + reg
## 5                        (model 10) ~ region*VPD_kPa_int + region*Solar_rad_Wm2_interpol + reg
## 3              (model 8) ~ region*VPD_kPa_int + region*Solar_rad_Wm2_interpol + SMI + region*mass
## 4                   (model 9) ~ region*VPD_kPa_int + region*Solar_rad_Wm2_interpol + region*mass
## 15
##     K      AICc Delta_AICc     ModelLik        AICcWt      Res.LL    Cum.Wt
## 11 22 4341.508   0.000000 1.000000e+00 9.202316e-01 -2147.829 0.9202316
## 12 21 4346.476   4.968639 8.338226e-02 7.673099e-02 -2151.395 0.9969626
## 13 20 4353.118  11.610312 3.011985e-03 2.771724e-03 -2155.794 0.9997343
## 14 19 4357.820  16.311809 2.870356e-04 2.641392e-04 -2159.219 0.9999985
## 7  29 4369.240  27.731954 9.507859e-07 8.749432e-07 -2154.009 0.9999993
## 8  28 4371.070  29.562367 3.807269e-07 3.503569e-07 -2156.034 0.9999997
## 9  27 4372.665  31.156848 1.715443e-07 1.578605e-07 -2157.937 0.9999998
## 10 26 4373.198  31.690000 1.314026e-07 1.209208e-07 -2159.306 1.0000000
## 2  37 4377.297  35.789635 1.691919e-08 1.556957e-08 -2149.006 1.0000000
## 6  30 4377.574  36.065982 1.473573e-08 1.356028e-08 -2157.061 1.0000000
## 1  41 4378.606  37.098343 8.794219e-09 8.092718e-09 -2145.042 1.0000000
## 5  31 4384.432  42.924320 4.776418e-10 4.395411e-10 -2159.372 1.0000000
## 3  33 4386.132  44.623845 2.041997e-10 1.879110e-10 -2157.973 1.0000000
## 4  32 4387.397  45.889237 1.084623e-10 9.981041e-11 -2159.732 1.0000000
## 15  3 4509.547 168.039322 3.241341e-37 2.982785e-37 -2251.752 1.0000000
```

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

```r
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
```

```r
CEWL_mod17p <- 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 + 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
## regionVentrum: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
## regionVentrum: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)
## regionVentrum
## regionHead
## regionDewlap                      ***
```

```
## 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
```
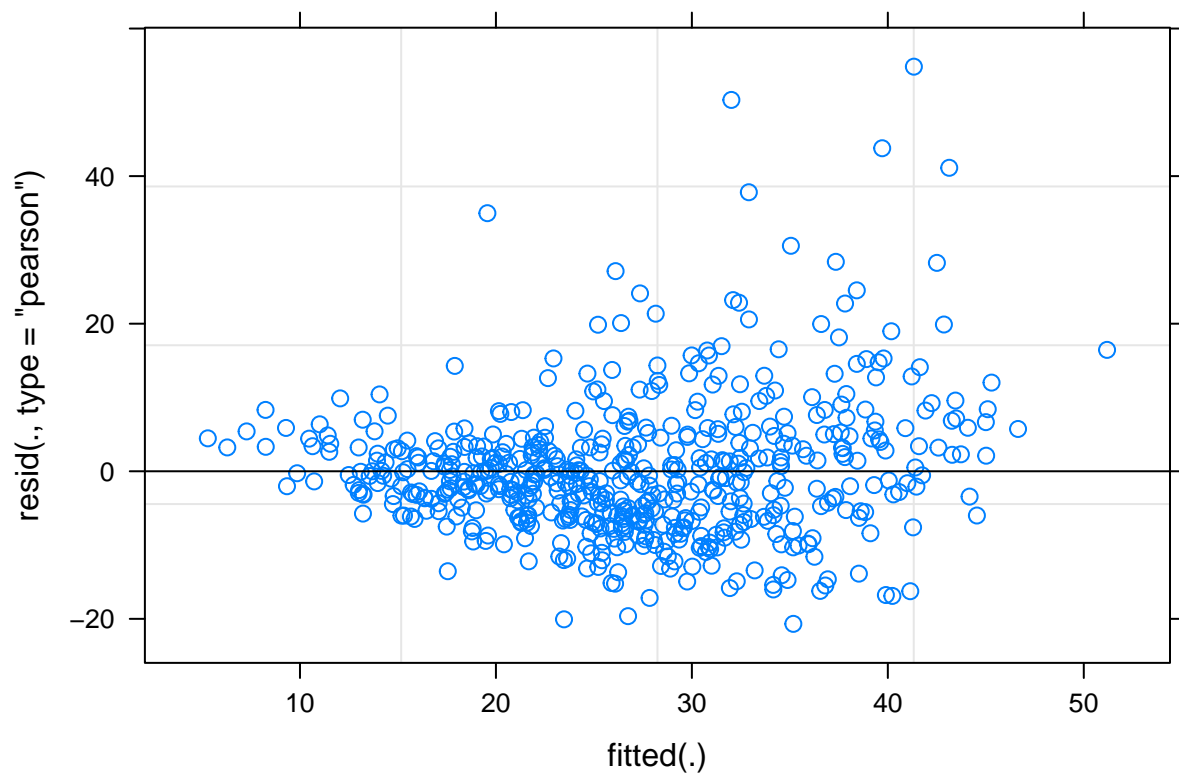
**Check LM Assumptions**

```
plot(CEWL_mod16)
```
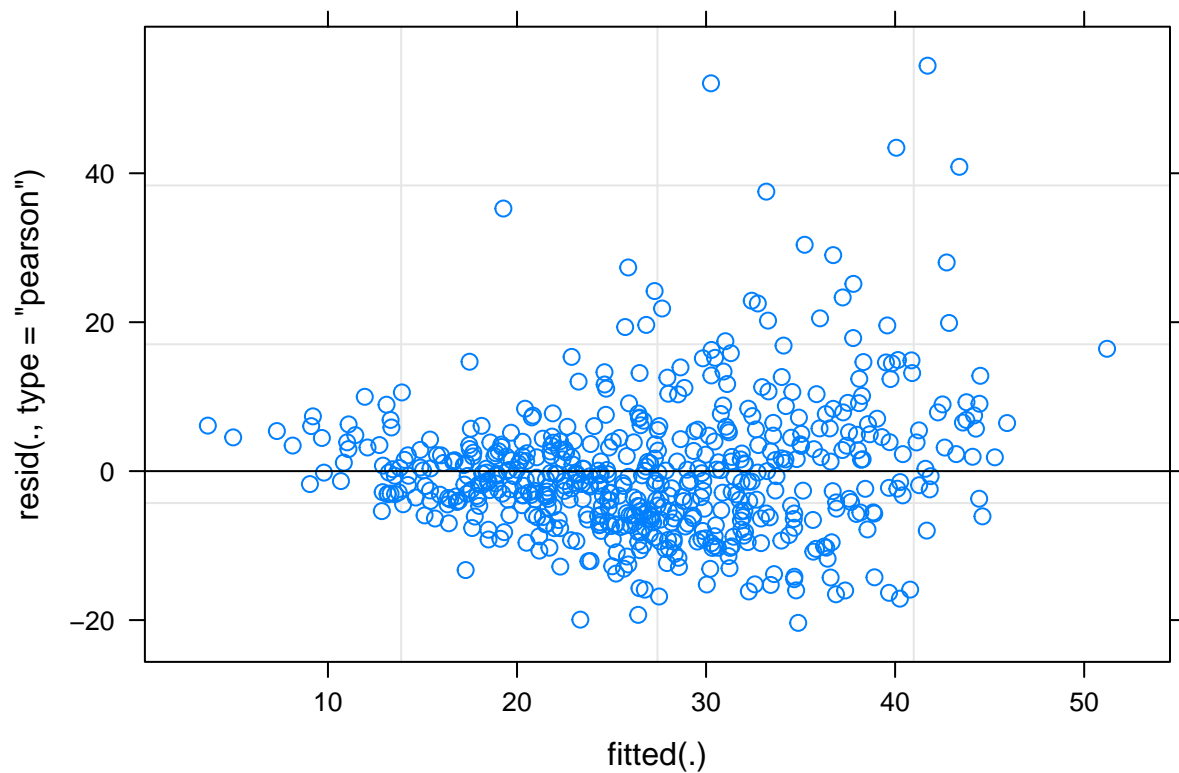


```
plot(CEWL_mod17)
```

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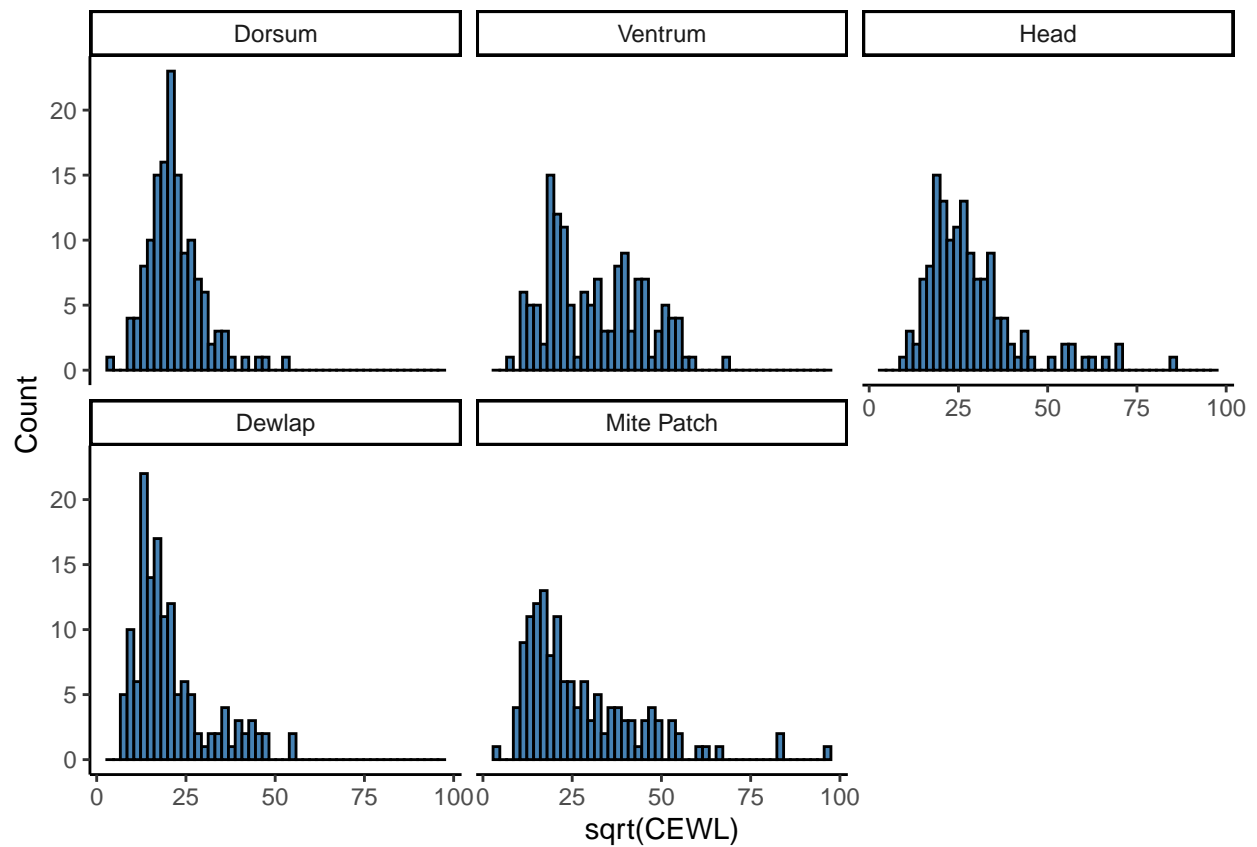
```
# sqrt(TEWL)
CEWL_data_full %>%
  ggplot(., aes(x = sqrt(TEWL_g_m2h))) +
  geom_histogram(color = "black", fill="steelblue", bins=50) +
  theme_classic() +
  xlab("sqrt(CEWL)") +
  ylab("Count") +
  facet_wrap(~region)
```
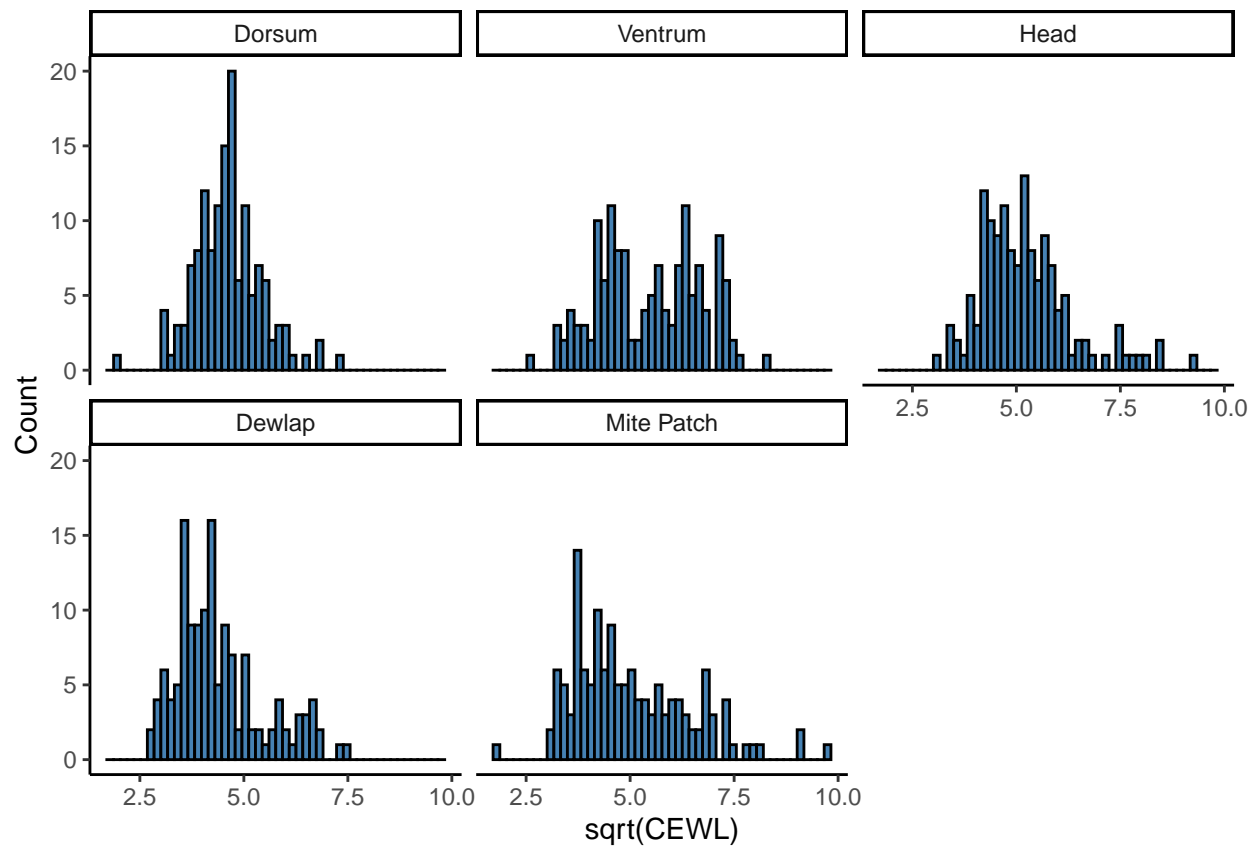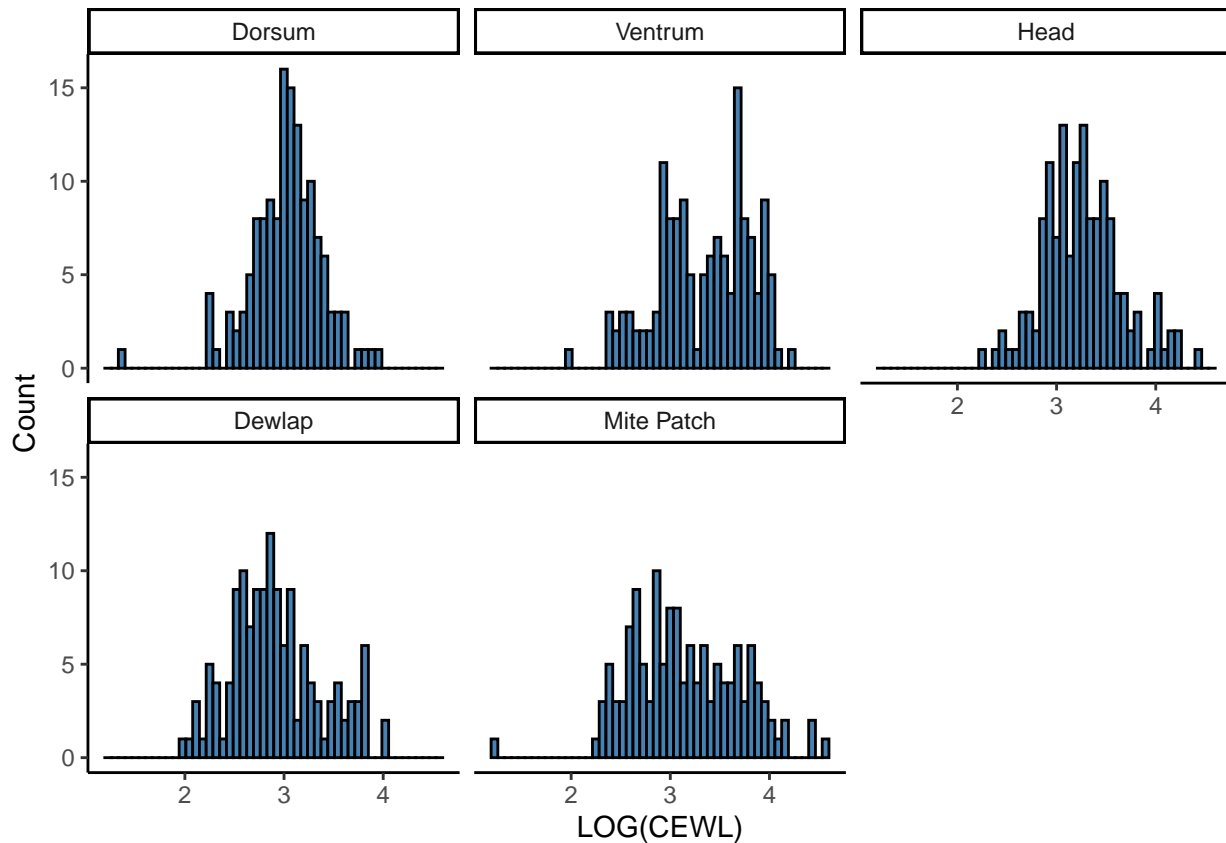
```
# log(TEWL)
CEWL_data_full %>%
  ggplot(., aes(x = log(TEWL_g_m2h))) +
  geom_histogram(color = "black", fill="steelblue", bins=50) +
  theme_classic() +
  xlab("LOG(CEWL)") +
  ylab("Count") +
  facet_wrap(~region)
```

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)
```
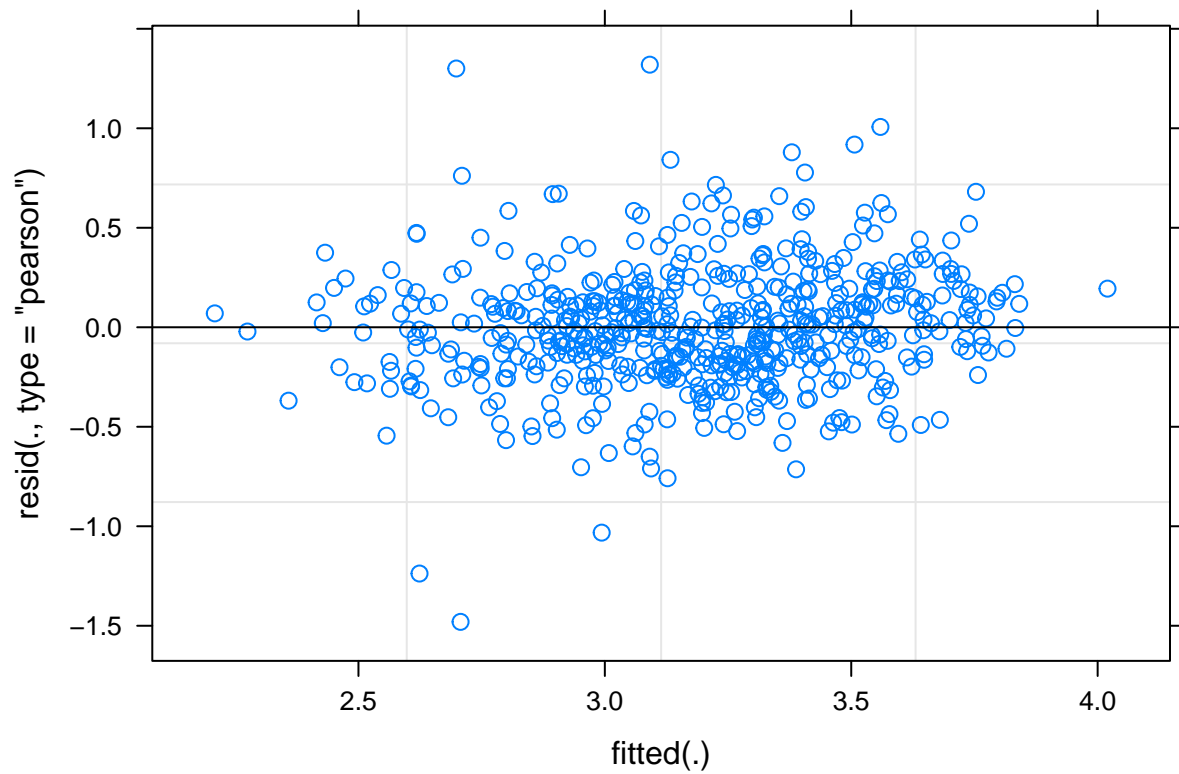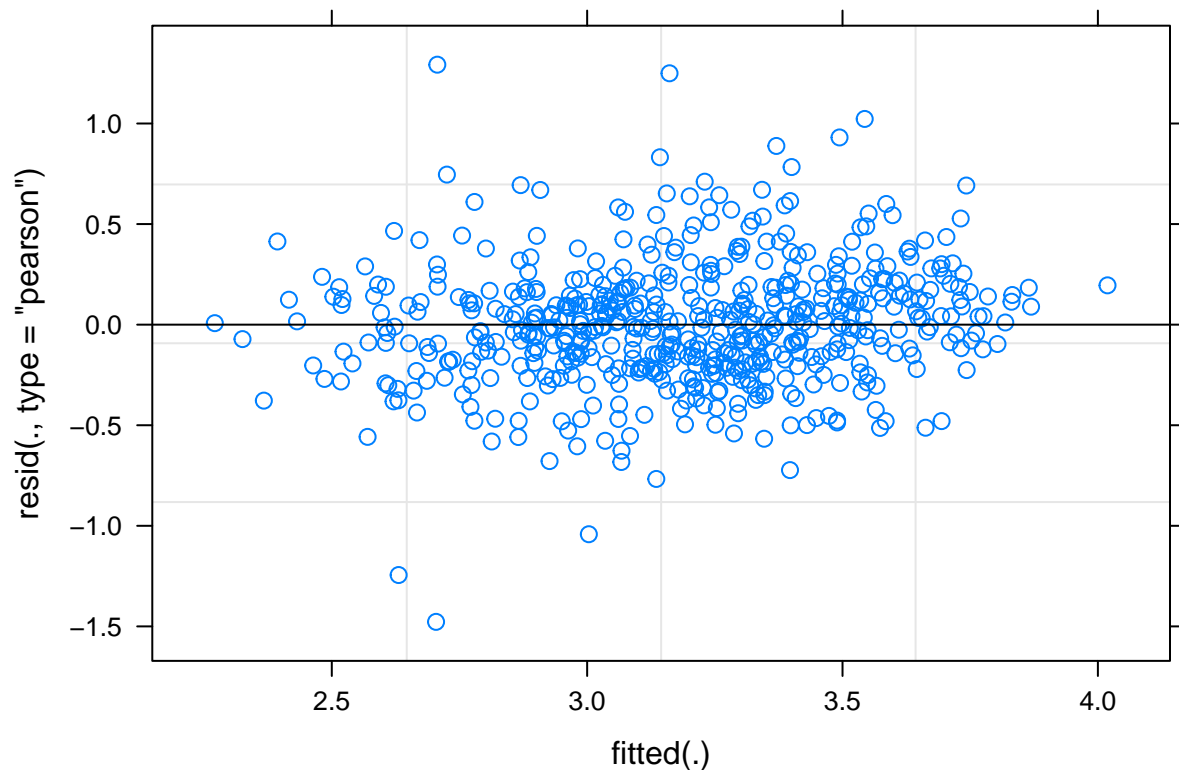
```
CEWL_mod17t <- lme4::lmer(data = CEWL_dat_sub1,
                          # response variable
                          log(TEWL_g_m2h) ~
                          # potential predictors
                          region * (VPD_kPa_int + mass_g) +
                          Solar_rad_Wm2_interpol +
                          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
```

```r
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
```

```
## regionVentrum: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
## regionVentrum: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)
## regionVentrum
## regionHead
## regionDewlap                   ***
## 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
```

**Export**

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

```r
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")
```