

# Cal Poly Herpetology CURE - Capture Data Analyses

Savannah Weaver

June 2021

## Contents

<b>Packages</b>	<b>1</b>
<b>Background and Goals</b>	<b>1</b>
<b>Data</b>	<b>1</b>
Compute Scaled Mass Index . . . . .	11
<b>Check Data Distributions</b>	<b>24</b>
Histograms & Q-Q Plots . . . . .	24
Conclusion . . . . .	41
<b>Basic Figures</b>	<b>41</b>
osmolality & hematocrit . . . . .	41
Osmolality Multi-Figure . . . . .	72
Hct Multi-Fig . . . . .	73
Hct-Osml ~ Sex . . . . .	75
What affects evaporative water loss? . . . . .	76
CEWL Multi-Figure . . . . .	106
<b>LMMs</b>	<b>108</b>
Hematocrit . . . . .	108
Hydration . . . . .	123
CEWL . . . . .	135

## Packages

## Background and Goals

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

## Data

### Morphometrics and Blood Data

This data was collected upon capture of each lizard.

Variables in this dataframe: - date - collection/capture time for each lizard - individual ID for each lizard - sock ID used to capture each lizard (removed, not relevant to analyses) - SVL = snout-vent length - mass in grams - sex - if female, whether or not gravid (with eggs) - which eye the blood sample was taken from - percent hematocrit = percent of blood that's red blood cells - osmolality = the concentration of solutes in the blood (this is the average of 1-3 replicates) - cloacal temperature at the time of CEWL measurement - processing time for each lizard, when all measurements were finished - hemolyzed = whether or not red blood cells burst and contaminated plasma

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

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

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

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

# check
summary(morpho_blood_dat)
```

##	date	collect_time	individual_ID
##	Min. :2021-04-05	Min. :2022-02-10 10:17:00	1 : 1
##	1st Qu.:2021-04-19	1st Qu.:2022-02-10 12:36:00	2 : 1
##	Median :2021-04-26	Median :2022-02-10 12:48:00	3 : 1
##	Mean :2021-04-27	Mean :2022-02-10 12:51:12	4 : 1
##	3rd Qu.:2021-05-10	3rd Qu.:2022-02-10 13:03:00	5 : 1

```
## Max. :2021-05-17 Max. :2022-02-10 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. :2022-02-10 12:44:00 N :85 Min. :2021-04-05 10:17:00
## 1st Qu.:2022-02-10 14:09:00 Y :39 1st Qu.:2021-04-19 12:49:00
## Median :2022-02-10 15:17:30 NA's:24 Median :2021-04-26 15:34:00
## Mean :2022-02-10 15:12:09 Mean :2021-04-28 20:28:01
## 3rd Qu.:2022-02-10 16:15:15 3rd Qu.:2021-05-10 12:44:00
## Max. :2022-02-10 17:38:00 Max. :2021-05-17 13:01:00
## NA's :8 NA's :3
## hold_time
## Min. : 21.0
## 1st Qu.: 95.0
## Median :141.5
## Mean :143.8
## 3rd Qu.:197.5
## Max. :268.0
## NA's :10
```

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

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

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

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

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

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

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

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

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

```
permit_stats <- morpho_blood_dat %>%  
  group_by(date, sex_M_F) %>%  
  summarise(n = n())
```

### Stats for Permit Report

```
## `summarise()` regrouping output by 'date' (override with `.groups` argument)
```

```
permit_stats
```

```
## # A tibble: 12 x 3  
## # Groups:   date [6]  
##   date      sex_M_F    n  
##   <date>    <fct>  <int>  
## 1 2021-04-05 F         4  
## 2 2021-04-05 M        25  
## 3 2021-04-19 F         9  
## 4 2021-04-19 M        14  
## 5 2021-04-26 F         8  
## 6 2021-04-26 M        18  
## 7 2021-05-03 F         4  
## 8 2021-05-03 M        15  
## 9 2021-05-10 F         9  
## 10 2021-05-10 M        14  
## 11 2021-05-17 F        14  
## 12 2021-05-17 M        14
```

```
# check total  
sum(permit_stats$n)
```

```
## [1] 148
```

```
# save  
write.csv(permit_stats, "./data/collection_summary.csv")
```

### CEWL Data

First, load it all in and merge.

Variables in this dataframe are: - date - time - date\_time combined variable - individual\_ID for each lizard measured - region = where on the body CEWL was measured - TEWL\_g\_m2h = CEWL measurement value in grams/sq-meter/hour - ambient\_temp\_C = temperature when and where measurement was taken - ambient\_RH\_percent = relative humidity when and where measurement was taken - e\_s\_kPa = saturation vapor pressure at a given temperature (calculated using the Clausius-Clapeyron equation from Riddell et al. 2017, cited in the published paper using this data) - e\_a\_kPa = actual ambient vapor pressure (e\_a = e\_s \* RH proportion) - VPD\_kPa = vapor pressure deficit, which is essentially the drying power of the air (VPD = e\_s - e\_a)

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

```

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

# week 2
CEWL_April_19 <- read.csv("../data/capture_CEWL/4-19-21-CEWL.csv",
                        na.strings=c("", "NA")) %>%
  dplyr::select(date = Date,
                Time, Status,
                ID = Comments,
                TEWL_g_m2h = TEWL..g..m2h.., # rename
                ambient_temp_C = AmbT..C., # rename
                ambient_RH_percent = AmbRH....
              )

# week 3
CEWL_April_26 <- read.csv("../data/capture_CEWL/4-26-21-CEWL.csv",
                        na.strings=c("", "NA")) %>%
  dplyr::select(date = Date,
                Time, Status,
                ID = Comments,
                TEWL_g_m2h = TEWL..g..m2h.., # rename
                ambient_temp_C = AmbT..C., # rename
                ambient_RH_percent = AmbRH....
              )

# week 4
CEWL_May_3 <- read.csv("../data/capture_CEWL/5-3-21-CEWL.csv",
                      na.strings=c("", "NA")) %>%
  dplyr::select(date = Date,
                Time, Status,
                ID = Comments,
                TEWL_g_m2h = TEWL..g..m2h.., # rename
                ambient_temp_C = AmbT..C., # rename
                ambient_RH_percent = AmbRH....
              )

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

```

```

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

# merge all CEWL datafiles & reformat
CEWL <- CEWL_April_05 %>% # week 1
  # join with weeks 2-6
  rbind(., CEWL_April_19,
        CEWL_April_26,
        CEWL_May_3,
        CEWL_May_10,
        CEWL_May_17
  ) %>%

# remove any unsuccessful measurements
dplyr::filter(Status == "Normal") %>%
# extract individual_ID and region separately from the "ID" variable
separate(ID, c("individual_ID", "region")) %>%
# reformat data
dplyr::mutate(# paste and format date-time variable
              CEWL_date_time = as.POSIXct(paste(date, Time),
                                             format = "%m/%d/%y %I:%M:%S %p"),

              # reformat date only
              date = as.Date(date, format = "%m/%d/%y"),
              # reformat time
              # format extracts just time after posix adds arbitrary date
              # but then it's a character again...
              Time = format(as.POSIXct(Time, format = "%I:%M:%S %p"),
                            format = "%H:%M:%S"),
              # format individual ID as a factor
              individual_ID = as.factor(individual_ID),
              # set body region as a factor variable after getting only the consistent characters due
              region = as.factor(substring(region, 1, 4)),
              # calculate VPD
              ambient_temp_K = ambient_temp_C + 273.15,
              e_s_kPa = 0.611*exp(((2500000/461.5)*
                                   ((1/273)-(1/ambient_temp_K)))),
              e_a_kPa = e_s_kPa * (ambient_RH_percent/100),
              VPD_kPa = e_s_kPa - e_a_kPa
  ) %>%

# remove cols not relevant to stats
dplyr::select(-Status) %>%
# remove any rows with missing values
dplyr::filter(complete.cases(.))
summary(CEWL)

```

```
##           date           Time           individual_ID  region
```

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

## CEWL Formatting

redo the levels for body region:

```
CEWL$region <- factor(CEWL$region,
                      levels = c("dors", "vent",
                                "head", "dewl", "mite"),
                      labels = c("Dorsum", "Ventrum", "Head",
                                "Dewlap", "Mite Patch")
                      )
unique(CEWL$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

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

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

## Extra CEWL Stats

Also get mean values by body region:

```

# calculate means
CEWL_means <- CEWL %>%
  group_by(region) %>%
  summarise(n_obs = n(),
            mean_CEWL = mean(TEWL_g_m2h),
            SD_CEWL = sd(TEWL_g_m2h),
            SEM_CEWL = SD_CEWL/sqrt(n_obs)
            ) %>%
  dplyr::select(region, mean_CEWL, SEM_CEWL)

## `summarise()` ungrouping output (override with `.groups` argument)

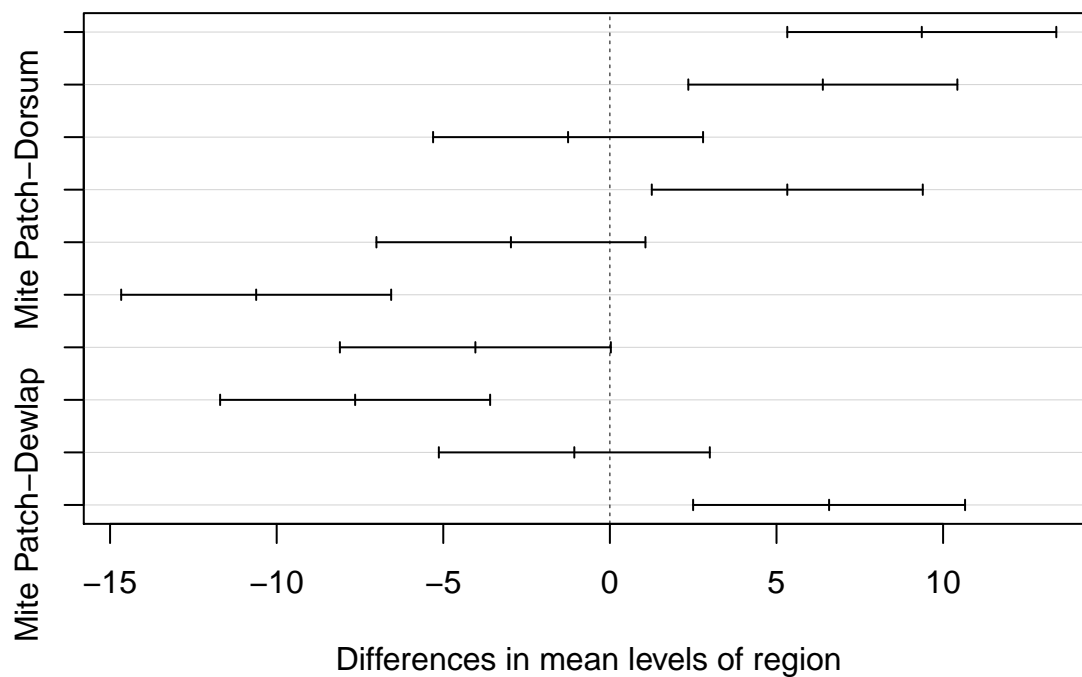
#arrange(mean_CEWL)
CEWL_means

## # A tibble: 5 x 3
##   region    mean_CEWL SEM_CEWL
##   <fct>      <dbl>    <dbl>
## 1 Dorsum      21.9     0.641
## 2 Ventrum     31.3     1.13
## 3 Head       28.3     1.08
## 4 Dewlap     20.6     0.895
## 5 Mite Patch  27.2     1.37

# pairwise ANOVA
CEWL_SLR <- lm(TEWL_g_m2h ~ region, data = CEWL)
CEWL_aov <- aov(CEWL_SLR)
CEWL_posthoc <- TukeyHSD(CEWL_aov)
plot(CEWL_posthoc)

```

### 95% family-wise confidence level





```
CEWL_posthoc_df <- data.frame(CEWL_posthoc[1]) %>%
  dplyr::select(Difference = region.diff,
               '95% confidence interval Lower limit' = region.lwr,
               '95% confidence interval Upper limit' = region.upr,
               'Adjusted p-value' = region.p.adj)
CEWL_posthoc_df
```

	Difference	95% confidence interval Lower limit	
Ventrum-Dorsum	9.360638	5.323763	
Head-Dorsum	6.390887	2.354011	
Dewlap-Dorsum	-1.254852	-5.306223	
Mite Patch-Dorsum	5.323511	1.257276	
Head-Ventrum	-2.969752	-7.006627	
Dewlap-Ventrum	-10.615491	-14.666861	
Mite Patch-Ventrum	-4.037127	-8.103362	
Dewlap-Head	-7.645739	-11.697109	
Mite Patch-Head	-1.067375	-5.133610	
Mite Patch-Dewlap	6.578364	2.497738	
	95% confidence interval Upper limit	Adjusted p-value	
Ventrum-Dorsum	13.39751386	1.762499e-09	
Head-Dorsum	10.42776209	1.662053e-04	
Dewlap-Dorsum	2.79651839	9.156911e-01	
Mite Patch-Dorsum	9.38974646	3.362987e-03	
Head-Ventrum	1.06712379	2.612293e-01	
Dewlap-Ventrum	-6.56411991	0.000000e+00	
Mite Patch-Ventrum	0.02910817	5.272558e-02	
Dewlap-Head	-3.59436813	3.176454e-06	
Mite Patch-Head	2.99885994	9.523881e-01	
Mite Patch-Dewlap	10.65898957	1.171627e-04	

```
write.csv(CEWL_posthoc_df, "./best_models/CEWL_pairwise_diffs.csv")
```

## Weather Data

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

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

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

The weather data is only every 15 minutes, but I want to match it to any minute measurement, so I need to

interpolate the values for each minute.

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

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

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

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

```

        RH_percent_interpol,
        VPD_kPa_int,
        Wind_mph_interpol,
        Solar_rad_Wm2_interpol)
summary(all_times_weather)

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

```

## Compute Scaled Mass Index

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

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

### Step 1: mass ~ SVL

plot:

```

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

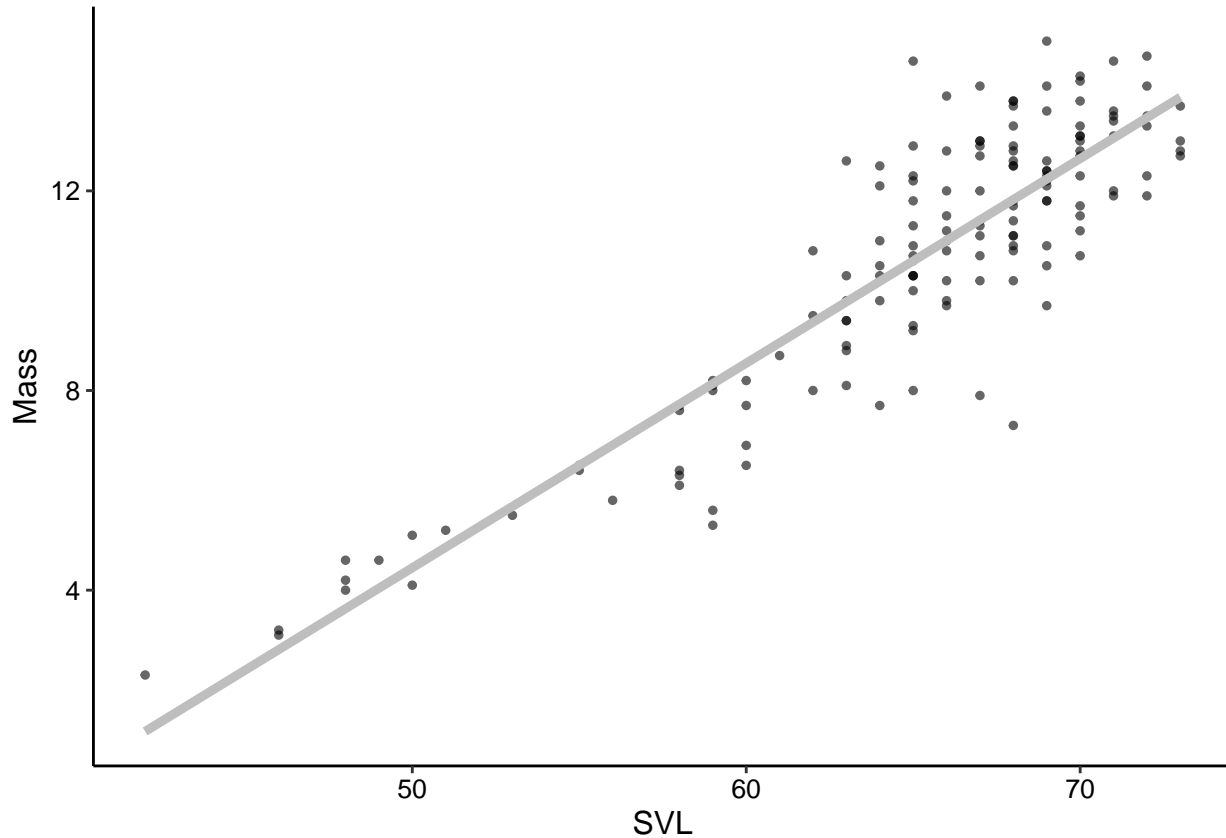
```

```

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

legend.text.align = 0
)

```



create a simple linear regression

```

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

```

```

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

```

```
## F-statistic: 547.7 on 1 and 146 DF, p-value: < 2.2e-16
```

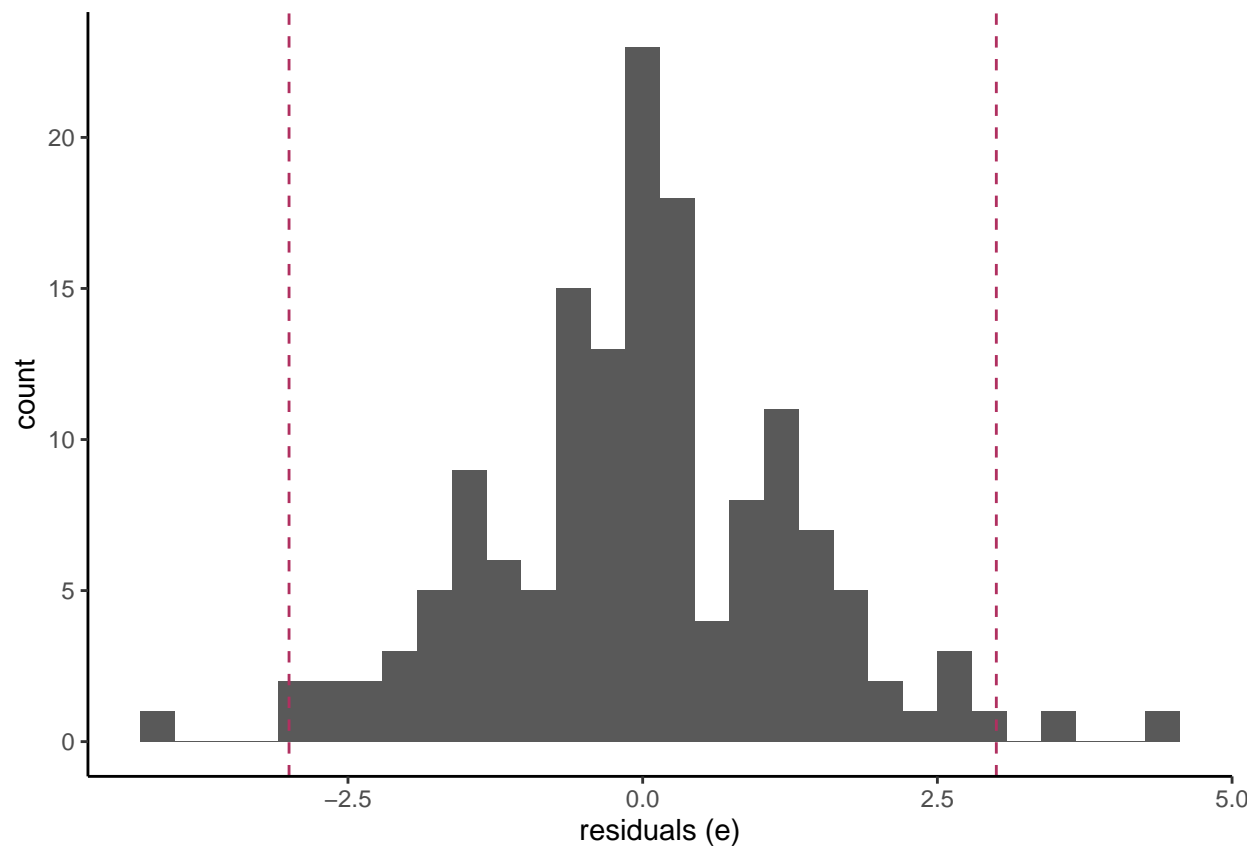
look for outliers by calculating residuals

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

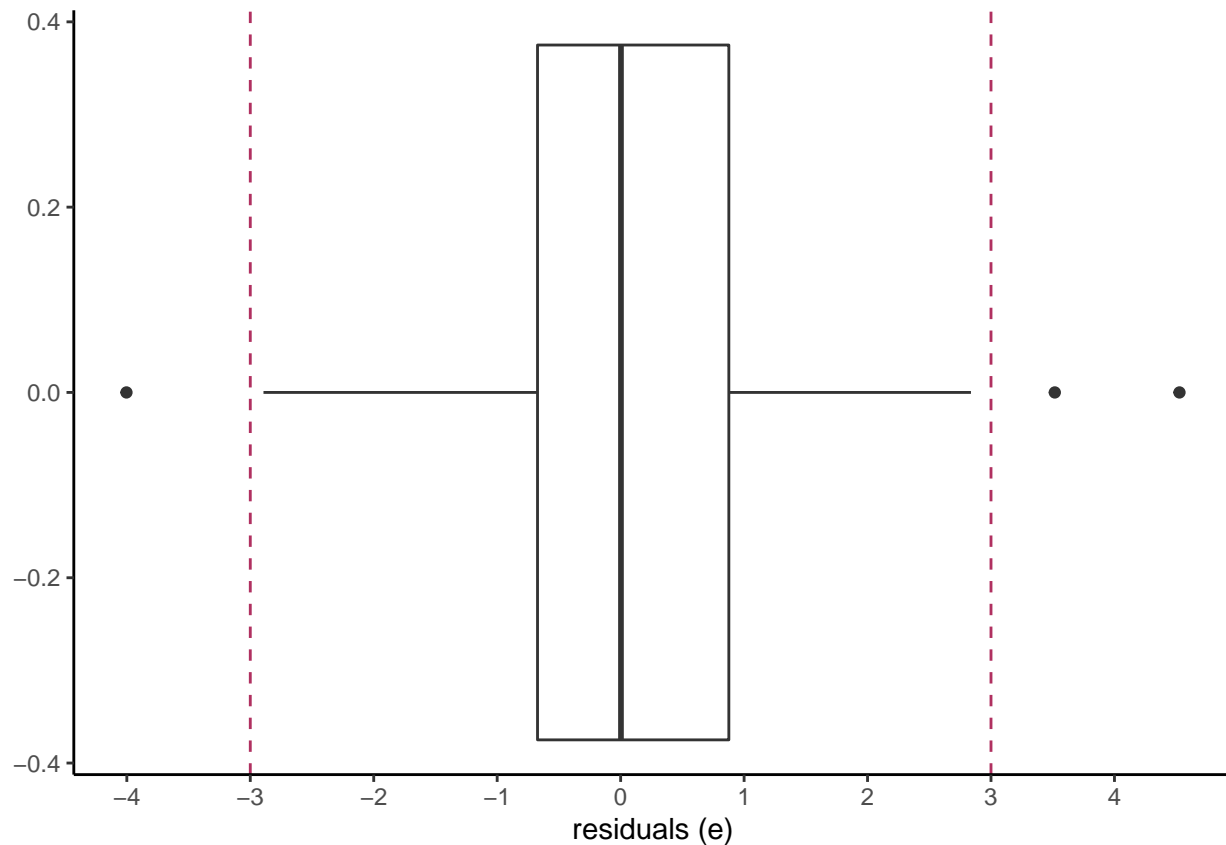
plot residuals

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

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



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



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

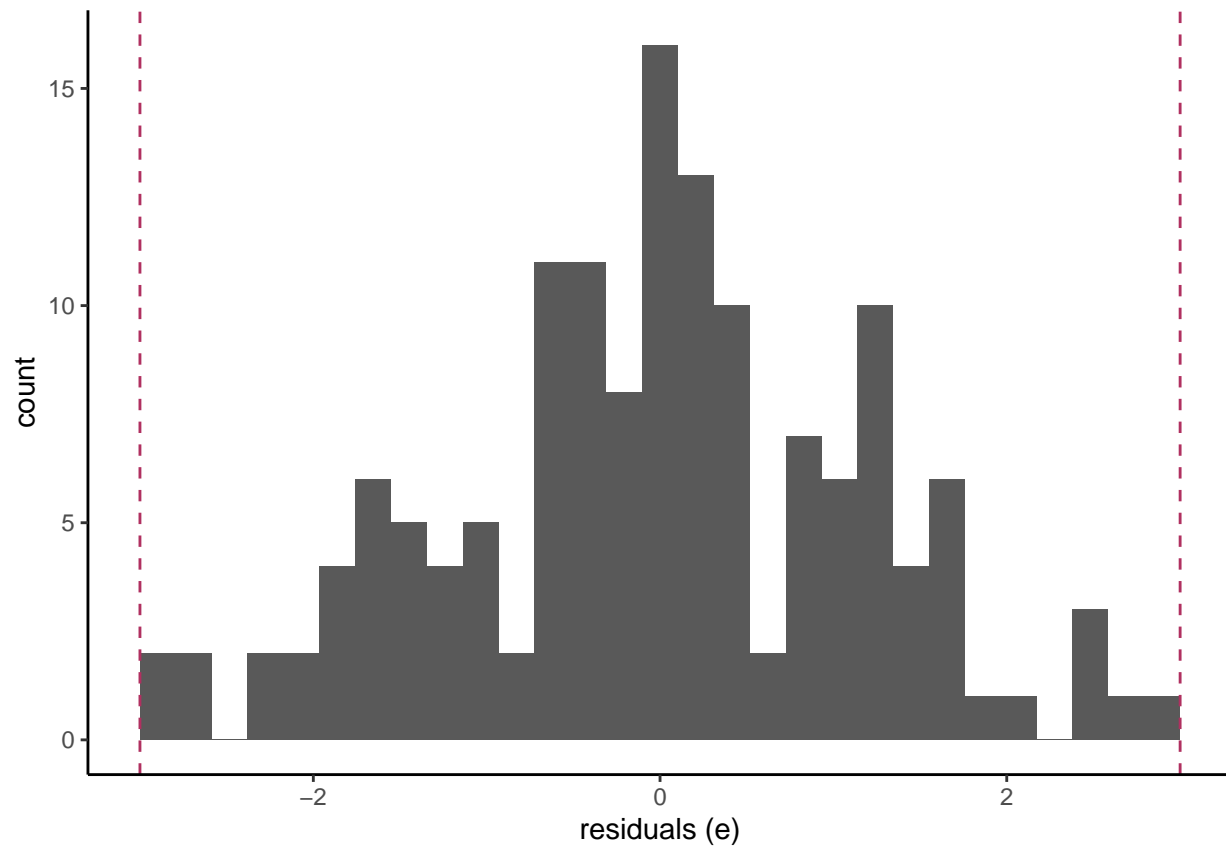
calculating residuals with outliers excluded

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

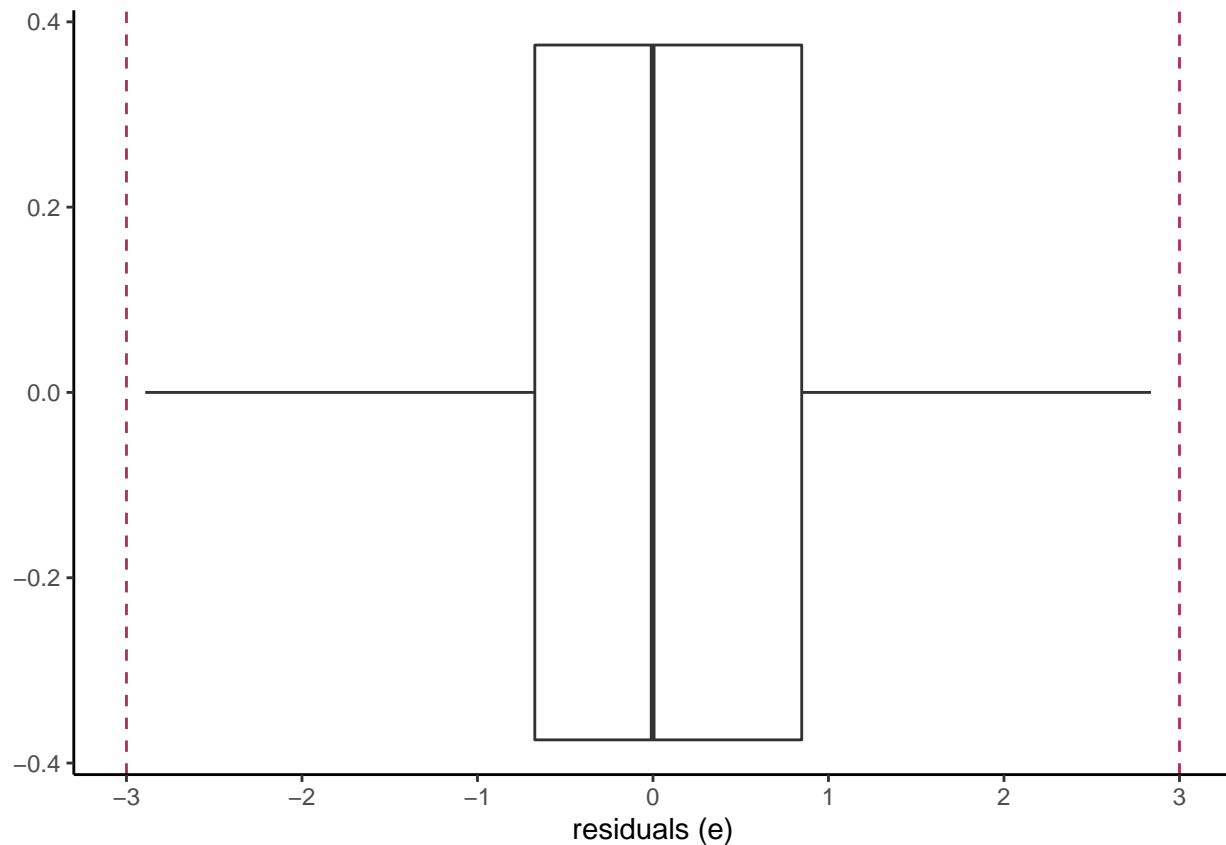
plot new residuals

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

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



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



And, check mean residual value:

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

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

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

Next, check for high leverage points:

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

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

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

```
##      date      collect_time individual_ID SVL_mm mass_g sex_M_F
## 1 2021-04-05 2022-02-10 10:38:00          4    48    4.2      M
```



```
## 2 2021-04-05 2022-02-10 10:17:00      5      50      4.1      M
## 3 2021-04-05 2022-02-10 10:47:00      6      48      4.6      M
## 4 2021-04-05 2022-02-10 10:42:00      8      42      2.3      M
## 5 2021-04-05 2022-02-10 13:27:00      9      46      3.1      F
## 6 2021-04-26 2022-02-10 12:32:00     55      46      3.2      F
## 7 2021-04-26 2022-02-10 12:47:00     62      51      5.2      M
## 8 2021-04-26 2022-02-10 12:40:00     65      48      4.0      M
## 9 2021-05-03 2022-02-10 12:36:00     85      49      4.6      M
## 10 2021-05-10 2022-02-10 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 2022-02-10 14:02:00      Y 2021-04-05 10:38:00      204
## 2             25 2022-02-10 13:59:00      Y 2021-04-05 10:17:00      222
## 3             24 2022-02-10 14:06:00      N 2021-04-05 10:47:00      199
## 4             23 2022-02-10 14:20:00      N 2021-04-05 10:42:00      218
## 5             23 2022-02-10 14:43:00    <NA> 2021-04-05 13:27:00       76
## 6             27 2022-02-10 13:16:00      N 2021-04-26 12:32:00       44
## 7             26 2022-02-10 14:28:00      N 2021-04-26 12:47:00      101
## 8             25 2022-02-10 15:26:00    <NA> 2021-04-26 12:40:00      166
## 9             24 2022-02-10 14:13:00      Y 2021-05-03 12:36:00       97
## 10            21 2022-02-10 17:15:00      Y 2021-05-10 13:10:00      245
##   y_hat      e row      H
## 1 3.62910 -0.57090   4 0.05776372
## 2 4.44886  0.34886   5 0.04645120
## 3 3.62910 -0.97090   6 0.05776372
## 4 1.16982 -1.13018   8 0.10020003
## 5 2.80934 -0.29066   9 0.07049270
## 6 2.80934 -0.39066  54 0.07049270
## 7 4.85874 -0.34126  60 0.04132611
## 8 3.62910 -0.37090  63 0.05776372
## 9 4.03898 -0.56102  83 0.05193040
## 10 4.44886 -0.65114 118 0.04645120
```

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

Check for influential points based on Cook's distance:

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

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

```

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

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

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

```

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

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

```

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

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

```

```

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

```

```

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

# check residuals values

```

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

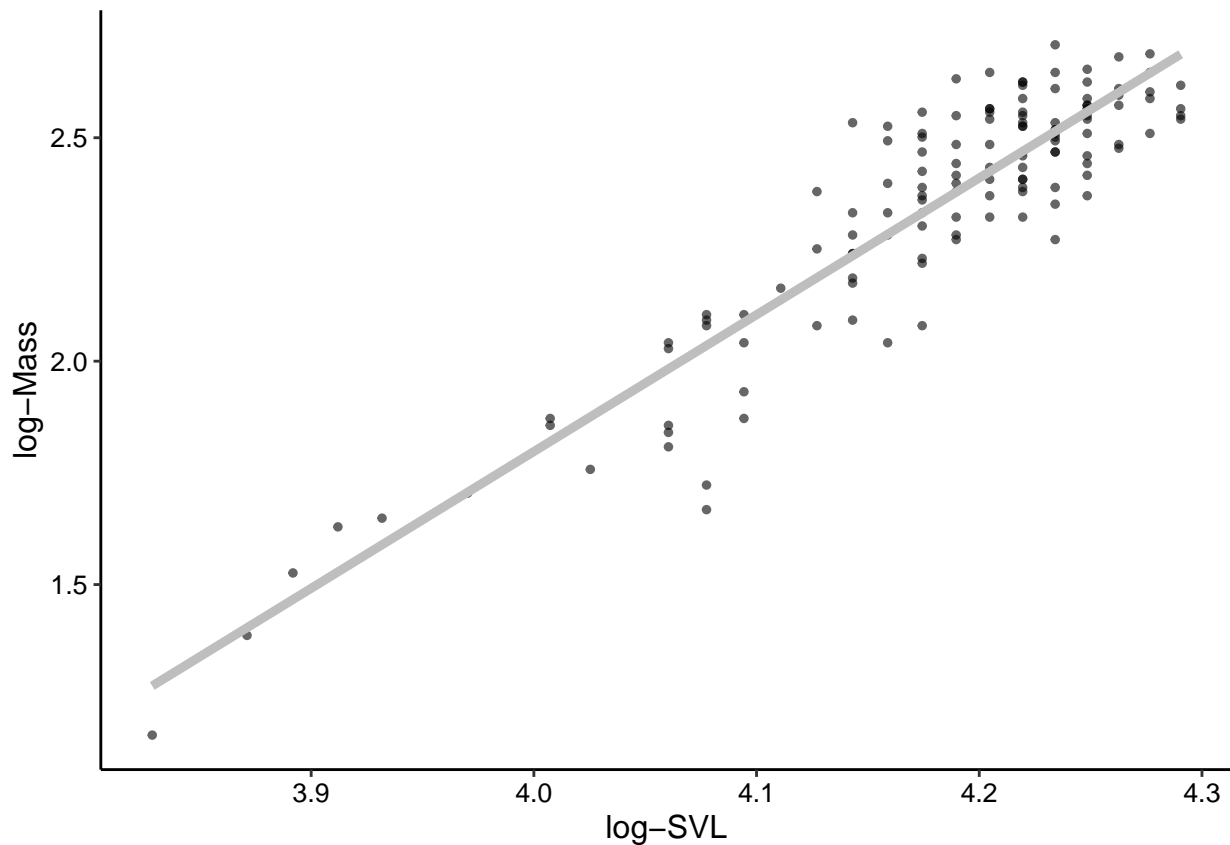
```
##           mean_res           med
## 1 4.654038e-17 0.001458016
```

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

## Step 2: make log-log relationship

plot and calculate SLR for filtered data

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



SLR

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

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

compute standardized major axis using this regression equation:

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

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

also get a value for L0:

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

### Step 3: calculate scaled mass index

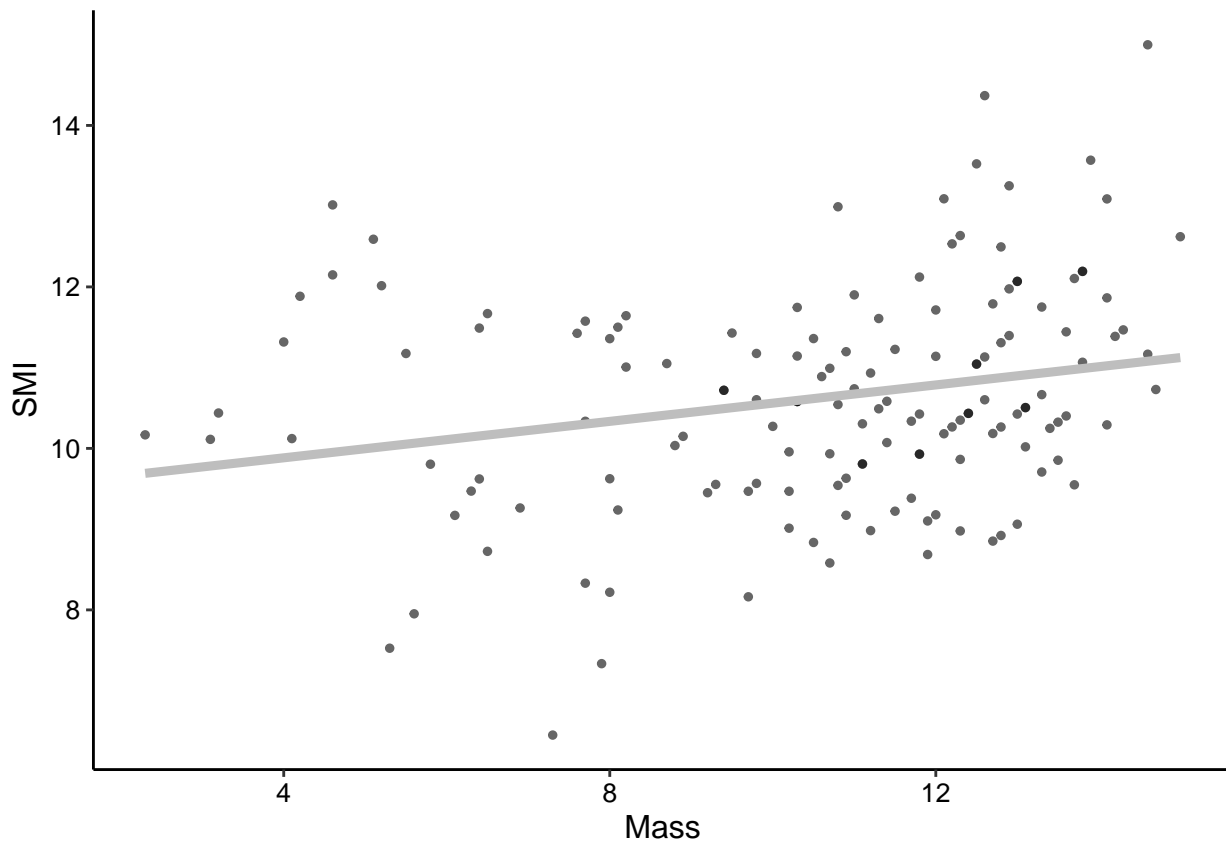
(And join weather data.)

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

### Check

Look at the difference between regular mass and SMI:

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



## Join Data

Add CEWL and morpho\_blood\_SMI data together.

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

```
##      date           Time      individual_ID      region
## Min.   :2021-04-05   Length:699      01      : 5   Dorsum    :141
## 1st Qu.:2021-04-19   Class :character 02      : 5   Ventrum   :141
## Median :2021-04-26   Mode  :character 03      : 5   Head      :141
## Mean   :2021-04-28                                     04      : 5   Dewlap    :139
## 3rd Qu.:2021-05-10                                     05      : 5   Mite Patch:137
## 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. :2022-02-10 11:29:00 Min. :46.00 Min. : 3.20
## 1st Qu.:1.541 1st Qu.:2022-02-10 12:37:00 1st Qu.:64.00 1st Qu.: 9.70
## Median :1.683 Median :2022-02-10 12:48:00 Median :67.00 Median :11.40
## Mean :1.673 Mean :2022-02-10 12:55:48 Mean :65.81 Mean :10.88
## 3rd Qu.:1.779 3rd Qu.:2022-02-10 13:02:15 3rd Qu.:69.00 3rd Qu.:12.80
## Max. :2.055 Max. :2022-02-10 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. :2022-02-10 12:44:00 N :368
## 1st Qu.:22.0 1st Qu.:2022-02-10 14:14:00 Y :179
## Median :23.0 Median :2022-02-10 15:25:00 NA's:152
## Mean :23.4 Mean :2022-02-10 15:16:48
## 3rd Qu.:25.0 3rd Qu.:2022-02-10 16:18:00
## Max. :28.0 Max. :2022-02-10 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

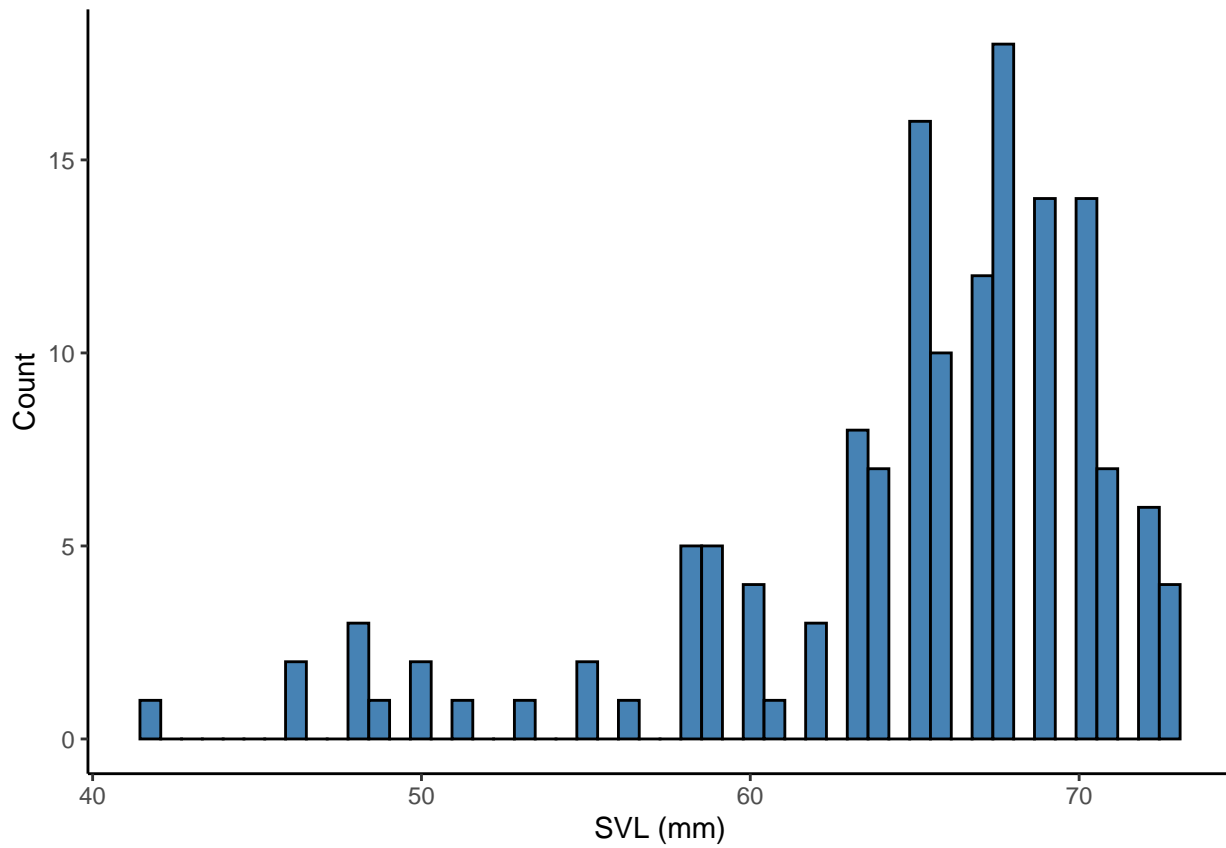
```

# Check Data Distributions

## Histograms & Q-Q Plots

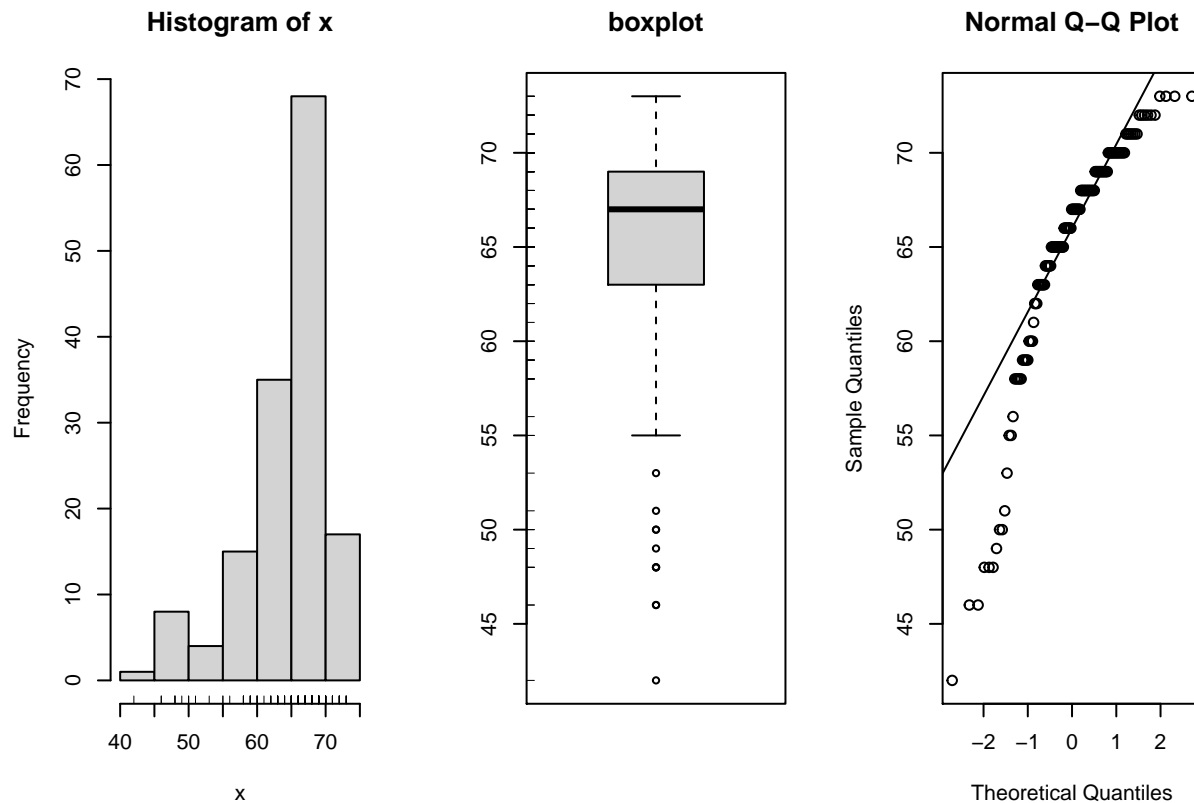
SVL

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



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



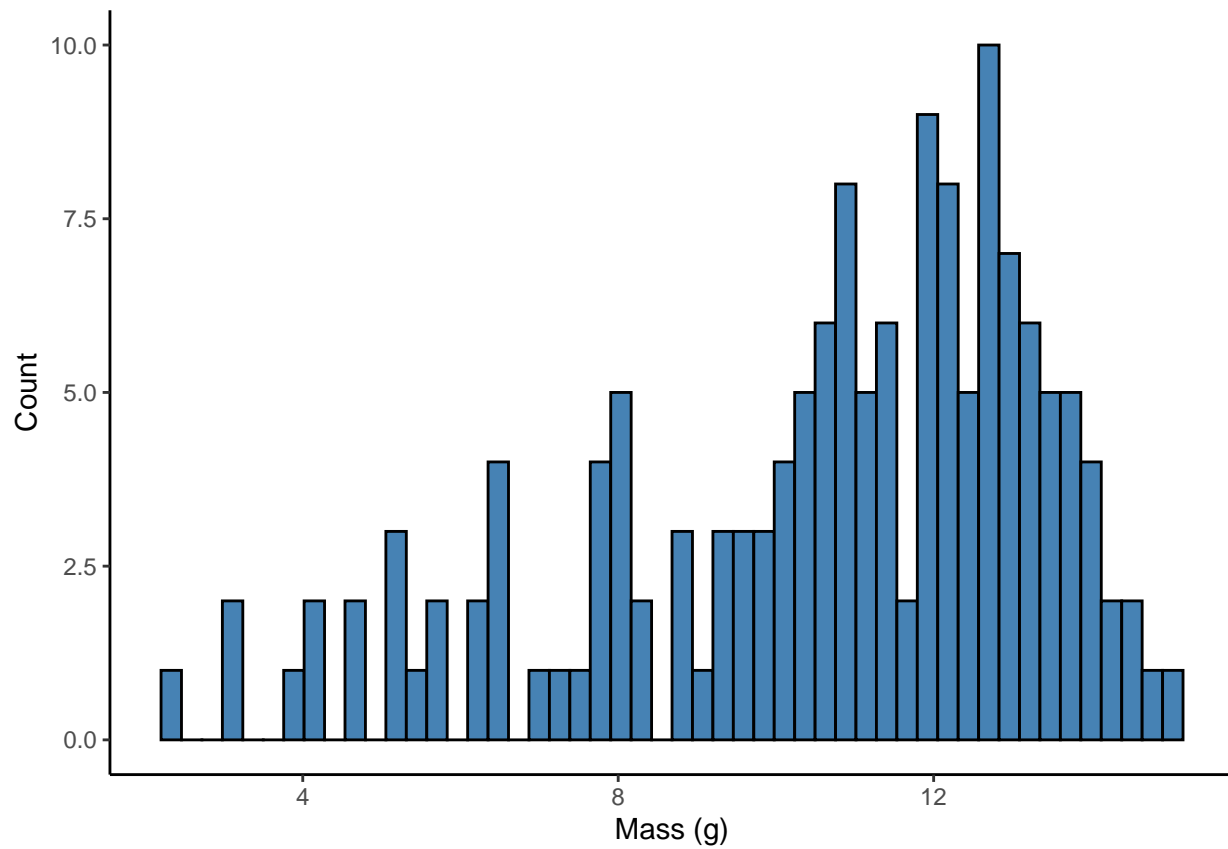


```
# Normality test if p > .05, data is normal. Data is not normal.
shapiro.test(morpho_blood_SMI$SVL_mm)
```

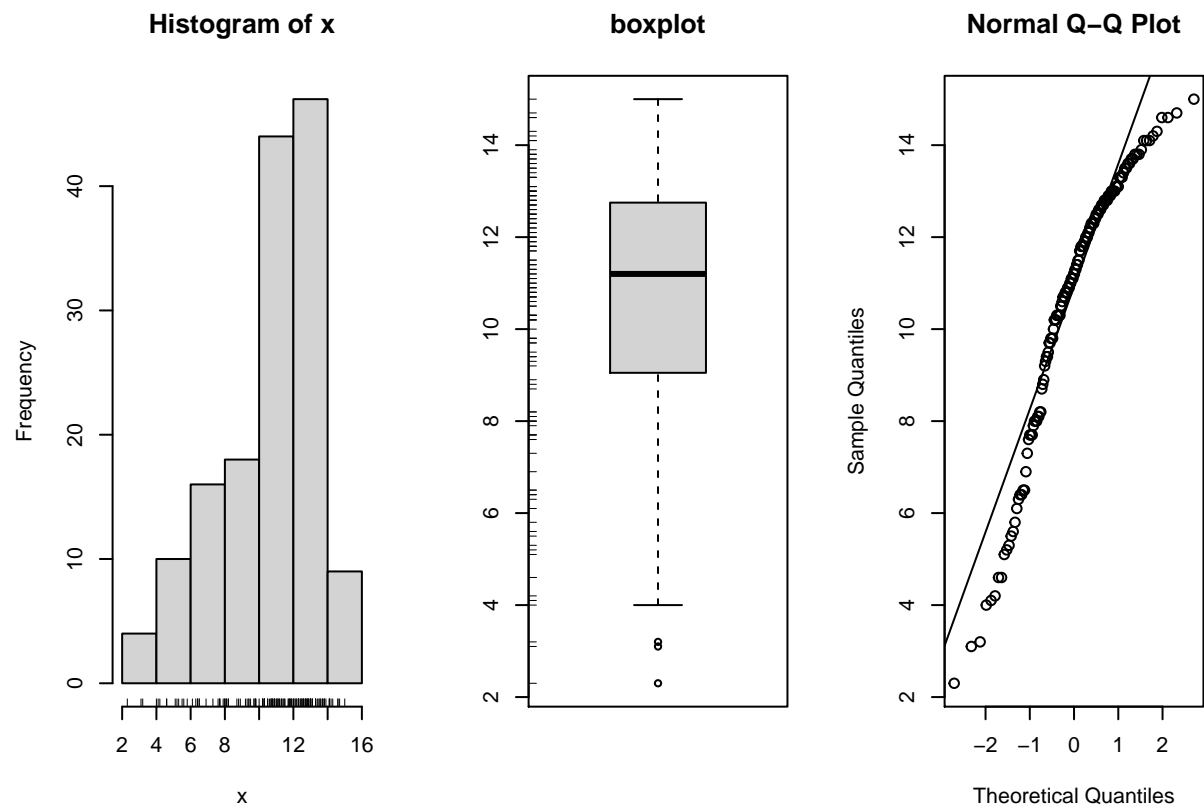
```
##
## Shapiro-Wilk normality test
##
## data: morpho_blood_SMI$SVL_mm
## W = 0.85469, p-value = 8.85e-11
```

Mass

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



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

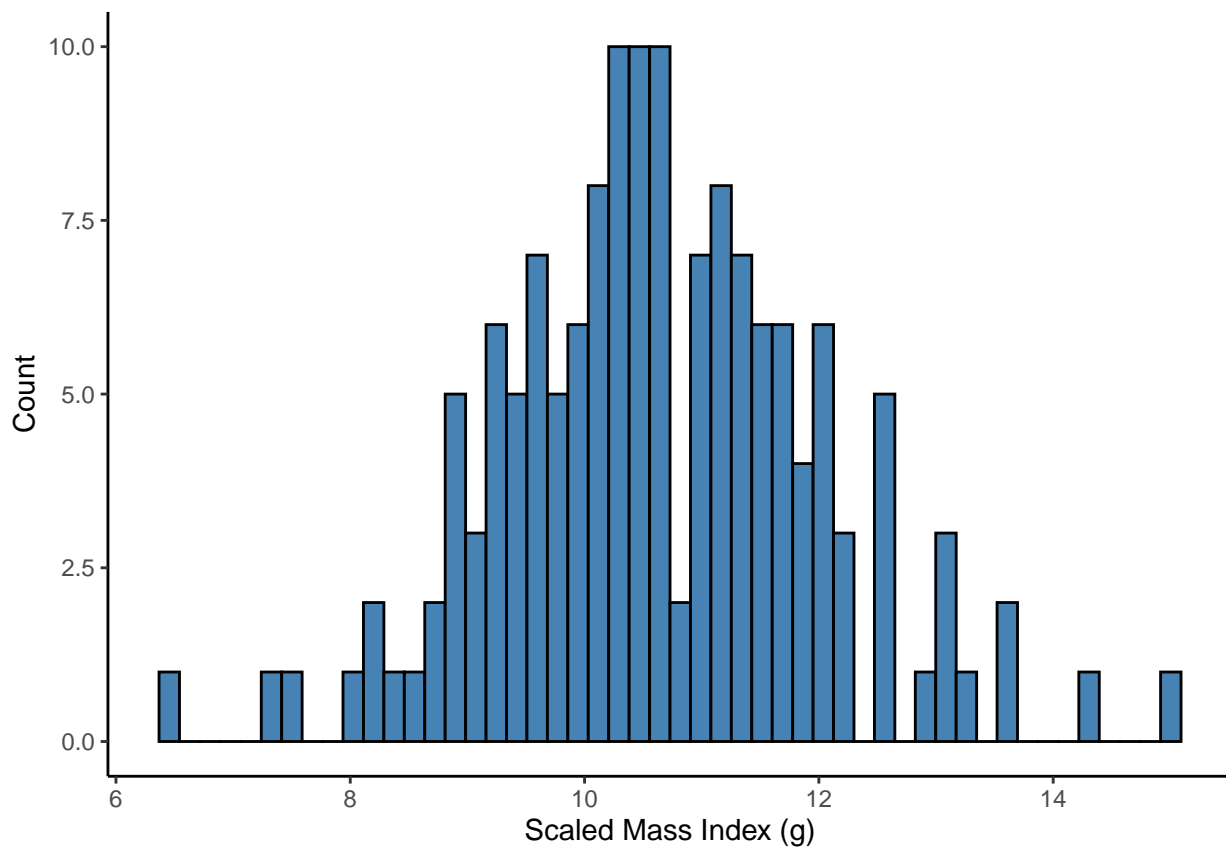


```
# Normality test if  $p > .05$ , data is normal. Data is not normal.  
shapiro.test(morpho_blood_SMI$mass_g)
```

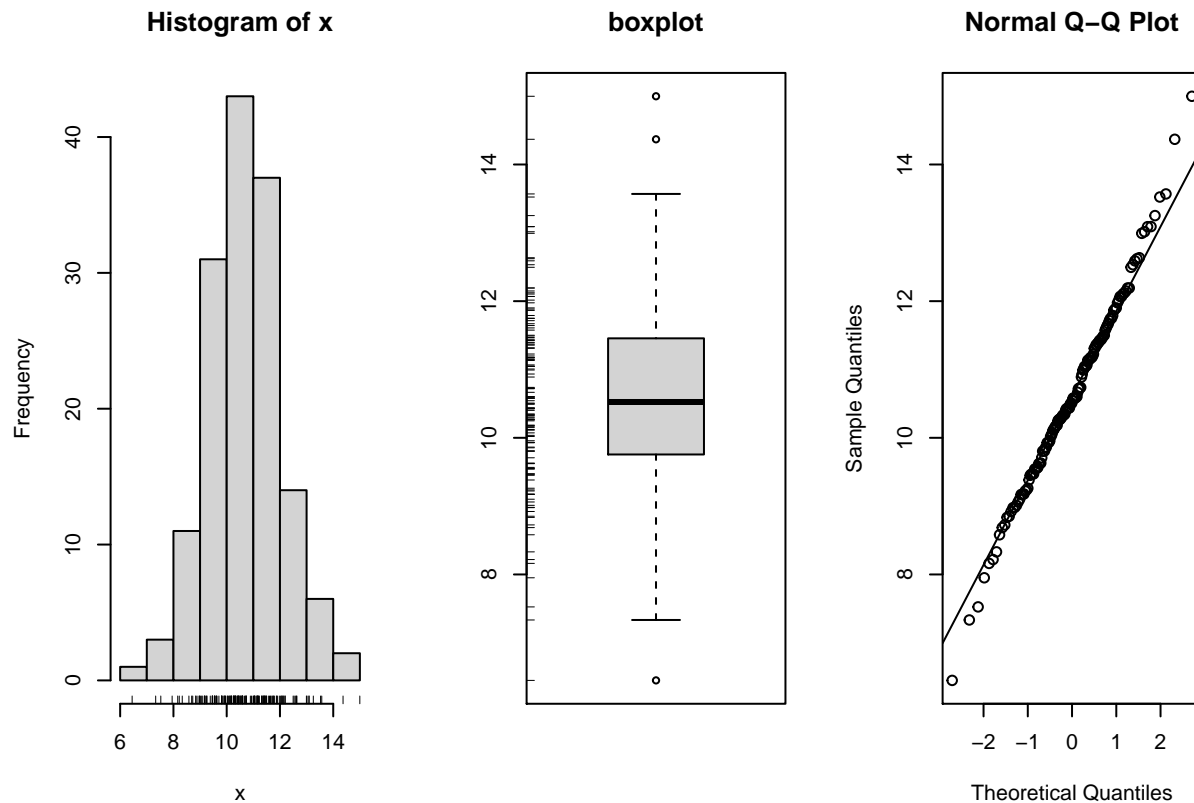
```
##  
## Shapiro-Wilk normality test  
##  
## data: morpho_blood_SMI$mass_g  
## W = 0.92517, p-value = 5.397e-07
```

SMI

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



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



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

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

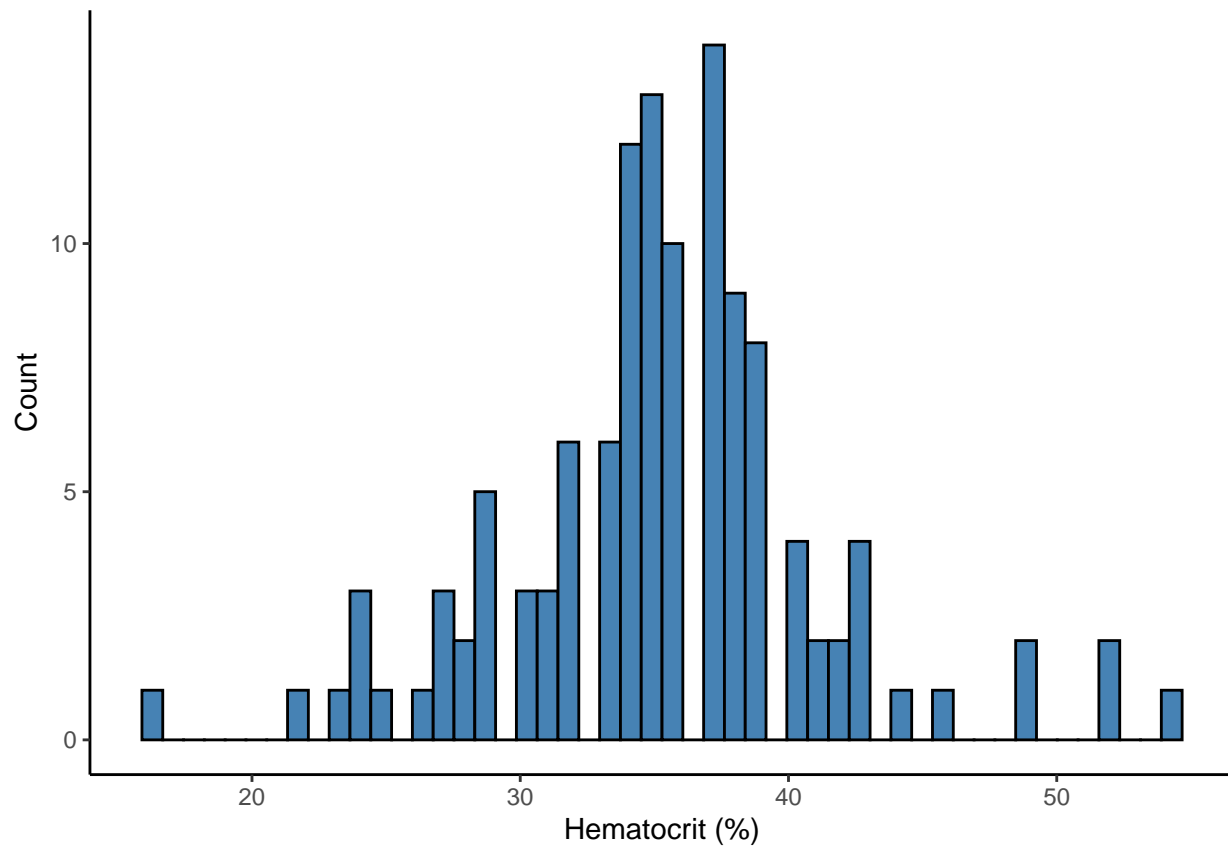
SMI is one of the few variables actually normally distributed!

## Hematocrit

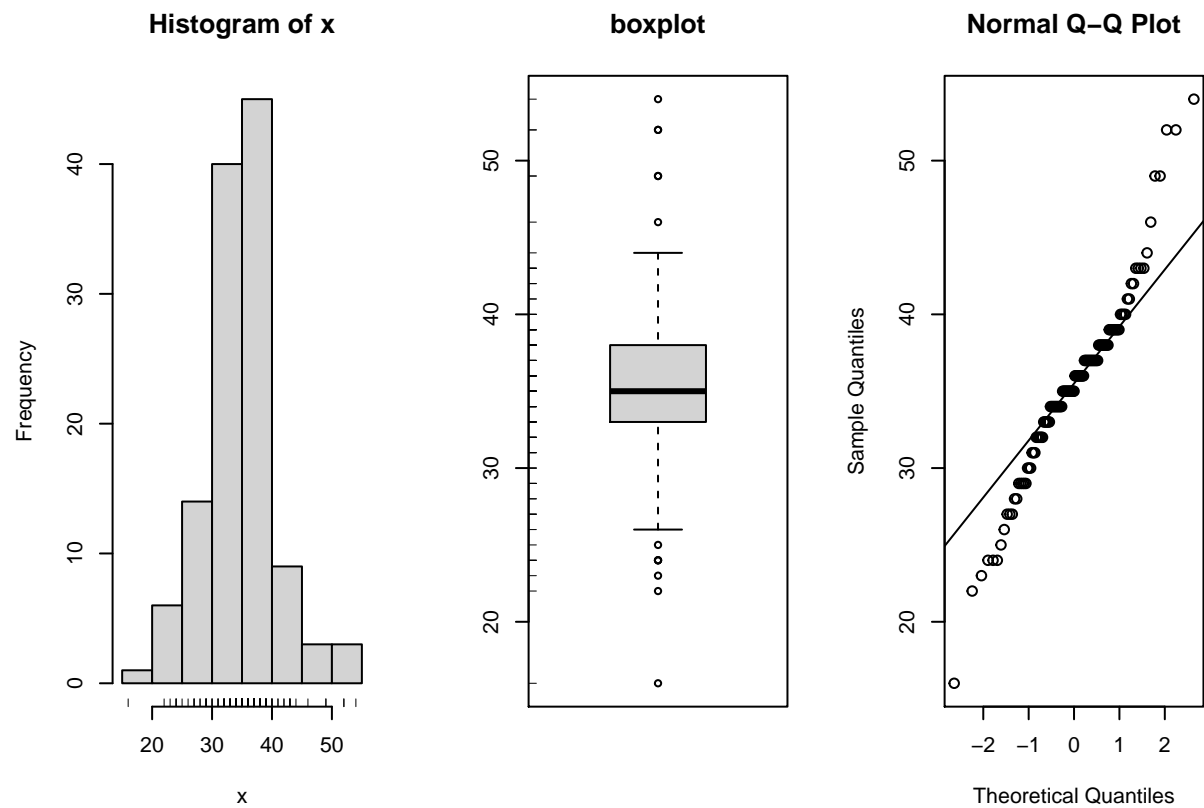
looks pretty normally distributed around ~35%, but not statistically normal

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

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



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



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

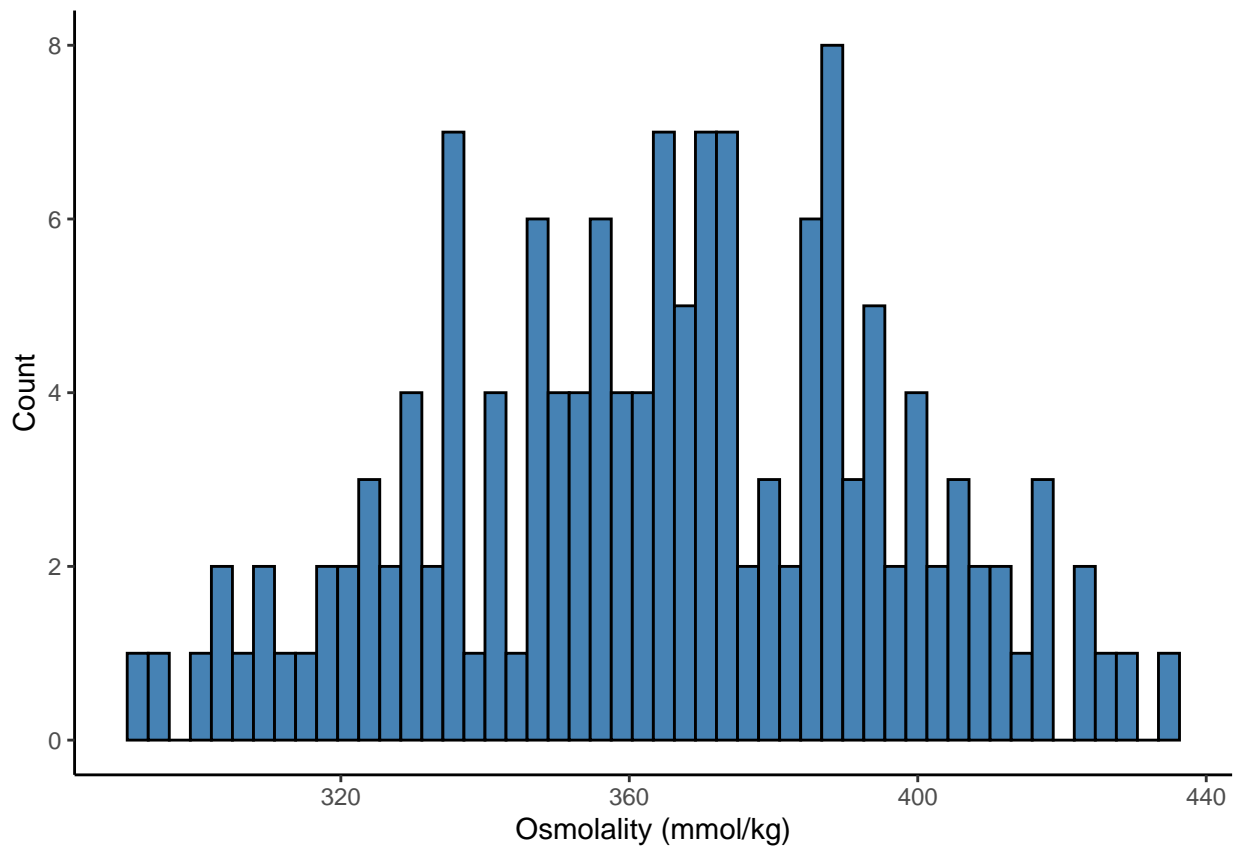
```
##
## Shapiro-Wilk normality test
##
## data: morpho_blood_SMI$hematocrit_percent
## W = 0.95933, p-value = 0.001056
```

## Osmolality

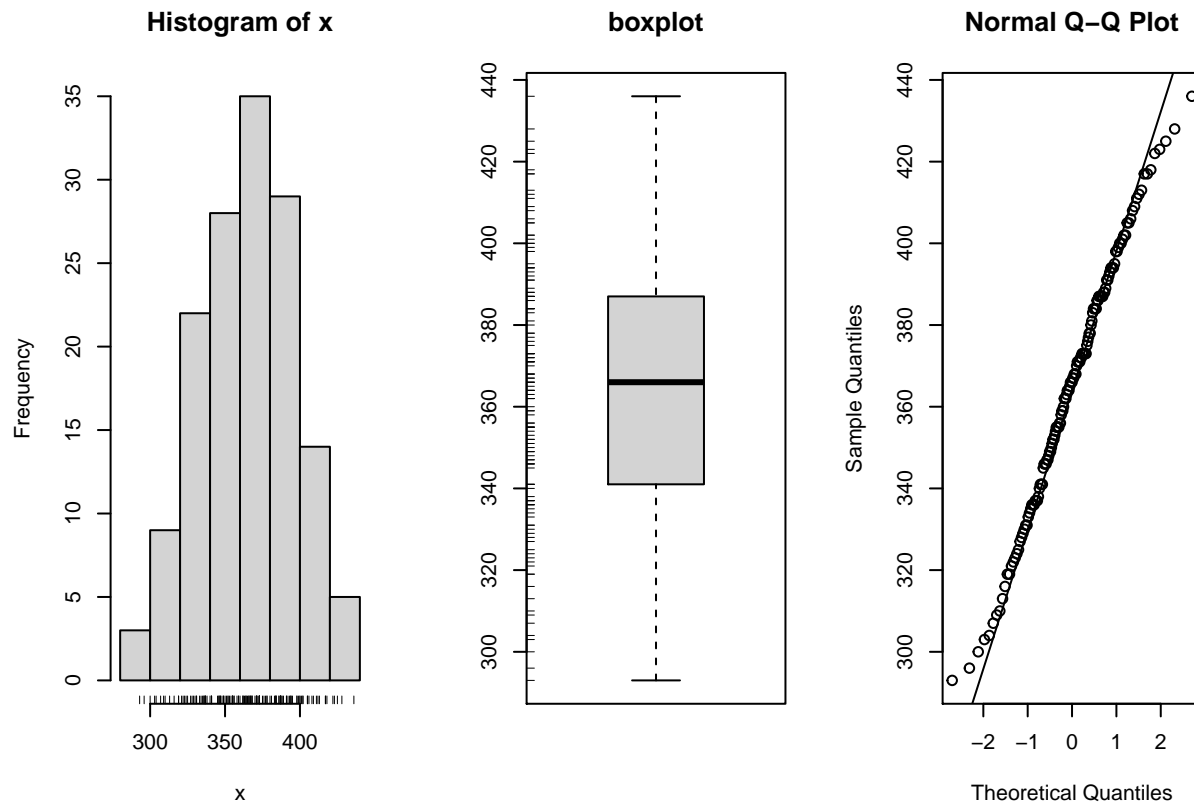
pretty normally distributed around ~370! :D

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

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



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



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

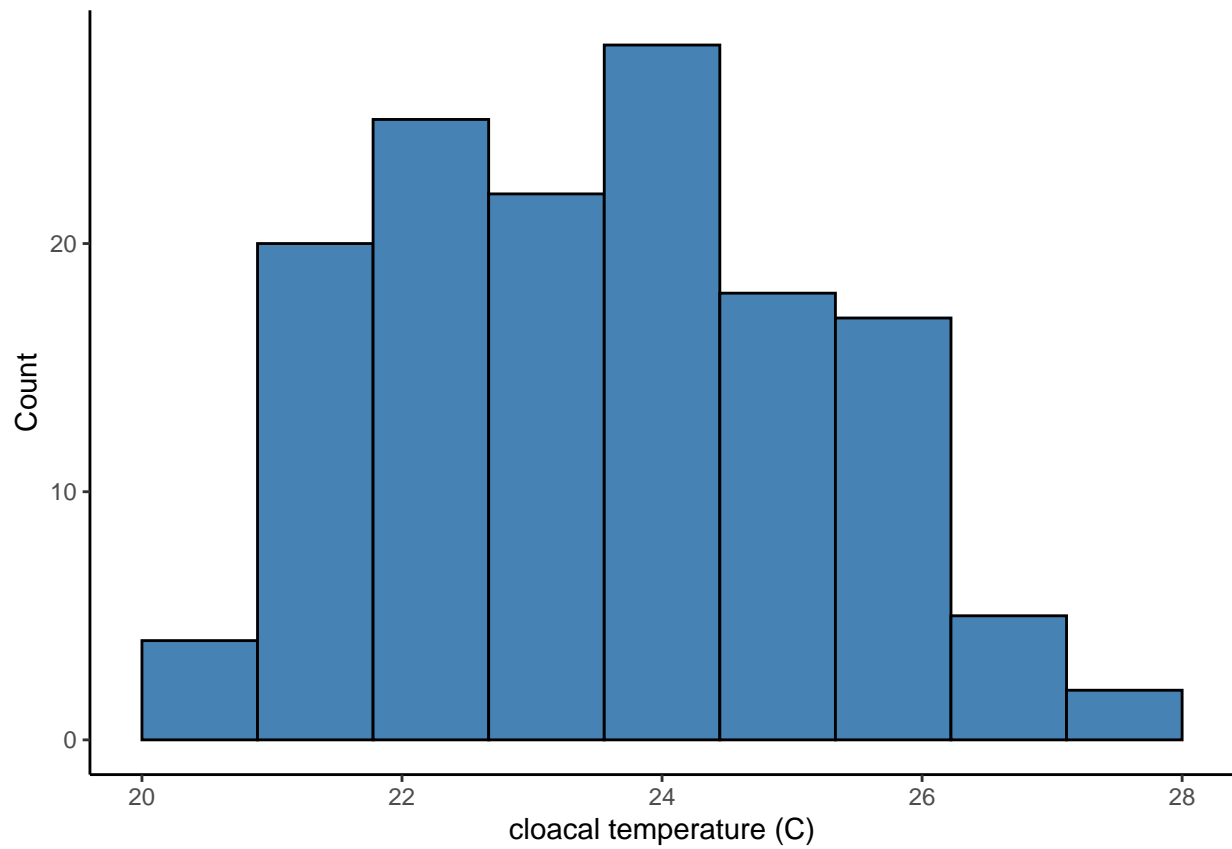
```
##
##  Shapiro-Wilk normality test
##
## data:  morpho_blood_SMI$osmolality_mmol_kg
## W = 0.99198, p-value = 0.5876
```

## Cloacal Temperature

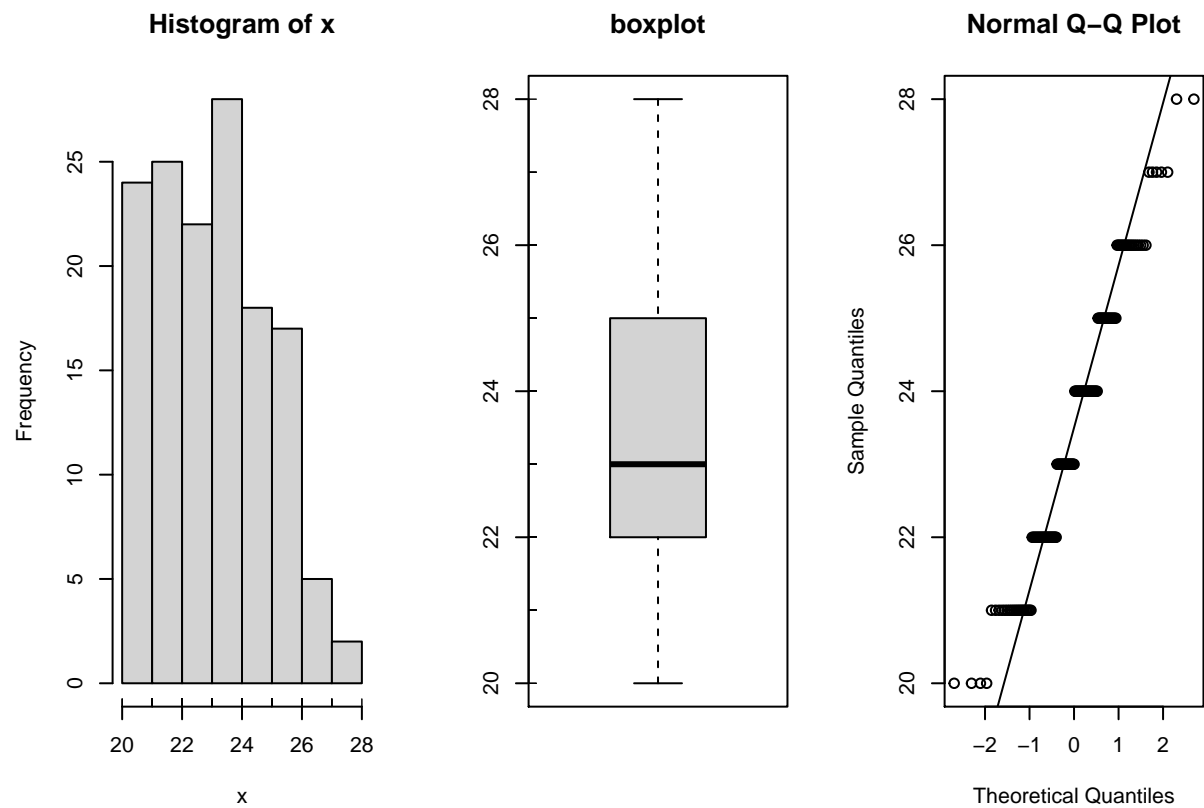
seems normally distributed, but not normal

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

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



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



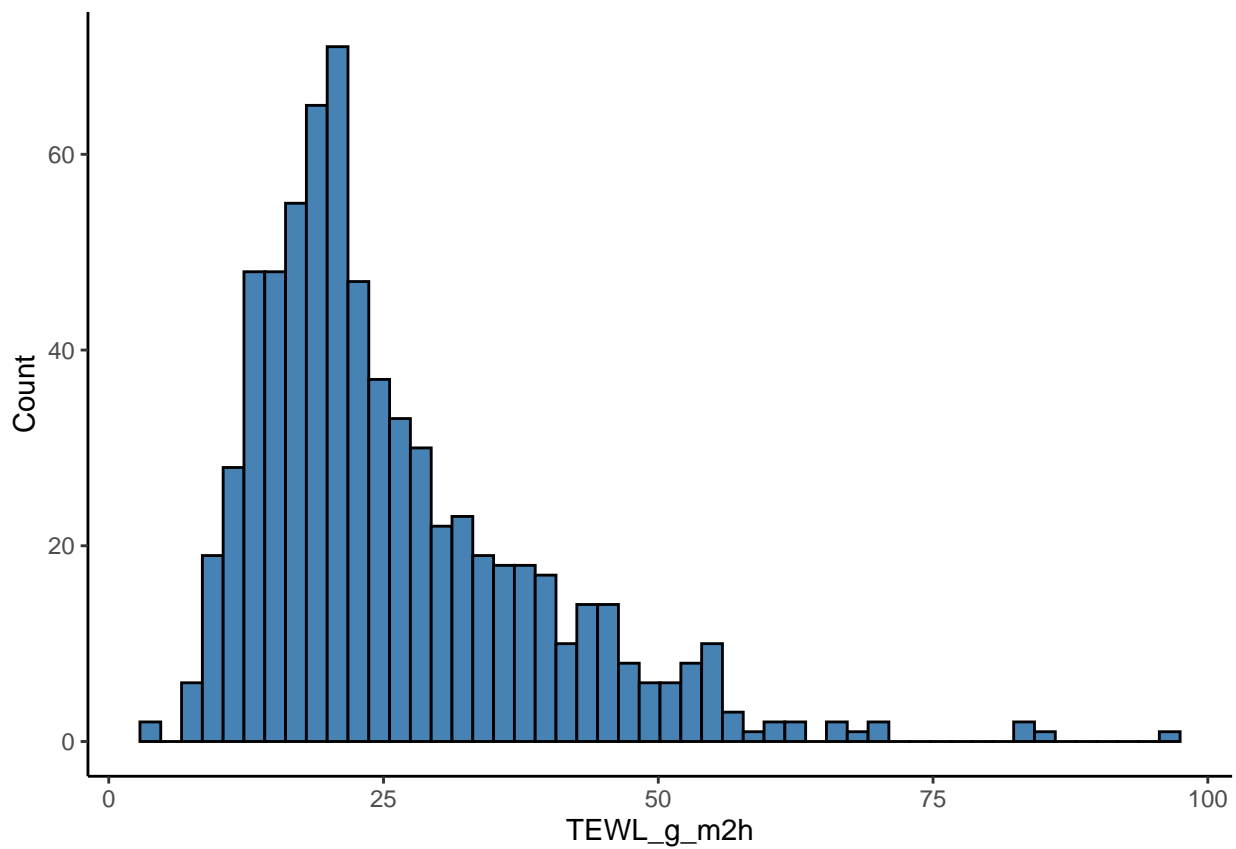


```
# Normality test if p > .05, data is normal. Data is not normal
shapiro.test(morpho_blood_SMI$cloacal_temp_C)
```

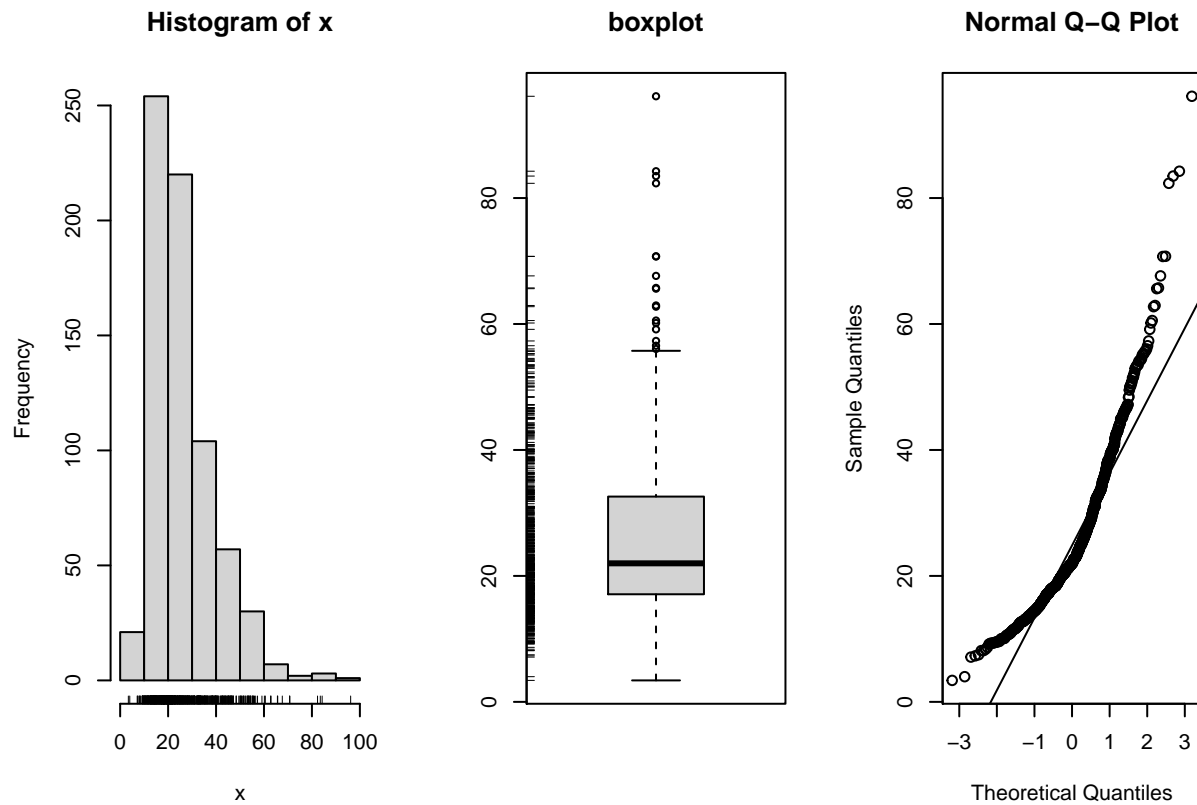
```
##
## Shapiro-Wilk normality test
##
## data: morpho_blood_SMI$cloacal_temp_C
## W = 0.95661, p-value = 0.0002007
```

## CEWL

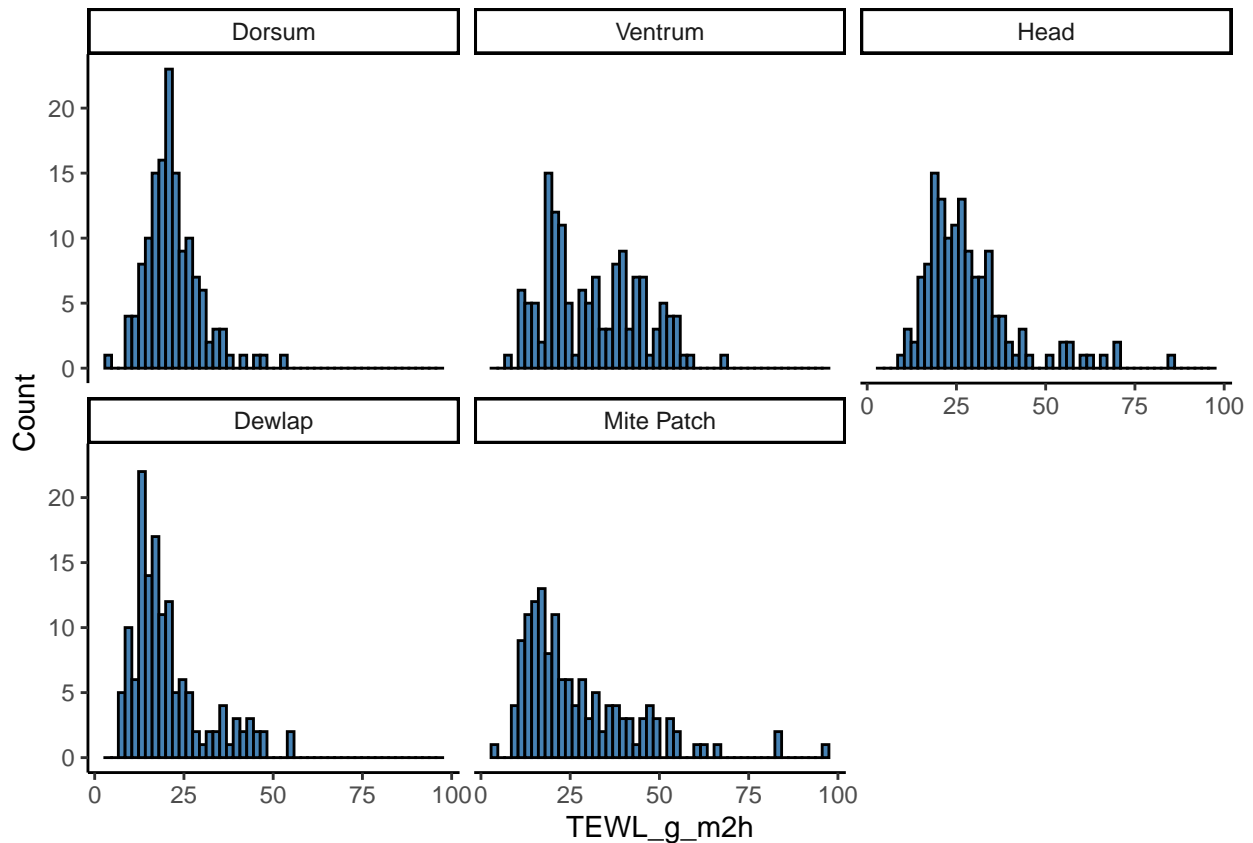
```
CEWL_data_full %>%
  ggplot(., aes(x = TEWL_g_m2h)) +
  geom_histogram(color = "black", fill="steelblue", bins=50) +
  theme_classic() +
  xlab("TEWL_g_m2h") +
  ylab("Count")
```



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



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



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

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

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

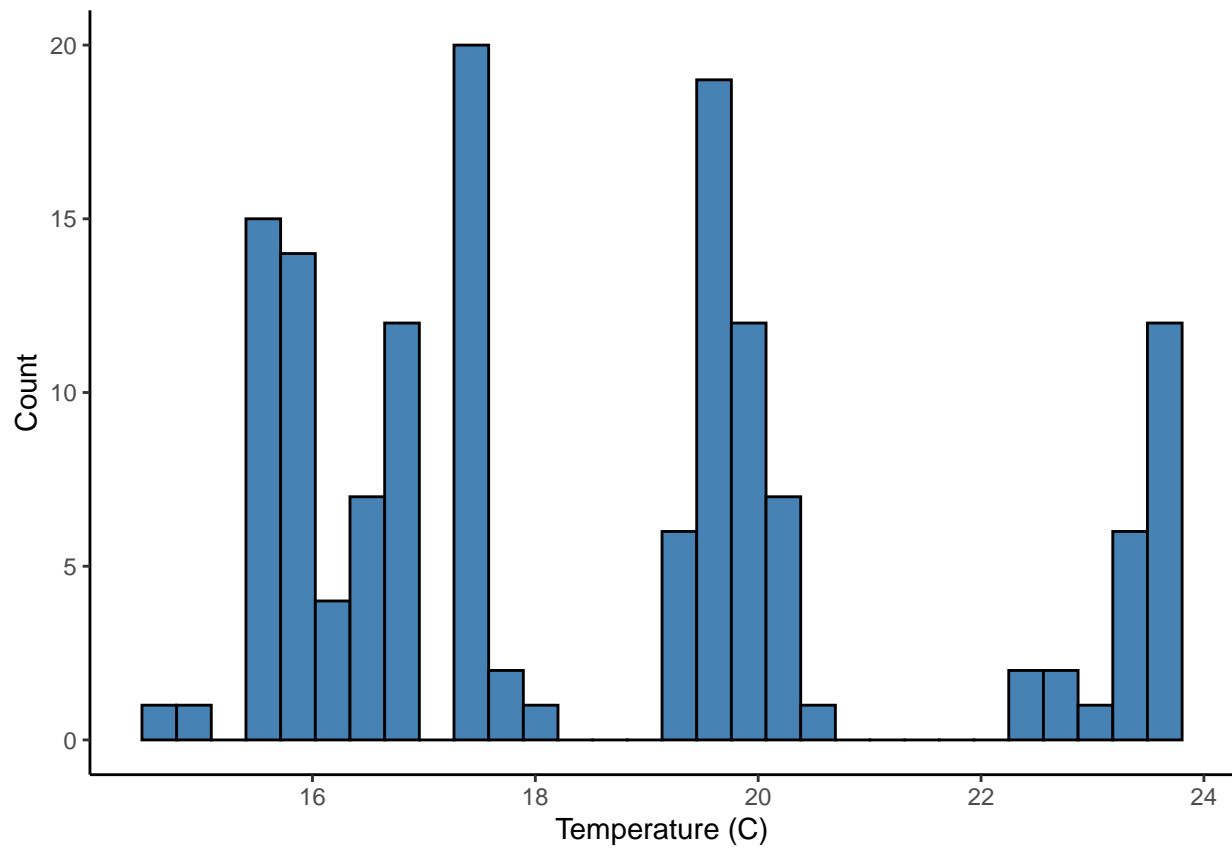
```
##
## Shapiro-Wilk normality test
##
## data: log(CEWL_data_full$TEWL_g_m2h)
## W = 0.99368, p-value = 0.004976
```

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

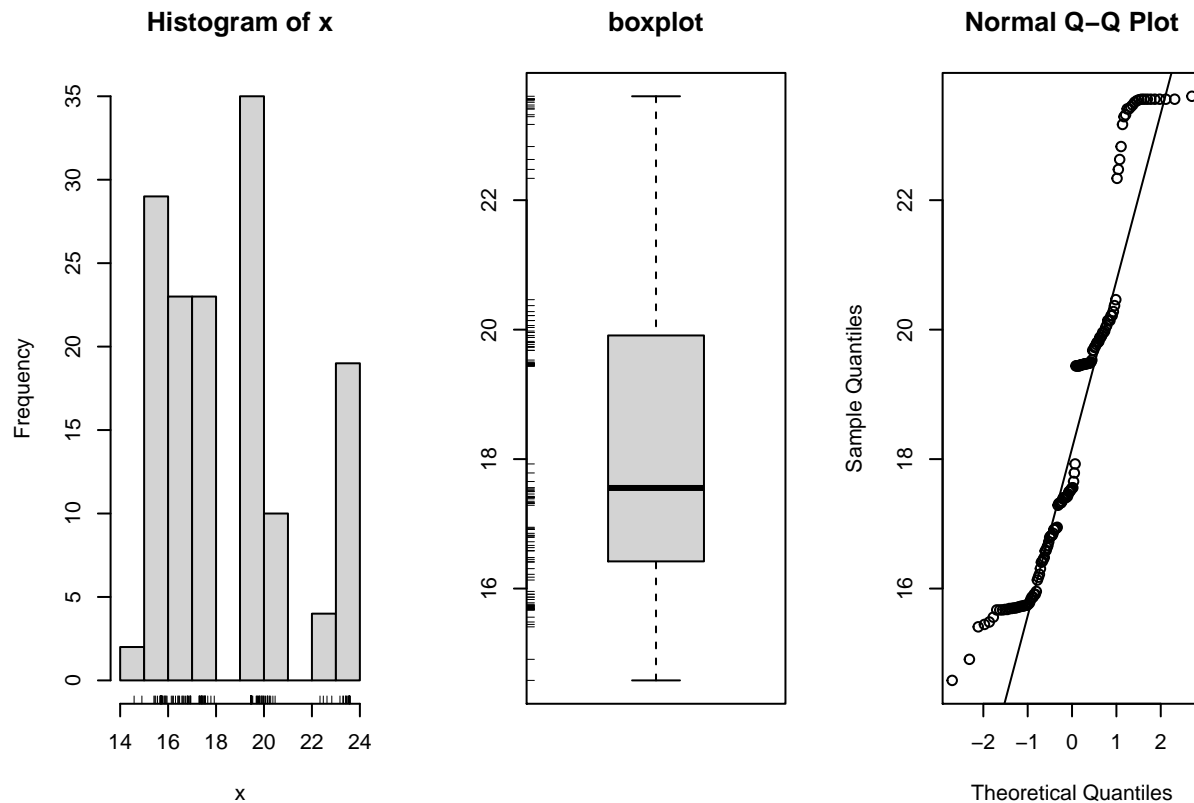
## Capture Temperature

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

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



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



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

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

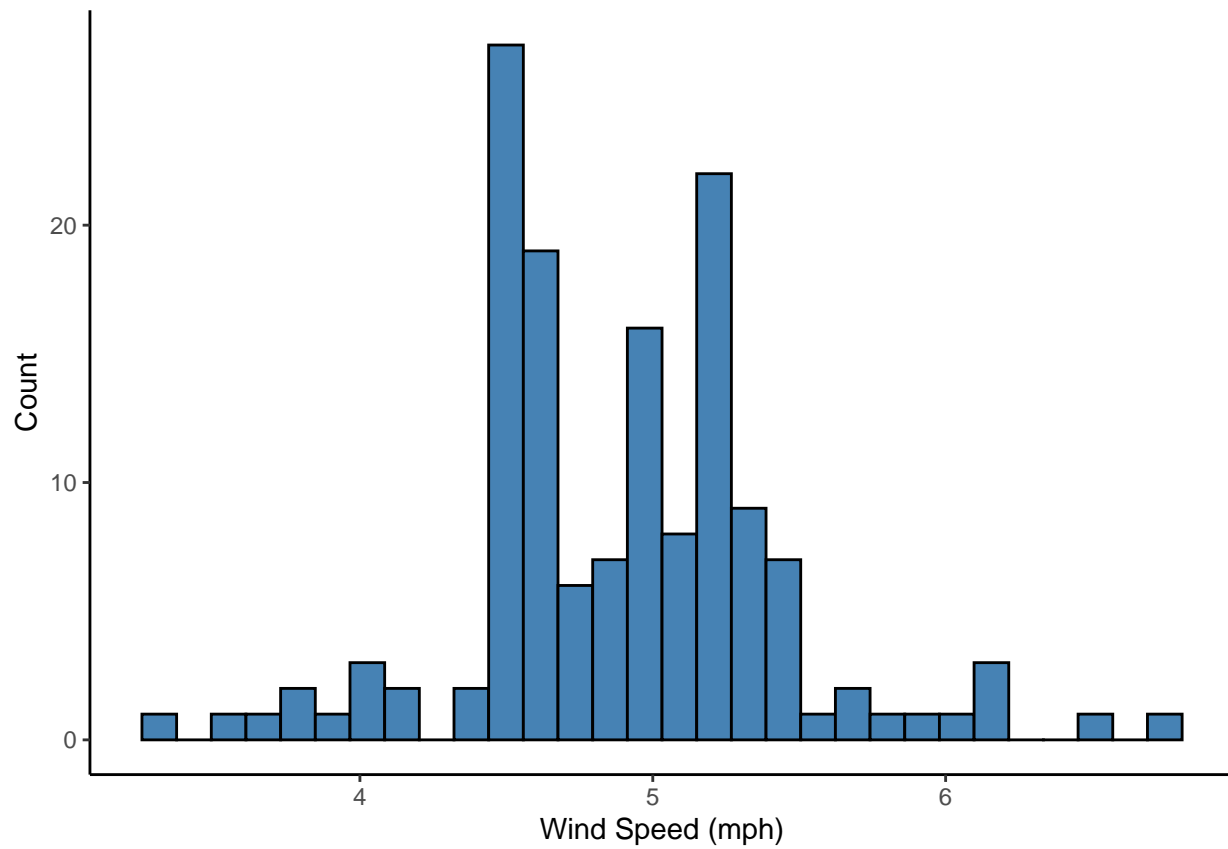
```
# log transform
shapiro.test(log(morpho_blood_SMI$temp_C_interpol))
```

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

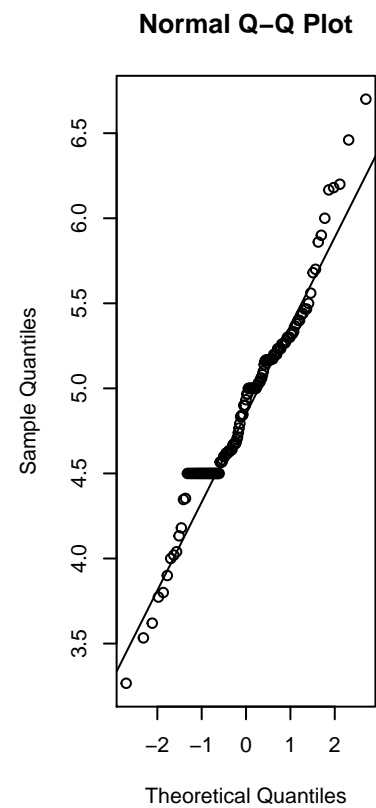
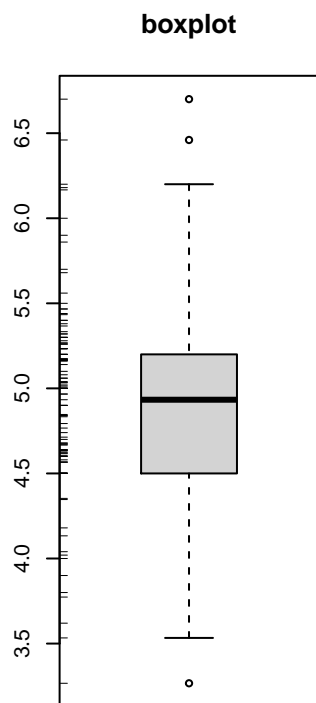
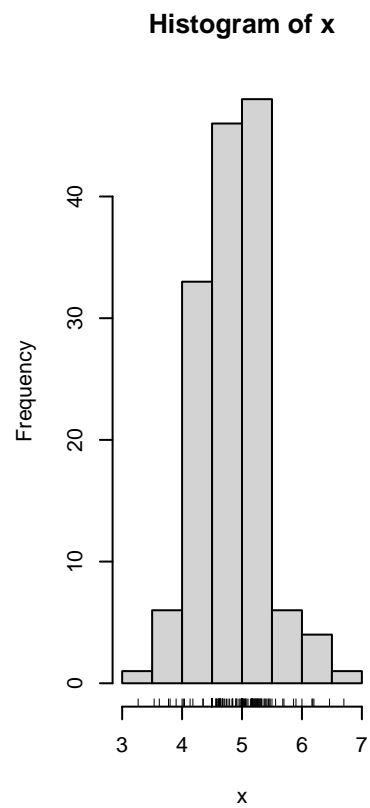
### Wind Speed at Capture

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

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



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



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

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

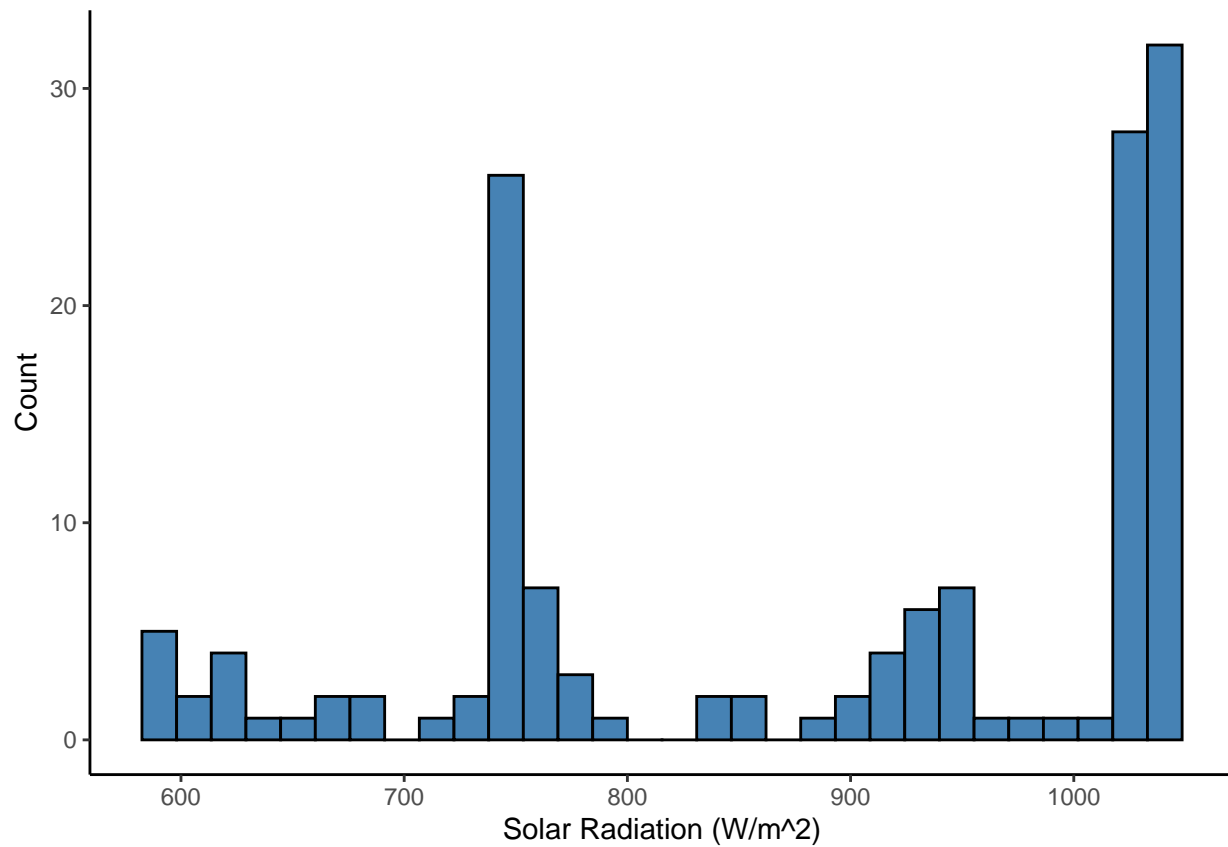
```
# ln transformation doesn't fix non normality  
shapiro.test(log(morpho_blood_SMI$Wind_mph_interpol))
```

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

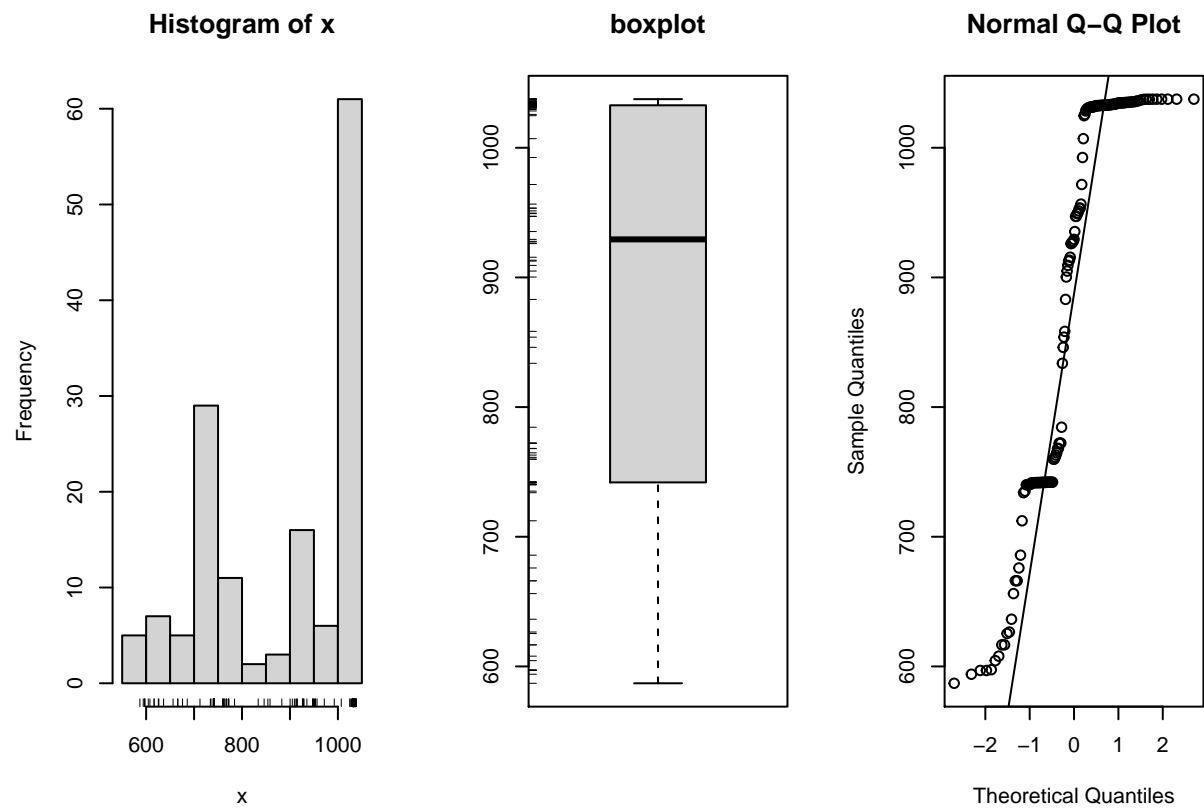
### Solar Radiation at Capture

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

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



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





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

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

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

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

## Conclusion

Osmolality and SMI were the only normally distributed variables.

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

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

## Basic Figures

### osmolality & hematocrit

Hct ~ SVL

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

```

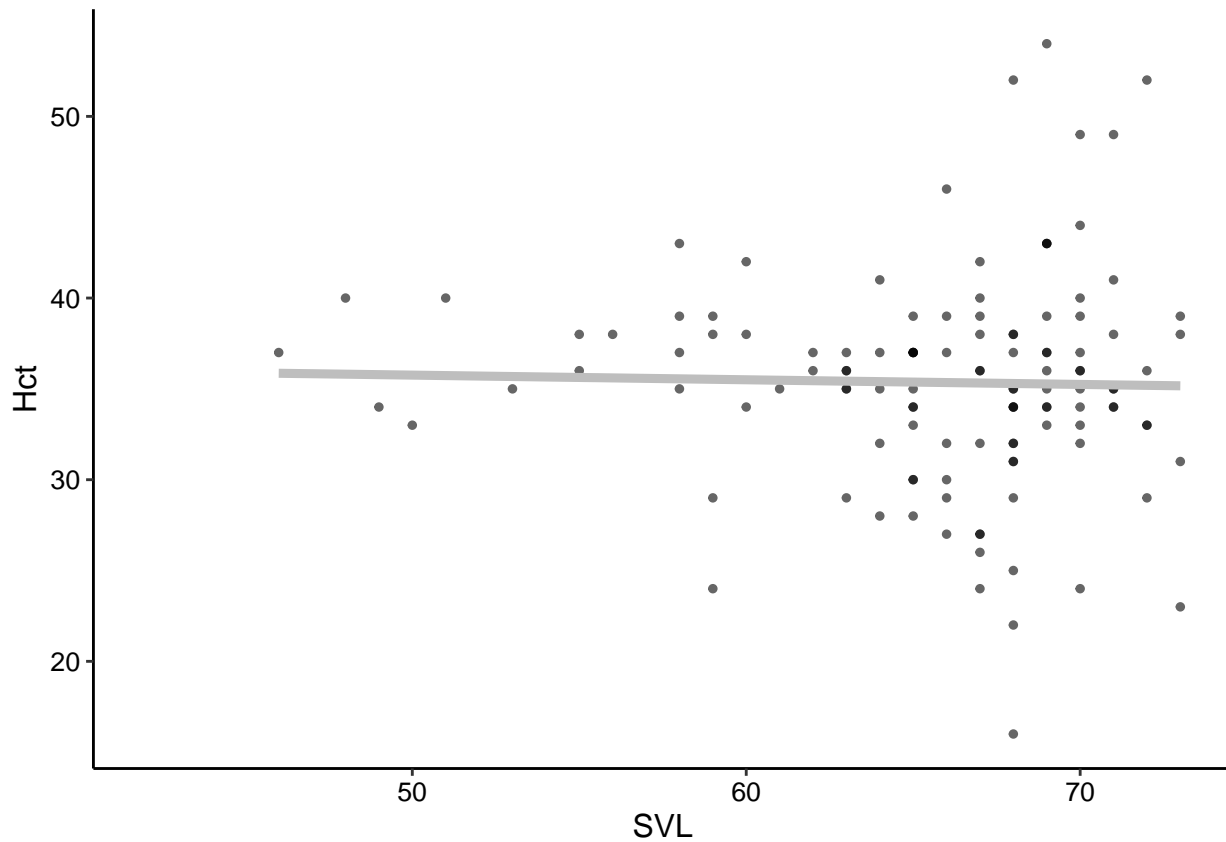
        family = "sans",
        size = 12),
axis.text = element_text(color = "black",
        family = "sans",
        size = 10),

legend.text.align = 0)

```

## Warning: Removed 27 rows containing non-finite values (stat\_smooth).

## Warning: Removed 27 rows containing missing values (geom\_point).



Osml ~ SVL

```

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

```

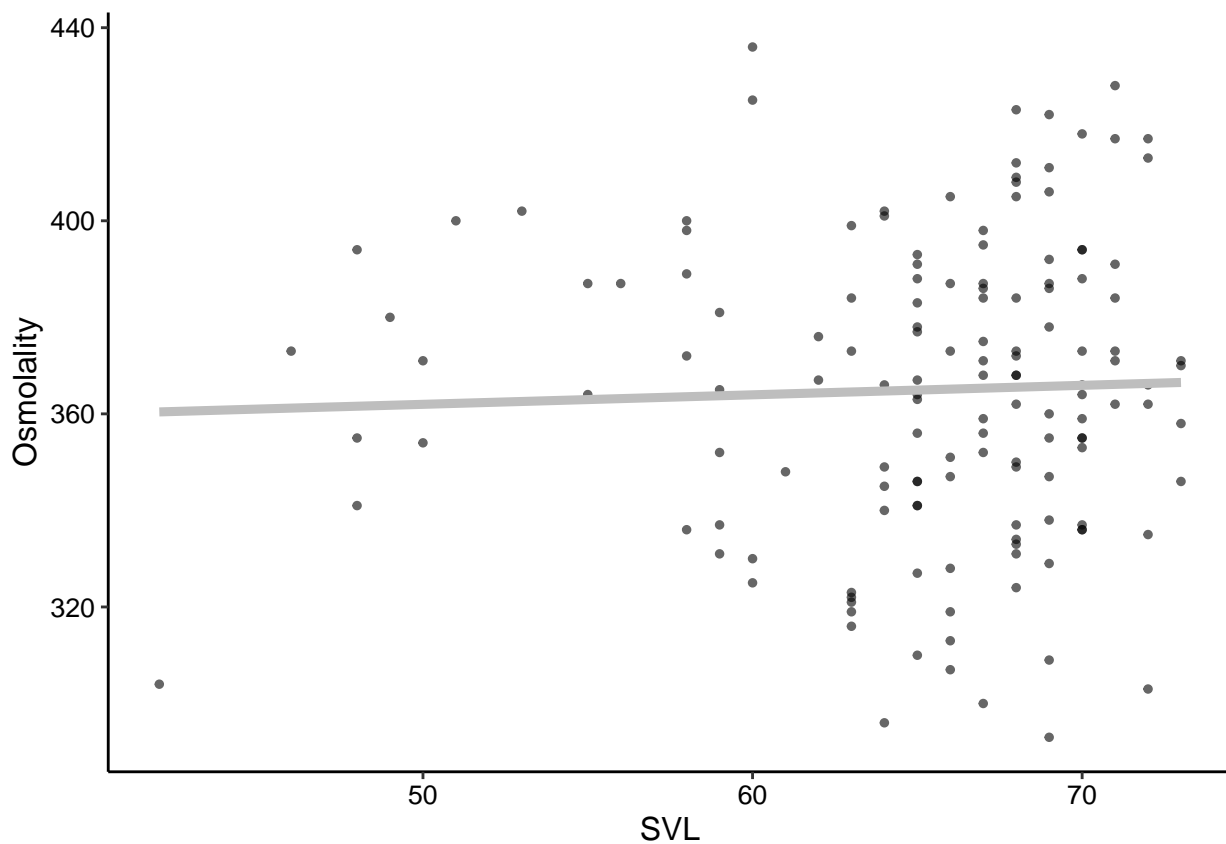
```

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

```

## Warning: Removed 3 rows containing non-finite values (stat\_smooth).

## Warning: Removed 3 rows containing missing values (geom\_point).



Hct ~ SMI

```

my_pnk <- RColorBrewer::brewer.pal(5, "Set2")[4]

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

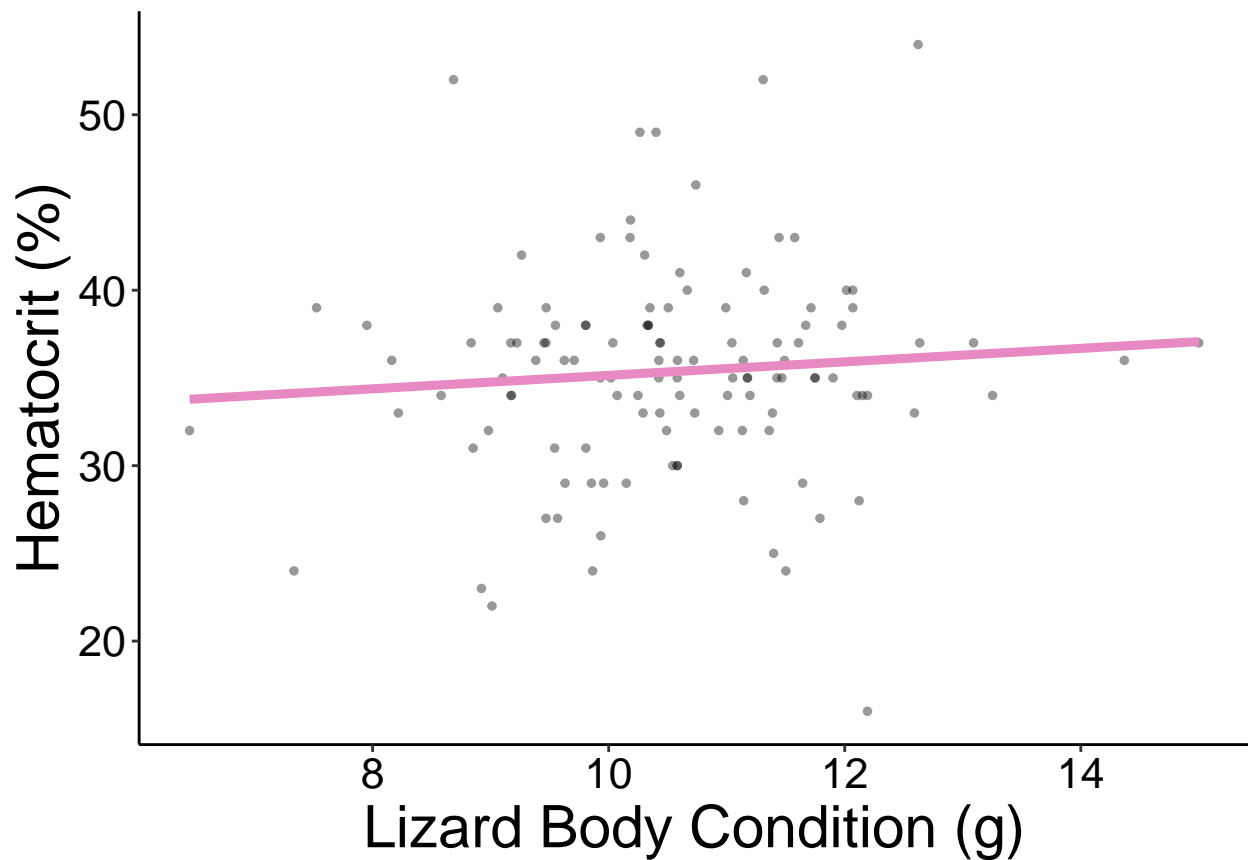
```

```

        alpha = 0.4) +
stat_smooth(aes(x = SMI,
                y = hematocrit_percent),
            formula = y ~ x,
            method = "lm",
            se = F,
            color = my_pnk,
            size = 1.6,
            alpha = 1 ) +
theme_classic() +
xlab("Lizard Body Condition (g)") +
ylab("Hematocrit (%)") +
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, #top
                          0.1, #right
                          0.1, #bottom
                          0.1 #left
                          ), "cm"),
) -> hct_SMI_fig
hct_SMI_fig

## 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 = 0.4) +
  stat_smooth(aes(x = SMI,
                 y = osmolality_mmol_kg),
            formula = y ~ x,
            method = "lm",
            se = F,
            color = my_pnk,
            size = 1.6,
            alpha = 1 ) +
  theme_classic() +
  xlab("Lizard Body Condition (g)") +
  #ylab("Osmolality (mmol/kg)") +
  ylab("") +
  #xlim(3, 7) +
  ylim(300, 450) +
  theme(text = element_text(color = "black",
                             family = "sans",
                             size = 22),
```

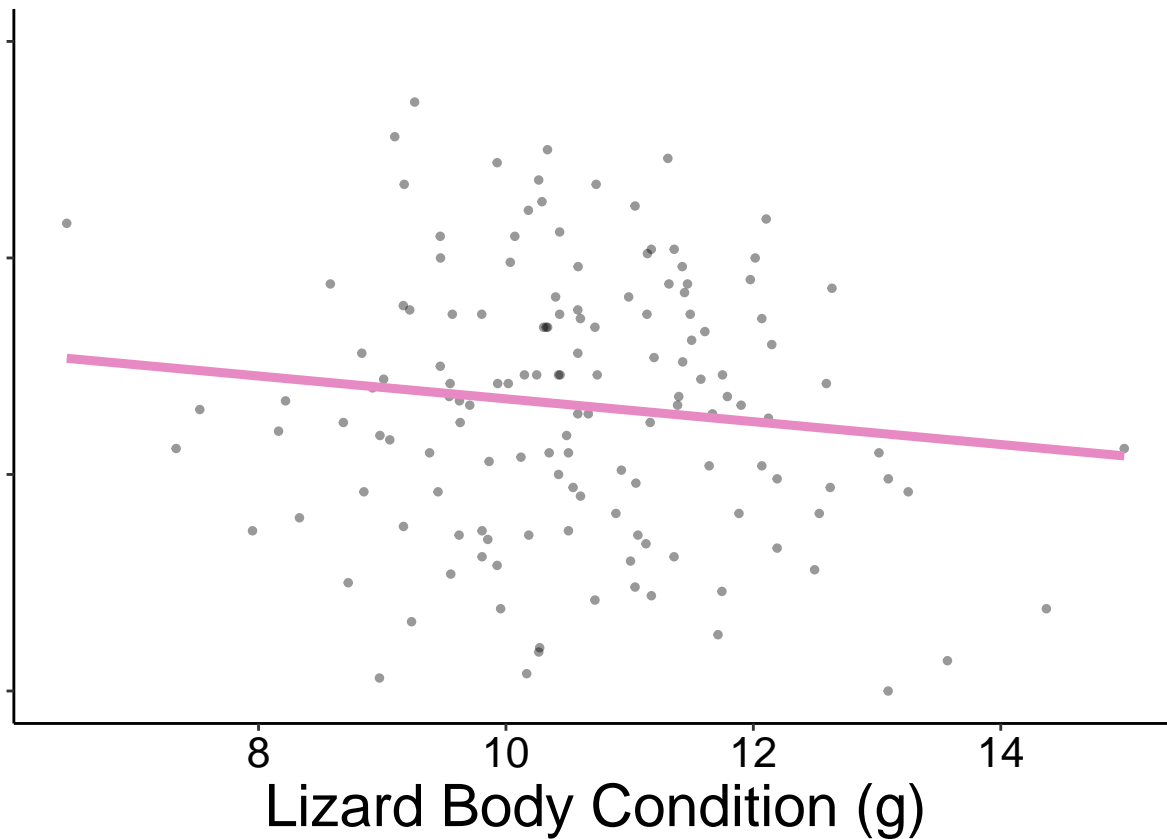
```

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, #top
                    0.1, #right
                    0.35, #bottom
                    0.1 #left
                    ), "cm"),
) -> osml_SMI_fig
osml_SMI_fig

```

## Warning: Removed 5 rows containing non-finite values (stat\_smooth).

## Warning: Removed 5 rows containing missing values (geom\_point).



Hct ~ Sex

males have significantly higher hematocrit %

```

# calculate means to overlay
hct_means <- morpho_blood_SMI %>%
  dplyr::filter(complete.cases(hematocrit_percent)) %>%
  group_by(sex_M_F) %>%
  summarise(mean_hct = mean(hematocrit_percent))

```

## `summarise()` ungrouping output (override with `.groups` argument)

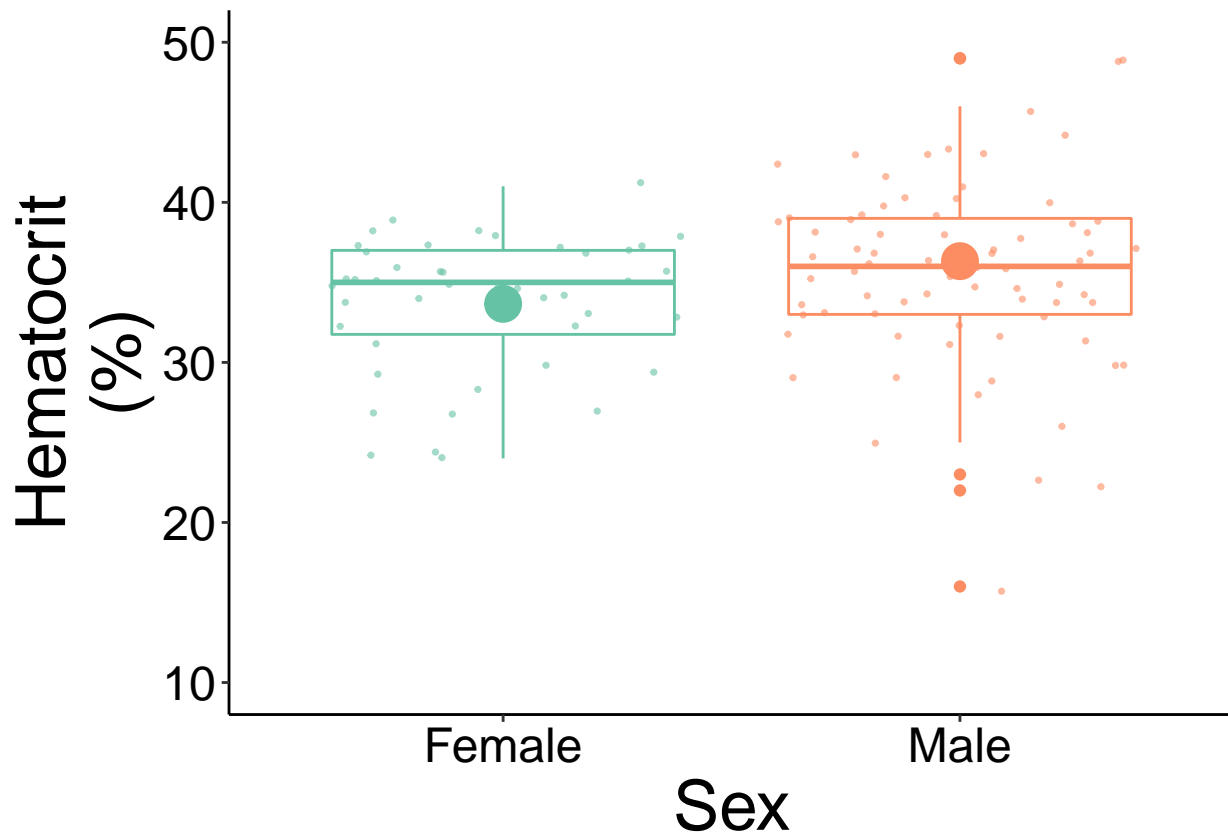
```

# graph
ggplot(data = morpho_blood_SMI) +
  geom_boxplot(aes(x = sex_M_F,
                  y = hematocrit_percent,
                  color = sex_M_F)) +
  geom_point(data = hct_means,
            aes(x = sex_M_F,
                y = mean_hct,
                color = sex_M_F),
            size = 6,
            #color = "black",
            alpha = 1) +
  geom_jitter(aes(x = sex_M_F,
                  y = hematocrit_percent,
                  color = sex_M_F),
            size = 0.6,
            alpha = 0.6) +
  theme_classic() +
  xlab("Sex") +
  ylab("Hematocrit\n(%)") +
  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 = 26),
        axis.text = element_text(color = "black",
                                   family = "sans",
                                   size = 18),
        legend.text.align = 0,
        legend.position = "none")
) -> hct_sex_fig
hct_sex_fig

```

## Warning: Removed 30 rows containing non-finite values (stat\_boxplot).

## Warning: Removed 30 rows containing missing values (geom\_point).



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

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

Osml ~ Sex

```
# calculate means to overlay
osml_means <- morpho_blood_SMI %>%
  dplyr::filter(complete.cases(osmolality_mmol_kg)) %>%
  group_by(sex_M_F) %>%
  summarise(mean_osml = mean(osmolality_mmol_kg))

## `summarise()` ungrouping output (override with `.groups` argument)

# graph
ggplot(data = morpho_blood_SMI) +
  geom_boxplot(aes(x = sex_M_F,
                  y = osmolality_mmol_kg,
                  color = sex_M_F)) +
  geom_point(data = osml_means,
            aes(x = sex_M_F,
                y = mean_osml,
```



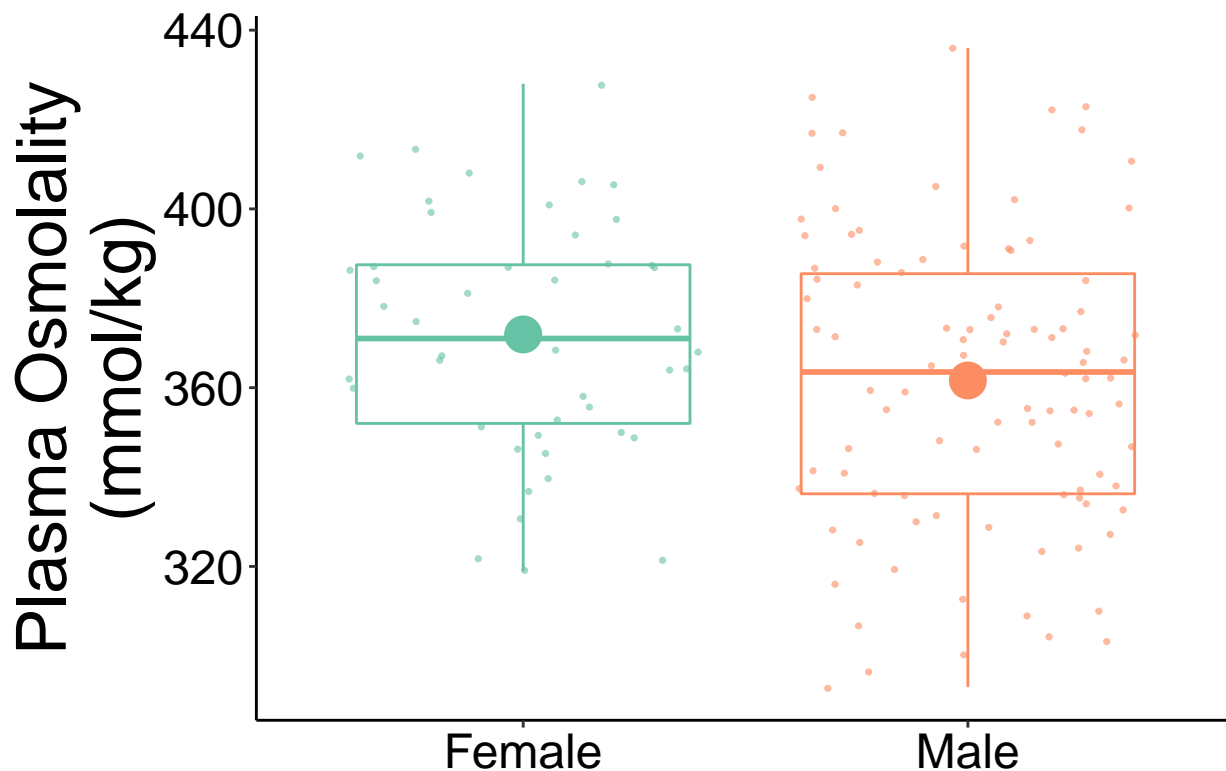
```

        color = sex_M_F),
    size = 6,
    #color = "black",
    alpha = 1) +
  geom_jitter(aes(x = sex_M_F,
    y = osmolality_mmol_kg,
    color = sex_M_F
    ),
    size = 0.6,
    alpha = 0.6) +
  theme_classic() +
  xlab("") +
  ylab("Plasma Osmolality\n(mmol/kg)") +
  scale_x_discrete(labels = c("F" = "Female",
    "M" = "Male")) +
  scale_color_brewer(palette = "Set2") +
  theme(text = element_text(color = "black",
    family = "sans",
    size = 26),
    axis.text = element_text(color = "black",
    family = "sans",
    size = 18),
    legend.text.align = 0,
    legend.position = "none"
  ) -> osml_sex_fig
osml_sex_fig

```

## Warning: Removed 3 rows containing non-finite values (stat\_boxplot).

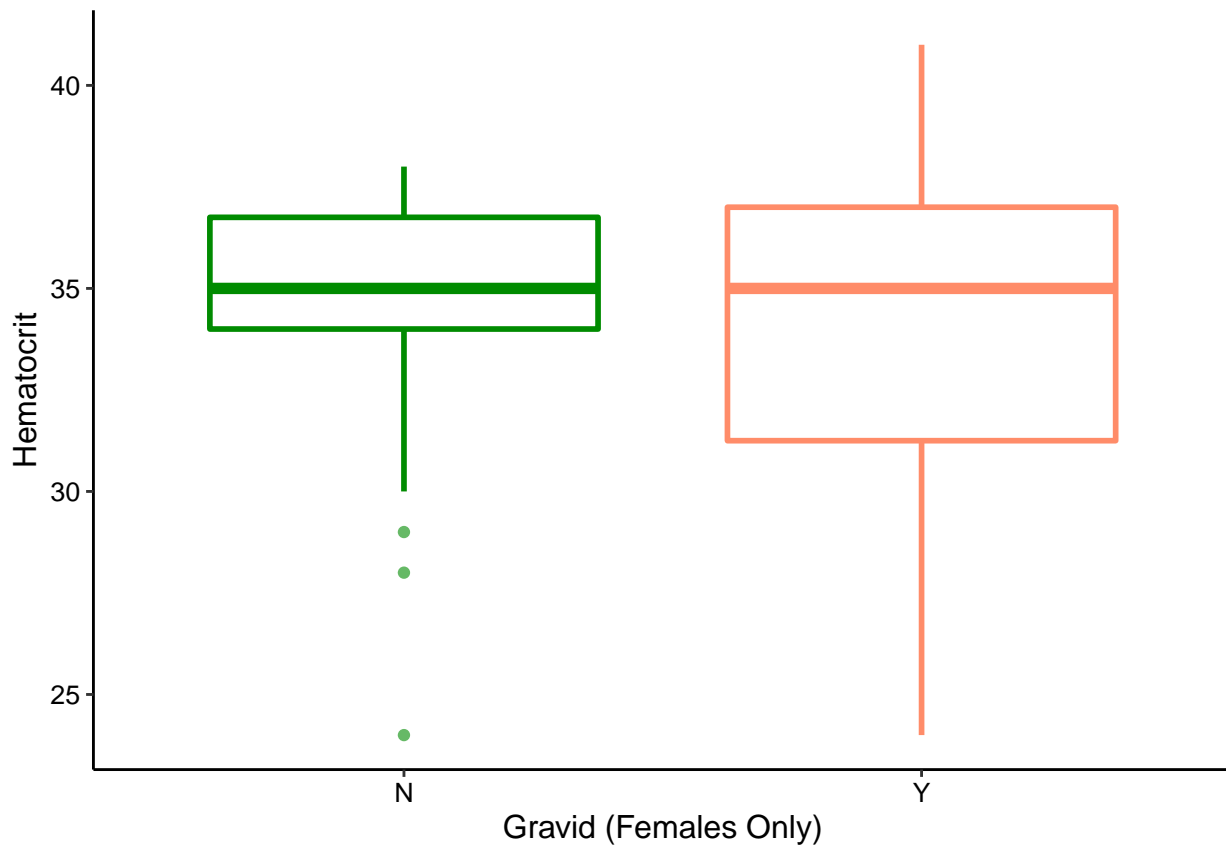
## Warning: Removed 3 rows containing missing values (geom\_point).



## Hct ~ Gravidity

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

## Warning: Removed 4 rows containing non-finite values (stat\_boxplot).



## Osml ~ Gravidity

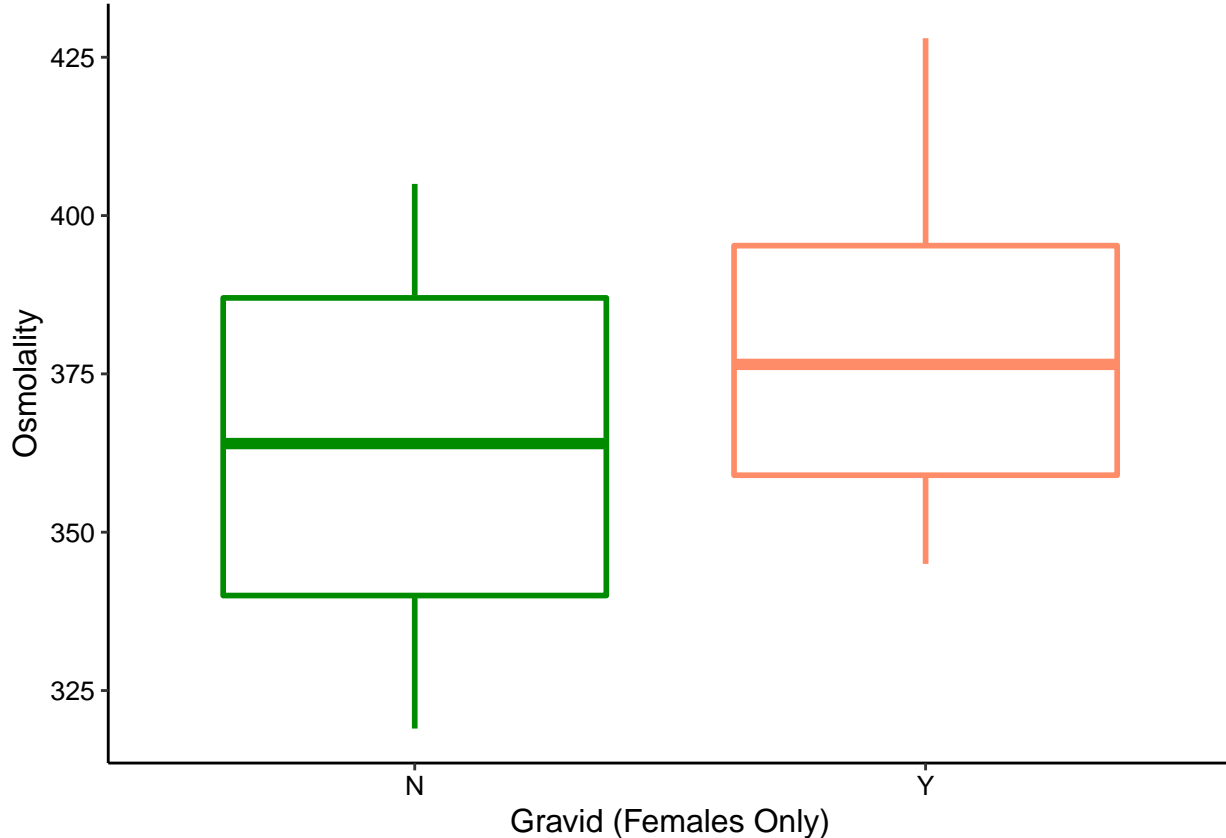
```
morpho_blood_SMI %>%
  dplyr::filter(sex_M_F == 'F') %>%
```

```

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

```

## Warning: Removed 1 rows containing non-finite values (stat\_boxplot).



### Hct ~ Sample Eye

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

```

morpho_blood_SMI %>%
  dplyr::filter(blood_sample_eye %in% c("R", "L")) %>%
  ggplot(data = .) +

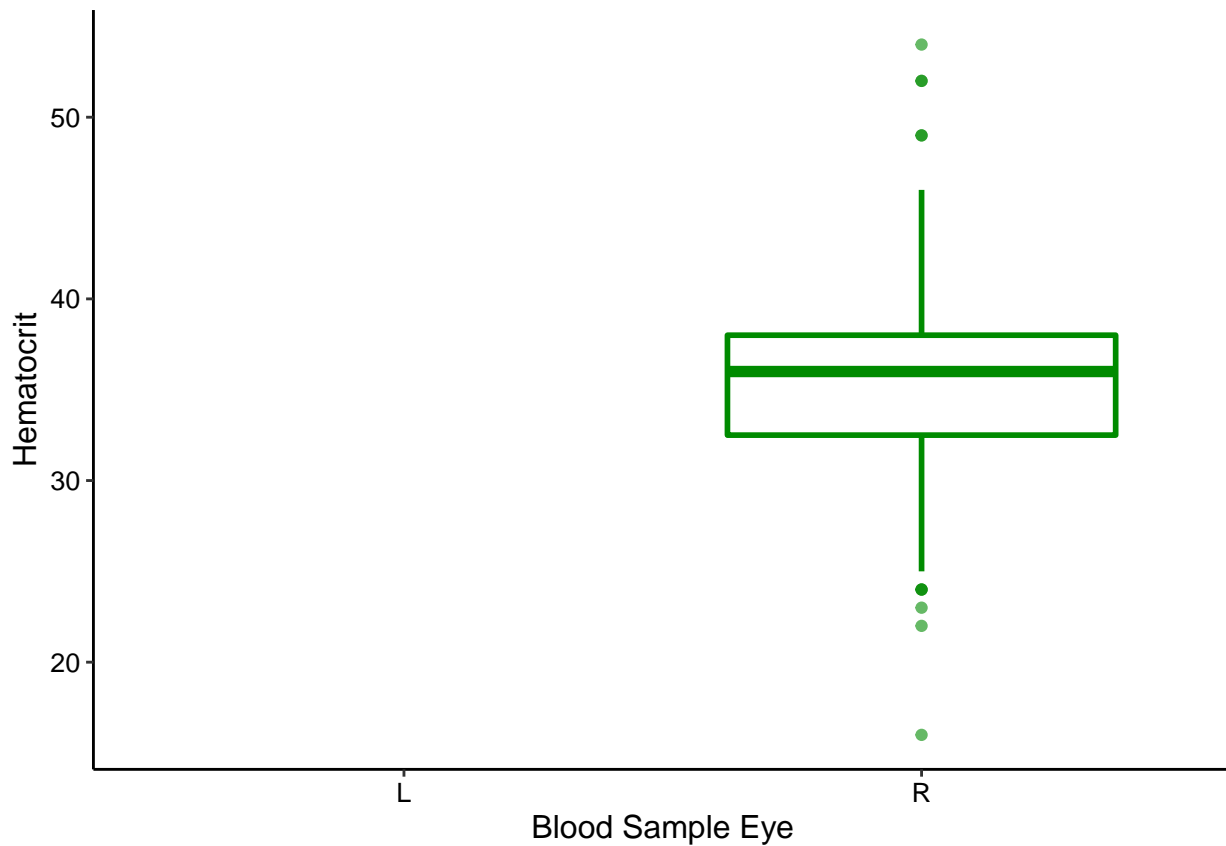
```

```

geom_boxplot(aes(x = blood_sample_eye,
                 y = hematocrit_percent,
                 color = blood_sample_eye
                 ),
             size = 1,
             alpha = 0.6) +
scale_colour_manual(name = "Blood Sample Eye",
                   values = c("green4", "salmon1") ) +
theme_classic() +
xlab("Blood Sample Eye") +
ylab("Hematocrit") +
theme(text = element_text(color = "black", family = "sans", size = 12),
      axis.text = element_text(color = "black", family = "sans", size = 10),
      legend.text.align = 0,
      legend.position = "none"
)

```

## Warning: Removed 27 rows containing non-finite values (stat\_boxplot).



Osml ~ Sample Eye

```

morpho_blood_SMI %>%
  dplyr::filter(blood_sample_eye %in% c("R", "L")) %>%
  ggplot(data = .) +
  geom_boxplot(aes(x = blood_sample_eye,
                  y = osmolality_mmol_kg,

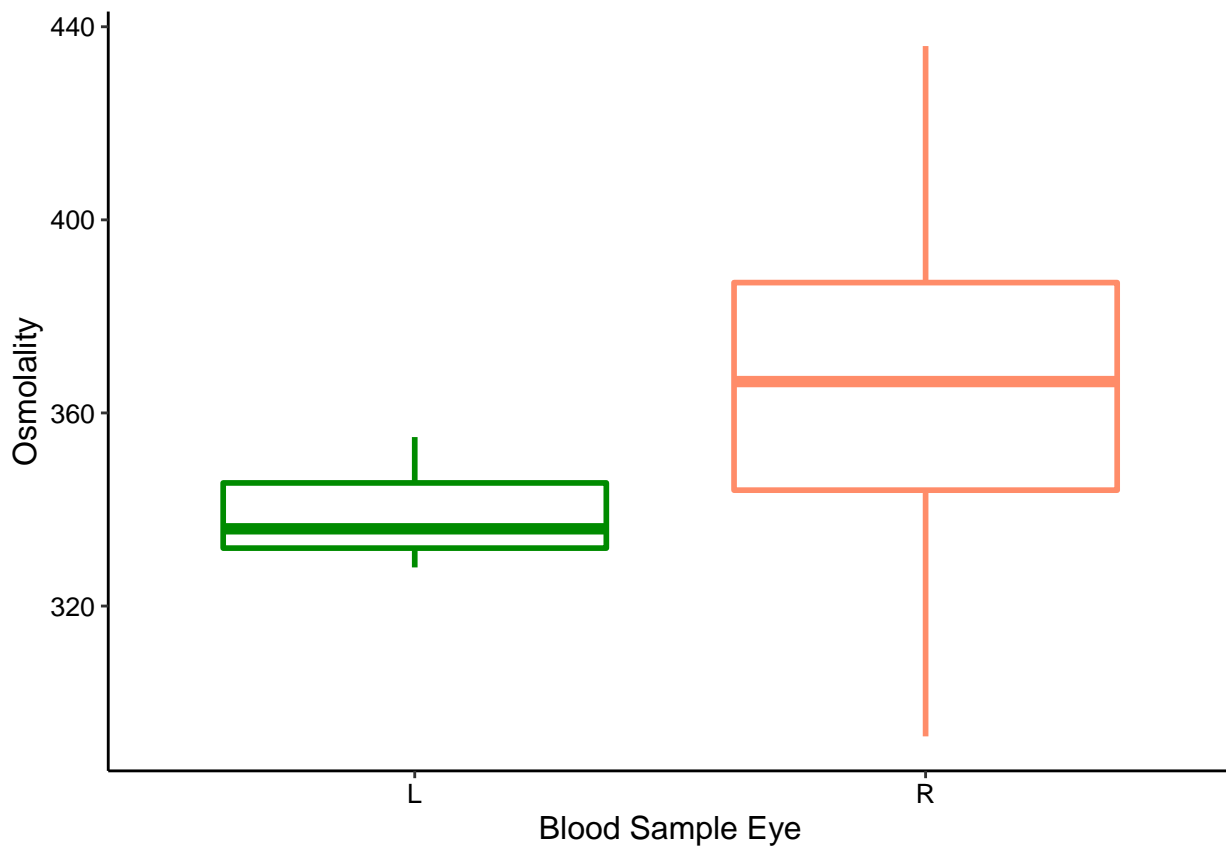
```

```

        color = blood_sample_eye
      ),
      size = 1,
      alpha = 0.6) +
scale_colour_manual(name = "Blood Sample Eye",
                    values = c("green4", "salmon1") ) +
theme_classic() +
xlab("Blood Sample Eye") +
ylab("Osmolality") +
theme(text = element_text(color = "black", family = "sans", size = 12),
      axis.text = element_text(color = "black", family = "sans", size = 10),
      legend.text.align = 0,
      legend.position = "none")

```

## Warning: Removed 3 rows containing non-finite values (stat\_boxplot).



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

**Hct ~ Hemolyzed/Not**

```

morpho_blood_SMI %>%
  dplyr::filter(hemolyzed %in% c("Y", "N")) %>%
  ggplot(data = .) +
  geom_boxplot(aes(x = hemolyzed,
                   y = hematocrit_percent,
                   color = hemolyzed)

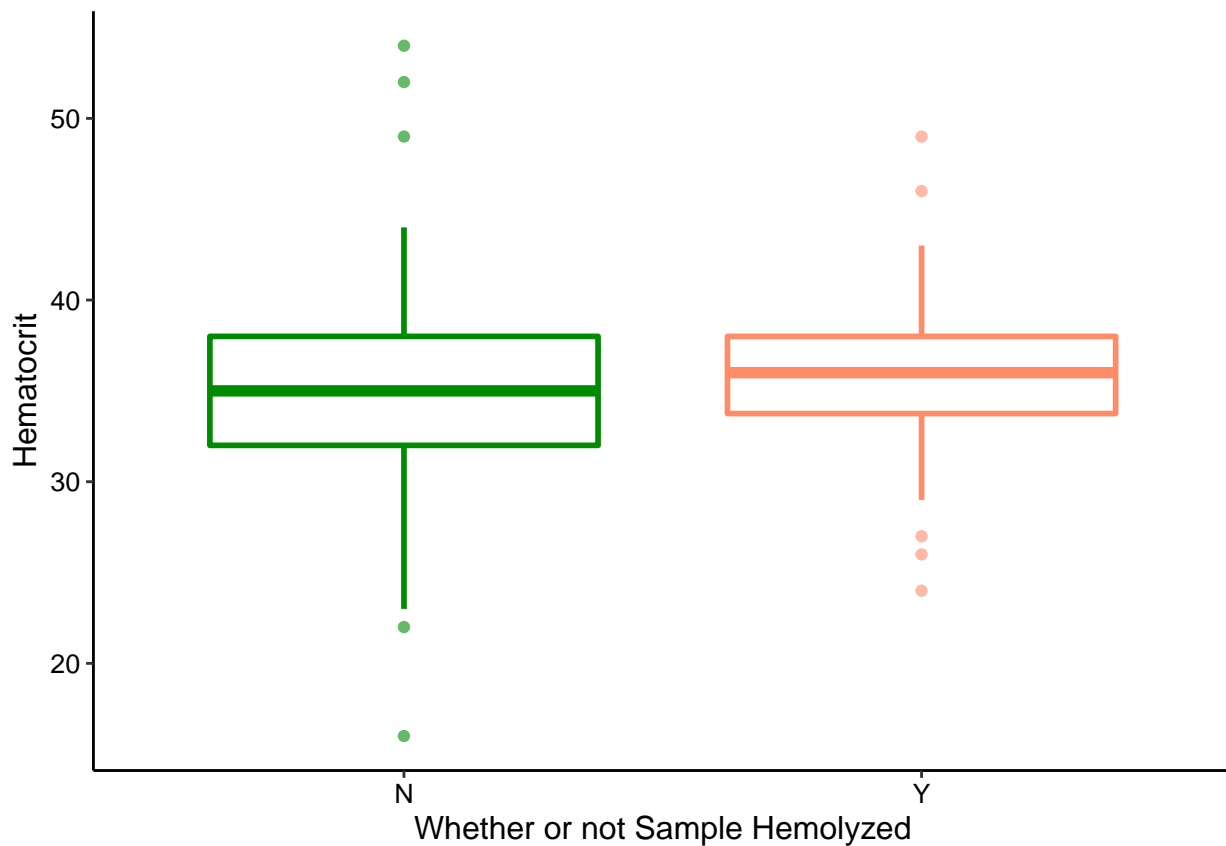
```

```

    ),
    size = 1,
    alpha = 0.6) +
scale_colour_manual(name = "Blood Sample Eye",
  values = c("green4", "salmon1", "green4", "salmon1") ) +
theme_classic() +
xlab("Whether or not Sample Hemolyzed") +
ylab("Hematocrit") +
theme(text = element_text(color = "black", family = "sans", size = 12),
  axis.text = element_text(color = "black", family = "sans", size = 10),
  legend.text.align = 0,
  legend.position = "none")

```

## Warning: Removed 25 rows containing non-finite values (stat\_boxplot).



Osml ~ Hemolyzed/Not

```

morpho_blood_SMI %>%
  dplyr::filter(hemolyzed %in% c("Y", "N")) %>%
  ggplot(data = .) +
  geom_boxplot(aes(x = hemolyzed,
    y = osmolality_mmol_kg,
    color = hemolyzed
  ),
  size = 1,
  alpha = 0.6) +

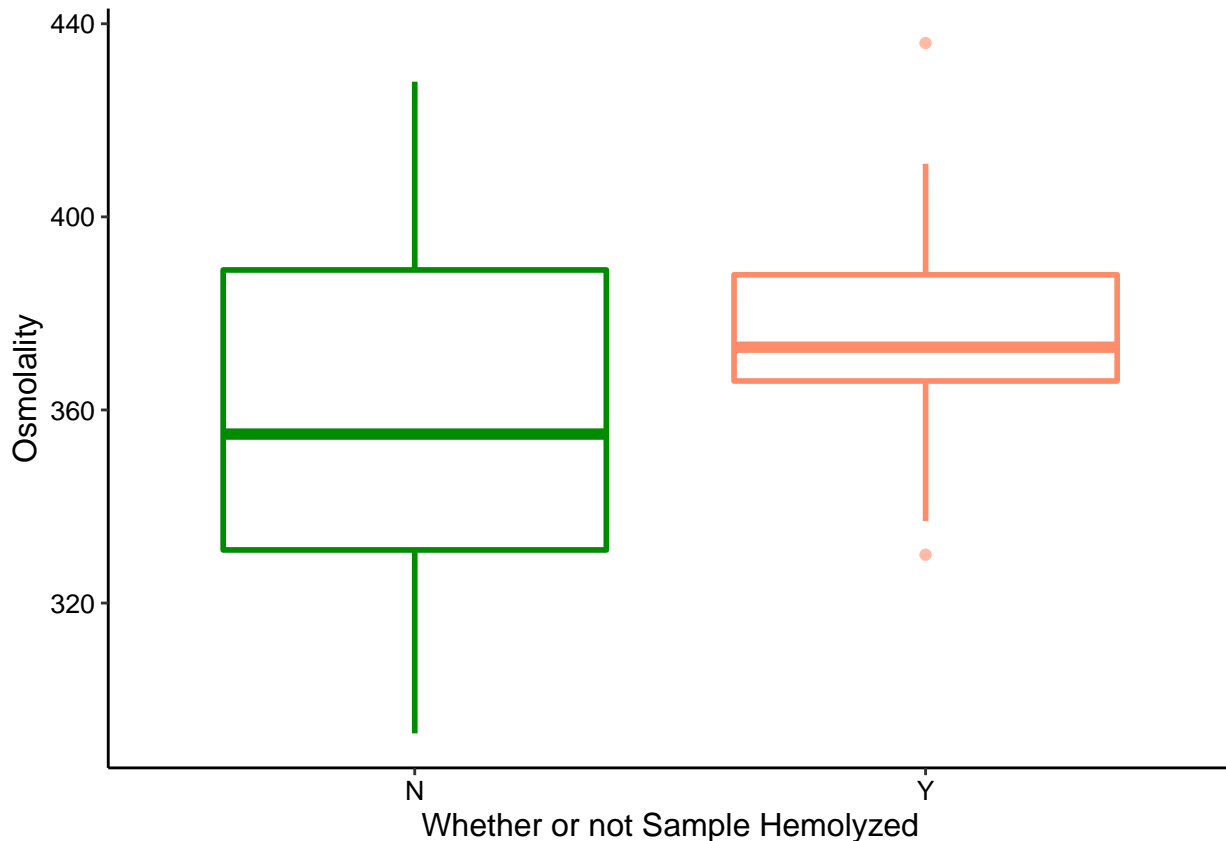
```

```

scale_colour_manual(name = "Blood Sample Eye",
                    values = c("green4", "salmon1", "green4", "salmon1") ) +
theme_classic() +
xlab("Whether or not Sample Hemolyzed") +
ylab("Osmolality") +
theme(text = element_text(color = "black", family = "sans", size = 12),
      axis.text = element_text(color = "black", family = "sans", size = 10),
      legend.text.align = 0,
      legend.position = "none")

```

## Warning: Removed 1 rows containing non-finite values (stat\_boxplot).



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

**Hct ~ Week**

```

morpho_blood_SMI %>%
  ggplot(data = .) +
  geom_boxplot(aes(x = as.factor(date),
                  y = hematocrit_percent,
                  color = as.factor(date)
                  ),
              size = 1,
              alpha = 0.6) +
  theme_classic() +

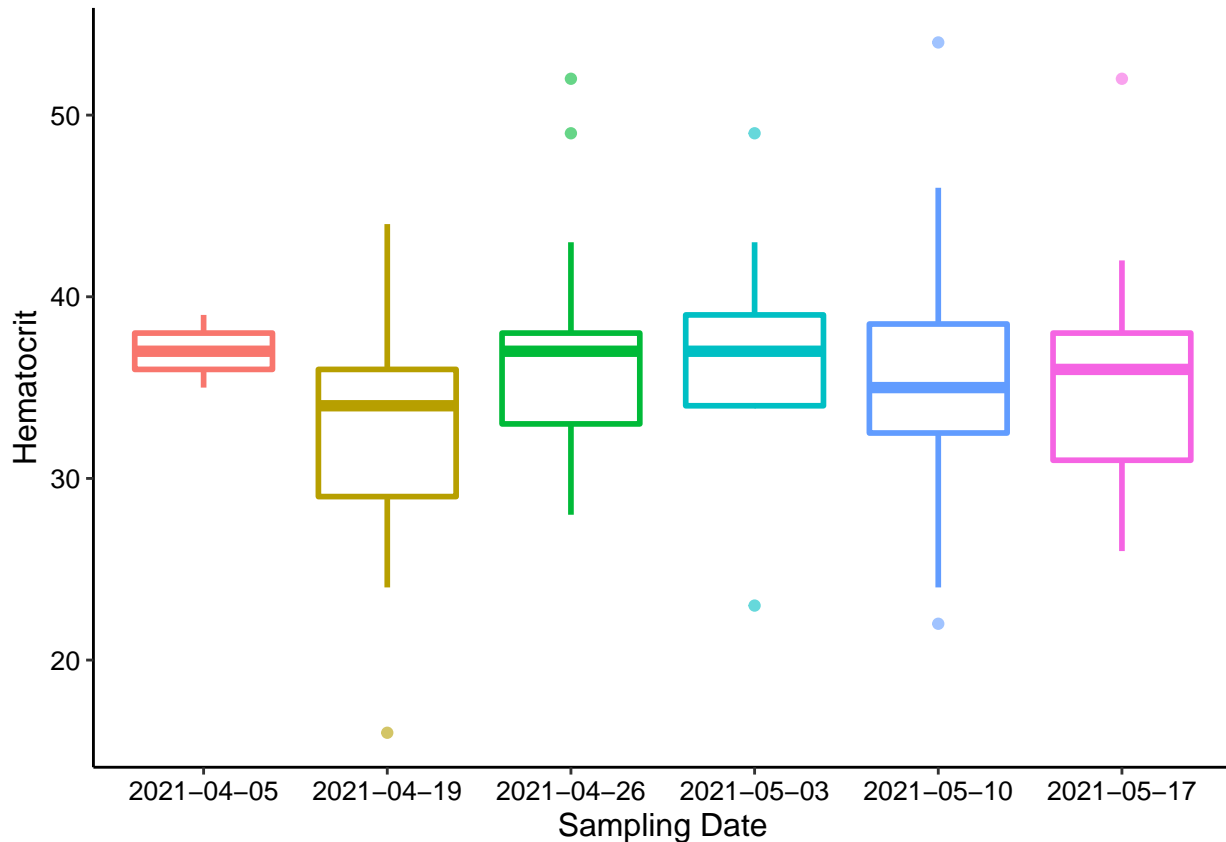
```

```

xlab("Sampling Date") +
ylab("Hematocrit") +
theme(text = element_text(color = "black", family = "sans", size = 12),
      axis.text = element_text(color = "black", family = "sans", size = 10),
      legend.text.align = 0,
      legend.position = "none")

```

## Warning: Removed 27 rows containing non-finite values (stat\_boxplot).



Osml ~ Week

```

# calculate means to overlay
weekly_means <- morpho_blood_SMI %>%
  dplyr::filter(complete.cases(osmolality_mmol_kg)) %>%
  group_by(d = as.factor(date)) %>%
  summarise(mean_osml = mean(osmolality_mmol_kg))

```

## `summarise()` ungrouping output (override with `.groups` argument)

```

# graph
ggplot(data = morpho_blood_SMI) +
  geom_boxplot(aes(x = as.factor(date),
                  y = osmolality_mmol_kg,
                  color = as.factor(date)),
            size = 1,
            alpha = 0.6) +
  geom_point(data = weekly_means,

```



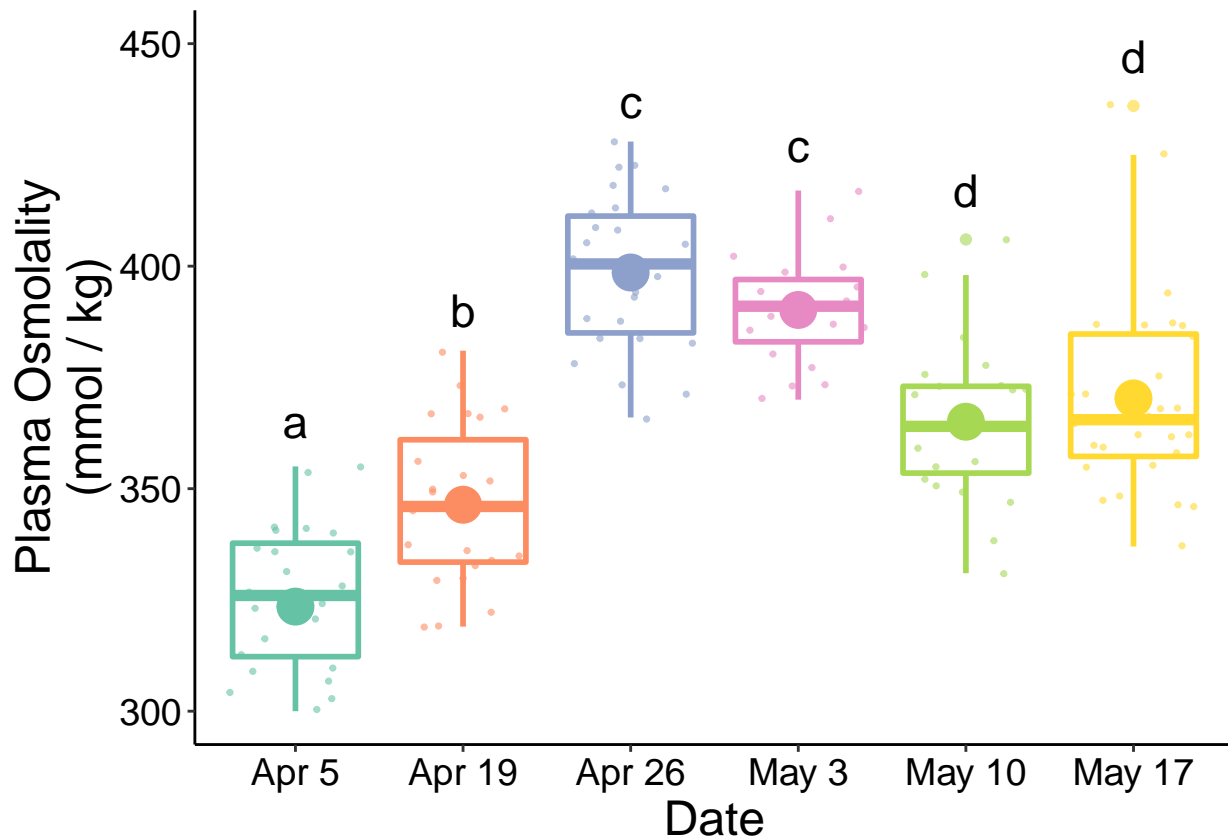
```

    aes(x = d,
        y = mean_osml,
        color = d),
    size = 6,
    #color = "black",
    alpha = 1) +
geom_jitter(aes(x = as.factor(date),
                y = osmolality_mmol_kg,
                color = as.factor(date)),
            size = 0.6,
            alpha = 0.6) +
theme_classic() +
xlab("Date") +
ylab("Plasma Osmolality\n(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).
```

```
## Warning: Removed 5 rows containing missing values (geom_point).
```



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

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

```
## Warning: Removed 5 rows containing missing values (geom_point).
```

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
Apr 5 vs Apr 19	12.5	5.0	20.0	0.001
Apr 5 vs Apr 26	25.0	17.5	32.5	<0.001
Apr 5 vs May 3	17.5	10.0	25.0	0.001
Apr 5 vs May 10	40.0	32.5	47.5	<0.001
Apr 5 vs May 17	47.5	40.0	55.0	<0.001
Apr 19 vs Apr 26	12.5	5.0	20.0	0.001
Apr 19 vs May 3	5.0	-2.5	12.5	0.001
Apr 19 vs May 10	22.5	15.0	30.0	<0.001
Apr 19 vs May 17	30.0	22.5	37.5	<0.001
Apr 26 vs May 3	5.0	-2.5	12.5	0.001
Apr 26 vs May 10	20.0	12.5	27.5	<0.001
Apr 26 vs May 17	27.5	20.0	35.0	<0.001
May 3 vs May 10	22.5	15.0	30.0	<0.001
May 3 vs May 17	30.0	22.5	37.5	<0.001
May 10 vs May 17	10.0	2.5	17.5	0.001

```
## 2021-04-19-2021-04-05 22.891304 7.979417 37.803191 0.0002634
## 2021-04-26-2021-04-05 75.076923 60.628732 89.525114 0.0000000
## 2021-05-03-2021-04-05 66.657895 50.935165 82.380624 0.0000000
## 2021-05-10-2021-04-05 41.543478 26.631591 56.455365 0.0000000
## 2021-05-17-2021-04-05 46.785714 32.597872 60.973557 0.0000000
## 2021-04-26-2021-04-19 52.185619 37.273732 67.097506 0.0000000
## 2021-05-03-2021-04-19 43.766590 27.616718 59.916462 0.0000000
## 2021-05-10-2021-04-19 18.652174 3.290581 34.013766 0.0078361
## 2021-05-17-2021-04-19 23.894410 9.234635 38.554185 0.0000857
## 2021-05-03-2021-04-26 -8.419028 -24.141758 7.303701 0.6342961
## 2021-05-10-2021-04-26 -33.533445 -48.445332 -18.621558 0.0000000
## 2021-05-17-2021-04-26 -28.291209 -42.479051 -14.103367 0.0000008
## 2021-05-10-2021-05-03 -25.114416 -41.264289 -8.964544 0.0002088
## 2021-05-17-2021-05-03 -19.872180 -35.356006 -4.388355 0.0039942
## 2021-05-17-2021-05-10 5.242236 -9.417539 19.902011 0.9059063
```

## Osmol ~ VPD

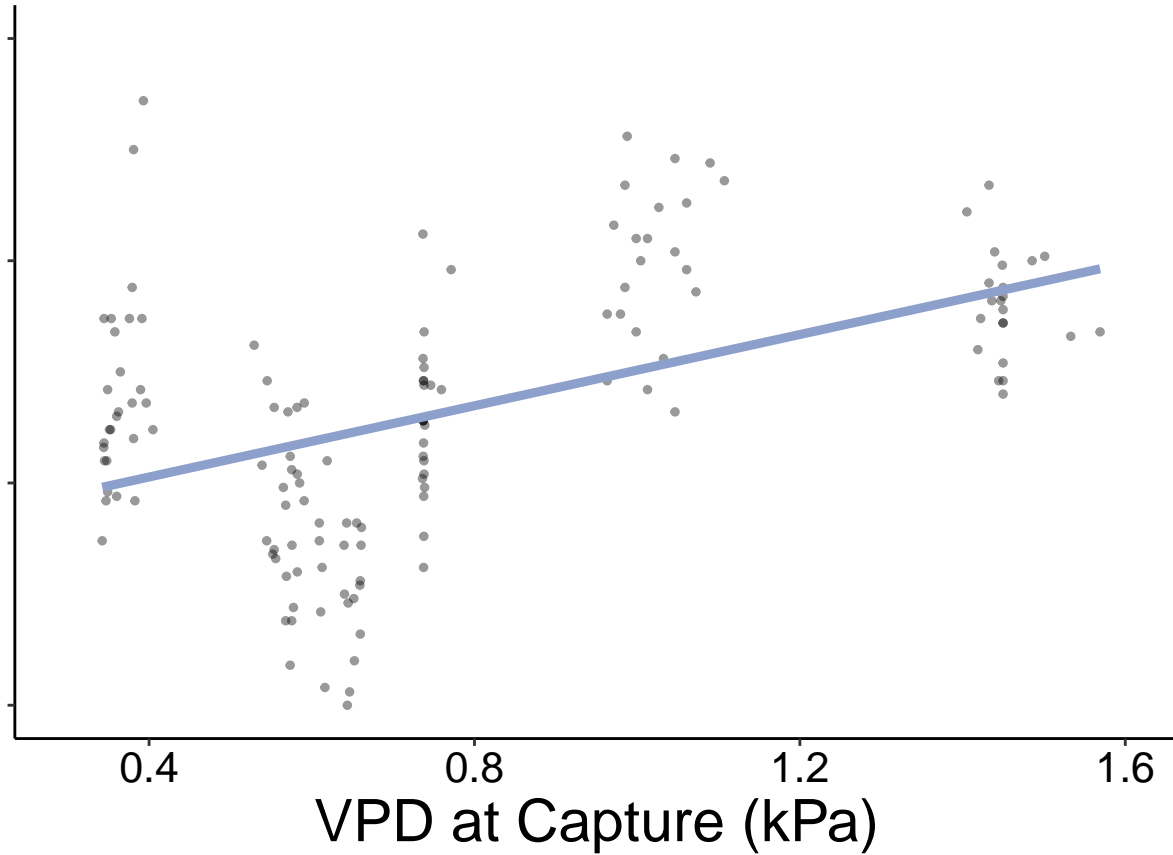
```
my_blu <- RColorBrewer::brewer.pal(5, "Set2")[3]

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_blu,
               size = 1.6,
               alpha = 1 ) +
    theme_classic() +
    xlab("VPD at Capture (kPa)") +
    #ylab("Plasma Osmolality\n(mmol / kg)") +
    ylab("") +
    xlim(0.3, 1.6) +
    ylim(300, 450) +
    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, #top
                              0.1, #right
                              0.1, #bottom
                              0.1 #left
                              ), "cm"))
```

```
) -> osml_vpd_fig
osml_vpd_fig
```

```
## Warning: Removed 8 rows containing non-finite values (stat_smooth).
```

```
## Warning: Removed 8 rows containing missing values (geom_point).
```



Hct ~ VPD

```
morpho_blood_SMI %>%
  ggplot(data = .) +
  geom_point(aes(x = VPD_kPa_int,
                 y = hematocrit_percent,
                 ),
            size = 1,
            alpha = 0.4) +
  stat_smooth(aes(x = VPD_kPa_int,
                 y = hematocrit_percent),
            formula = y ~ x,
            method = "lm",
            se = F,
            color = my_blu,
            size = 1.6,
            alpha = 1 ) +
  theme_classic() +
  xlab("VPD at Capture (kPa)") +
```

```

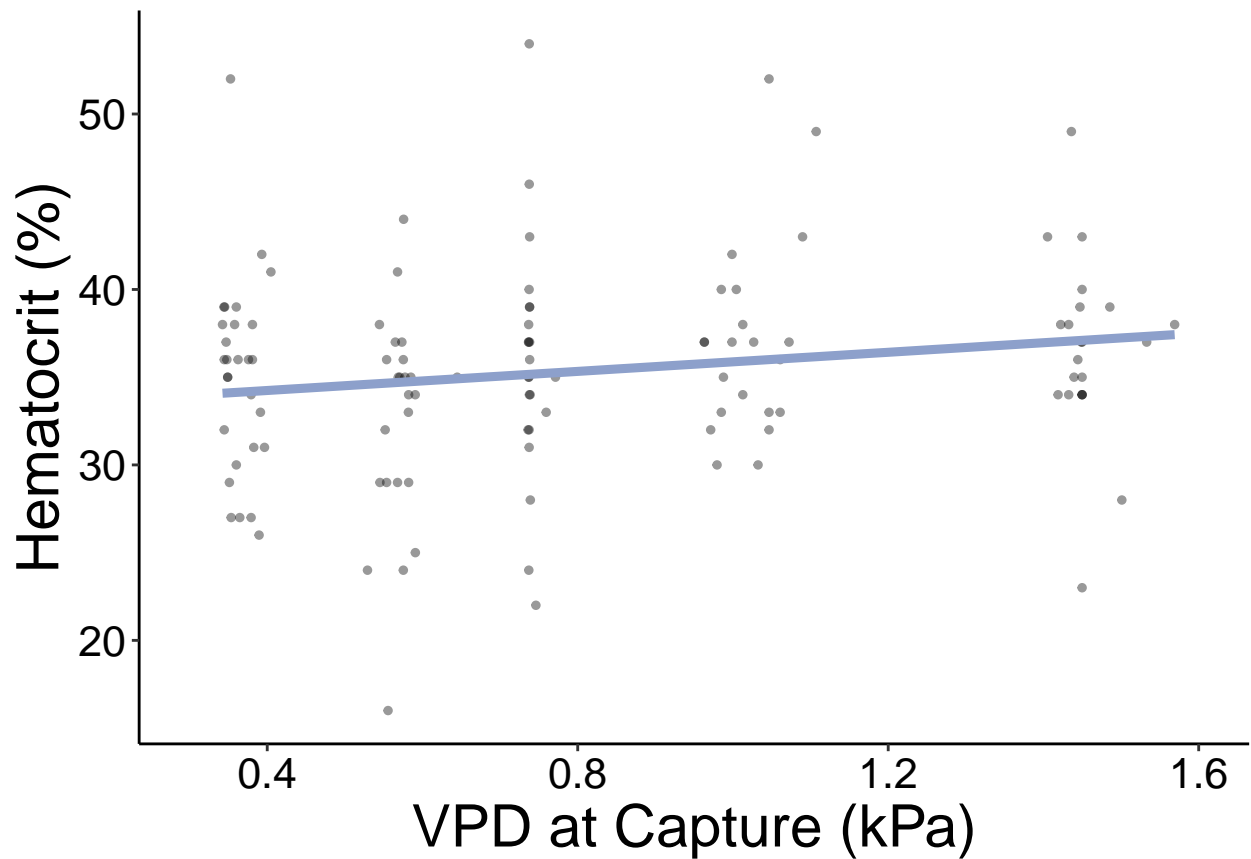
ylab("Hematocrit (%)") +
xlim(0.3, 1.6) +
theme(text = element_text(color = "black",
                           family = "sans",
                           size = 22),
      axis.text = element_text(color = "black",
                                family = "sans",
                                size = 16),
      legend.text.align = 0,
      plot.margin = unit(c(0.1, #top
                           0.1, #right
                           0.1, #bottom
                           0.1 #left
                           ), "cm"))

) -> hct_vpd_fig
hct_vpd_fig

```

## Warning: Removed 29 rows containing non-finite values (stat\_smooth).

## Warning: Removed 29 rows containing missing values (geom\_point).



Osml ~ Wind

```

my_lime <- RColorBrewer::brewer.pal(5, "Set2")[5]

morpho_blood_SMI %>%

```

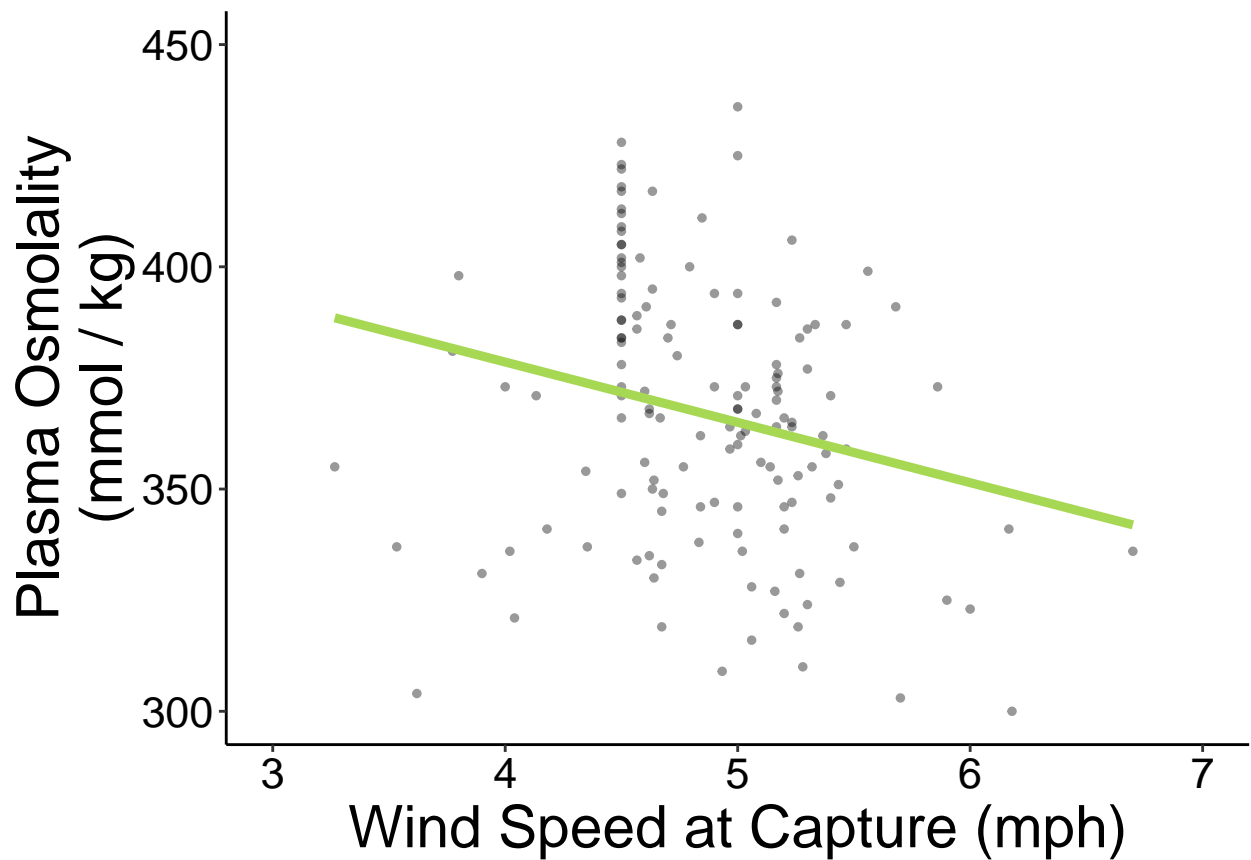
```

ggplot(data = .) +
  geom_point(aes(x = Wind_mph_interpol,
                 y = osmolality_mmol_kg,
                 ),
            size = 1,
            alpha = 0.4) +
  stat_smooth(aes(x = Wind_mph_interpol,
                  y = osmolality_mmol_kg),
              formula = y ~ x,
              method = "lm",
              se = F,
              color = my_lime,
              size = 1.6,
              alpha = 1 ) +
  theme_classic() +
  xlab("Wind Speed at Capture (mph)") +
  ylab("Plasma Osmolality\n(mmol / kg)") +
  xlim(3, 7) +
  ylim(300, 450) +
  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, #top
                             0.1, #right
                             0.1, #bottom
                             0.1 #left
                             ), "cm"))
) -> osml_wind_fig
osml_wind_fig

```

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

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



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

Hct ~ VPD

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

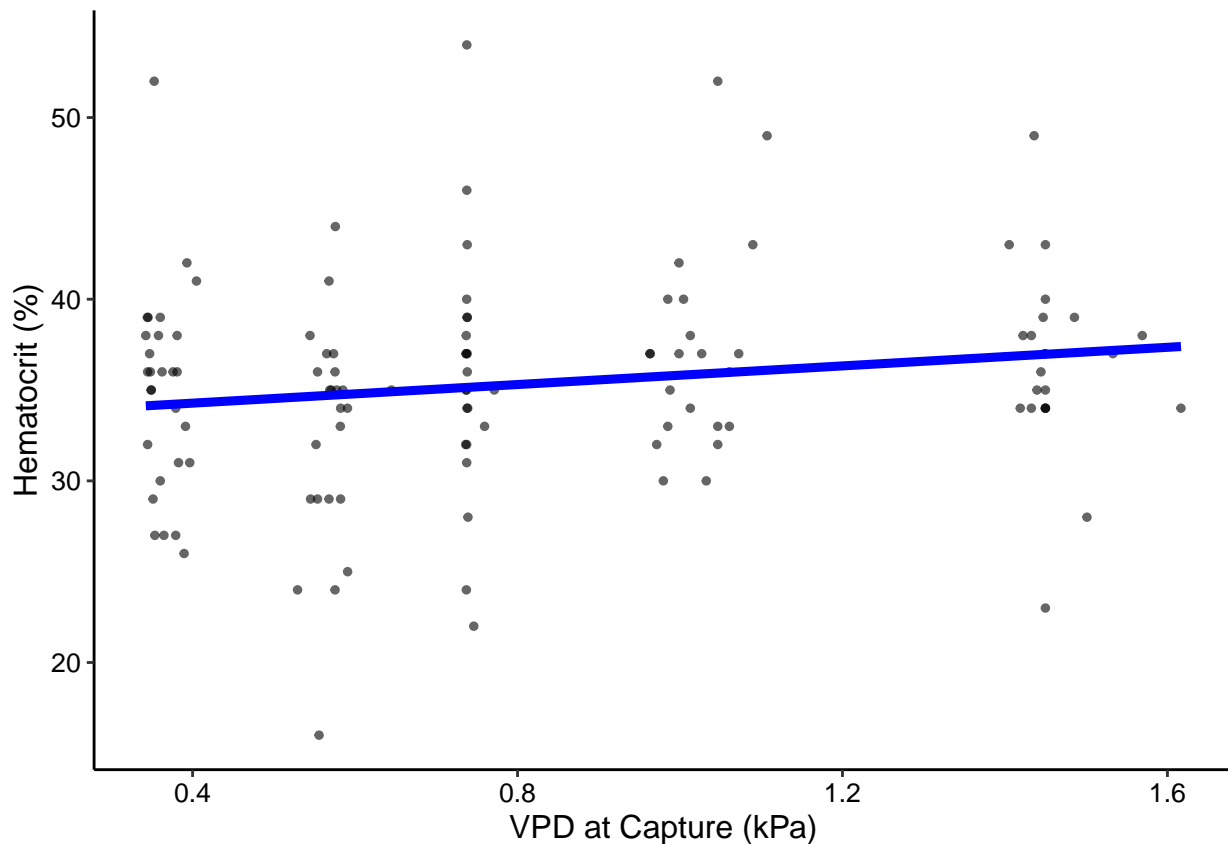
```

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

```

## Warning: Removed 28 rows containing non-finite values (stat\_smooth).

## Warning: Removed 28 rows containing missing values (geom\_point).



Hct ~ Temperature

```

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

```



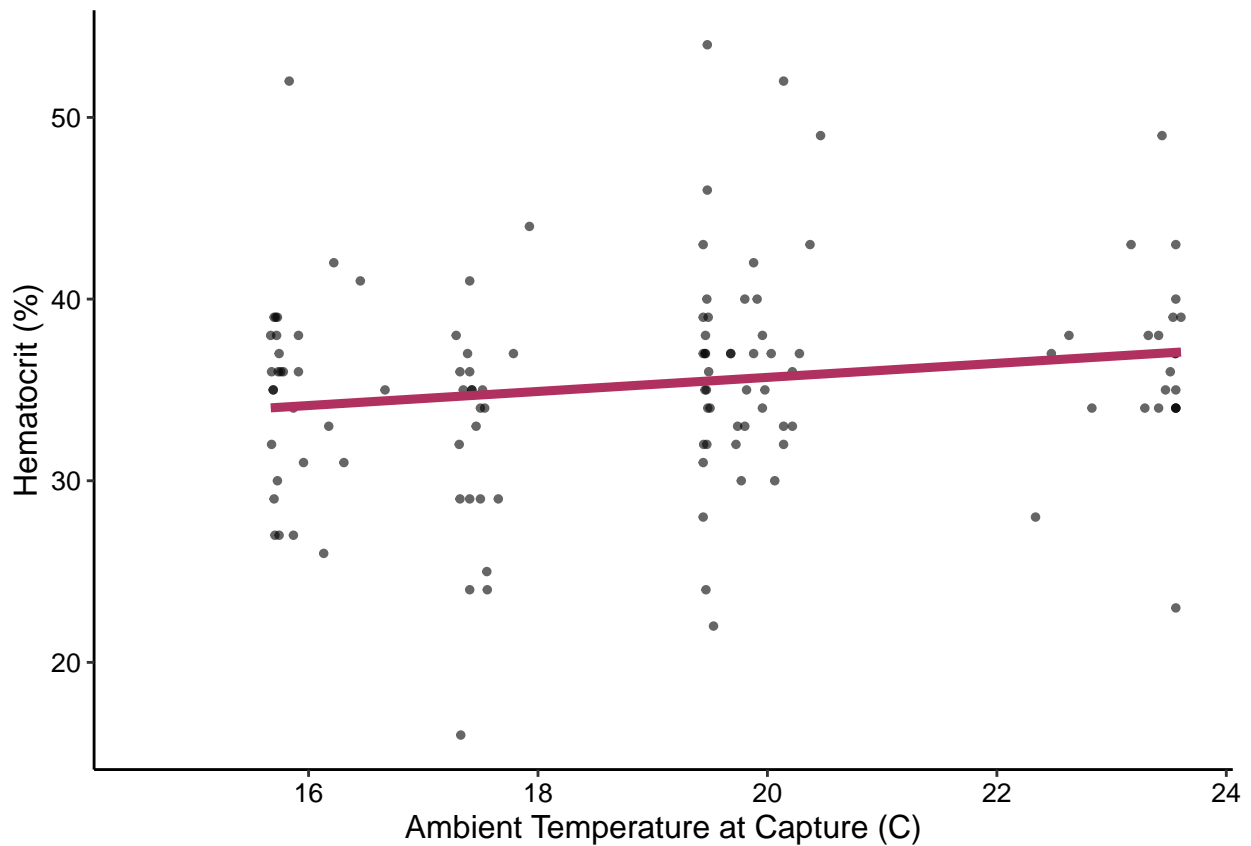
```

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

```

## Warning: Removed 28 rows containing non-finite values (stat\_smooth).

## Warning: Removed 28 rows containing missing values (geom\_point).



Osml ~ Temperature

```

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

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

```

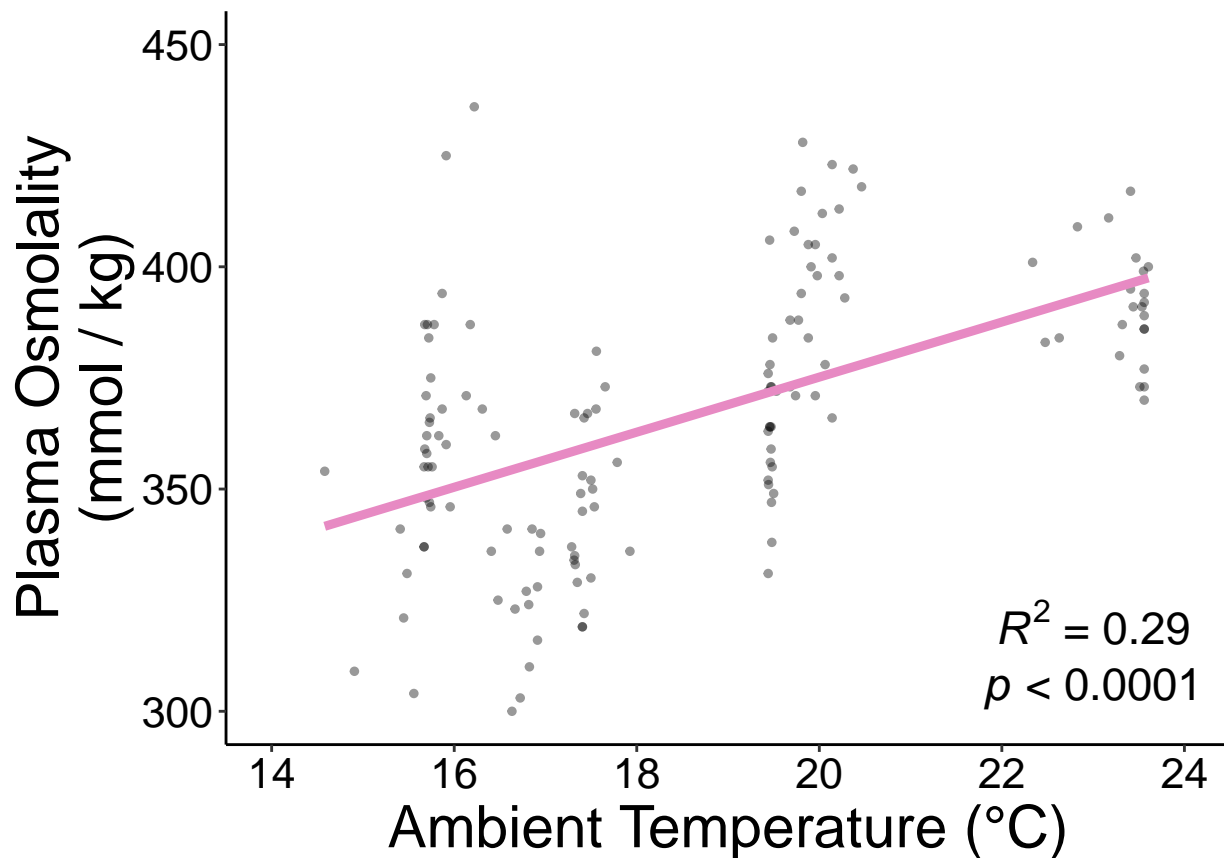
```

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

```

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

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



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

#### Osml ~ Solar Radiation

```
my_orng <- RColorBrewer::brewer.pal(5, "Set2")[2]

morpho_blood_SMI %>%
  ggplot(data = .) +
  geom_point(aes(x = Solar_rad_Wm2_interpol,
                 y = osmolality_mmol_kg),
             size = 1,
             alpha = 0.4) +
  stat_smooth(aes(x = Solar_rad_Wm2_interpol,
                  y = osmolality_mmol_kg),
              formula = y ~ x,
              method = "lm",
              se = F,
              color = my_orng,
              size = 1.6,
              alpha = 1) +
```

```

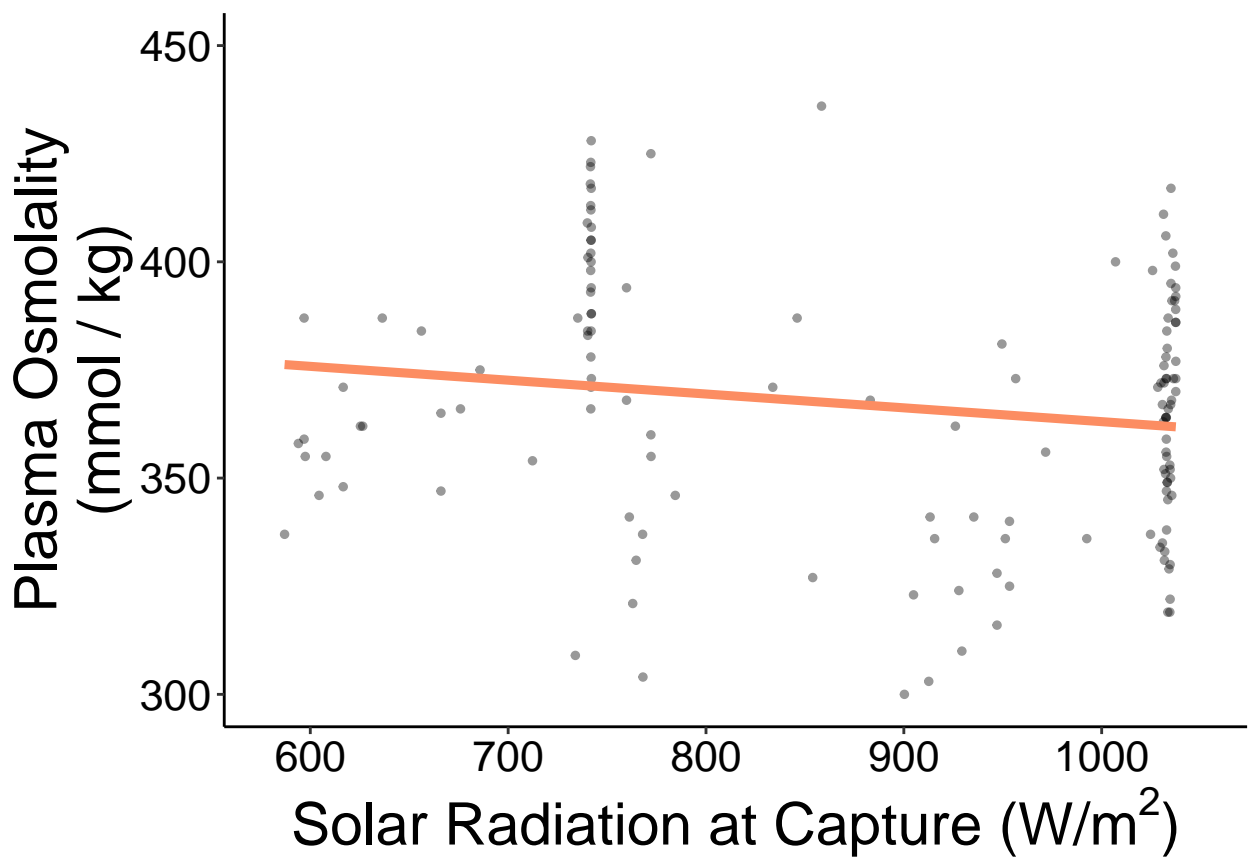
theme_classic() +
xlab(bquote('Solar Radiation at Capture ( $W/m^2$ )')) +
ylab("Plasma Osmolality\n(mmol / kg)") +
xlim(580, 1050) +
ylim(300,450) +
theme(text = element_text(color = "black",
                             family = "sans",
                             size = 22),
      axis.text = element_text(color = "black",
                                family = "sans",
                                size = 16),
      legend.text.align = 0,
      plot.margin = unit(c(0.1, #top
                           0.1, #right
                           0, #bottom
                           0.1 #left
                           ), "cm"))

) -> osml_sorad_fig
osml_sorad_fig

```

## Warning: Removed 7 rows containing non-finite values (stat\_smooth).

## Warning: Removed 7 rows containing missing values (geom\_point).

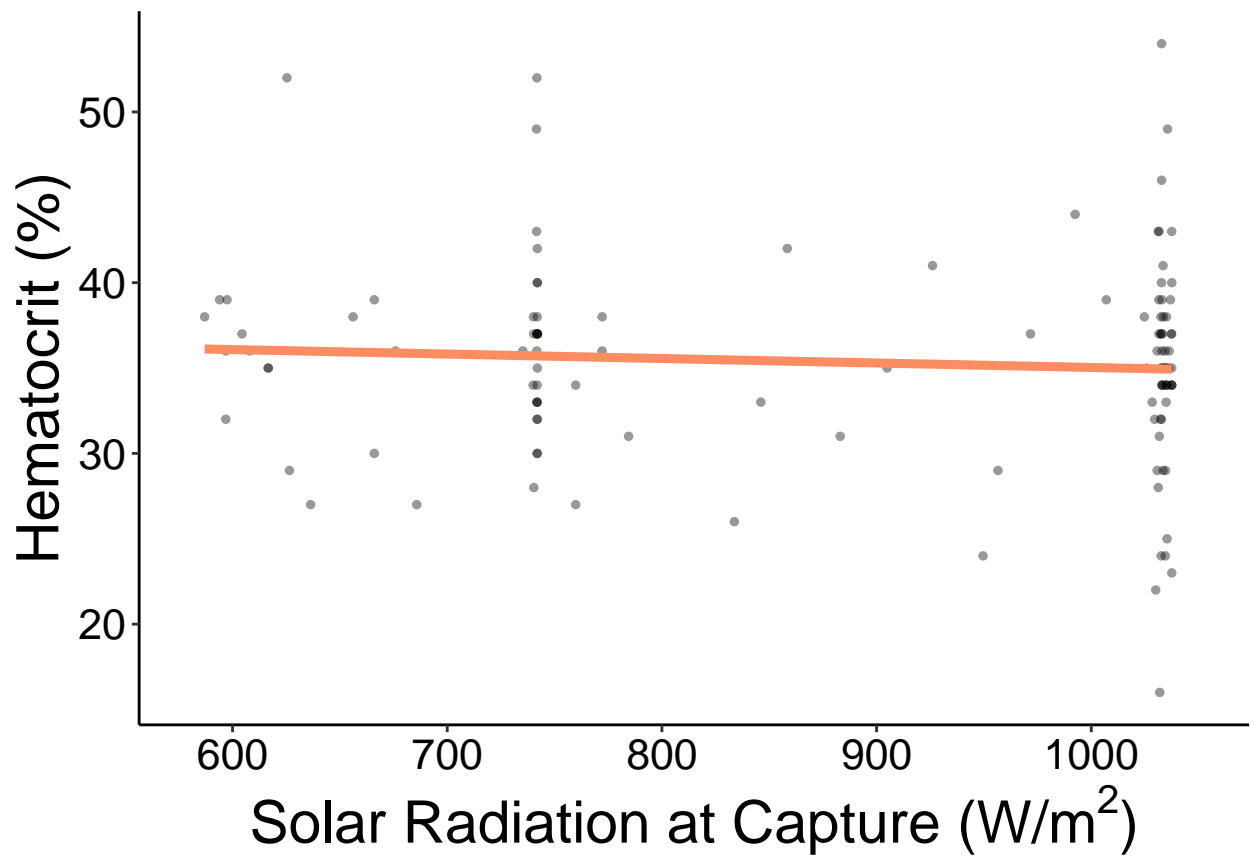


## Hct ~ Solar Radiation

```
morpho_blood_SMI %>%
  ggplot(data = .) +
  geom_point(aes(x = Solar_rad_Wm2_interpol,
                 y = hematocrit_percent),
             size = 1,
             alpha = 0.4) +
  stat_smooth(aes(x = Solar_rad_Wm2_interpol,
                  y = hematocrit_percent),
              formula = y ~ x,
              method = "lm",
              se = F,
              color = my_orng,
              size = 1.6,
              alpha = 1) +
  theme_classic() +
  xlab(bquote('Solar Radiation at Capture (W/'*m^2*')')) +
  ylab("Hematocrit (%)") +
  xlim(580, 1050) +
  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, #top
                             0.1, #right
                             0, #bottom
                             0.1 #left
                             ), "cm"))

) -> hct_sorad_fig
hct_sorad_fig

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



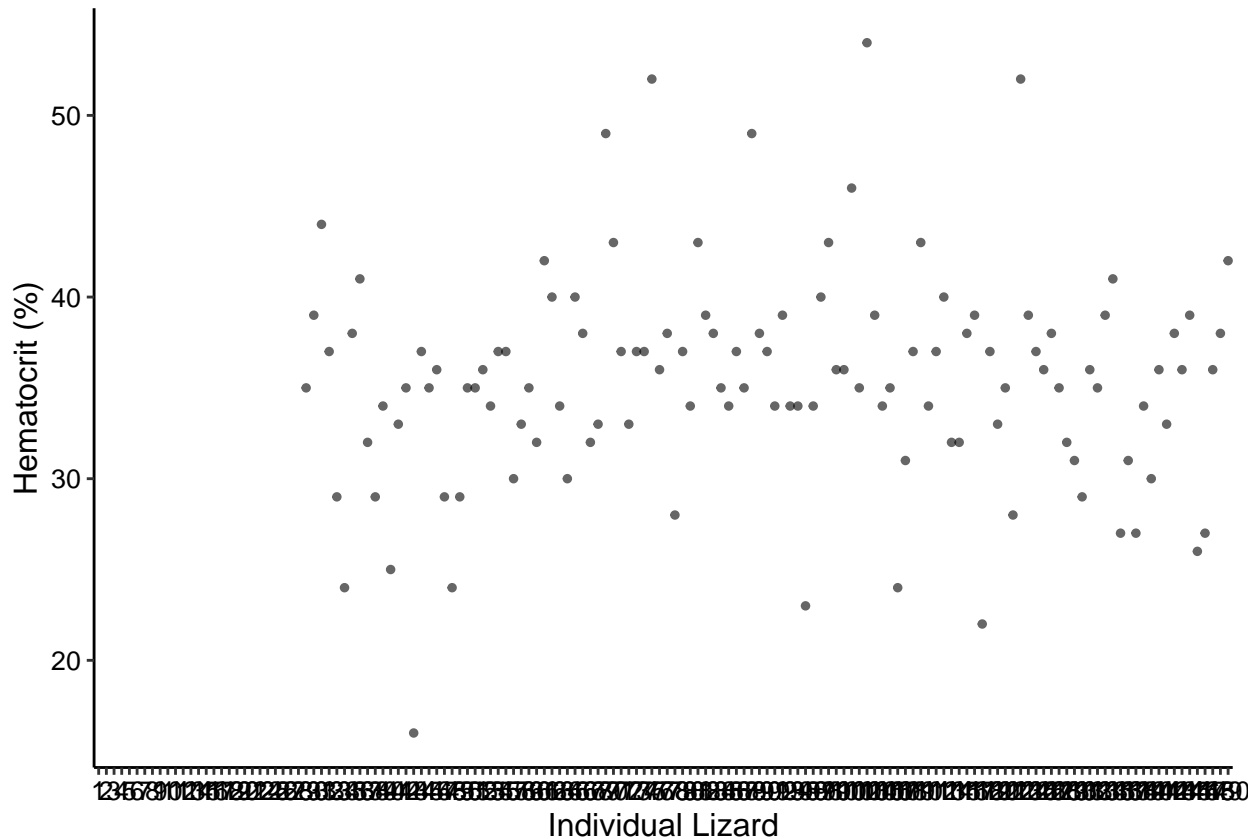
Hct ~ Individual

```
morpho_blood_SMI %>%
  ggplot(data = .) +
  geom_point(aes(x = individual_ID,
                 y = hematocrit_percent,
                 ),
            size = 1,
            alpha = 0.6) +
  stat_smooth(aes(x = individual_ID,
                 y = hematocrit_percent,
                 ),
            formula = y ~ x,
            method = "lm",
            color = "gray",
            se = F,
            size = 1.6,
            alpha = 1 ) +
  theme_classic() +
  xlab("Individual Lizard") +
  ylab("Hematocrit (%)") +
  theme(text = element_text(color = "black",
                             family = "sans",
                             size = 12),
        axis.text = element_text(color = "black",
                                   family = "sans",
```

```
size = 10),
legend.text.align = 0)
```

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

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



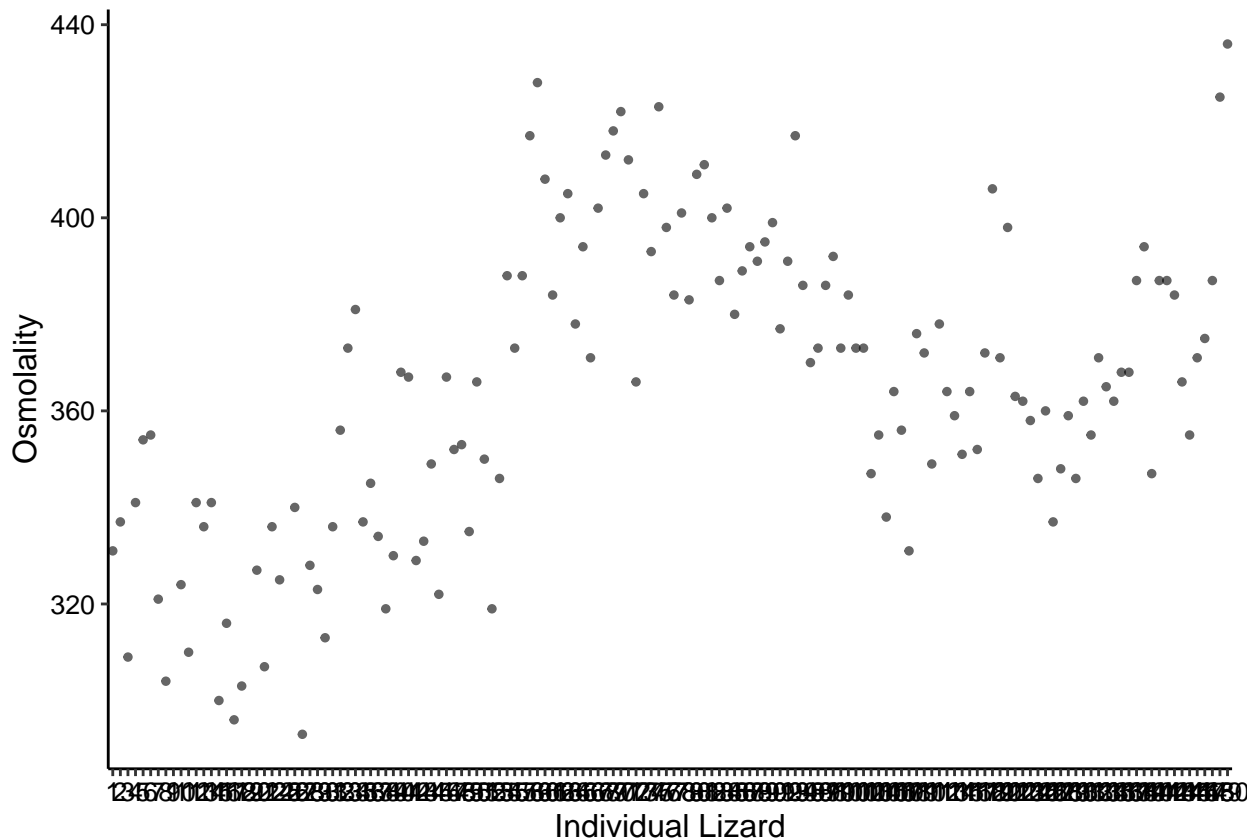
Osml ~ Individual

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

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

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

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



## Osmolality Multi-Figure

Based on reviewer comments & model revisions, this should include: VPD, wind, and sorad at capture, body condition, and sex. I'll do the 4 continuous variables in one multi-fig, then do the fig for sex separately bc its categorical.

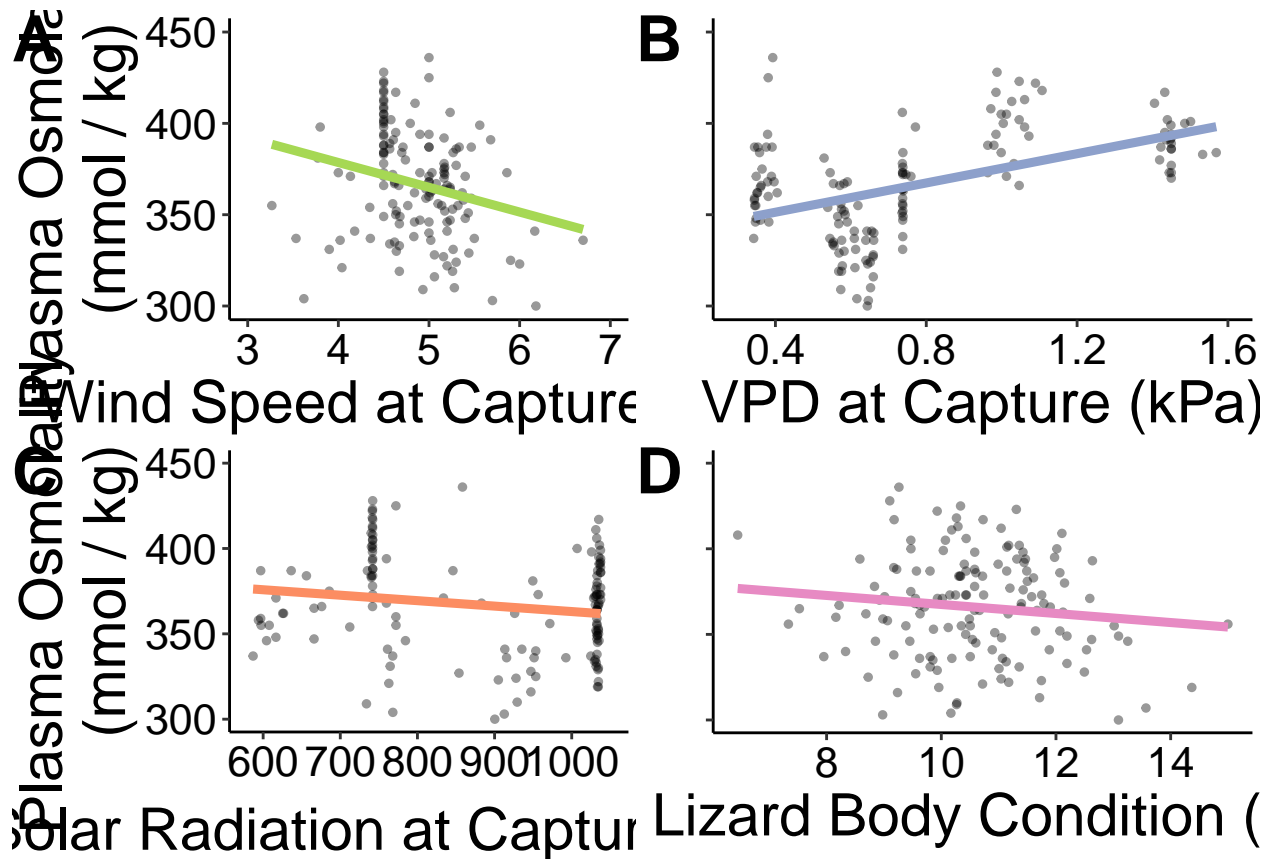
```
ggarrange(osml_wind_fig, osml_vpd_fig,
          osml_sorad_fig, osml_SMI_fig,
          ncol = 2, nrow = 2,
          labels = c("A", "B", "C", "D"),
          hjust = 0, vjust = 1.1,
          font.label = list(size = 24, face = "bold", color = "black")
          ) -> osml_multi_fig
```

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



```
## Warning: Removed 7 rows containing missing values (geom_point).
## Warning: Removed 8 rows containing non-finite values (stat_smooth).
## Warning: Removed 8 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).
## Warning: Removed 5 rows containing non-finite values (stat_smooth).
## Warning: Removed 5 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 = 8)
```

## Hct Multi-Fig

VPD, sorad, body condition, and sex should be plotted. I'm doing ~sex jointly with osmolality, which leaves the 3 continuous variables. hct\_vpd\_fig

```
ggarrange(hct_vpd_fig,
          hct_sorad_fig,
```

```

hct_SMI_fig,
ncol = 1, nrow = 3,
labels = c("A", "B", "C"),
hjust = 0, vjust = 1.1,
font.label = list(size = 24, face = "bold", color = "black")
) -> hct_multi_fig

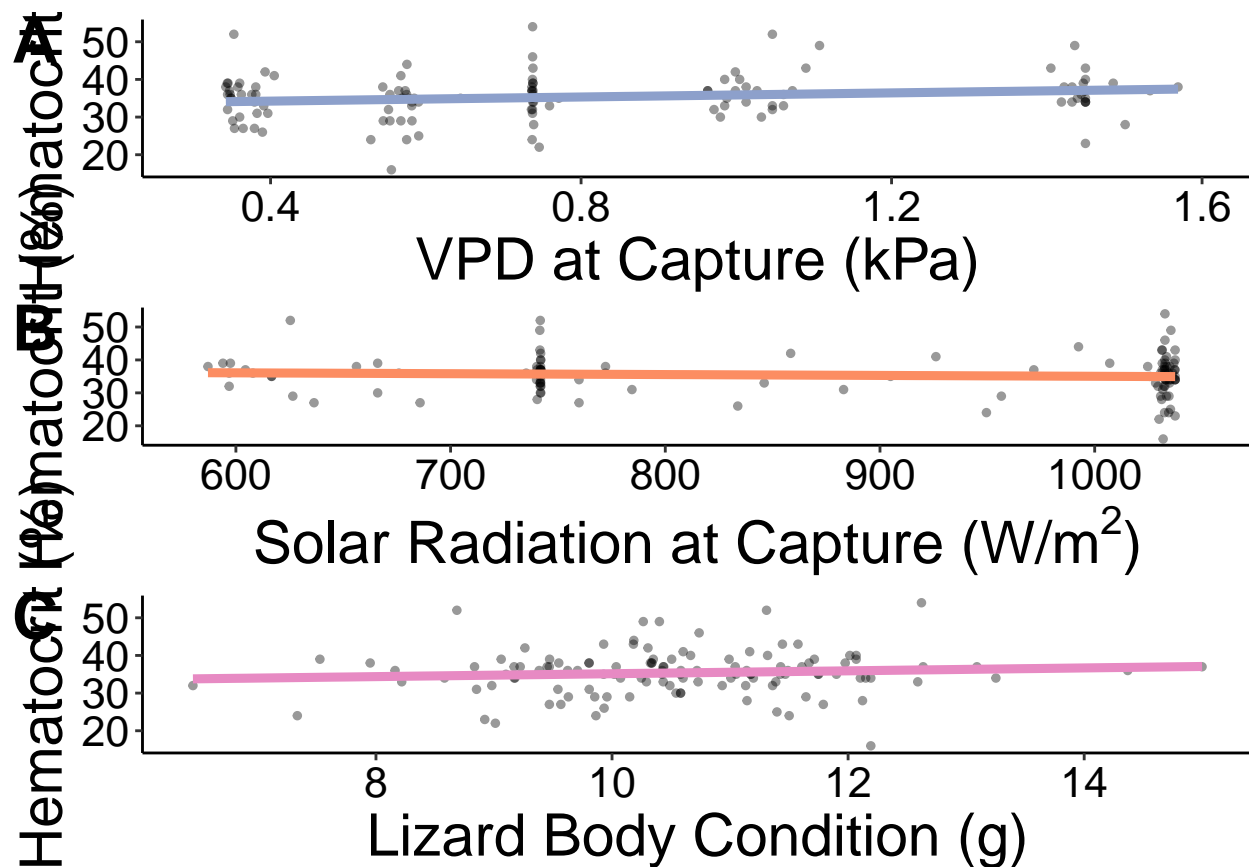
```

```

## Warning: Removed 29 rows containing non-finite values (stat_smooth).
## Warning: Removed 29 rows containing missing values (geom_point).
## Warning: Removed 28 rows containing non-finite values (stat_smooth).
## Warning: Removed 28 rows containing missing values (geom_point).
## Warning: Removed 27 rows containing non-finite values (stat_smooth).
## Warning: Removed 27 rows containing missing values (geom_point).

```

```
hct_multi_fig
```



```

# export figure
ggsave(filename = "hct_multi_fig.jpeg",
plot = hct_multi_fig,
path = "./final_figures",
device = "jpeg",
dpi = 1200,
width = 6, height = 12)

```

## Hct-Osml ~ Sex

```
ggarrange(osml_sex_fig, hct_sex_fig,
  ncol = 1, nrow = 2,
  labels = c("A", "B"),
  hjust = 0, vjust = 1.1,
  font.label = list(size = 24, face = "bold", color = "black")
) -> sex_multi_fig
```

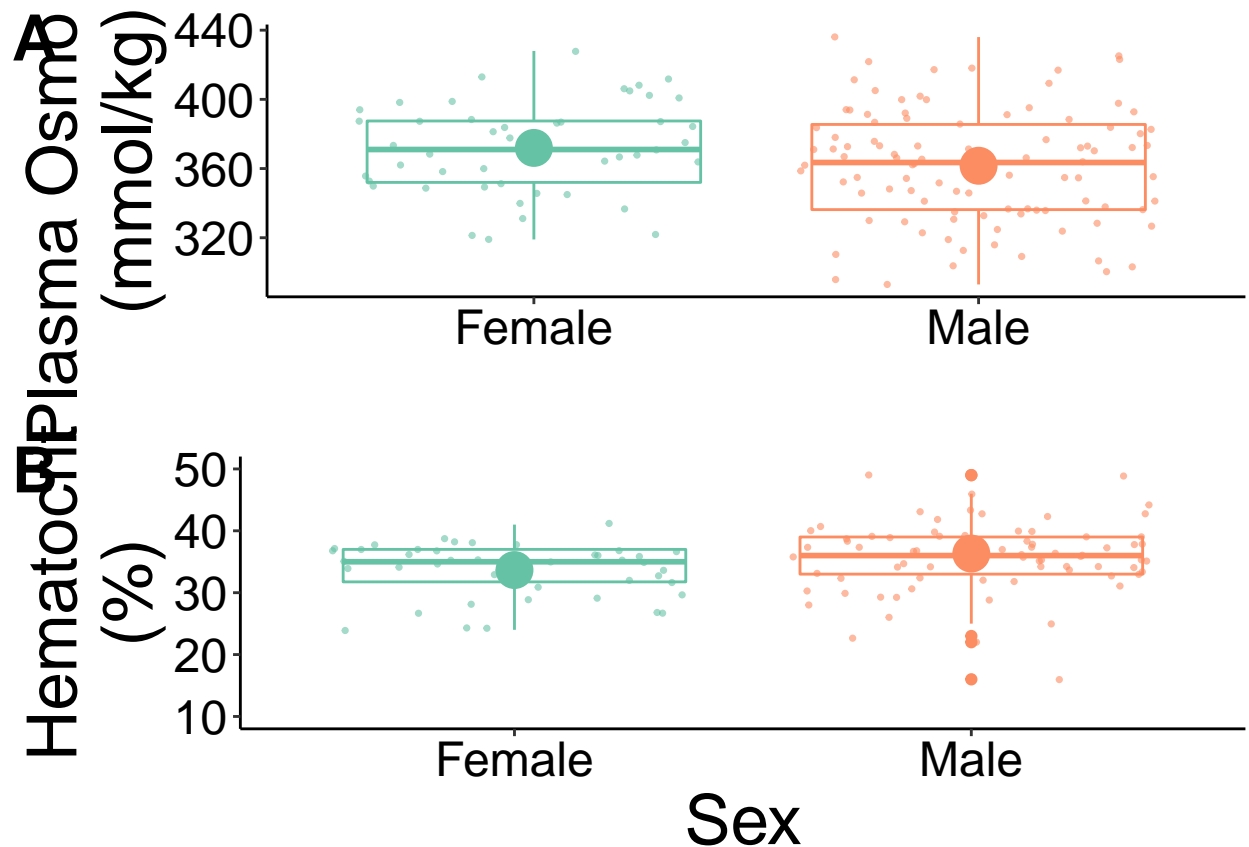
## Warning: Removed 3 rows containing non-finite values (stat\_boxplot).

## Warning: Removed 3 rows containing missing values (geom\_point).

## Warning: Removed 30 rows containing non-finite values (stat\_boxplot).

## Warning: Removed 30 rows containing missing values (geom\_point).

sex\_multi\_fig



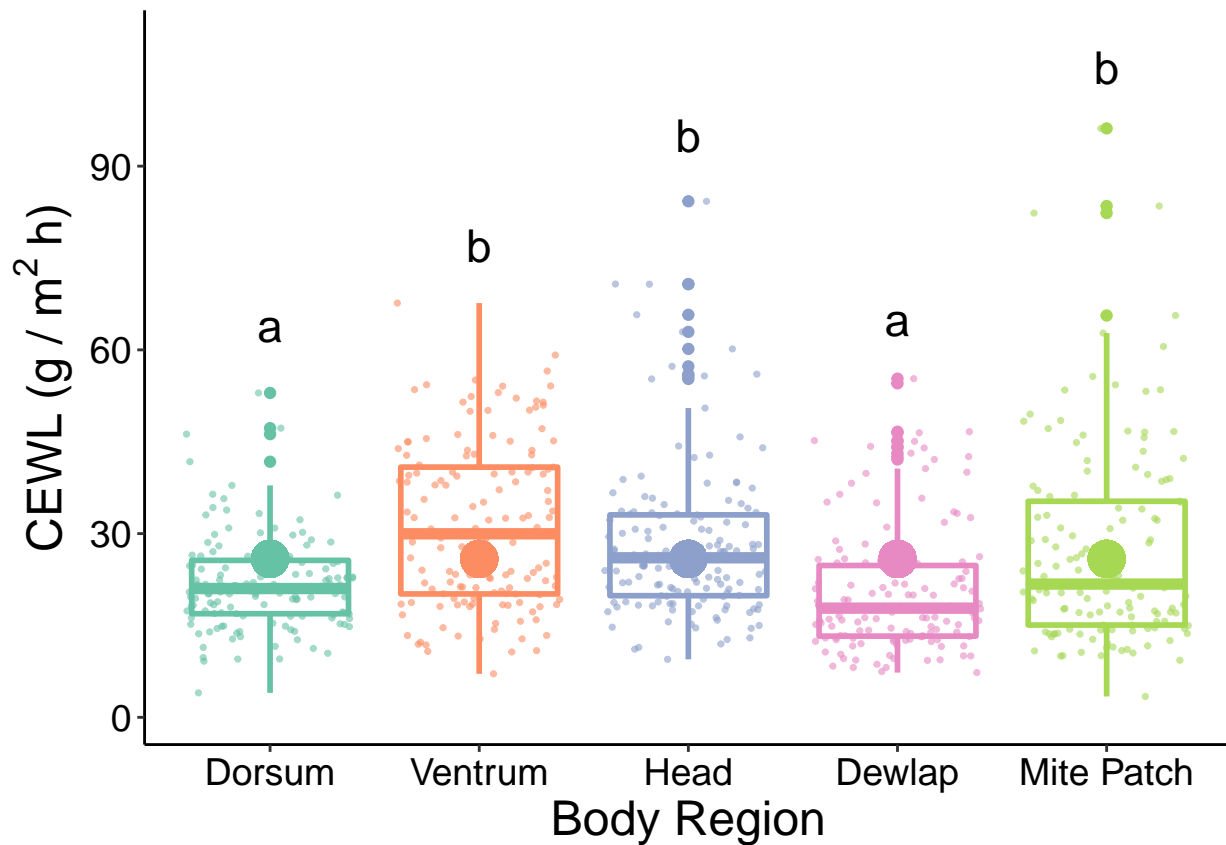
```
# export figure
ggsave(filename = "sex_multi_fig.jpeg",
  plot = sex_multi_fig,
  path = "./final_figures",
  device = "jpeg",
  dpi = 1200,
  width = 5, height = 9)
```

## 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 = 0.6) +
  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 = "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, 110) +
  theme(text = element_text(color = "black",
                             family = "sans",
                             size = 18),
        axis.text = element_text(color = "black",
                                   family = "sans",
                                   size = 14),
        legend.text.align = 0,
        legend.position = "none"
  ) -> CEWL_region_fig
CEWL_region_fig
```



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

### Body Region Ratios

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

by_region_CEWL <- CEWL_mite %>%
```

```

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

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

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

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

```

```

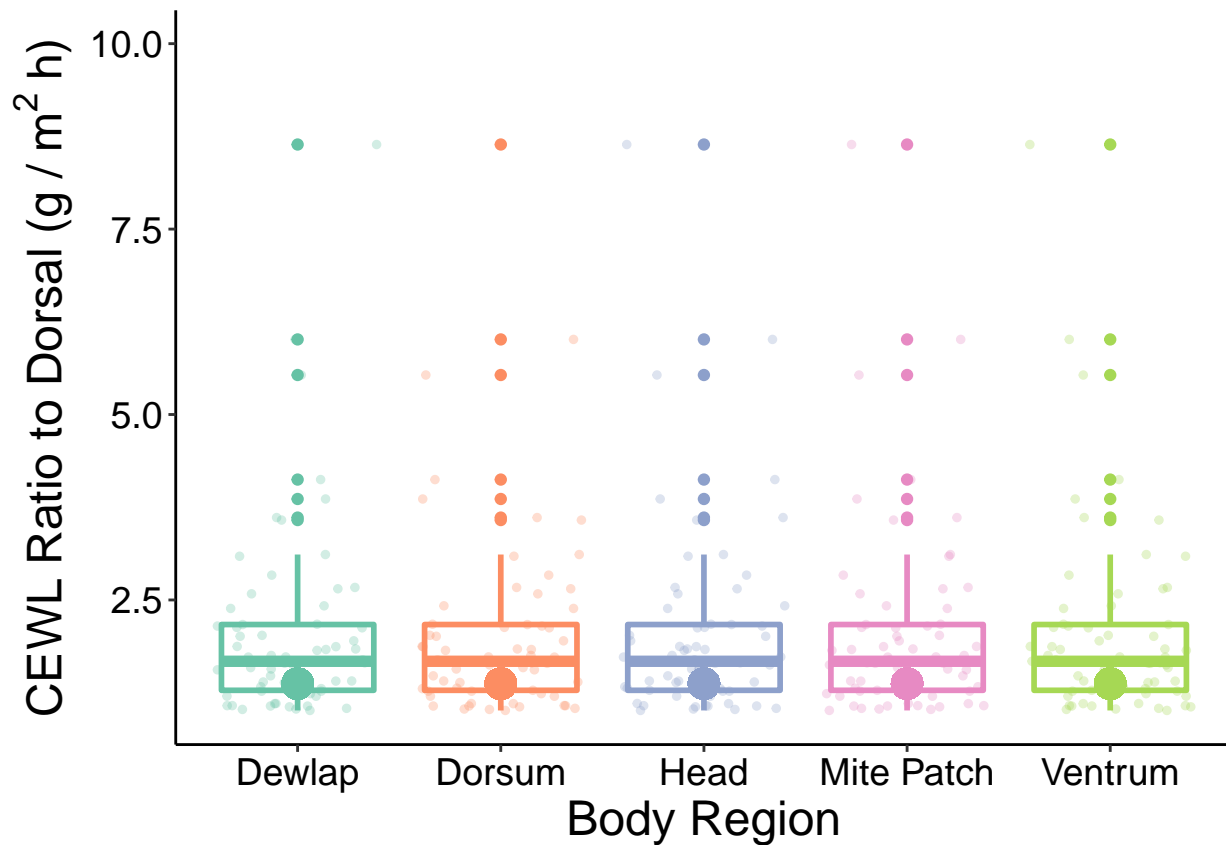
xlab("Body Region") +
ylab(bquote('CEWL Ratio to Dorsal (g / '*m^2~h*')')) +
annotate("text", x = 1, y = 64, label = "a", size = 6) +
annotate("text", x = 2, y = 77, label = "b", size = 6) +
annotate("text", x = 3, y = 95, label = "b", size = 6) +
annotate("text", x = 4, y = 65, label = "a", size = 6)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

```

```

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

```



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

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

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

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

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

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

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

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

CEWL ~ Osmolality

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



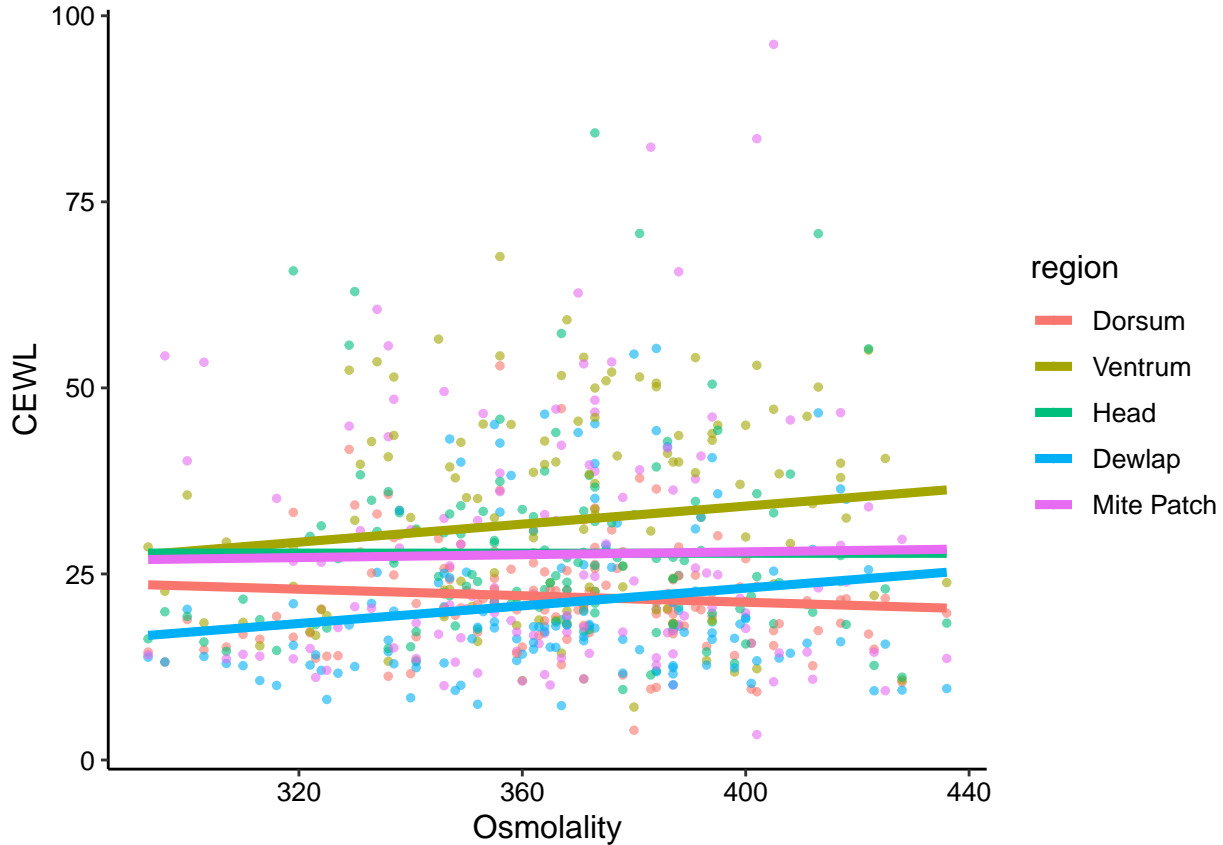
```

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

```

## Warning: Removed 49 rows containing non-finite values (stat\_smooth).

## Warning: Removed 49 rows containing missing values (geom\_point).



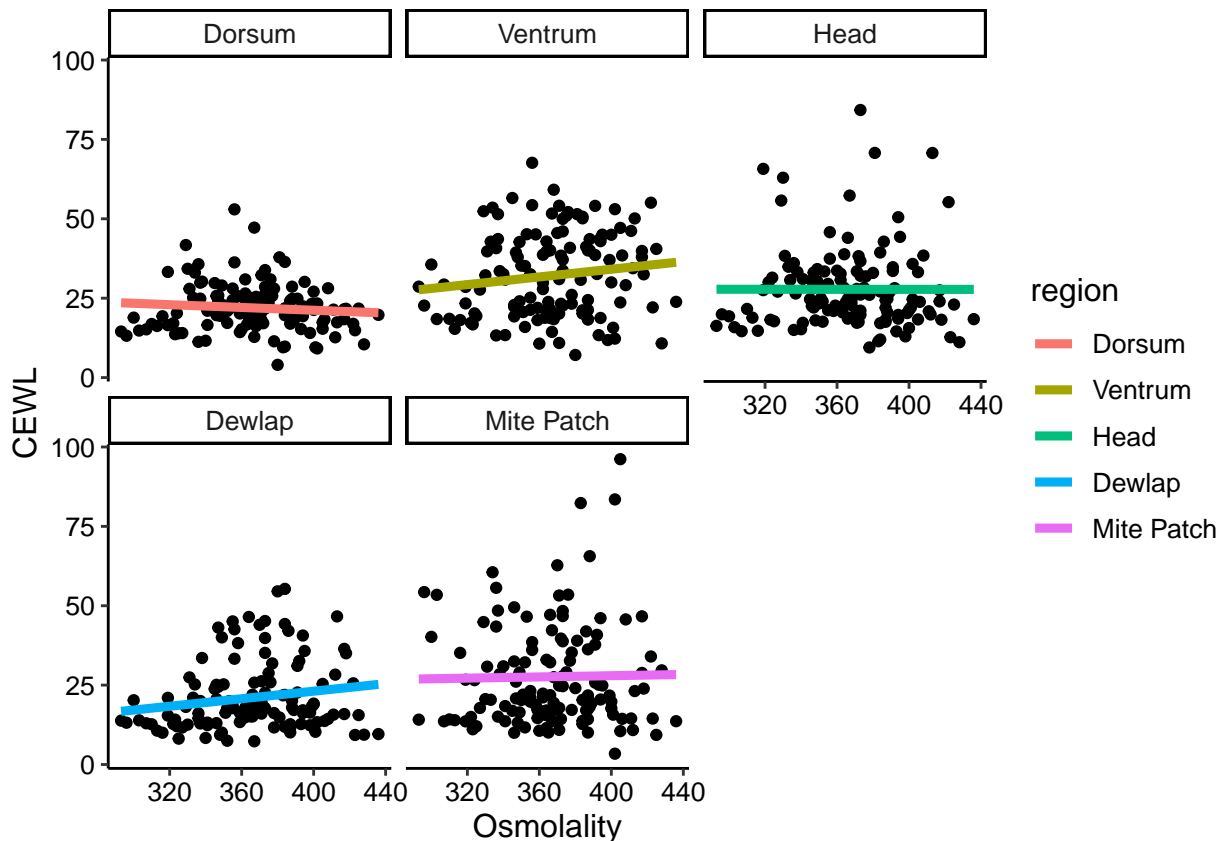
```

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

```

## Warning: Removed 49 rows containing non-finite values (stat\_smooth).

## Warning: Removed 49 rows containing missing values (geom\_point).

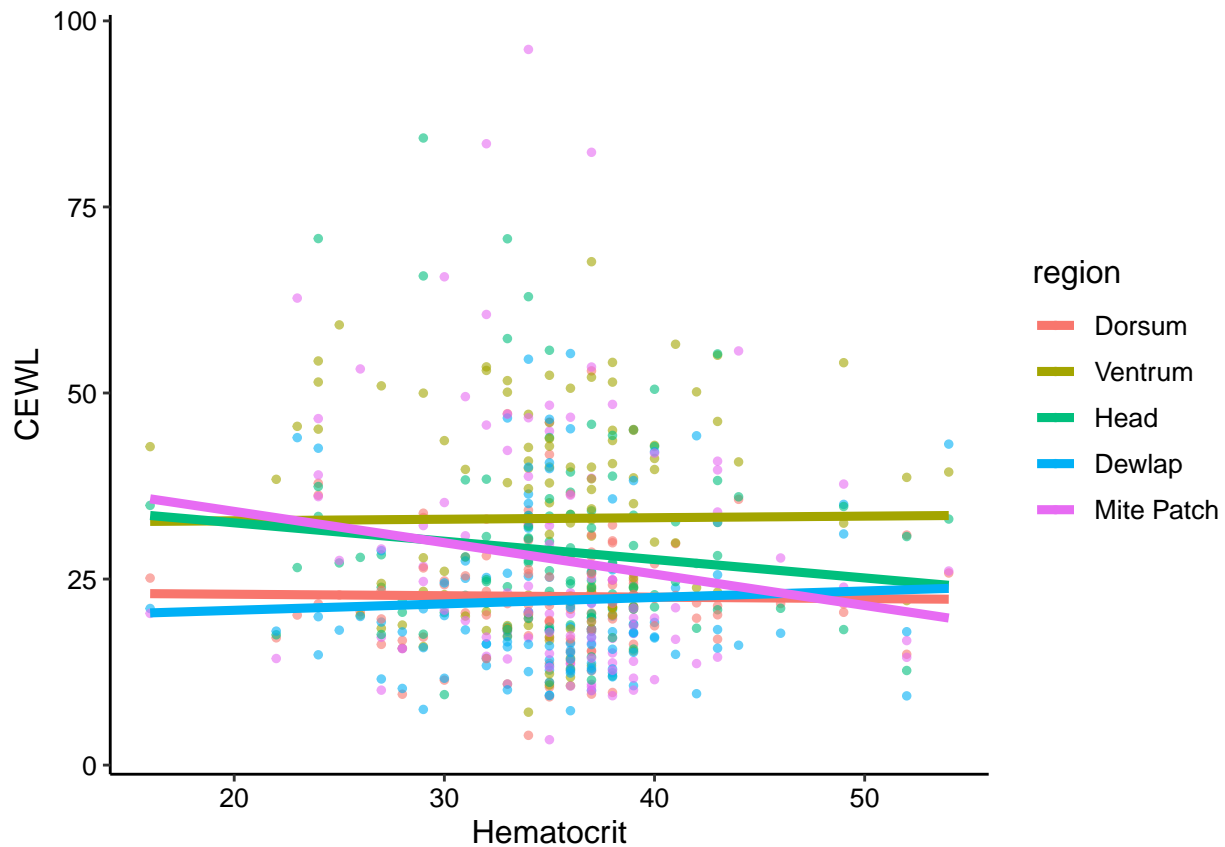


## CEWL ~ Hematocrit

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

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

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



CEWL ~ Cloacal Temperature

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

```

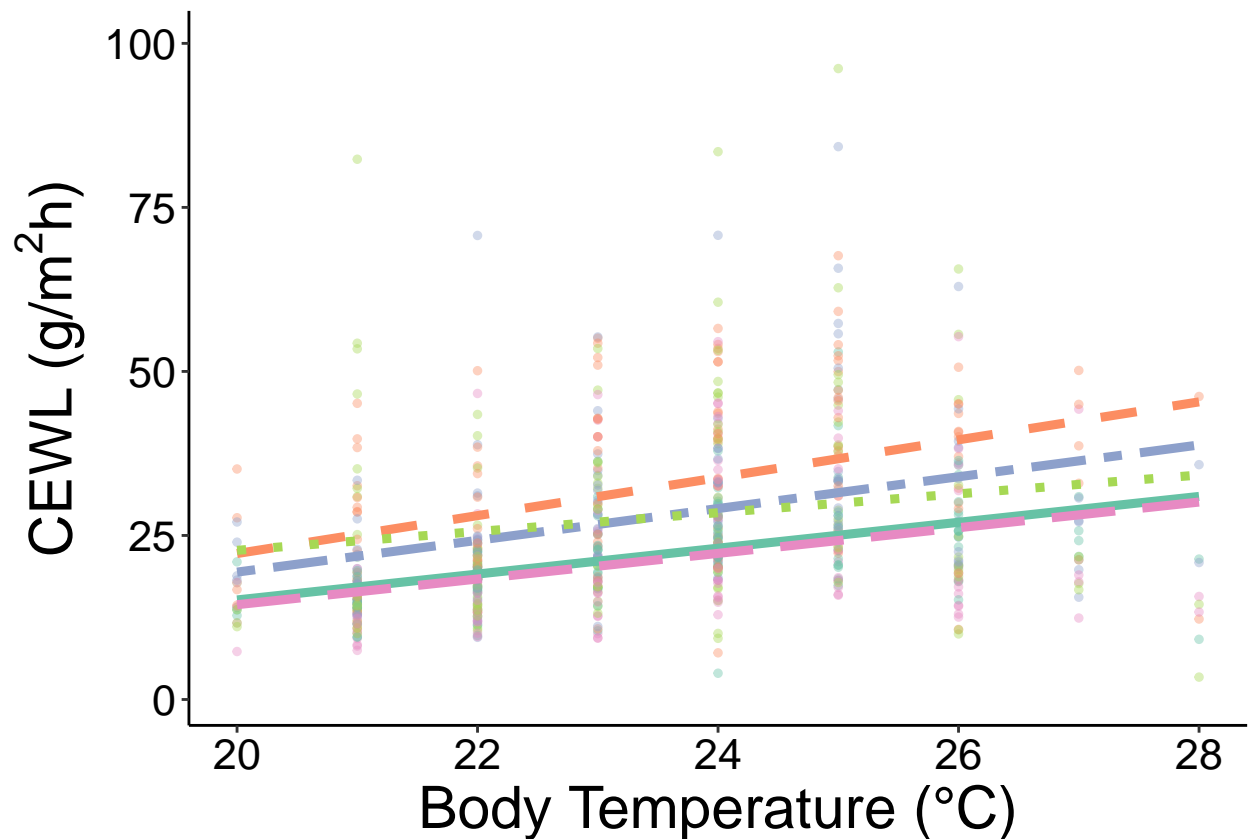
scale_linetype_manual(values = c("solid", "dashed",
                                "twodash", "longdash", "dotted")) +

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, #top
                           0.1, #right
                           0.35, #bottom
                           0.1 #left
                           ), "cm"),
      legend.text.align = 0,
      legend.position = "none") -> clotemp_CEWL_fig
clotemp_CEWL_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.tif",

```

```
#      plot = CEWL_ctemp_fig,
#      path = "./final_figures",
#      device = "tiff",
#      dpi = 1200,
#      width = 6, height = 4)
```

## CEWL ~ Capture Temperature

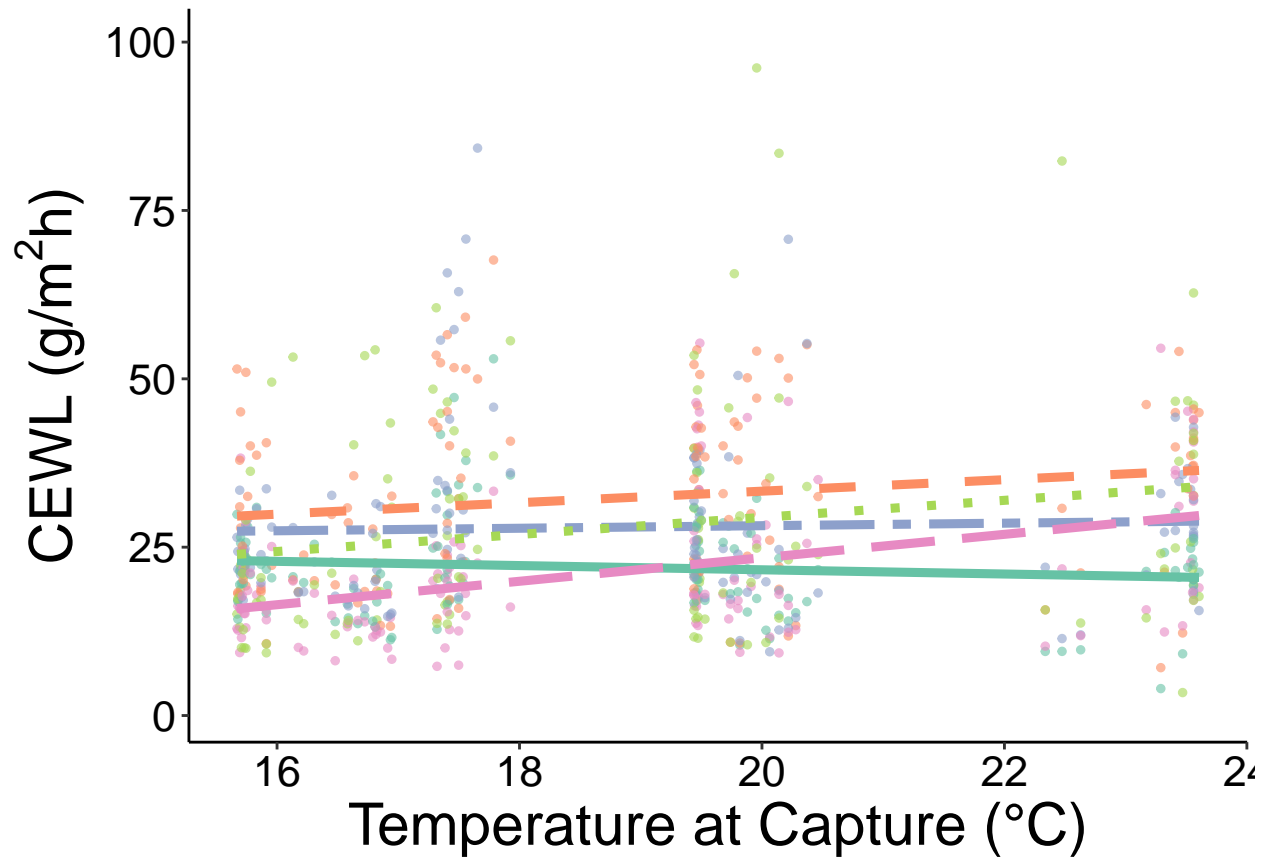
```
CEWL_data_full %>%
  ggplot(data = .) +
  geom_point(aes(x = temp_C_interpol,
                 y = TEWL_g_m2h,
                 color = region
                 ),
             size = 1,
             alpha = 0.6) +
  stat_smooth(aes(x = temp_C_interpol,
                  y = TEWL_g_m2h,
                  color = region,
                  linetype = region
                  ),
              formula = y ~ x,
              method = "lm",
              se = F,
              size = 1.6,
              alpha = 1 ) +
  scale_color_brewer(palette = "Set2") +
  scale_linetype_manual(values = c("solid", "dashed",
                                   "twodash", "longdash", "dotted")) +

  theme_classic() +
  xlab("Temperature at Capture (°C)") +
  #ylab("") +
  ylim(1, 100) +
  #xlim(16, 24) +
  ylab(bquote('CEWL (g/*m2*h)')) +
  theme(text = element_text(color = "black",
                             family = "sans",
                             size = 22),
        axis.text = element_text(color = "black",
                                   family = "sans",
                                   size = 16),
        #axis.text.y = element_blank(),
        legend.text = element_text(color = "black",
                                    family = "sans",
                                    size = 26),
        plot.margin = unit(c(0.1, #top
                             0.1, #right
                             0.1, #bottom
                             0.1 #left
                             ), "cm"),
        legend.text.align = 0,
        legend.position = "none"
  ) -> cap_temp_CEWL_fig
```

```
cap_temp_CEWL_fig
```

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

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



CEWL ~ Capture VPD

```
CEWL_data_full %>%  
  ggplot(data = .) +  
  geom_jitter(aes(x = VPD_kPa_int,  
                  y = TEWL_g_m2h,  
                  color = region  
                ),  
             size = 1,  
             alpha = 0.4) +  
  stat_smooth(aes(x = VPD_kPa_int,  
                  y = TEWL_g_m2h,  
                  color = region,  
                  linetype = region  
                ),  
             formula = y ~ x,  
             method = "lm",  
             se = F,  
             size = 1.6,  
             alpha = 1 ) +
```

```

theme_classic() +
xlab("VPD at Capture (kPa)") +
ylab(bquote('CEWL (g/*m2*h)')) +
#ylab("") +
scale_color_brewer(palette = "Set2",
                    name = "") +
scale_linetype_manual(values = c("solid", "dashed",
                                "twodash", "longdash", "dotted")) +

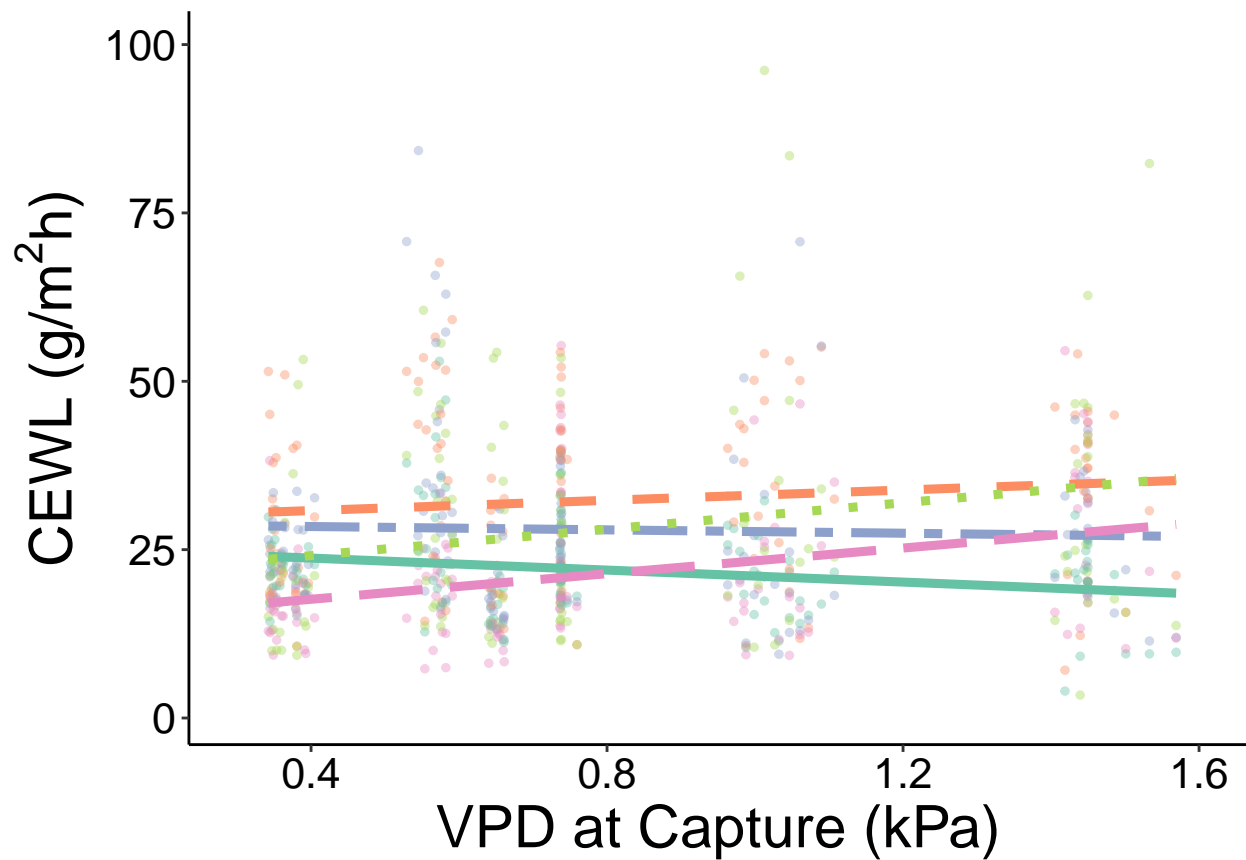
ylim(1, 100) +
xlim(0.3, 1.6) +
theme(text = element_text(color = "black",
                           family = "sans",
                           size = 22),
      axis.text = element_text(color = "black",
                                family = "sans",
                                size = 16),
      #axis.text.y = element_blank(),
      legend.text = element_text(color = "black",
                                  family = "sans",
                                  size = 26),
      legend.text.align = 0,
      plot.margin = unit(c(0.1, #top
                           0.1, #right
                           0.1, #bottom
                           0.1 #left
                           ), "cm"),
      legend.position = "none"
      #legend.position = c(0.15, 0.85)
      ) -> cap_vpd_CEWL_fig
cap_vpd_CEWL_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,
                  linetype = region
                 ),
            formula = y ~ x,
            method = "lm",
            se = F,
```

```

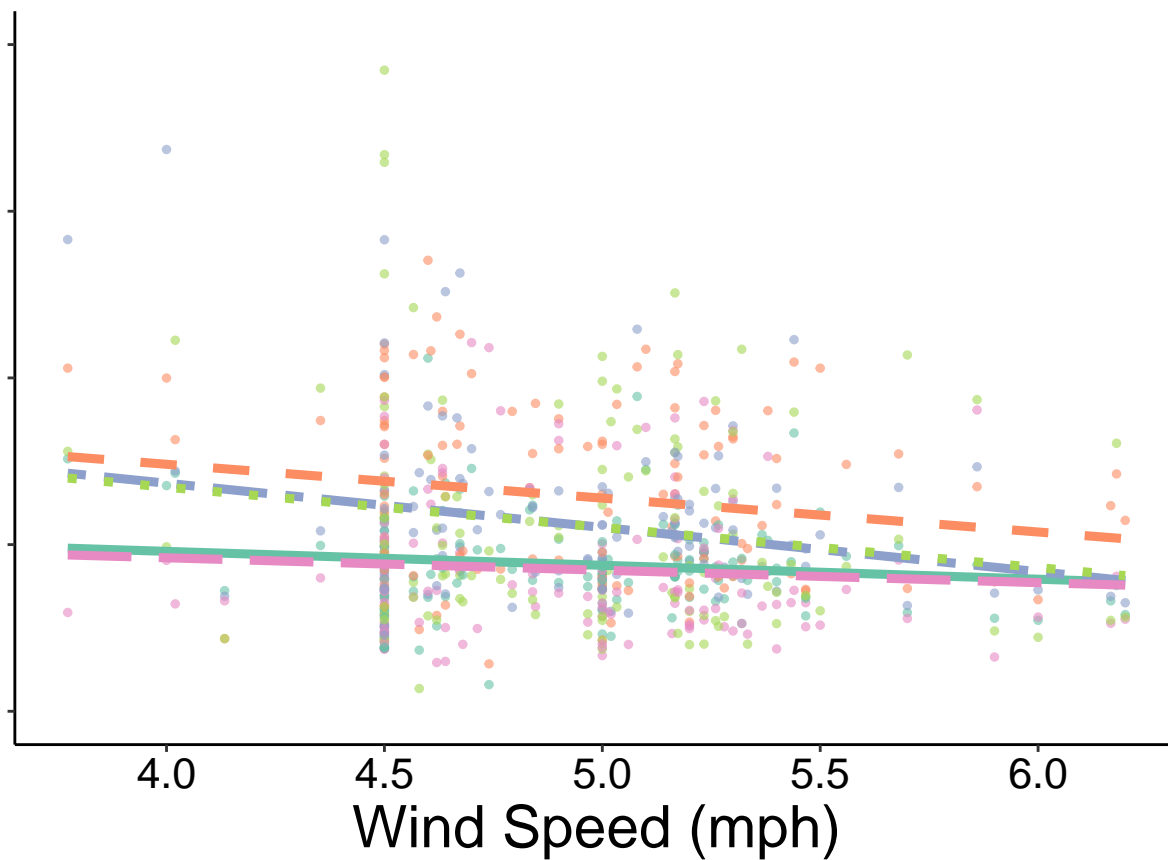
        size = 1.6,
        alpha = 1 ) +
theme_classic() +
scale_color_brewer(palette = "Set2") +
scale_linetype_manual(values = c("solid", "dashed",
                                "twodash", "longdash", "dotted")) +

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(0.1,0.1,0.1,0.1), "cm"),
      legend.text.align = 0,
      legend.position = "none"
) -> cap_wind_CEWL_fig
cap_wind_CEWL_fig

```

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

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



CEWL ~ Solar Rad

```
CEWL_data_full %>%
  ggplot(data = .) +
  geom_point(aes(x = Solar_rad_Wm2_interpol,
                 y = TEWL_g_m2h,
                 color = region
                ),
            size = 1,
            alpha = 0.6) +
  stat_smooth(aes(x = Solar_rad_Wm2_interpol,
                  y = TEWL_g_m2h,
                  color = region,
                  linetype = region
                 ),
            formula = y ~ x,
            method = "lm",
            se = F,
            size = 1.6,
            alpha = 1 ) +
  theme_classic() +
  scale_color_brewer(palette = "Set2") +
  scale_linetype_manual(values = c("solid", "dashed",
                                   "twodash", "longdash", "dotted")) +
  xlab(bquote('Solar Radiation at Capture (W/'*m^2*')')) +
  #ylab(bquote('CEWL (g/'*m^2*'h)')) +
```

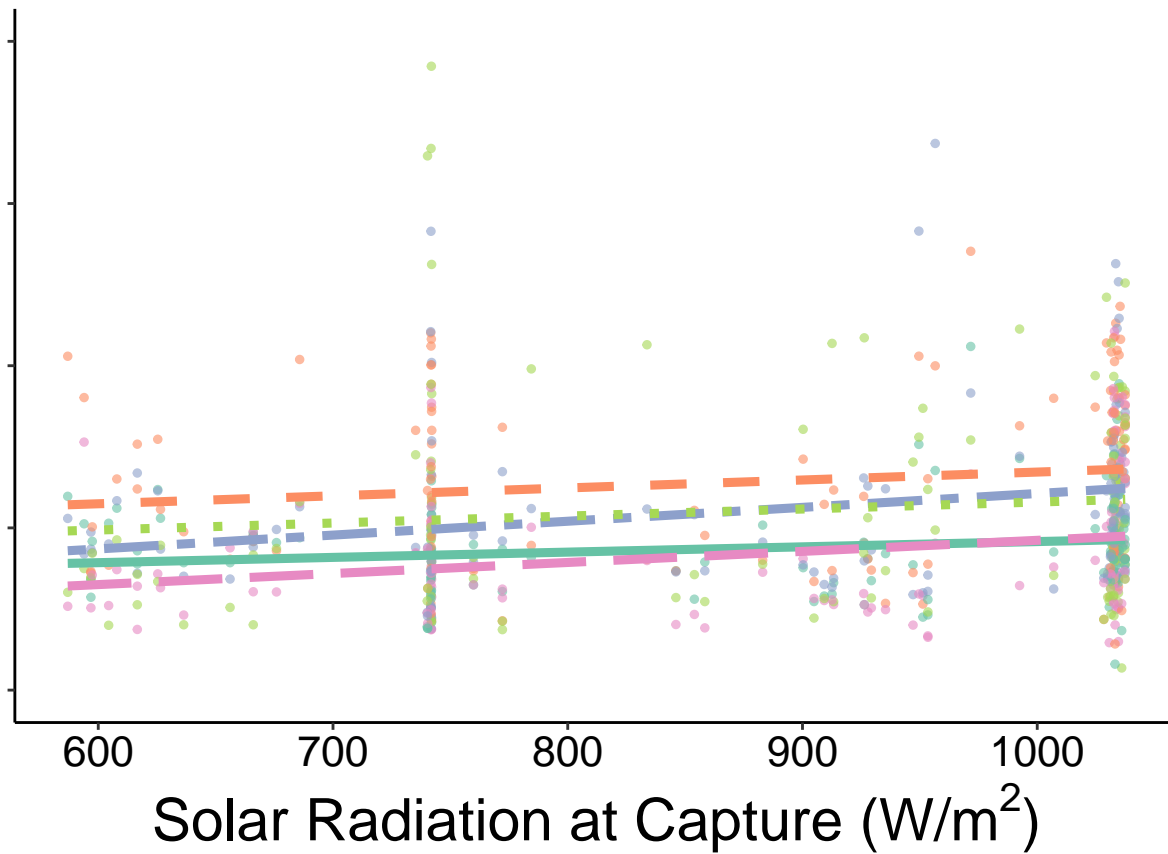
```

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, #top
                          0.1, #right
                          0, #bottom
                          0.1 #left
                          ), "cm"),
      legend.text.align = 0,
      legend.position = "none"
) -> cap_sorad_CEWL_fig
cap_sorad_CEWL_fig

```

## Warning: Removed 59 rows containing non-finite values (stat\_smooth).

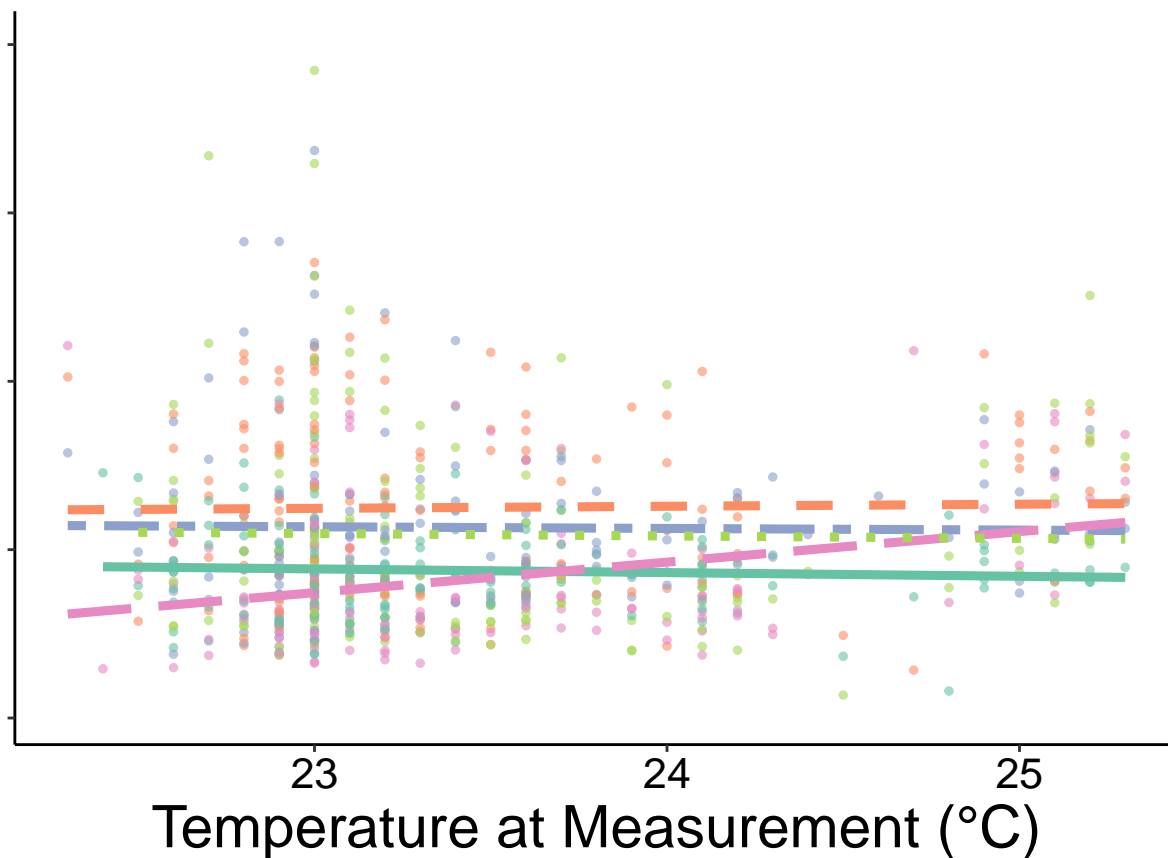
## Warning: Removed 59 rows containing missing values (geom\_point).



## 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,
                  linetype = region
                  ),
              formula = y ~ x,
              method = "lm",
              se = F,
              size = 1.6,
              alpha = 1 ) +
  scale_color_brewer(palette = "Set2") +
  scale_linetype_manual(values = c("solid", "dashed",
                                   "twodash", "longdash", "dotted")) +

  theme_classic() +
  xlab("Temperature at Measurement (°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),
        axis.text.y = element_blank(),
        legend.text = element_text(color = "black",
                                    family = "sans",
                                    size = 26),
        plot.margin = unit(c(0.1, #top
                             0.1, #right
                             0.1, #bottom
                             0.1 #left
                             ), "cm"),
        legend.text.align = 0,
        legend.position = "none"
  ) -> msmt_temp_CEWL_fig
msmt_temp_CEWL_fig
```



#### CEWL ~ Measurement VPD

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

```
CEWL_data_full %>%
  ggplot(data = .) +
  geom_jitter(aes(x = VPD_kPa,
                  y = TEWL_g_m2h,
                  color = region
                ),
             size = 1,
             alpha = 0.4) +
  stat_smooth(aes(x = VPD_kPa,
                  y = TEWL_g_m2h,
                  color = region,
                  linetype = region
                ),
             formula = y ~ x,
             method = "lm",
             se = F,
             size = 1.6,
             alpha = 1) +
  theme_classic() +
  xlab("VPD at Measurement (kPa)") +
  #ylab(bquote('CEWL (g/'*m^2*'h)')) +
  ylab("") +
```

```

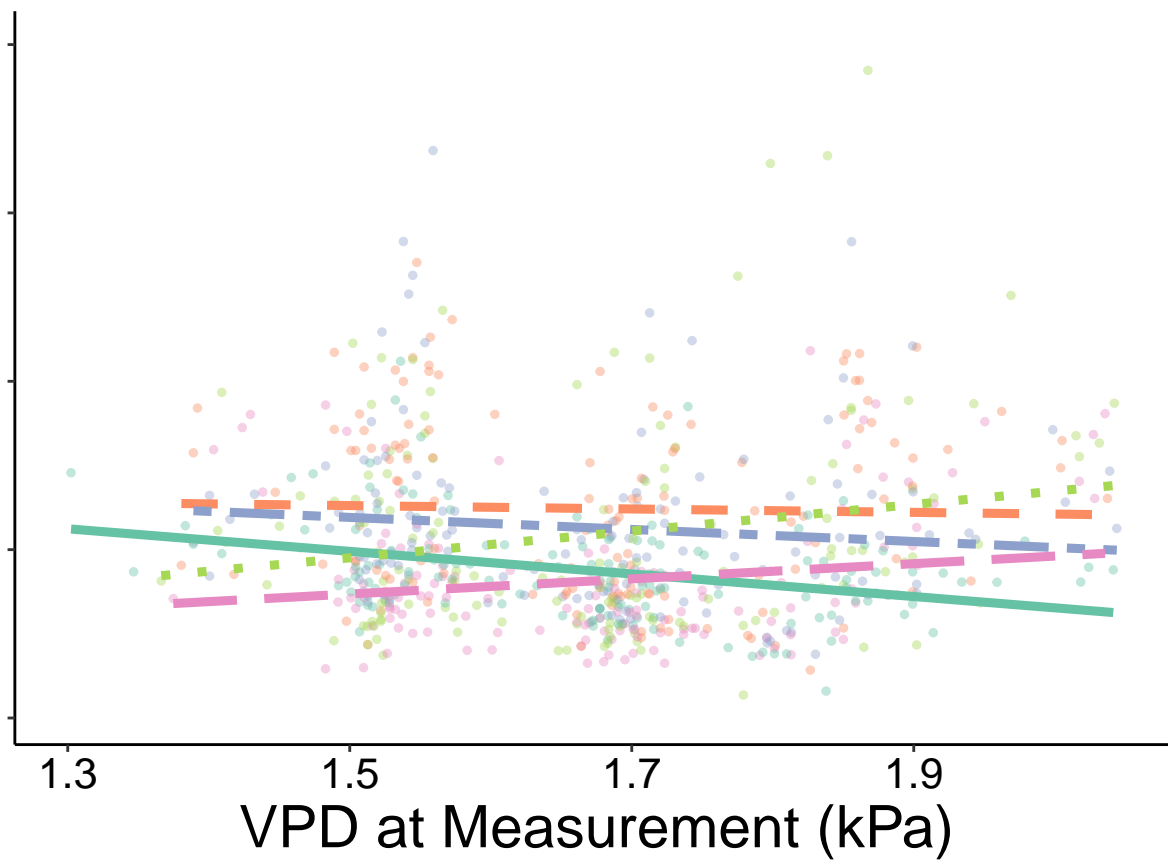
scale_color_brewer(palette = "Set2",
                   name = "") +
scale_linetype_manual(values = c("solid", "dashed",
                                "twodash", "longdash", "dotted")) +

ylim(1, 100) +
xlim(1.3, 2.05) +
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(),
      legend.text.align = 0,
      plot.margin = unit(c(0.1, #top
                           0.1, #right
                           0.1, #bottom
                           0.1 #left
                           ), "cm"),
      legend.position = "none"
      #legend.position = c(0.15, 0.85)
      ) -> msmt_VPD_CEWL_fig
msmt_VPD_CEWL_fig

```

```
## Warning: Removed 4 rows containing non-finite values (stat_smooth).
```

```
## Warning: Removed 4 rows containing missing values (geom_point).
```



CEWL ~ Individual

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

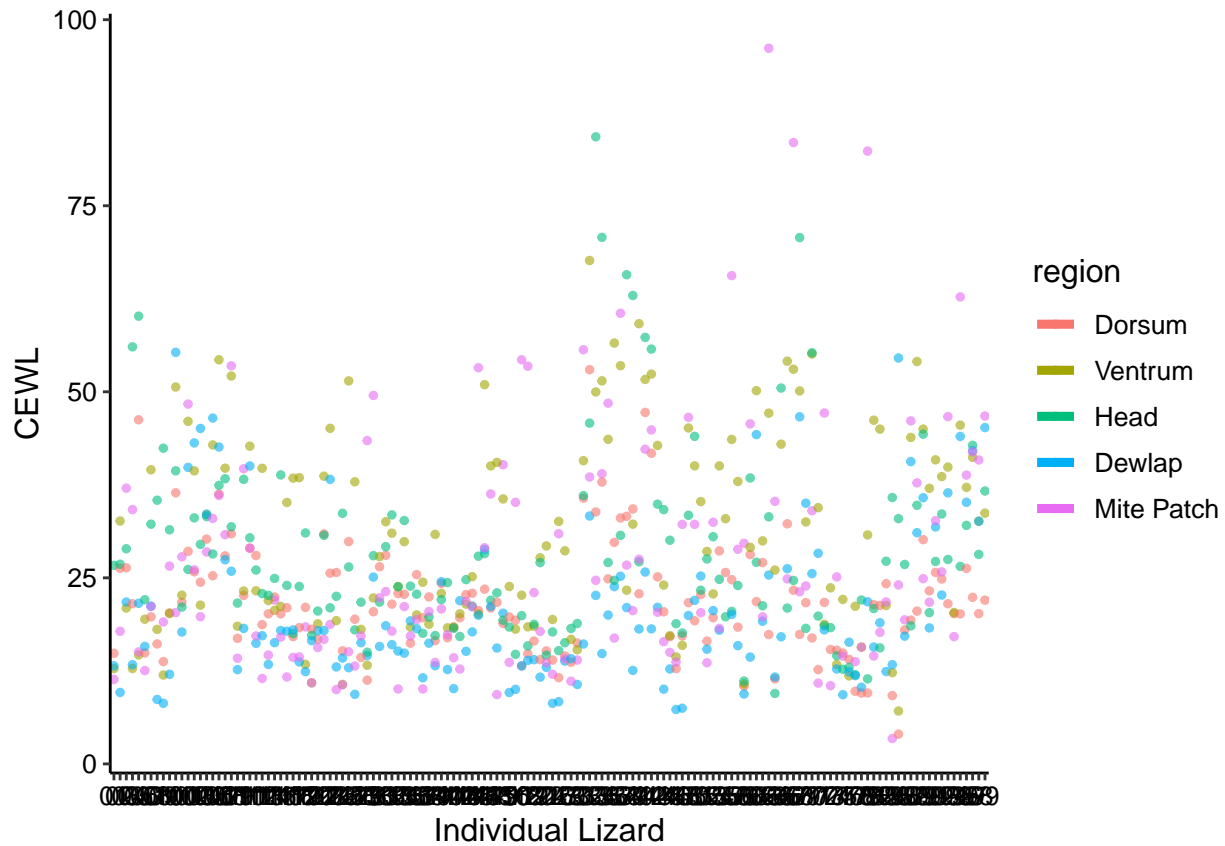
  # just to get a better look
  # ylim(5, 40) +
```



```

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

```



CEWL ~ SVL

```

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

```

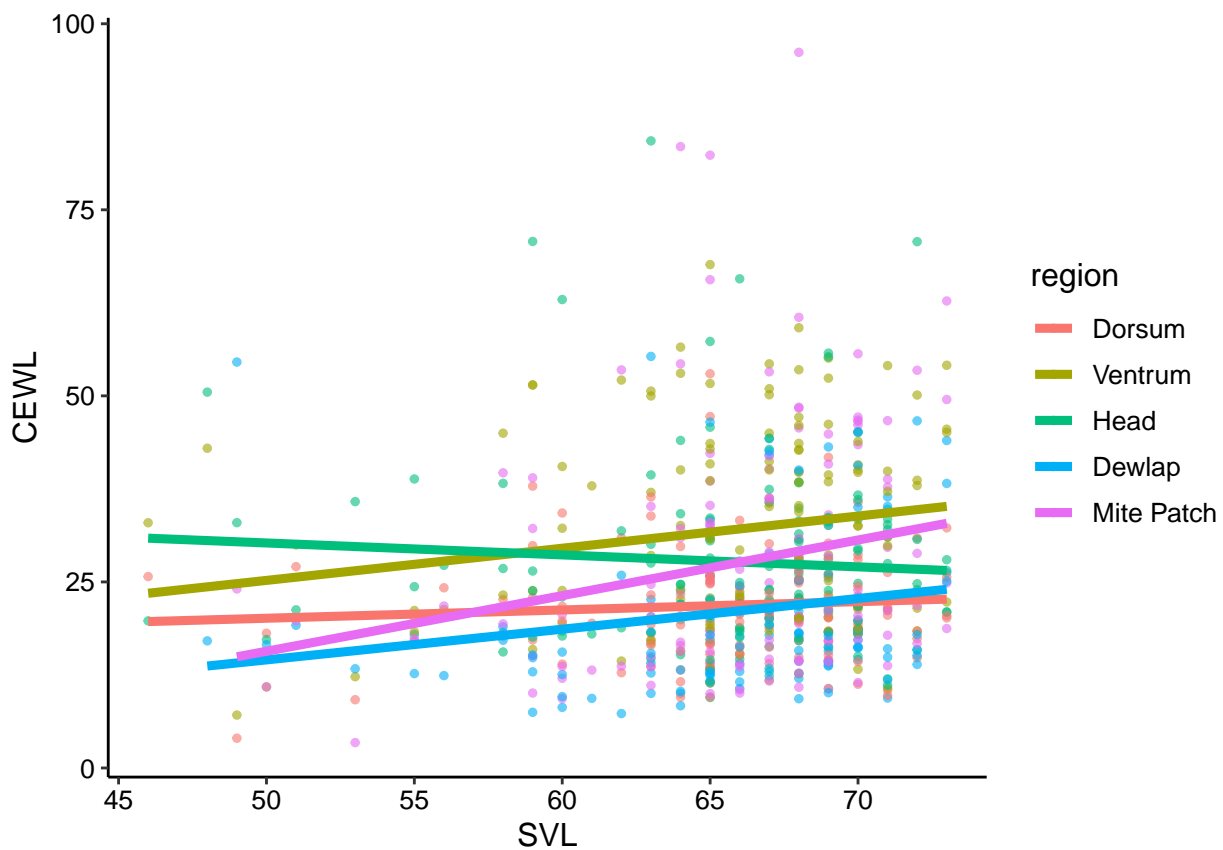
```

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

```

## Warning: Removed 44 rows containing non-finite values (stat\_smooth).

## Warning: Removed 44 rows containing missing values (geom\_point).



CEWL ~ SMI

```

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

```

```

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

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

```

```

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

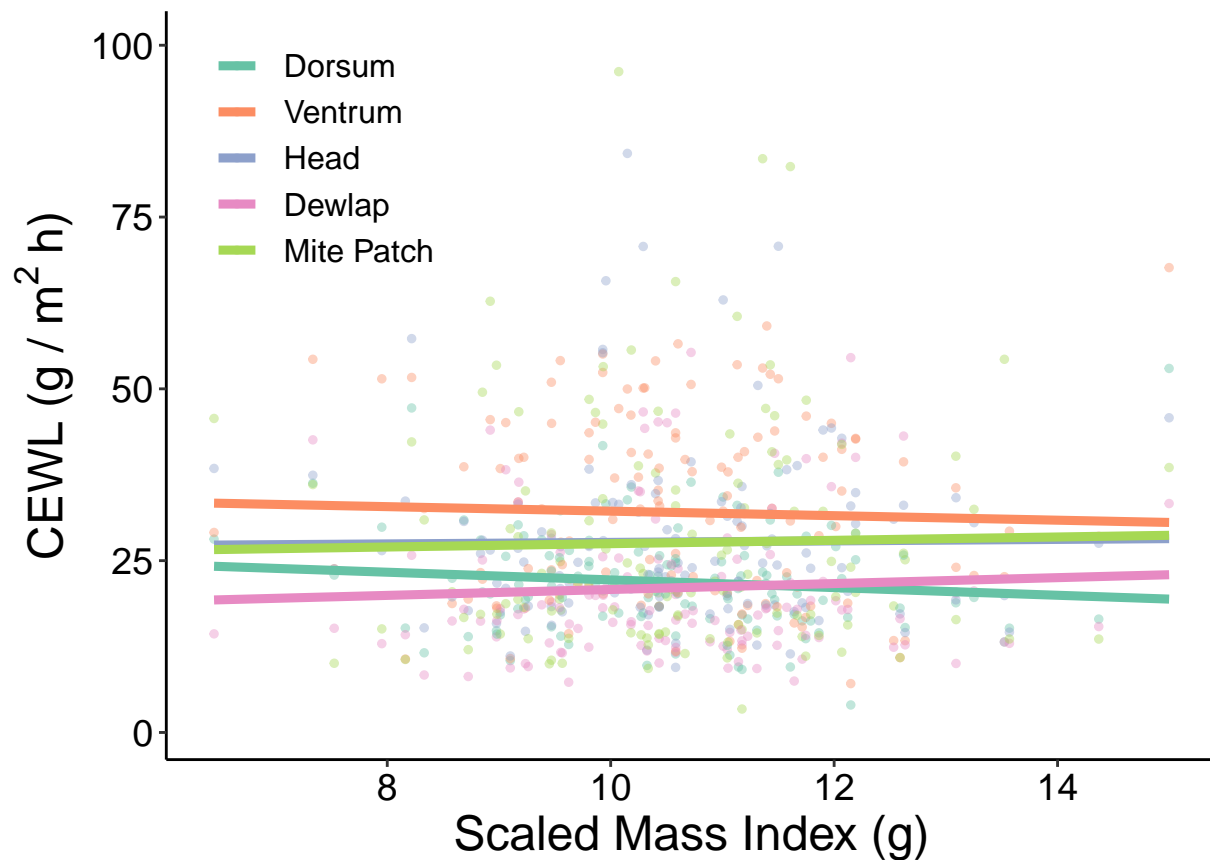
```

```
CEWL_SMI_fig
```

```

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

```



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

### CEWL ~ Mass

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

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

```

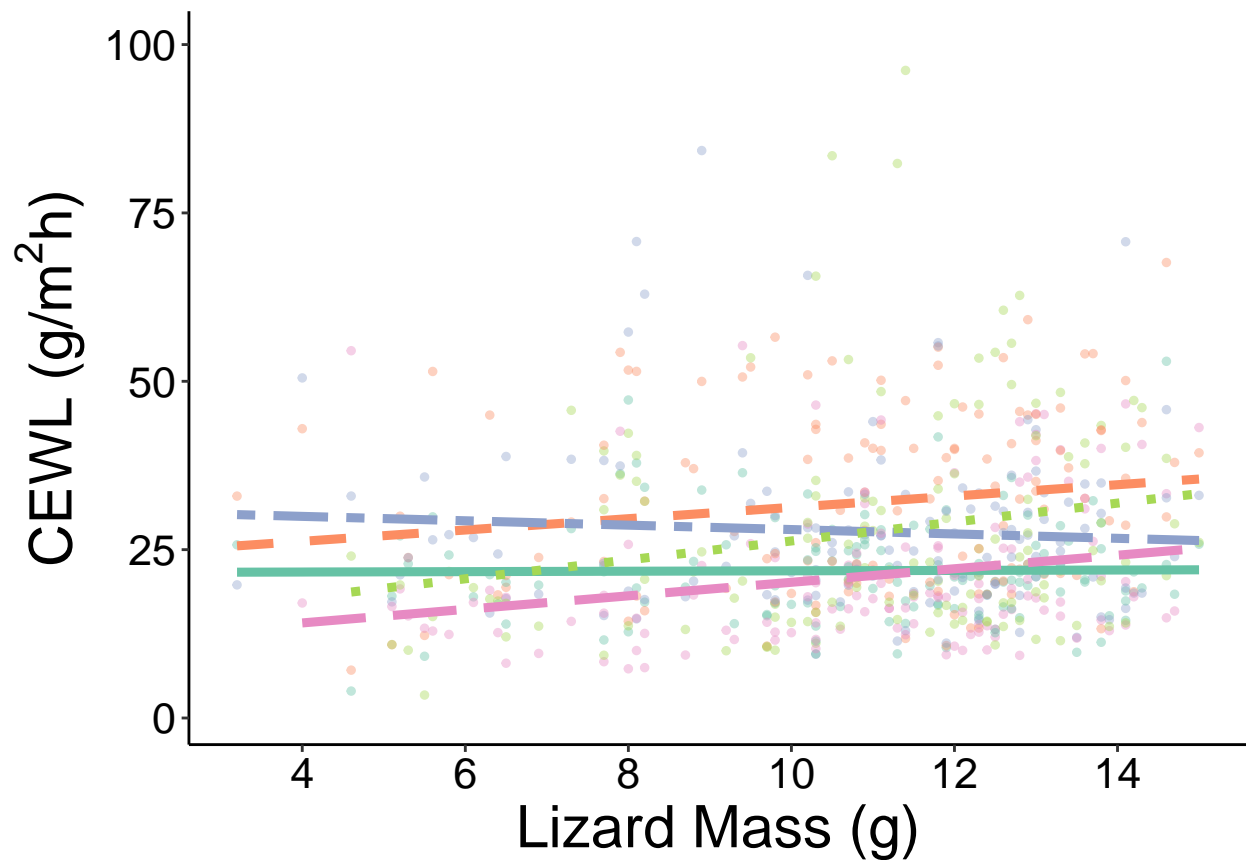
      se = F,
      size = 1.6,
      alpha = 1 ) +
theme_classic() +
xlab("Lizard Mass (g)") +
#ylab("") +
ylab(bquote('CEWL (g/'*m^2*'h)')) +
#annotate("text", x = 1, y = 65, label = "a", size = 6) +
scale_color_brewer(palette = "Set2",
                    name = "") +
scale_linetype_manual(name = "",
                      values = c("solid", "dashed",
                                "twodash", "longdash", "dotted")) +

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, #top
                           0.1, #right
                           0.1, #bottom
                           0.1 #left
                           ), "cm"),
      legend.text.align = 0,
      #legend.position = c(0.5, 0.6),
      legend.position = "none"
    ) -> mass_CEWL_fig
mass_CEWL_fig

```

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

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



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

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

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

```
# export legend
ggsave(filename = "CEWL_body_reg_legend.jpeg",
        plot = CEWL_legend,
        path = "./final_figures",
        device = "jpeg",
        dpi = 1200,
        width = 3, height = 3)
```

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

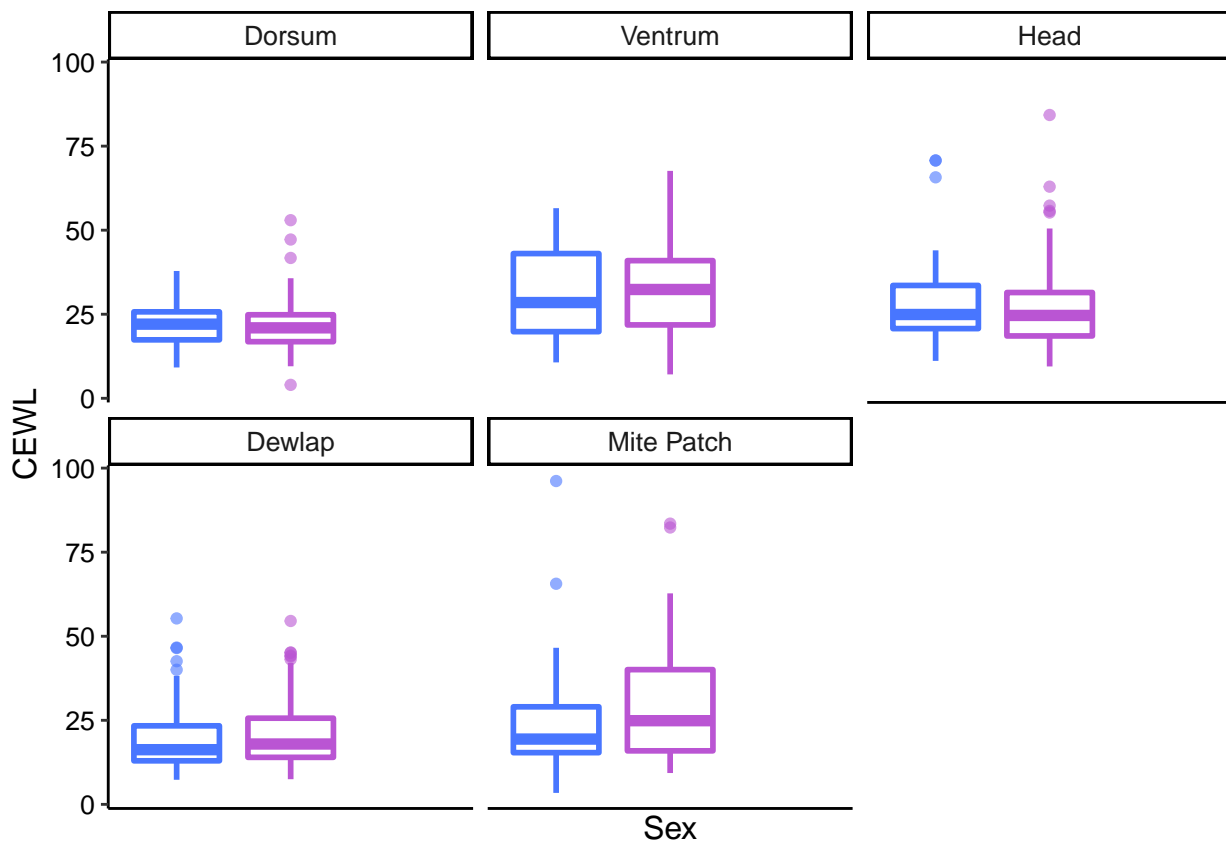
CEWL ~ Sex

```
CEWL_data_full %>%
  ggplot(data = .) +
```

```

geom_boxplot(aes(x = sex_M_F,
                 y = TEWL_g_m2h,
                 color = sex_M_F
                 ),
             size = 1,
             alpha = 0.6) +
facet_wrap(~region) +
scale_color_manual(values = c("royalblue1", "mediumorchid")) +
scale_x_discrete(breaks = c(1,2,3)) +
theme_classic() +
xlab("Sex") +
ylab("CEWL") +
theme(text = element_text(color = "black", family = "sans", size = 12),
      axis.text = element_text(color = "black", family = "sans", size = 10),
      legend.text.align = 0,
      legend.position = "none")

```



CEWL ~ Gravity

```

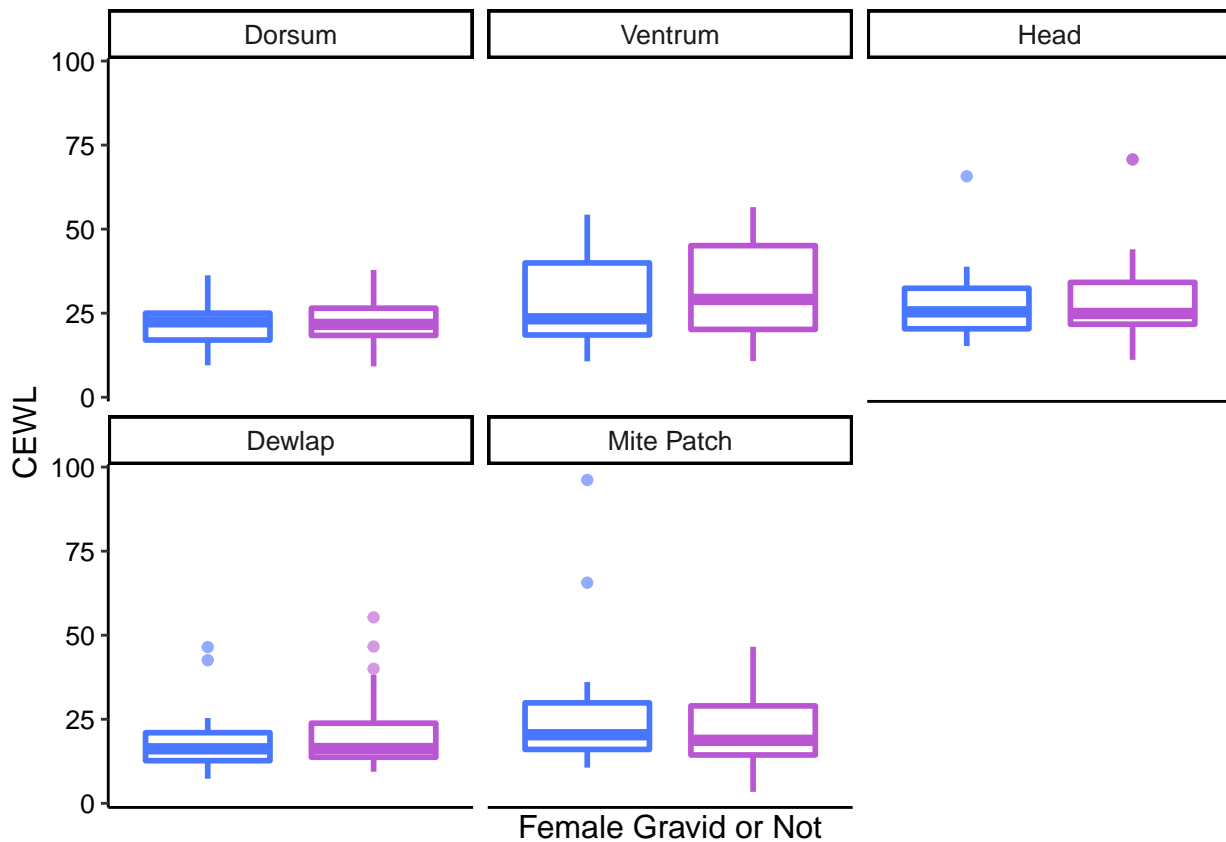
CEWL_data_full %>%
  dplyr::filter(sex_M_F == "F") %>%
  ggplot(data = .) +
  geom_boxplot(aes(x = gravid_Y_N,
                   y = TEWL_g_m2h,
                   color = gravid_Y_N
                   ),

```

```

    size = 1,
    alpha = 0.6) +
facet_wrap(~region) +
scale_color_manual(values = c("royalblue1", "mediumorchid")) +
scale_x_discrete(breaks = c(1,2,3)) +
theme_classic() +
xlab("Female Gravid or Not") +
ylab("CEWL") +
theme(text = element_text(color = "black", family = "sans", size = 12),
      axis.text = element_text(color = "black", family = "sans", size = 10),
      legend.text.align = 0,
      legend.position = "none")

```



CEWL ~ Week

```

CEWL_data_full %>%
  ggplot(data = .) +
  geom_boxplot(aes(x = as.factor(date),
                  y = TEWL_g_m2h,
                  color = as.factor(date)
                  ),
    size = 1,
    alpha = 0.6) +
  facet_wrap(~region) + # could not figure out how to change facet labels without changing underlying d
  scale_color_manual(values = c("royalblue1", "mediumorchid", "seagreen4",
                                "royalblue1", "mediumorchid", "seagreen4")) +

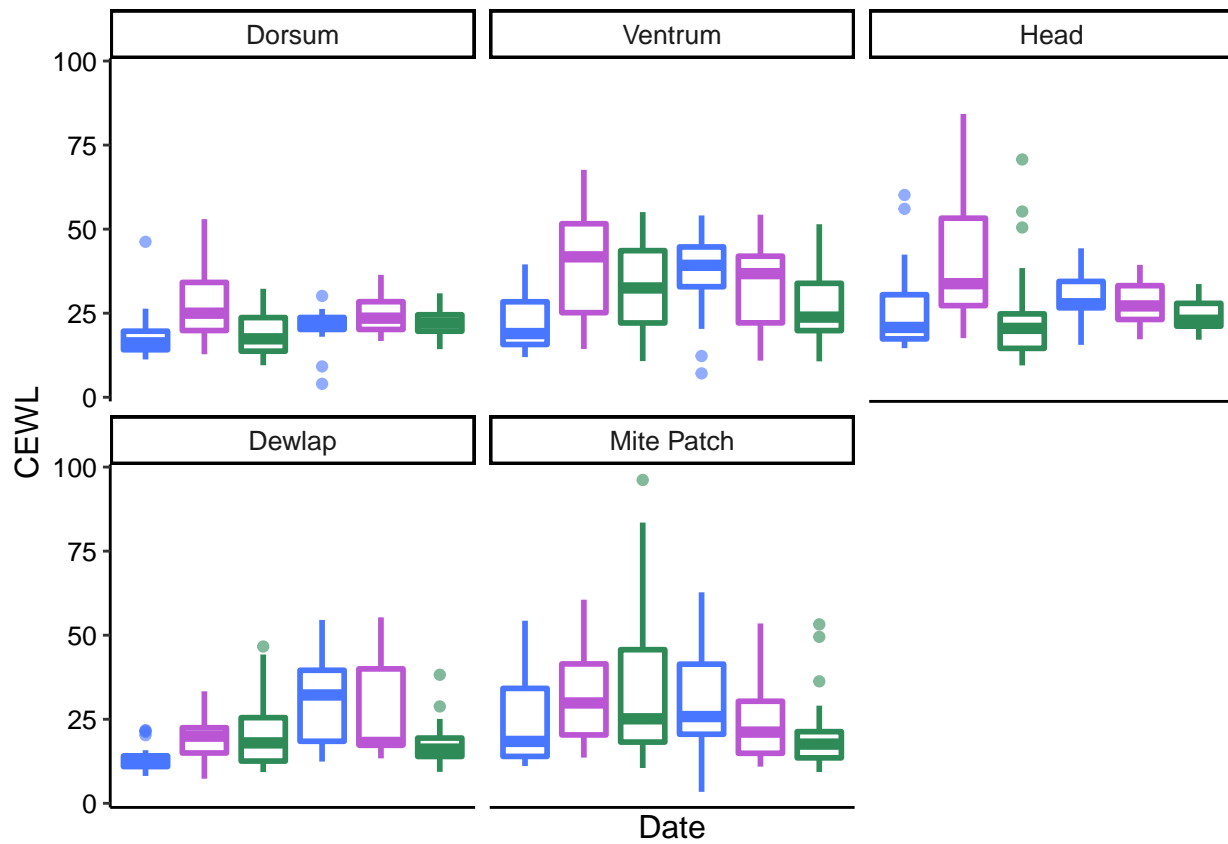
```



```

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

```



CEWL ~ holding time

```

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

```

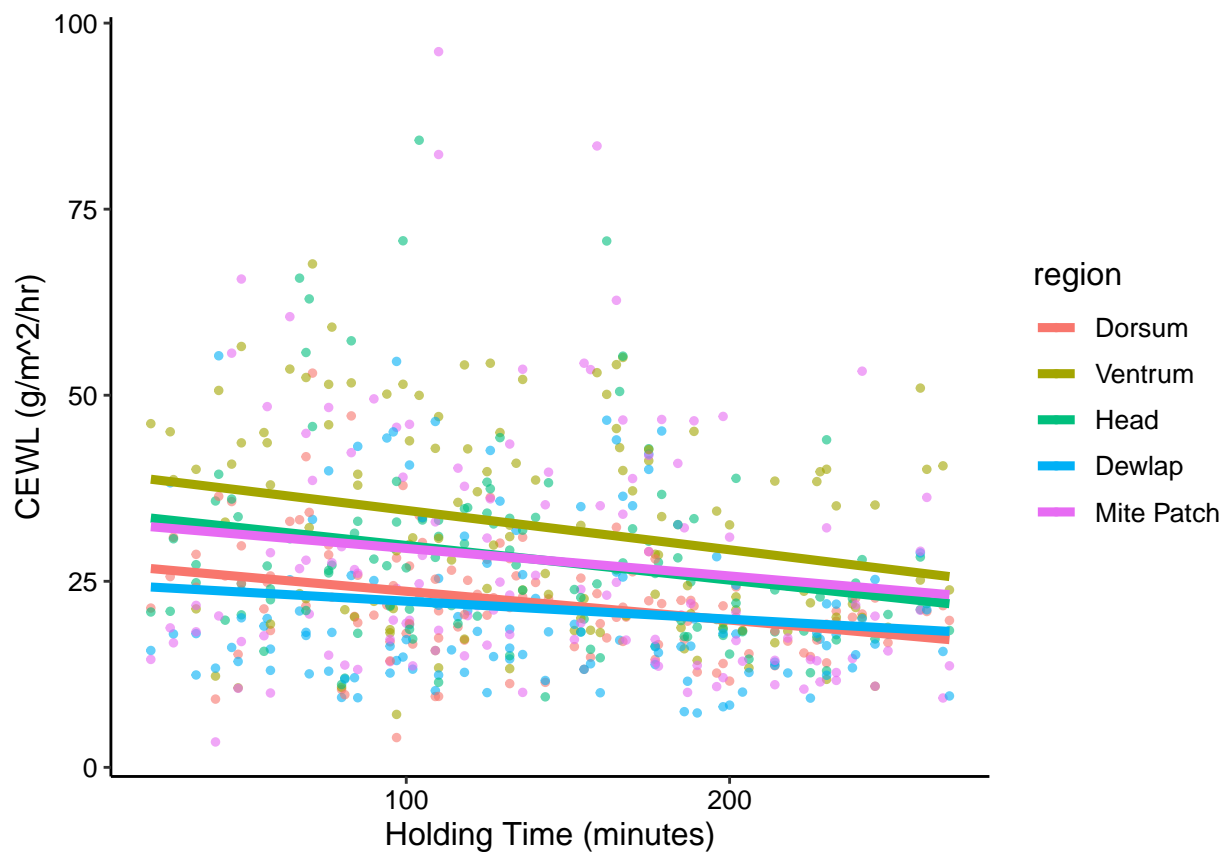
```

      size = 1.6,
      alpha = 1 ) +
theme_classic() +
xlab("Holding Time (minutes)") +
ylab("CEWL (g/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

Based on reviewer comments & model revisions, this should include: capture VPD and temp, mass, sorad, clotemp, msmt VPD & temp. 7 variables total. Used to be 6...

```

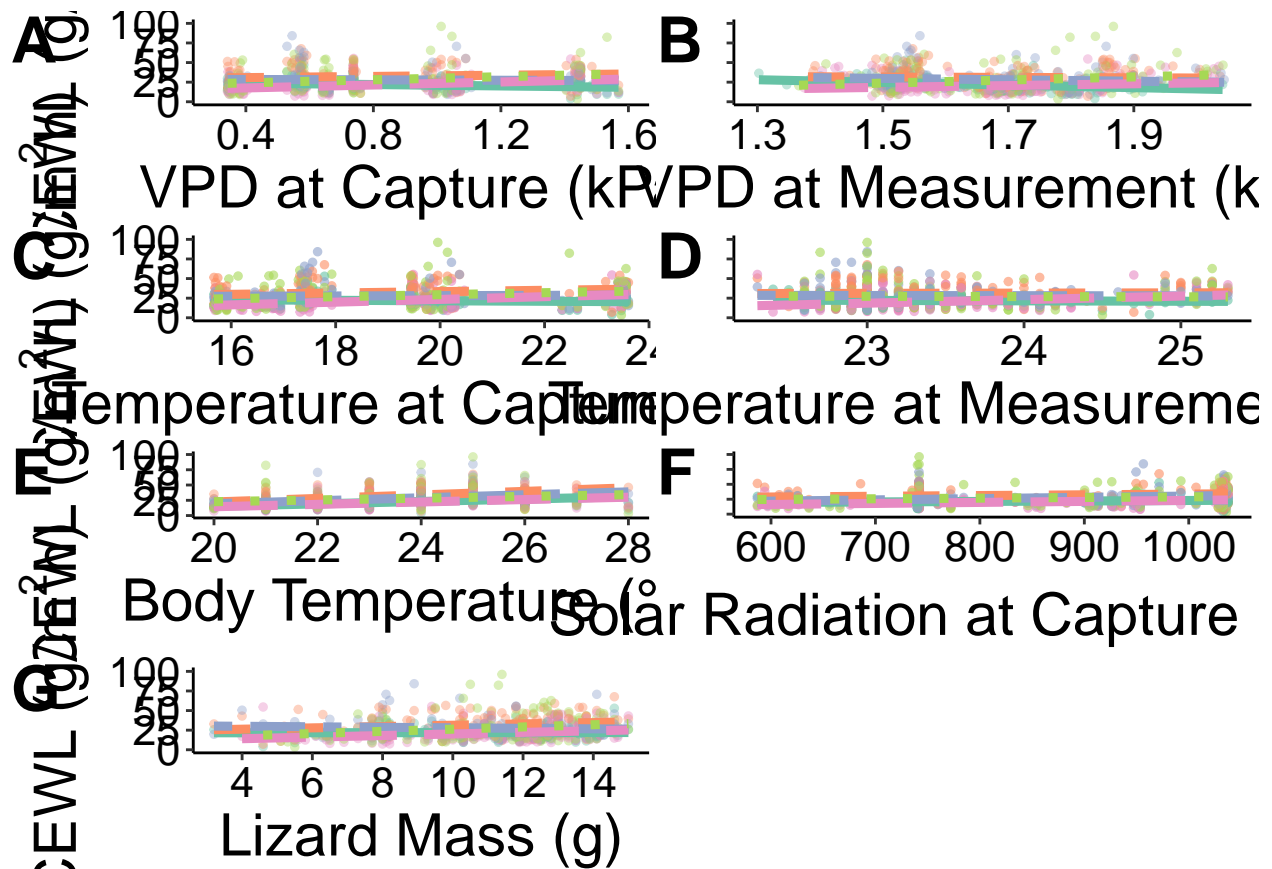
ggarrange(cap_vpd_CEWL_fig, msmt_VPD_CEWL_fig,
          cap_temp_CEWL_fig, msmt_temp_CEWL_fig,
          clotemp_CEWL_fig, cap_sorad_CEWL_fig,
          mass_CEWL_fig,
          labels = c("A", "B", "C", "D", "E", "F", "G"),
          font.label = list(size = 24, face = "bold", color = "black"),

```

```
ncol = 2, nrow = 4,
widths = c(1.072, 1),
hjust = 0, vjust = 1.1
#common.legend = TRUE, # add on later
#legend = c(0,0)
) -> CEWL_multi_fig
```

```
## Warning: Removed 59 rows containing non-finite values (stat_smooth).
## Warning: Removed 59 rows containing missing values (geom_point).
## Warning: Removed 4 rows containing non-finite values (stat_smooth).
## Warning: Removed 4 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 59 rows containing non-finite values (stat_smooth).
## Warning: Removed 59 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 = 16)
```

## 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:

```
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:

```
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)    30.18293    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 capture',
                  '(model 5) ~ sex, VPD at capture, solar radiation at capture, SMI, wind speed at capture',
                  '(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')

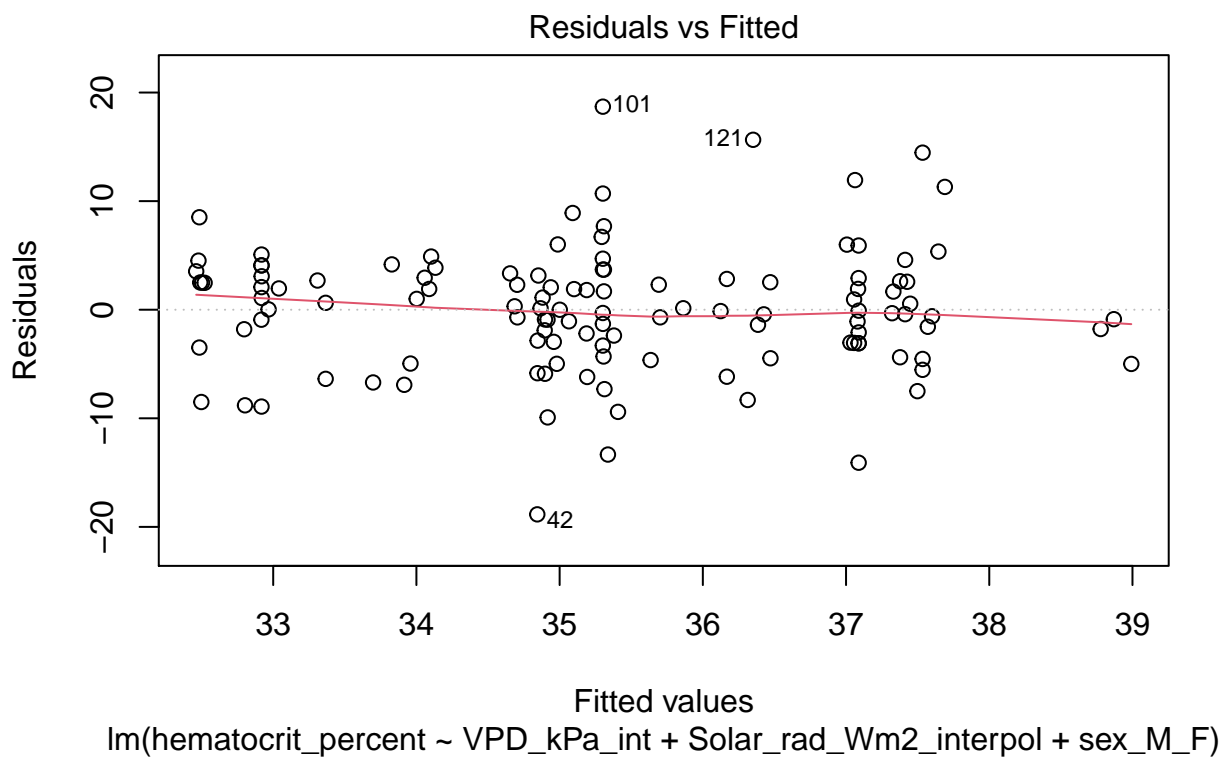
#calculate AIC of each model
hct_AICc <- data.frame(aictab(cand.set = hct_models,
                             modnames = hct_mod_names))
hct_AICc

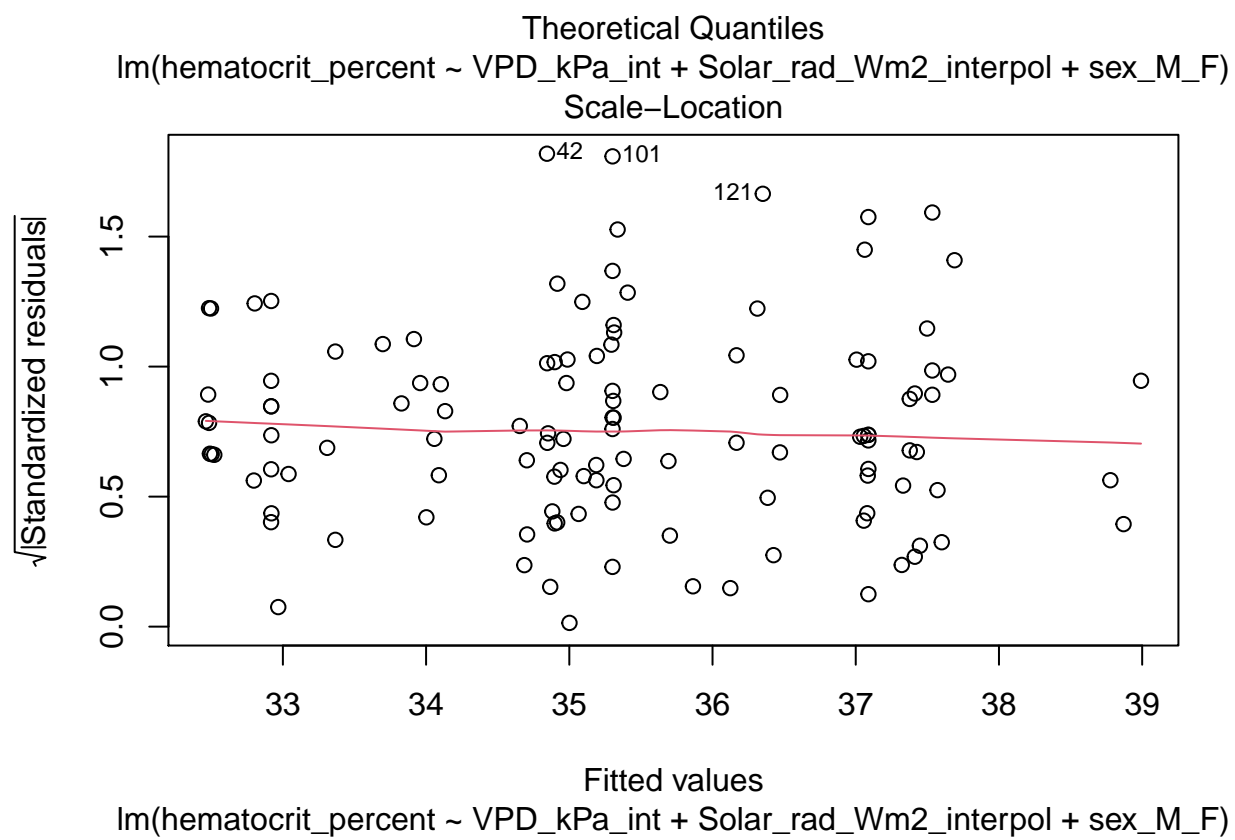
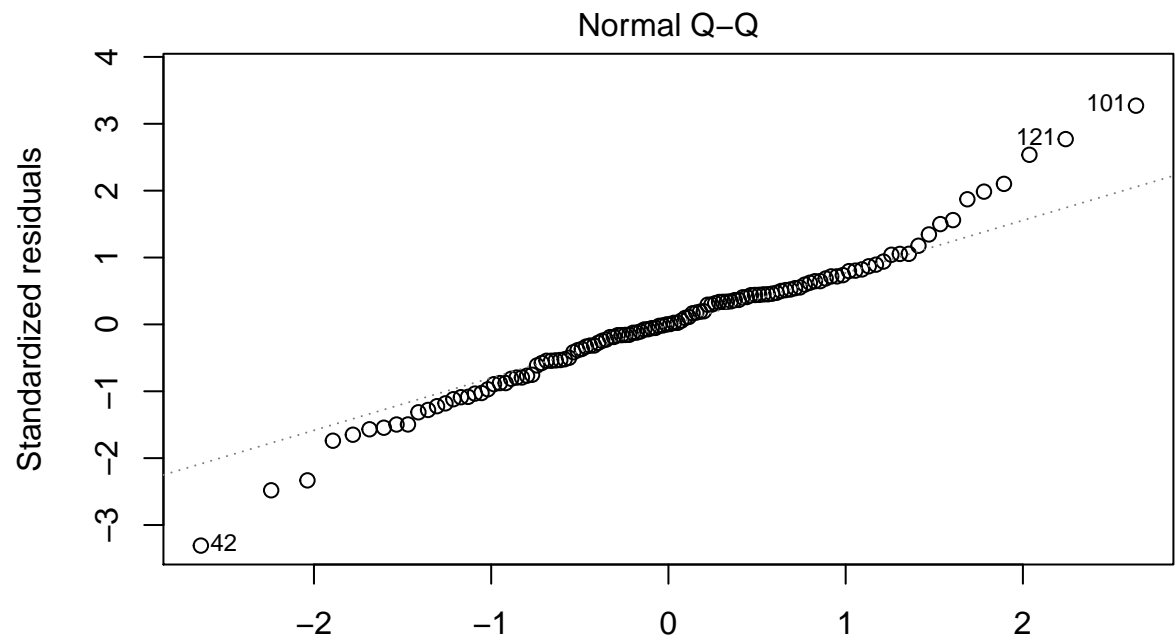
##                                     Modnames
## 4                                (model 7) ~ sex, VPD at capture, solar radiation at capture
## 5                                (model 8) ~ sex, VPD at capture
## 3                                (model 6) ~ sex, VPD at capture, solar radiation at capture, SMI
## 2    (model 5) ~ sex, VPD at capture, solar radiation at capture, SMI, wind speed at capture
## 6                                (model 9) ~ sex
```

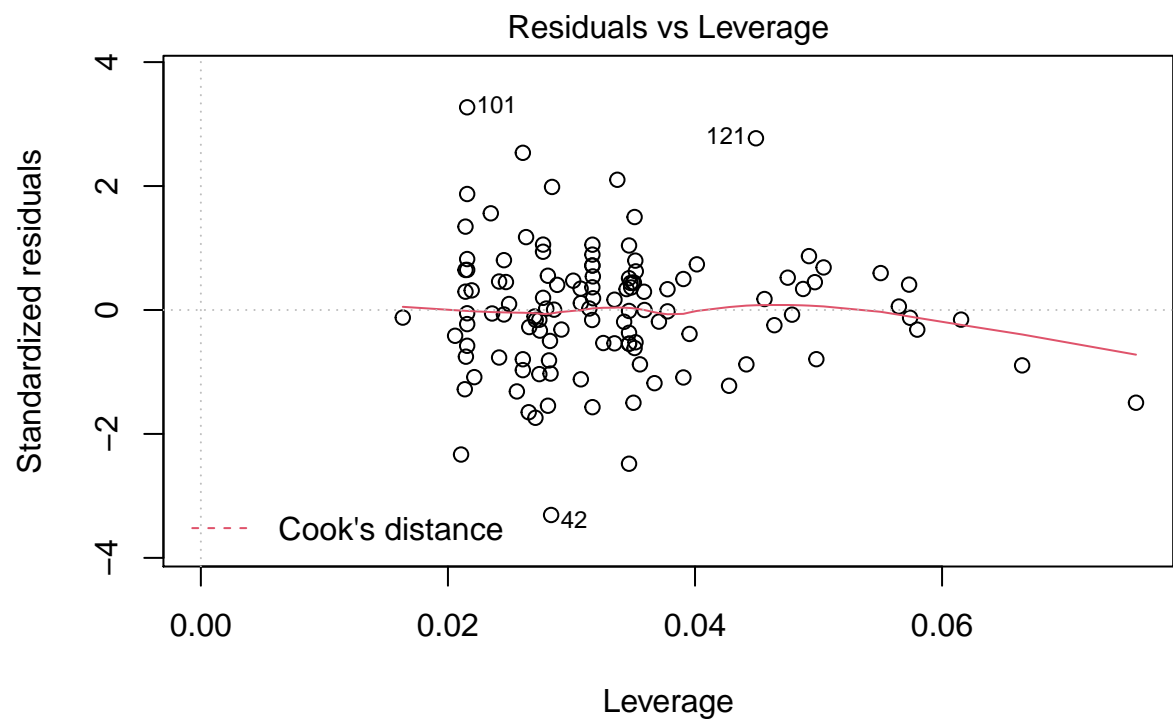
```
## 1 (model 4) ~ sex, VPD at capture, solar radiation at capture, SMI, wind speed at capture, mass
## 7 null model
##      K      AICc Delta_AICc   ModelLik      AICcWt      LL      Cum.Wt
## 4 5 768.0253 0.00000000 1.000000000 0.369737267 -378.7495 0.3697373
## 5 4 768.0500 0.02461668 0.987767098 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)
```

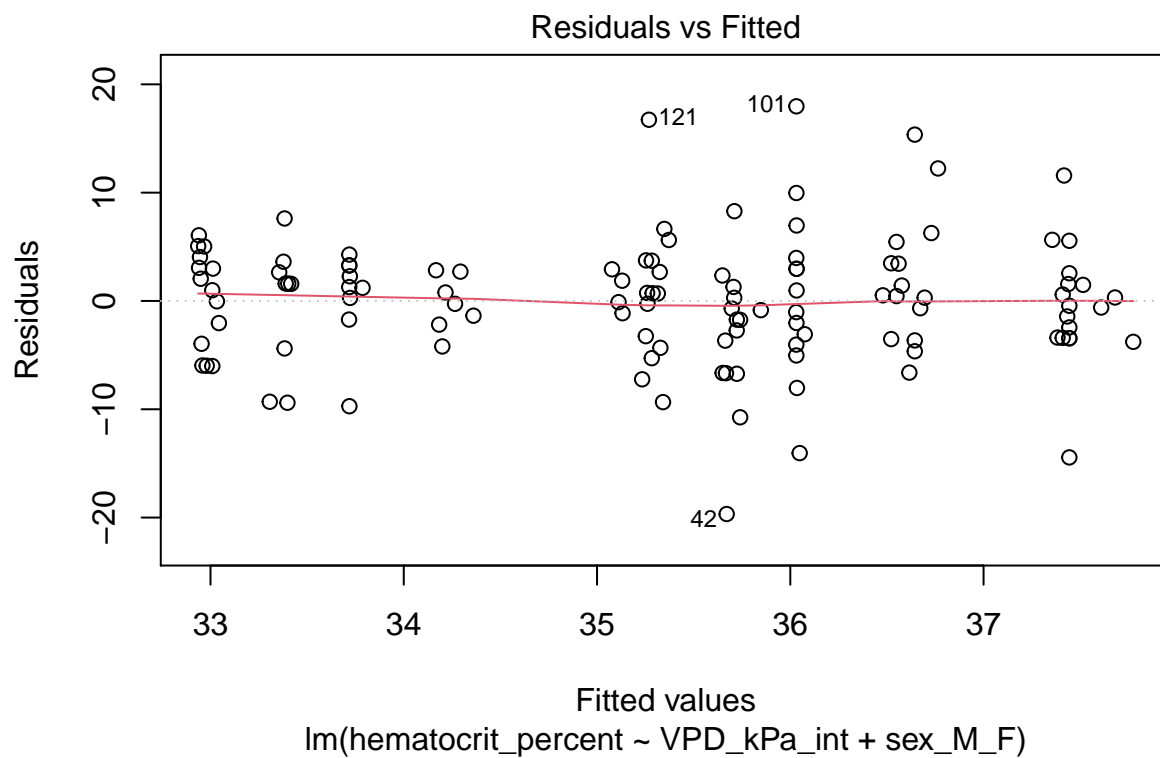


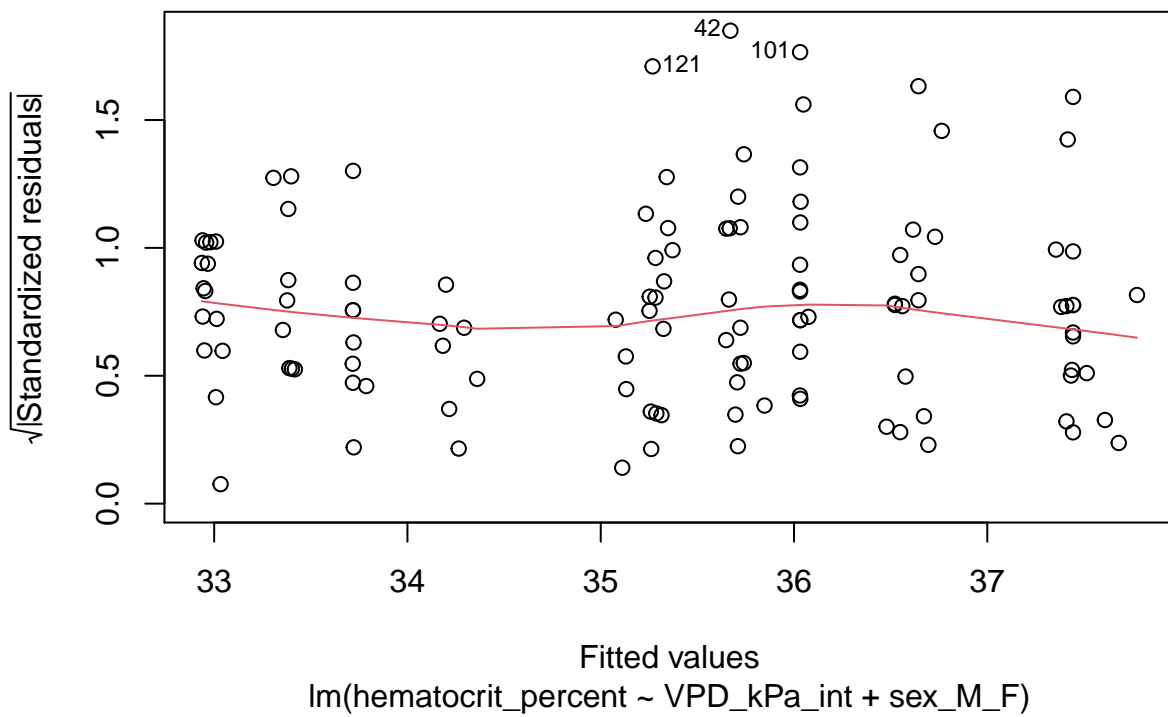
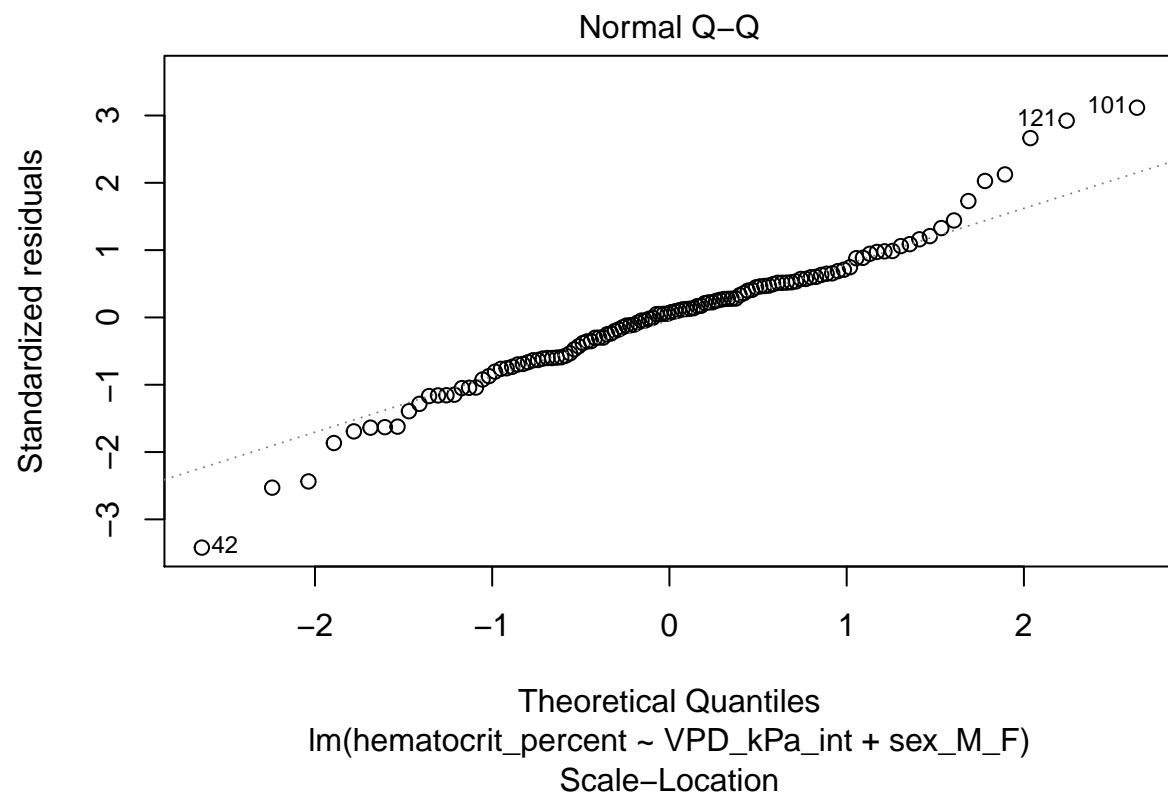


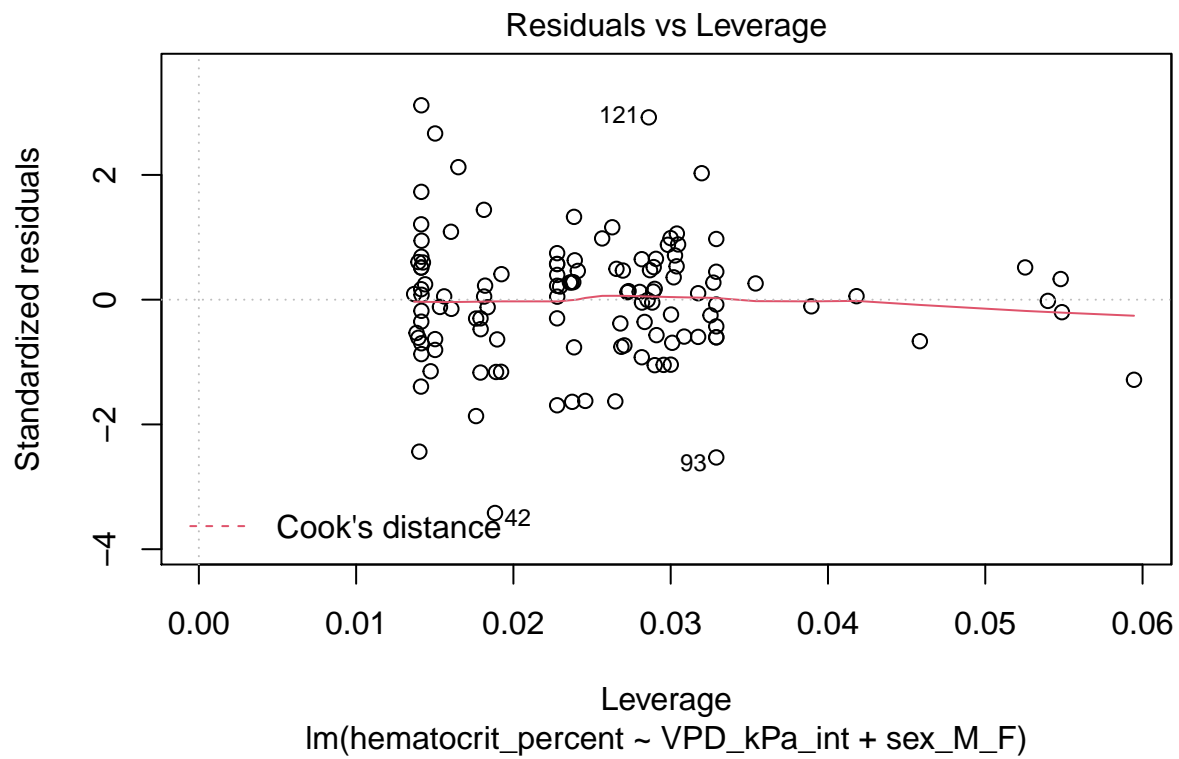


lm(hematocrit\_percent ~ VPD\_kPa\_int + Solar\_rad\_Wm2\_interpol + sex\_M\_F)

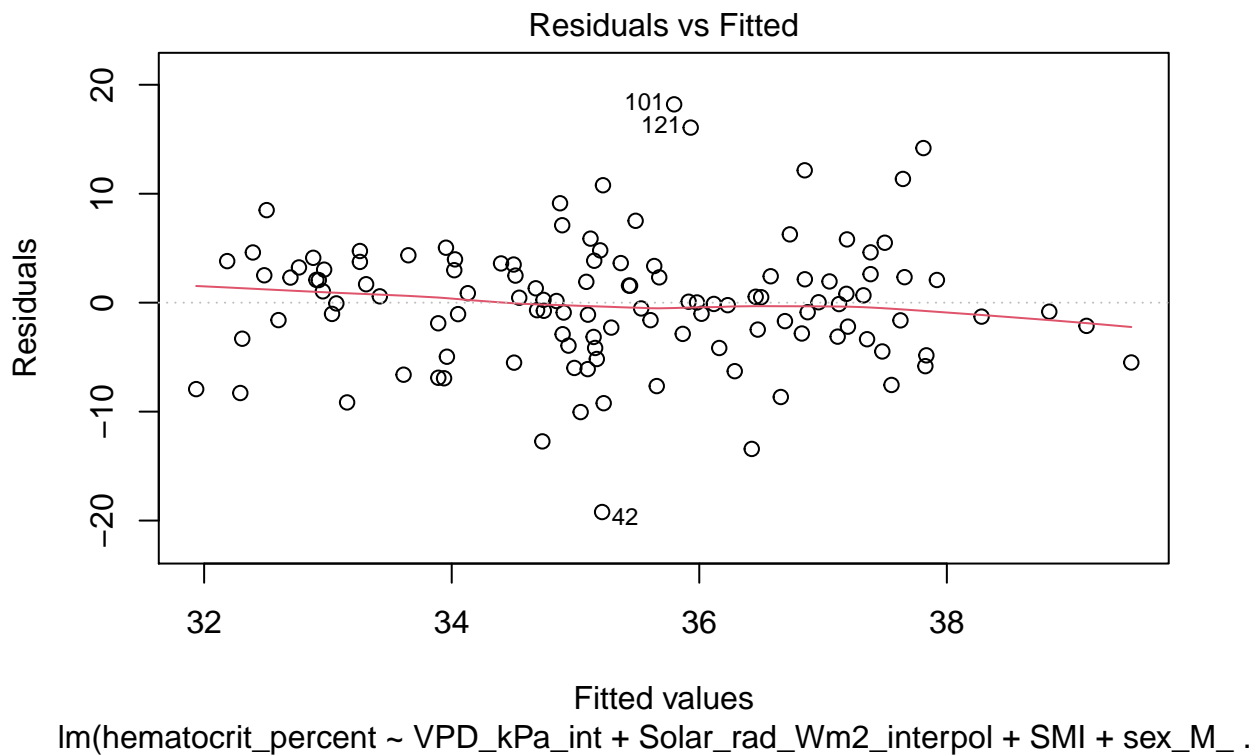
```
plot(hct_mod8)
```



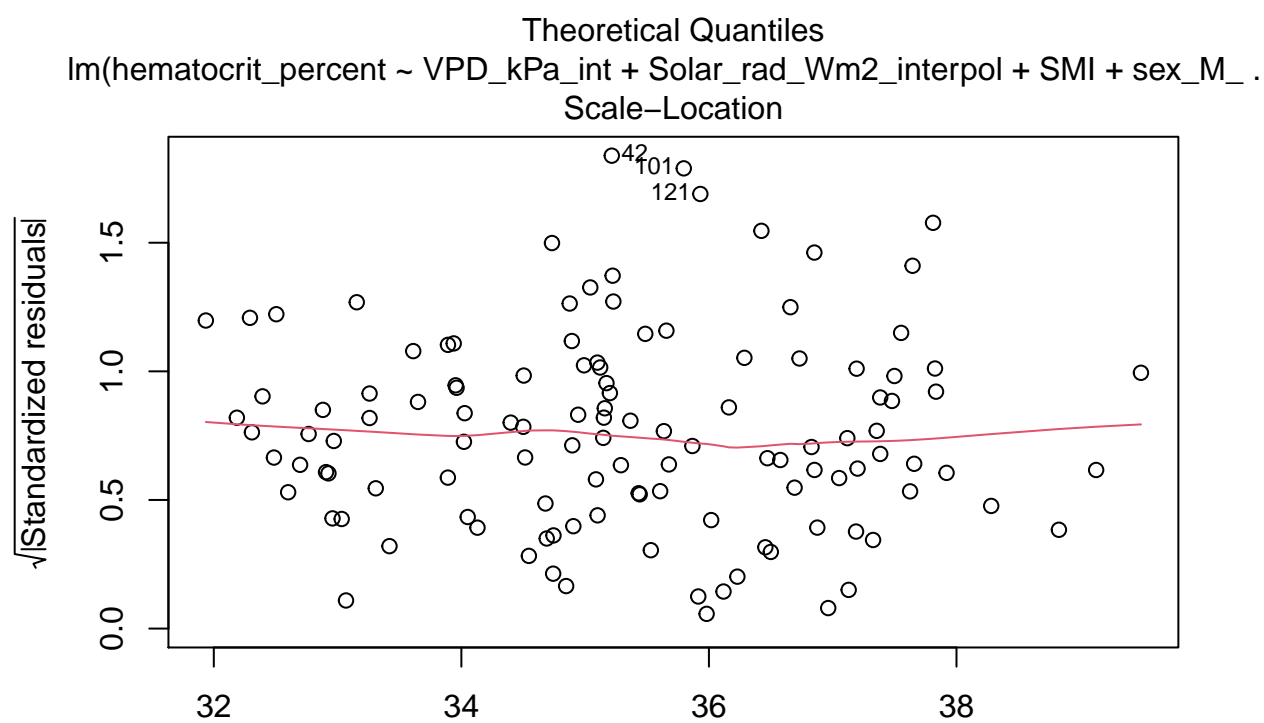
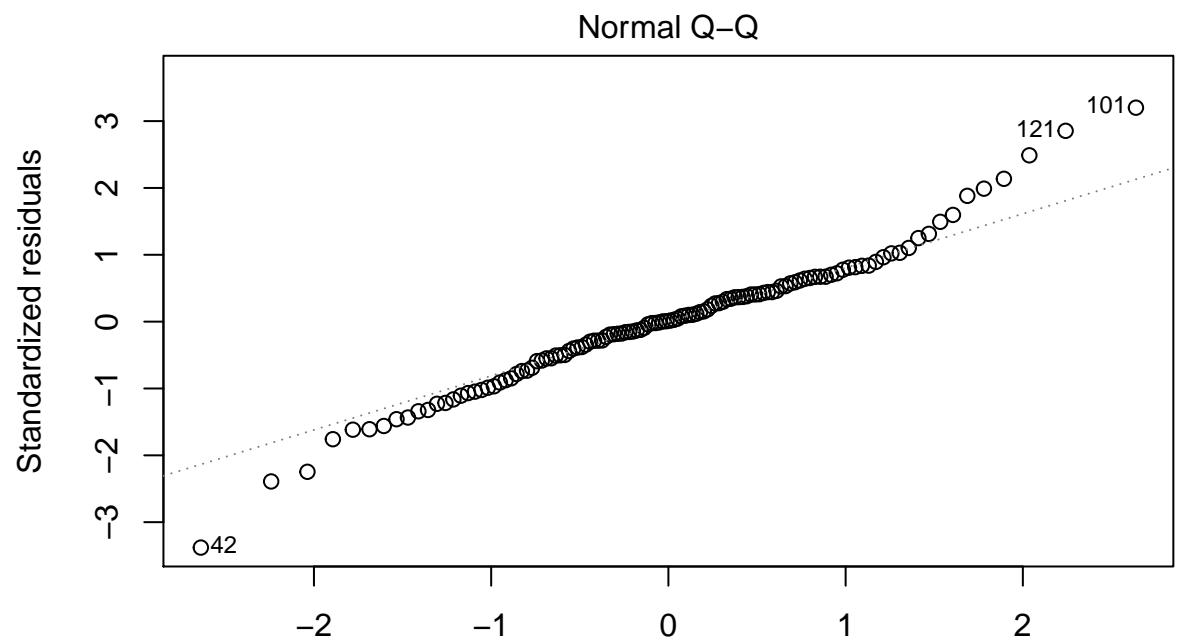


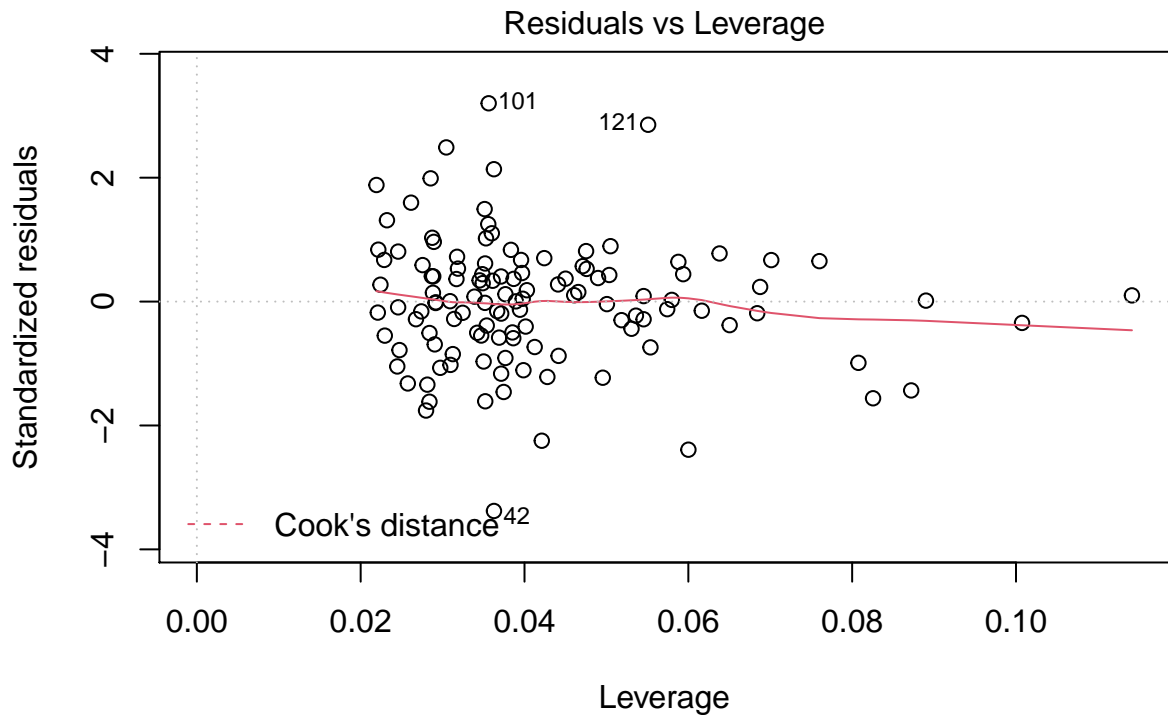


```
plot(hct_mod6)
```









lm(hematocrit\_percent ~ VPD\_kPa\_int + Solar\_rad\_Wm2\_interpol + SMI + sex\_M\_ .

```
vif(hct_mod7)
```

```
##          VPD_kPa_int Solar_rad_Wm2_interpol          sex_M_F
##          1.119482          1.084479          1.043912
```

```
vif(hct_mod8)
```

```
## VPD_kPa_int    sex_M_F
##    1.041939    1.041939
```

```
vif(hct_mod6)
```

```
##          VPD_kPa_int Solar_rad_Wm2_interpol          SMI
##          1.120944          1.164583          1.129005
##          sex_M_F
##          1.073387
```

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")
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_kPa_ 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_kPa_:_C_  0.598 -0.986  -0.448 -0.148  0.291  0.059  0.039 -0.042  0.035
```

use VIF to look for multicollinearity:

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

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

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

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

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

drop mass.

```
# model 3
hydrat_mod3 <- lme4::lmer(data = morpho_blood_SMI,
```

```

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

```

```

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

```

drop temperature

```

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

```

```

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

```

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

```
summary(hydrat_mod4)
```

```

## Linear mixed model fit by REML ['lmerMod']
## Formula:
## osmolality_mmol_kg ~ VPD_kPa_int + Wind_mph_interpol + Solar_rad_Wm2_interpol +
## SMI + SVL_mm + sex_M_F + (1 | date) + (1 | hemoalyzed)
## Data: morpho_blood_SMI
##
## REML criterion at convergence: 1026.9
##

```

```
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.22452 -0.63811  0.06486  0.65425  2.72400
##
## Random effects:
##   Groups      Name      Variance Std.Dev.
##   date      (Intercept) 930.06   30.497
##   hemolyzed (Intercept)  19.33    4.397
##   Residual                284.66   16.872
## Number of obs: 121, groups:  date, 6; hemolyzed, 2
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)    385.41079   37.34722  10.320
## VPD_kPa_int      4.10087   15.42376   0.266
## Wind_mph_interpol -11.58238   3.56118  -3.252
## Solar_rad_Wm2_interpol  0.05656   0.03674   1.540
## SMI              -0.63969   1.24862  -0.512
## SVL_mm           -0.07346   0.29247  -0.251
## sex_M_FM         -4.92854   3.61752  -1.362
##
## Correlation of Fixed Effects:
##              (Intr) VPD_P_ Wnd_m_ S__W2_ SMI      SVL_mm
## VPD_kPa_int -0.141
## Wnd_mph_ntr -0.005  0.039
## Slr_rd_Wm2_ -0.591 -0.135 -0.404
## SMI          -0.420 -0.153 -0.024  0.030
## SVL_mm       -0.335 -0.072 -0.213 -0.133  0.229
## sex_M_FM     0.182 -0.034  0.007 -0.100 -0.216 -0.141
```

```
drop1(hydrat_mod4)
```

```
## Single term deletions
##
## Model:
## osmolality_mmol_kg ~ VPD_kPa_int + Wind_mph_interpol + Solar_rad_Wm2_interpol +
##      SMI + SVL_mm + sex_M_F + (1 | date) + (1 | hemolyzed)
##              npar      AIC
## <none>                1066.0
## VPD_kPa_int            1 1064.2
## Wind_mph_interpol      1 1074.2
## Solar_rad_Wm2_interpol  1 1065.9
## SMI                    1 1064.3
## SVL_mm                  1 1064.1
## sex_M_F                 1 1066.0
```

```
drop SVL:
```

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

```

                                (1|date) + (1|hemolyzed))
summary(hydrat_mod5)

## Linear mixed model fit by REML ['lmerMod']
## Formula:
## osmolality_mmol_kg ~ VPD_kPa_int + Wind_mph_interpol + Solar_rad_Wm2_interpol +
##      SMI + sex_M_F + (1 | date) + (1 | hemolyzed)
##      Data: morpho_blood_SMI
##
## REML criterion at convergence: 1026.3
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.21547 -0.65331  0.05192  0.63351  2.76644
##
## Random effects:
##   Groups      Name      Variance Std.Dev.
##   date      (Intercept) 920.9     30.347
##   hemolyzed (Intercept)  20.5      4.528
##   Residual                282.2    16.800
## Number of obs: 121, groups:  date, 6; hemolyzed, 2
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)    382.20594   35.04299  10.907
## VPD_kPa_int      3.82691   15.31564   0.250
## Wind_mph_interpol -11.76568    3.46435  -3.396
## Solar_rad_Wm2_interpol  0.05539    0.03626   1.528
## SMI             -0.57016    1.21036  -0.471
## sex_M_FM        -5.05674    3.56580  -1.418
##
## Correlation of Fixed Effects:
##              (Intr) VPD_P_ Wnd_m_ S_W2_ SMI
## VPD_kPa_int -0.176
## Wnd_mph_ntr -0.083  0.024
## Slr_rd_Wm2_ -0.680 -0.146 -0.446
## SMI         -0.374 -0.141  0.027  0.062
## sex_M_FM     0.144 -0.045 -0.024 -0.121 -0.190
drop1(hydrat_mod5)

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

```

```

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

summary(hydrat_mod6)

## Linear mixed model fit by REML ['lmerMod']
## Formula: osmolality_mmol_kg ~ Wind_mph_interpol + Solar_rad_Wm2_interpol +
##          SMI + sex_M_F + (1 | date) + (1 | hemolyzed)
## Data: morpho_blood_SMI
##
## REML criterion at convergence: 1033.7
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.21786 -0.66082  0.05462  0.63355  2.76432
##
## Random effects:
##   Groups      Name      Variance Std.Dev.
##   date      (Intercept) 933.36   30.551
##   hemolyzed (Intercept)  20.58    4.536
##   Residual                279.66   16.723
## Number of obs: 121, groups:  date, 6; hemolyzed, 2
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)    383.46657   34.42551  11.139
## Wind_mph_interpol -11.79963    3.44895  -3.421
## Solar_rad_Wm2_interpol  0.05708    0.03576   1.596
## SMI             -0.52561    1.19286  -0.441
## sex_M_FM        -5.01920    3.54614  -1.415
##
## Correlation of Fixed Effects:
##              (Intr) Wnd_m_ S__W2_ SMI
## Wnd_mph_ntr -0.079
## Slr_rd_Wm2_ -0.724 -0.448
## SMI         -0.409  0.030  0.043
## sex_M_FM    0.139 -0.022 -0.129 -0.199

drop1(hydrat_mod6)

## Single term deletions
##
## Model:
## osmolality_mmol_kg ~ Wind_mph_interpol + Solar_rad_Wm2_interpol +
##          SMI + sex_M_F + (1 | date) + (1 | hemolyzed)
##              npar      AIC
## <none>              1062.2
## Wind_mph_interpol      1 1071.4
## Solar_rad_Wm2_interpol  1 1062.5

```



```
## SMI                      1 1060.5
## sex_M_F                  1 1062.3
```

drop SMI:

```
# model 7
hydrat_mod7 <- lme4::lmer(data = morpho_blood_SMI,
                          # response variable
                          osmolality_mmol_kg ~
                            Wind_mph_interpol + Solar_rad_Wm2_interpol +
                            sex_M_F +
                          # random effects
                          (1|date) + (1|hemolyzed))

summary(hydrat_mod7)

## Linear mixed model fit by REML ['lmerMod']
## Formula: osmolality_mmol_kg ~ Wind_mph_interpol + Solar_rad_Wm2_interpol +
##       sex_M_F + (1 | date) + (1 | hemolyzed)
## Data: morpho_blood_SMI
##
## REML criterion at convergence: 1036.1
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.17326 -0.70062  0.01535  0.58677  2.78981
##
## Random effects:
## Groups      Name                Variance Std.Dev.
## date      (Intercept)          949.18   30.809
## hemolyzed (Intercept)          19.82    4.452
## Residual                        277.51   16.659
## Number of obs: 121, groups: date, 6; hemolyzed, 2
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)   377.04913   31.38254  12.015
## Wind_mph_interpol  -11.77287    3.43552  -3.427
## Solar_rad_Wm2_interpol  0.05809    0.03566   1.629
## sex_M_FM        -5.33018    3.46222  -1.540
##
## Correlation of Fixed Effects:
##              (Intr) Wnd_m_ S__W2_
## Wnd_mph_ntr  -0.071
## Slr_rd_Wm2_ -0.774 -0.451
## sex_M_FM      0.064 -0.017 -0.123

drop1(hydrat_mod7)

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

```
## Solar_rad_Wm2_interpol    1 1060.7
## sex_M_F                  1 1060.8
```

drop sex:

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

summary(hydrat_mod8)

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

drop1(hydrat_mod8)
```

```
## Single term deletions
##
## Model:
## osmolality_mmol_kg ~ Wind_mph_interpol + Solar_rad_Wm2_interpol +
##          (1 | date) + (1 | hemolyzed)
##              npar      AIC
## <none>              1060.8
## Wind_mph_interpol      1 1069.9
## Solar_rad_Wm2_interpol  1 1060.6
```

drop solar radiation:

```
# model 9
hydrat_mod9 <- lme4::lmer(data = morpho_blood_SMI,
  # response variable
  osmolality_mmol_kg ~
  Wind_mph_interpol +
  # random effects
  (1|date) + (1|hemolyzed))
```

finally, test the null model

```
hydrat_mod_null <- lme4::lmer(data = morpho_blood_SMI,
  osmolality_mmol_kg ~ 1 +
  (1|date) + (1|hemolyzed))
```

## Selection

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

```
hydrat_models <- list(hydrat_mod4, hydrat_mod5, hydrat_mod6,
  hydrat_mod7, hydrat_mod8, hydrat_mod9,
  hydrat_mod_null)

#specify model names
hydrat_mod_names <- c('(model 4) ~ VPD, Wind, Solar, SMI, SVL, sex',
  '(model 5) ~ VPD, Wind, Solar, SMI, sex',
  '(model 6) ~ Wind, Solar, SMI, sex',
  '(model 7) ~ Wind, Solar, sex',
  '(model 8) ~ Wind, Solar',
  '(model 9) ~ Wind',
  'null model')

#calculate AIC of each model
hydrat_AICc <- data.frame(aictab(cand.set = hydrat_models,
  modnames = hydrat_mod_names))
```

```
## Warning in aictab.AIClmerMod(cand.set = hydrat_models, modnames = hydrat_mod_names):
## Model selection for fixed effects is only appropriate with ML estimation:
## REML (default) should only be used to select random effects for a constant set of fixed effects
hydrat_AICc
```

##		Modnames	K	AICc	Delta_AICc
## 2	(model 5) ~ VPD, Wind, Solar, SMI, sex	9	1045.969	0.000000	
## 1	(model 4) ~ VPD, Wind, Solar, SMI, SVL, sex	10	1048.910	2.941314	
## 6	(model 9) ~ Wind	5	1050.348	4.379199	
## 3	(model 6) ~ Wind, Solar, SMI, sex	8	1050.986	5.017215	
## 4	(model 7) ~ Wind, Solar, sex	7	1051.072	5.103056	
## 5	(model 8) ~ Wind, Solar	6	1055.500	9.531431	
## 7	null model	4	1078.070	32.101007	
##	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:

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

summary(hydrat_mod5p)

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula:
## osmolality_mmol_kg ~ VPD_kPa_int + Wind_mph_interpol + Solar_rad_Wm2_interpol +
## SMI + sex_M_F + (1 | date) + (1 | hemolyzed)
## Data: morpho_blood_SMI
##
## REML criterion at convergence: 1026.3
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.21547 -0.65331  0.05192  0.63351  2.76644
##
## Random effects:
## Groups      Name                Variance Std.Dev.
## date      (Intercept)    920.9      30.347
## hemolyzed (Intercept)    20.5       4.528
## Residual                    282.2     16.800
## Number of obs: 121, groups: date, 6; hemolyzed, 2
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)    382.20594   35.04299   59.29144  10.907 8.44e-16 ***
## VPD_kPa_int      3.82691   15.31564   72.68400   0.250 0.803393
## Wind_mph_interpol -11.76568    3.46435  114.19881  -3.396 0.000941 ***
## Solar_rad_Wm2_interpol  0.05539    0.03626   86.94121   1.528 0.130190
## SMI              -0.57016    1.21036  110.48891  -0.471 0.638520
## sex_M_FM        -5.05674    3.56580  109.47729  -1.418 0.158996
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) VPD_P_ Wnd_m_ S_W2_ SMI
## VPD_kPa_int  -0.176
## Wnd_mph_ntr  -0.083  0.024
## Slr_rd_Wm2_  -0.680 -0.146 -0.446
## SMI           -0.374 -0.141  0.027  0.062
## sex_M_FM      0.144 -0.045 -0.024 -0.121 -0.190

hydrat_mod4p <- lmerTest::lmer(data = morpho_blood_SMI,
  # response variable
  osmolality_mmol_kg ~
```

```

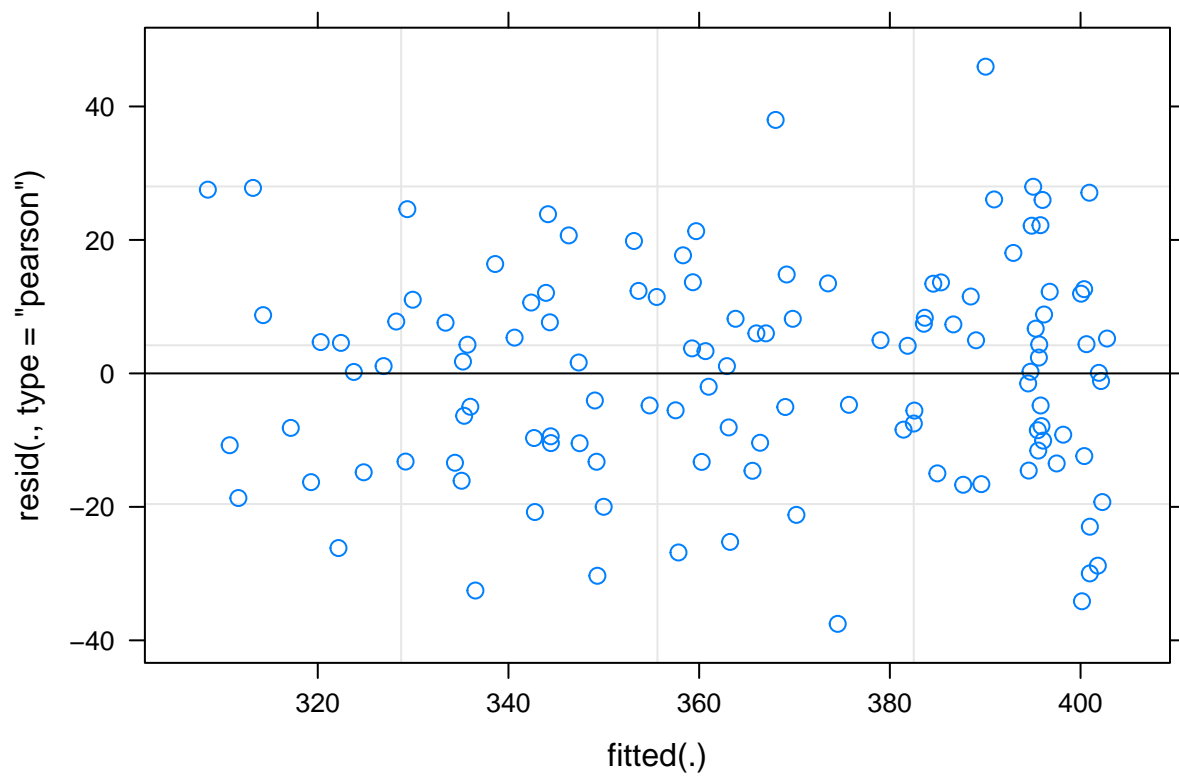
      VPD_kPa_int +
      Wind_mph_interpol + Solar_rad_Wm2_interpol +
      SMI + SVL_mm + sex_M_F +
      # random effects
      (1|date) + (1|hemolyzed))
summary(hydrat_mod4p)

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula:
## osmolality_mmol_kg ~ VPD_kPa_int + Wind_mph_interpol + Solar_rad_Wm2_interpol +
##      SMI + SVL_mm + sex_M_F + (1 | date) + (1 | hemolyzed)
##      Data: morpho_blood_SMI
##
## REML criterion at convergence: 1026.9
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.22452 -0.63811  0.06486  0.65425  2.72400
##
## Random effects:
##      Groups      Name      Variance Std.Dev.
##      date      (Intercept) 930.06   30.497
##      hemolyzed (Intercept)  19.33    4.397
##      Residual                284.66   16.872
## Number of obs: 121, groups:  date, 6; hemolyzed, 2
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)    385.41079    37.34722   71.15211  10.320  8.8e-16 ***
## VPD_kPa_int      4.10087    15.42376   72.07437   0.266  0.79109
## Wind_mph_interpol -11.58238    3.56118  112.70287  -3.252  0.00151 **
## Solar_rad_Wm2_interpol  0.05656    0.03674   85.31715   1.540  0.12737
## SMI              -0.63969    1.24862  109.24695  -0.512  0.60946
## SVL_mm          -0.07346    0.29247  109.90093  -0.251  0.80215
## sex_M_FM        -4.92854    3.61752  108.48257  -1.362  0.17589
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) VPD_P_ Wnd_m_ S_W2_ SMI      SVL_mm
## VPD_kPa_int  -0.141
## Wnd_mph_ntr  -0.005  0.039
## Slr_rd_Wm2_  -0.591 -0.135 -0.404
## SMI           -0.420 -0.153 -0.024  0.030
## SVL_mm        -0.335 -0.072 -0.213 -0.133  0.229
## sex_M_FM      0.182 -0.034  0.007 -0.100 -0.216 -0.141

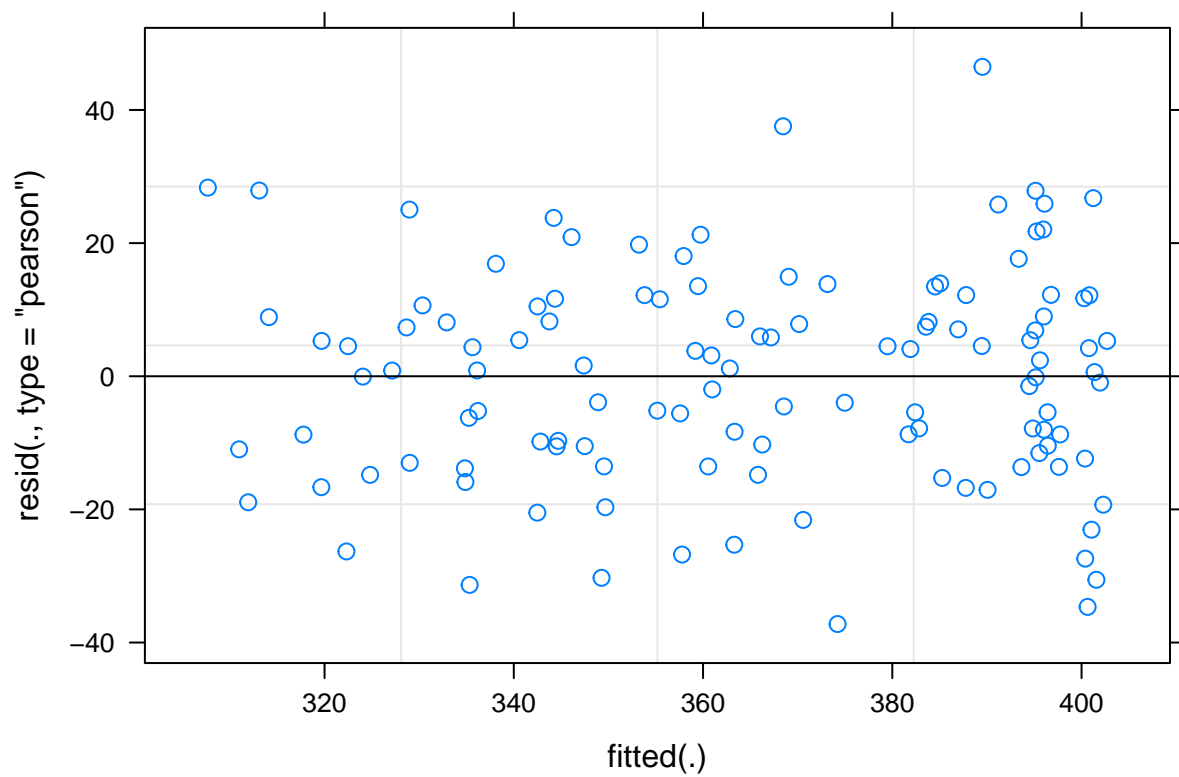
```

## Check LM Assumptions

```
plot(hydrat_mod4)
```



```
plot(hydrat_mod5)
```



```
vif(hydrat_mod4)
```

```
##          VPD_kPa_int      Wind_mph_interpol Solar_rad_Wm2_interpol
```

```
##          1.056725          1.323659          1.334494
##          SMI          SVL_mm          sex_M_F
##          1.122785          1.212112          1.088032
```

```
vif(hydrat_mod5)
```

```
##          VPD_kPa_int          Wind_mph_interpol Solar_rad_Wm2_interpol
##          1.051181          1.263170          1.310640
##          SMI          sex_M_F
##          1.064047          1.066248
```

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

```

```
## rescaling

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

drop region\*SMI interaction:

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

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

```
summary(CEWL_mod7)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: TEWL_g_m2h ~ region * (VPD_kPa_int + Solar_rad_Wm2_interpol +
##   mass_g + sex_M_F) + SVL_mm + SMI + hematocrit_percent + osmolality_mmol_kg +
##   cloacal_temp_C + hold_time + ambient_temp_C + temp_C_interpol +
##   VPD_kPa + Wind_mph_interpol + (1 | individual_ID)
## Data: CEWL_dat_sub1
##
## REML criterion at convergence: 4298
##
## Scaled residuals:
```

```

##      Min      1Q  Median      3Q      Max
## -2.0010 -0.5518 -0.1184  0.4093  5.3989
##
## Random effects:
##   Groups      Name      Variance Std.Dev.
## individual_ID (Intercept) 28.96    5.382
## Residual                99.25    9.962
## Number of obs: 570, groups: individual_ID, 116
##
## Fixed effects:
##
##              Estimate Std. Error t value
## (Intercept)      -5.149e+01  7.962e+01  -0.647
## regionVentrum      -5.594e+00  8.998e+00  -0.622
## regionHead         -2.535e+00  9.020e+00  -0.281
## regionDewlap       -2.051e+01  9.204e+00  -2.229
## regionMite Patch   -9.271e+00  9.287e+00  -0.998
## VPD_kPa_int        -5.157e+01  1.719e+01  -3.000
## Solar_rad_Wm2_interpol  1.296e-02  9.670e-03   1.340
## mass_g             -5.396e-01  2.205e+00  -0.245
## sex_M_FM           1.739e+00  2.329e+00   0.747
## SVL_mm             3.853e-01  1.051e+00   0.367
## SMI                7.305e-01  2.196e+00   0.333
## hematocrit_percent  -2.837e-01  1.241e-01  -2.287
## osmolality_mmol_kg  -1.080e-02  3.969e-02  -0.272
## cloacal_temp_C      2.314e+00  5.952e-01   3.888
## hold_time          -7.852e-03  1.694e-02  -0.463
## ambient_temp_C      -5.553e+00  1.661e+00  -3.343
## temp_C_interpol      5.925e+00  2.438e+00   2.431
## VPD_kPa             2.766e+01  1.122e+01   2.465
## Wind_mph_interpol    1.632e+00  2.342e+00   0.697
## regionVentrum:VPD_kPa_int  7.379e+00  3.665e+00   2.014
## regionHead:VPD_kPa_int  1.870e+00  3.677e+00   0.509
## regionDewlap:VPD_kPa_int  1.433e+01  3.691e+00   3.882
## regionMite Patch:VPD_kPa_int  1.628e+01  3.673e+00   4.431
## regionVentrum:Solar_rad_Wm2_interpol -9.398e-04  8.519e-03  -0.110
## regionHead:Solar_rad_Wm2_interpol  1.315e-02  8.520e-03   1.543
## regionDewlap:Solar_rad_Wm2_interpol -1.927e-03  8.574e-03  -0.225
## regionMite Patch:Solar_rad_Wm2_interpol -1.304e-02  8.621e-03  -1.513
## regionVentrum:mass_g  9.639e-01  5.268e-01   1.830
## regionHead:mass_g    -3.112e-01  5.228e-01  -0.595
## regionDewlap:mass_g  1.033e+00  5.334e-01   1.937
## regionMite Patch:mass_g  1.039e+00  5.412e-01   1.920
## regionVentrum:sex_M_FM  9.875e-01  2.831e+00   0.349
## regionHead:sex_M_FM   -2.227e+00  2.852e+00  -0.781
## regionDewlap:sex_M_FM  -1.484e+00  2.865e+00  -0.518
## regionMite Patch:sex_M_FM  2.383e+00  2.847e+00   0.837
##
## Correlation matrix not shown by default, as p = 35 > 12.
## Use print(x, correlation=TRUE) or
##      vcov(x)      if you need it
##
## fit warnings:
## Some predictor variables are on very different scales: consider rescaling

```



```
drop1(CEWL_mod7)
```

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

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

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

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

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

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

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

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

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

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

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

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

## 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
## regionVentrums: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
## regionVentrums: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
## regionVentrums: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

## 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

## 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
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
## regionVentrums: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
## regionVentrums: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
## regionVentrums: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

```

```
## 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)
##
```

	npars	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
## regionVentrurn                     -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
## regionVentrurn: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
## regionVentrurn: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
## regionVentrurn:mass_g               9.944e-01  5.154e-01   1.929
## regionHead:mass_g                   -3.901e-01  5.114e-01  -0.763
## regionDewlap:mass_g                 9.735e-01  5.230e-01   1.862
## regionMite Patch:mass_g             1.112e+00  5.303e-01   2.097
##
## Correlation matrix not shown by default, as p = 25 > 12.
## Use print(x, correlation=TRUE) or
##      vcov(x)          if you need it
##
## fit warnings:
## Some predictor variables are on very different scales: consider rescaling
drop1(CEWL_mod14)

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

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

```

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

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

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

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

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

drop hematocrit:

```
CEWL_mod15 <- lme4::lmer(data = CEWL_dat_sub1,
  # response variable
  TEWL_g_m2h ~
  # potential predictors
  region * (VPD_kPa_int + Solar_rad_Wm2_interpol +
  mass_g) +
  cloacal_temp_C +
  ambient_temp_C + temp_C_interpol + VPD_kPa +
  # random effect
  (1|individual_ID))
```

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

```
summary(CEWL_mod15)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: TEWL_g_m2h ~ region * (VPD_kPa_int + Solar_rad_Wm2_interpol +
##      mass_g) + cloacal_temp_C + ambient_temp_C + temp_C_interpol +
##      VPD_kPa + (1 | individual_ID)
## Data: CEWL_dat_sub1
##
```

```

## REML criterion at convergence: 4318.6
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.9727 -0.5678 -0.1167  0.3925  5.2412
##
## Random effects:
##   Groups             Name             Variance Std.Dev.
## individual_ID (Intercept) 29.27      5.410
## Residual                  99.10      9.955
## Number of obs: 570, groups: individual_ID, 116
##
## Fixed effects:
##
##              Estimate Std. Error t value
## (Intercept)      -3.296e+01  2.994e+01  -1.101
## regionVentrum      -5.605e+00  8.987e+00  -0.624
## regionHead         -2.427e+00  9.008e+00  -0.269
## regionDewlap       -2.044e+01  9.193e+00  -2.224
## regionMite Patch   -9.316e+00  9.269e+00  -1.005
## VPD_kPa_int        -4.300e+01  1.600e+01  -2.688
## Solar_rad_Wm2_interpol  1.788e-02  8.862e-03   2.017
## mass_g             2.651e-01  4.201e-01   0.631
## cloacal_temp_C      2.305e+00  3.830e-01   6.017
## ambient_temp_C     -4.598e+00  1.326e+00  -3.468
## temp_C_interpol     4.384e+00  2.247e+00   1.951
## VPD_kPa            2.498e+01  1.030e+01   2.424
## regionVentrum:VPD_kPa_int  7.574e+00  3.611e+00   2.098
## regionHead:VPD_kPa_int  1.283e+00  3.609e+00   0.355
## regionDewlap:VPD_kPa_int  1.394e+01  3.623e+00   3.848
## regionMite Patch:VPD_kPa_int  1.677e+01  3.618e+00   4.633
## regionVentrum:Solar_rad_Wm2_interpol -8.689e-04  8.504e-03  -0.102
## regionHead:Solar_rad_Wm2_interpol  1.285e-02  8.503e-03   1.511
## regionDewlap:Solar_rad_Wm2_interpol -2.101e-03  8.557e-03  -0.246
## regionMite Patch:Solar_rad_Wm2_interpol -1.270e-02  8.602e-03  -1.477
## regionVentrum:mass_g  1.002e+00  5.155e-01   1.943
## regionHead:mass_g    -3.836e-01  5.115e-01  -0.750
## regionDewlap:mass_g   9.819e-01  5.231e-01   1.877
## regionMite Patch:mass_g  1.116e+00  5.304e-01   2.105
##
## Correlation matrix not shown by default, as p = 24 > 12.
## Use print(x, correlation=TRUE) or
##      vcov(x)          if you need it
##
## fit warnings:
## Some predictor variables are on very different scales: consider rescaling
drop1(CEWL_mod15)

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

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

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

```

```

## rescaling

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

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

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

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

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

## Linear mixed model fit by REML ['lmerMod']
## Formula:
## TEWL_g_m2h ~ region * (VPD_kPa_int + mass_g) + Solar_rad_Wm2_interpol +
##   cloacal_temp_C + ambient_temp_C + temp_C_interpol + VPD_kPa +
##   (1 | individual_ID)
##   Data: CEWL_dat_sub1
##
## REML criterion at convergence: 4295.7
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.0352 -0.5858 -0.1210  0.3869  5.4385
##
## Random effects:
##   Groups             Name             Variance Std.Dev.

```

```

## individual_ID (Intercept) 29.06 5.391
## Residual 100.21 10.011
## Number of obs: 570, groups: individual_ID, 116
##
## Fixed effects:
##
## Estimate Std. Error t value
## (Intercept) -32.909846 29.607707 -1.112
## regionVentrum -6.228368 6.247217 -0.997
## regionHead 7.364134 6.247501 1.179
## regionDewlap -22.083459 6.358260 -3.473
## regionMite Patch -19.373854 6.413066 -3.021
## VPD_kPa_int -42.543813 15.976119 -2.663
## mass_g 0.268075 0.421516 0.636
## Solar_rad_Wm2_interpol 0.017407 0.006995 2.488
## cloacal_temp_C 2.296740 0.383048 5.996
## ambient_temp_C -4.526612 1.325540 -3.415
## temp_C_interpol 4.329559 2.246854 1.927
## VPD_kPa 24.691304 10.305080 2.396
## regionVentrum:VPD_kPa_int 7.467234 3.453473 2.162
## regionHead:VPD_kPa_int 2.943301 3.450477 0.853
## regionDewlap:VPD_kPa_int 13.663075 3.456064 3.953
## regionMite Patch:VPD_kPa_int 14.968835 3.438133 4.354
## regionVentrum:mass_g 0.996443 0.518135 1.923
## regionHead:mass_g -0.359870 0.514148 -0.700
## regionDewlap:mass_g 0.981930 0.525960 1.867
## regionMite Patch:mass_g 1.131285 0.533287 2.121
##
## Correlation matrix not shown by default, as p = 20 > 12.
## Use print(x, correlation=TRUE) or
## vcov(x) if you need it
drop1(CEWL_mod16)

## Single term deletions
##
## Model:
## TEWL_g_m2h ~ region * (VPD_kPa_int + mass_g) + Solar_rad_Wm2_interpol +
## cloacal_temp_C + ambient_temp_C + temp_C_interpol + VPD_kPa +
## (1 | individual_ID)
## npar AIC
## <none> 4369.9
## Solar_rad_Wm2_interpol 1 4374.4
## cloacal_temp_C 1 4401.3
## ambient_temp_C 1 4379.8
## temp_C_interpol 1 4371.8
## VPD_kPa 1 4373.9
## region:VPD_kPa_int 4 4390.4
## region:mass_g 4 4375.8

drop temp at capture:
CEWL_mod17 <- lme4::lmer(data = CEWL_dat_sub1,
# response variable
TEWL_g_m2h ~
# potential predictors

```

```

        region * (VPD_kPa_int + mass_g) +
        Solar_rad_Wm2_interpol +
        cloacal_temp_C +
        ambient_temp_C + VPD_kPa +
        # random effect
        (1|individual_ID))
summary(CEWL_mod17)

## Linear mixed model fit by REML ['lmerMod']
## Formula:
## TEWL_g_m2h ~ region * (VPD_kPa_int + mass_g) + Solar_rad_Wm2_interpol +
##      cloacal_temp_C + ambient_temp_C + VPD_kPa + (1 | individual_ID)
##      Data: CEWL_dat_sub1
##
## REML criterion at convergence: 4302.8
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.0661 -0.5956 -0.1231  0.3725  5.4784
##
## Random effects:
##      Groups             Name             Variance Std.Dev.
## individual_ID (Intercept)  30.39         5.512
## Residual                  100.17        10.009
## Number of obs: 570, groups: individual_ID, 116
##
## Fixed effects:
##
##              Estimate Std. Error t value
## (Intercept)      4.097965  22.870441   0.179
## regionVentrum     -6.107394   6.245885  -0.978
## regionHead        7.471656   6.246290   1.196
## regionDewlap     -22.025097   6.357613  -3.464
## regionMite Patch -19.424710   6.412131  -3.029
## VPD_kPa_int     -12.733030   4.057068  -3.138
## mass_g           0.291158   0.423411   0.688
## Solar_rad_Wm2_interpol 0.022793   0.006491   3.511
## cloacal_temp_C    2.343638   0.387322   6.051
## ambient_temp_C   -3.147068   1.129079  -2.787
## VPD_kPa          14.409836   8.940416   1.612
## regionVentrum:VPD_kPa_int 7.476906   3.452851   2.165
## regionHead:VPD_kPa_int  2.939064   3.449868   0.852
## regionDewlap:VPD_kPa_int 13.660303   3.455489   3.953
## regionMite Patch:VPD_kPa_int 14.966590   3.437480   4.354
## regionVentrum:mass_g    0.987961   0.518046   1.907
## regionHead:mass_g     -0.365361   0.514064  -0.711
## regionDewlap:mass_g    0.980463   0.525926   1.864
## regionMite Patch:mass_g 1.139601   0.533206   2.137
##
## Correlation matrix not shown by default, as p = 19 > 12.
## Use print(x, correlation=TRUE) or
##      vcov(x)          if you need it

```

```
drop1(CEWL_mod17)
```

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

drop ambient VPD at msmt:

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

```
## Linear mixed model fit by REML ['lmerMod']
## Formula:
## TEWL_g_m2h ~ region * (VPD_kPa_int + mass_g) + Solar_rad_Wm2_interpol +
##   cloacal_temp_C + ambient_temp_C + (1 | individual_ID)
##   Data: CEWL_dat_sub1
##
## REML criterion at convergence: 4311.6
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.1109 -0.5796 -0.1096  0.3721  5.5173
##
## Random effects:
##   Groups             Name             Variance Std.Dev.
## individual_ID (Intercept)  31.36         5.6
## Residual                  100.07        10.0
## Number of obs: 570, groups: individual_ID, 116
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)      8.787318  22.888471   0.384
## regionVentrum     -5.968820   6.242171  -0.956
## regionHead         7.613204   6.242608   1.220
## regionDewlap     -21.887146   6.354175  -3.445
## regionMite Patch  -19.374143   6.409004  -3.023
```

```

## VPD_kPa_int          -8.185200   2.928817  -2.795
## mass_g               0.355432   0.422858   0.841
## Solar_rad_Wm2_interpol 0.014955   0.004342   3.444
## cloacal_temp_C       2.320429   0.390650   5.940
## ambient_temp_C      -2.191820   0.968373  -2.263
## regionVentrums: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
## regionVentrums: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 + region*mass_g + cloaca',
  '(model 7) ~ region*VPD_kPa_int + region*Solar_rad_Wm2_interpol + SMI + region*mass_g + cloaca',
  '(model 8) ~ region*VPD_kPa_int + region*Solar_rad_Wm2_interpol + SMI + region*mass_g + cloaca',
  '(model 9) ~ region*VPD_kPa_int + region*Solar_rad_Wm2_interpol + region*mass_g + cloaca',
  '(model 10) ~ region*VPD_kPa_int + region*Solar_rad_Wm2_interpol + region*mass_g + cloaca',
  '(model 11) ~ region*VPD_kPa_int + region*Solar_rad_Wm2_interpol + region*mass_g + cloaca',
  '(model 12) ~ region*VPD_kPa_int + region*Solar_rad_Wm2_interpol + region*mass_g + cloaca',
  '(model 13) ~ region*VPD_kPa_int + region*Solar_rad_Wm2_interpol + region*mass_g + cloaca',
  '(model 14) ~ region*VPD_kPa_int + region*Solar_rad_Wm2_interpol + region*mass_g + cloaca',
  '(model 15) ~ region*VPD_kPa_int + region*Solar_rad_Wm2_interpol + region*mass_g + cloaca',
  '(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 + region*Solar_rad_Wm2_interpol + region*SMI + region*mass_g + cloaca
## 8 (model 13) ~ region*VPD_kPa_int + region*Solar_rad_Wm2_interpol + region*SMI + region*mass_g + cloaca
## 9 (model 14) ~ region*VPD_kPa_int + region*Solar_rad_Wm2_interpol + region*SMI + region*mass_g + cloaca
## 10 (model 15) ~ region*VPD_kPa_int + region*Solar_rad_Wm2_interpol + region*mass_g + cloaca
## 2 (model 7) ~ region*VPD_kPa_int + region*Solar_rad_Wm2_interpol + SMI + region*mass_g + cloaca
## 6 (model 11) ~ region*VPD_kPa_int + region*Solar_rad_Wm2_interpol + region*mass_g + cloaca
## 1 (model 6a) ~ region*VPD_kPa_int + region*Solar_rad_Wm2_interpol + region*SMI + region*mass_g + cloaca
## 5 (model 10) ~ region*VPD_kPa_int + region*Solar_rad_Wm2_interpol + region*mass_g + cloaca
## 3 (model 8) ~ region*VPD_kPa_int + region*Solar_rad_Wm2_interpol + SMI + region*mass_g + cloaca
## 4 (model 9) ~ region*VPD_kPa_int + region*Solar_rad_Wm2_interpol + region*mass_g + cloaca
## 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:

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

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula:
## TEWL_g_m2h ~ region * (VPD_kPa_int + mass_g) + Solar_rad_Wm2_interpol +
##   cloacal_temp_C + ambient_temp_C + temp_C_interpol + VPD_kPa +
##   (1 | individual_ID)
## Data: CEWL_dat_sub1
##
## REML criterion at convergence: 4295.7
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.0352 -0.5858 -0.1210  0.3869  5.4385
##
## Random effects:
## Groups           Name          Variance Std.Dev.
## individual_ID (Intercept) 29.06      5.391
## Residual                100.21    10.011
## Number of obs: 570, groups: individual_ID, 116
##
## Fixed effects:
##              Estimate Std. Error    df t value Pr(>|t|)
## (Intercept)   -32.909846  29.607707 114.999468  -1.112  0.268659
## regionVentrum    -6.228368   6.247217 444.802904  -0.997  0.319315
## regionHead       7.364134   6.247501 444.836608   1.179  0.239135
## regionDewlap   -22.083459   6.358260 449.172834  -3.473  0.000564
## regionMite Patch -19.373854   6.413066 445.592471  -3.021  0.002664
## VPD_kPa_int    -42.543813  15.976119 112.305198  -2.663  0.008884
## mass_g           0.268075   0.421516 450.541075   0.636  0.525113
## Solar_rad_Wm2_interpol  0.017407   0.006995 107.447880   2.488  0.014364
## cloacal_temp_C   2.296740   0.383048 107.357738   5.996 2.76e-08
## ambient_temp_C  -4.526612   1.325540 111.836286  -3.415  0.000890
```

```

## temp_C_interpol      4.329559    2.246854 107.335445    1.927 0.056631
## VPD_kPa              24.691304   10.305080 114.154457    2.396 0.018199
## regionVentrum:VPD_kPa_int    7.467234    3.453473 442.945754    2.162 0.031134
## regionHead:VPD_kPa_int      2.943301    3.450477 443.066029    0.853 0.394113
## regionDewlap:VPD_kPa_int    13.663075    3.456064 443.729837    3.953 8.97e-05
## regionMite Patch:VPD_kPa_int 14.968835    3.438133 442.150933    4.354 1.66e-05
## regionVentrum:mass_g        0.996443    0.518135 446.636242    1.923 0.055099
## regionHead:mass_g         -0.359870    0.514148 445.253712   -0.700 0.484333
## regionDewlap:mass_g        0.981930    0.525960 450.744396    1.867 0.062561
## regionMite Patch:mass_g      1.131285    0.533287 446.743940    2.121 0.034443
##
## (Intercept)
## regionVentrum
## regionHead
## regionDewlap          ***
## regionMite Patch      **
## VPD_kPa_int           **
## mass_g
## Solar_rad_Wm2_interpol  *
## cloacal_temp_C        ***
## ambient_temp_C        ***
## temp_C_interpol       .
## VPD_kPa               *
## regionVentrum:VPD_kPa_int  *
## regionHead:VPD_kPa_int
## regionDewlap:VPD_kPa_int  ***
## regionMite Patch:VPD_kPa_int ***
## regionVentrum:mass_g    .
## regionHead:mass_g
## regionDewlap:mass_g    .
## regionMite Patch:mass_g  *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## Correlation matrix not shown by default, as p = 20 > 12.
## Use print(x, correlation=TRUE) or
##     vcov(x)           if you need it

```

```

CEWL_mod17p <- lmerTest::lmer(data = CEWL_dat_sub1,
                              # response variable
                              TEWL_g_m2h ~
                              # 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

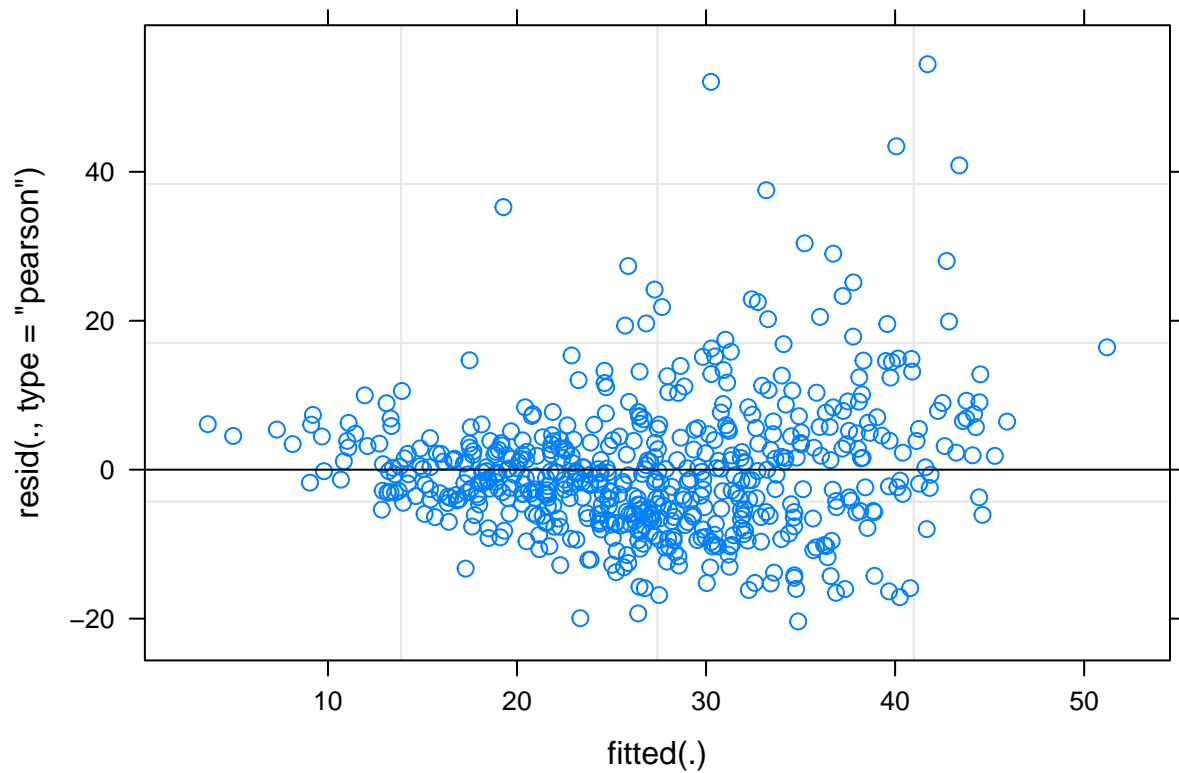
```

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

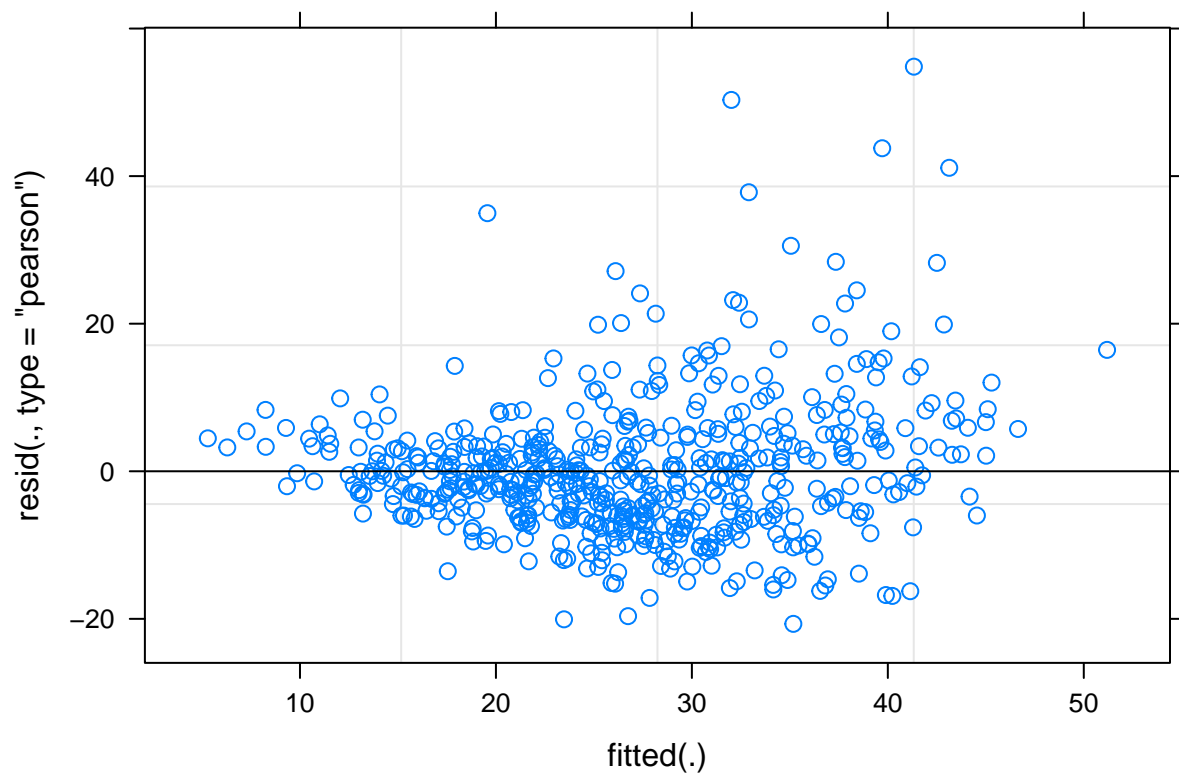
##
## Correlation matrix not shown by default, as p = 19 > 12.
## Use print(x, correlation=TRUE) or
##     vcov(x)           if you need it
```

### Check LM Assumptions

```
plot(CEWL_mod16)
```



```
plot(CEWL_mod17)
```

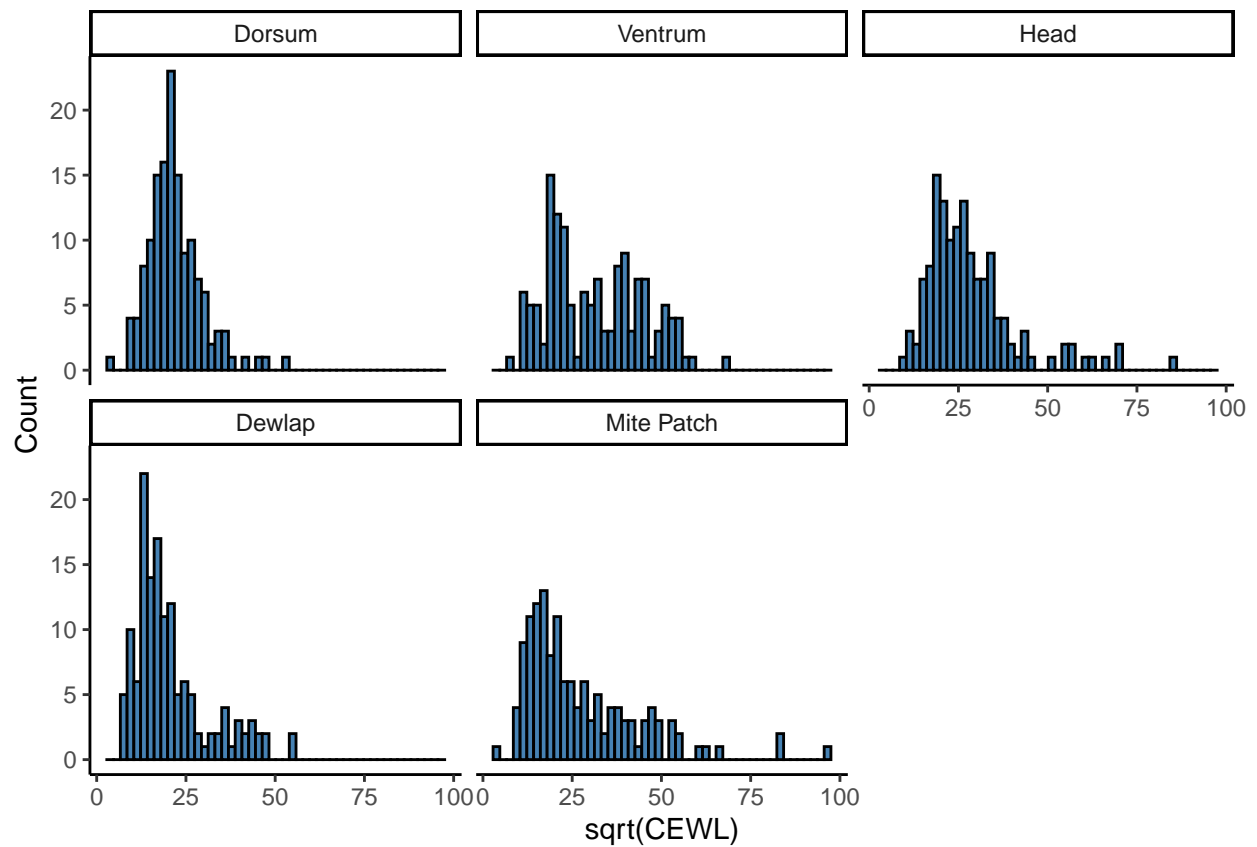


Both have fanning, which indicates that linearity and equal error variance are not satisfied.

### Test Transformations

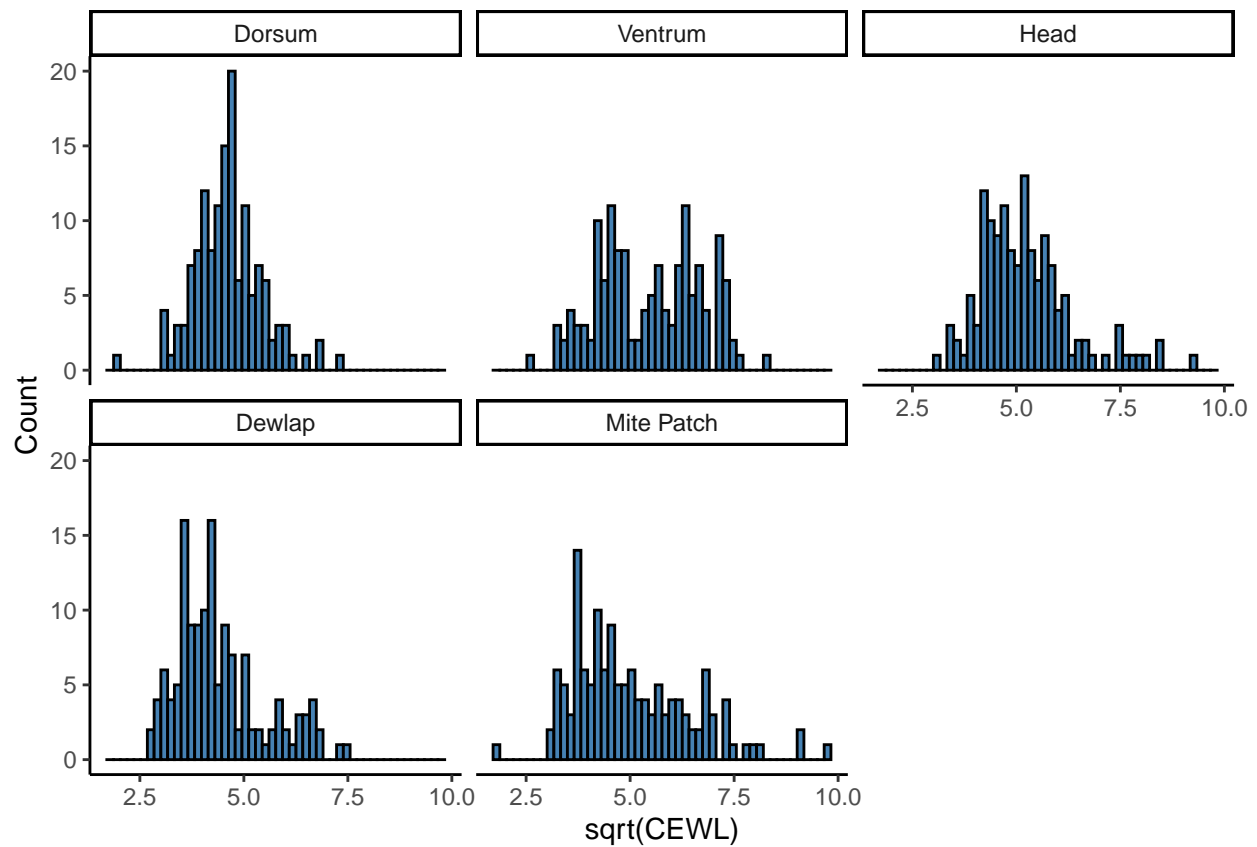
Can I improve satisfaction of LM assumptions by transforming the dependent variable? In particular, conditions of linearity and normality are not met.

```
# 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)
```

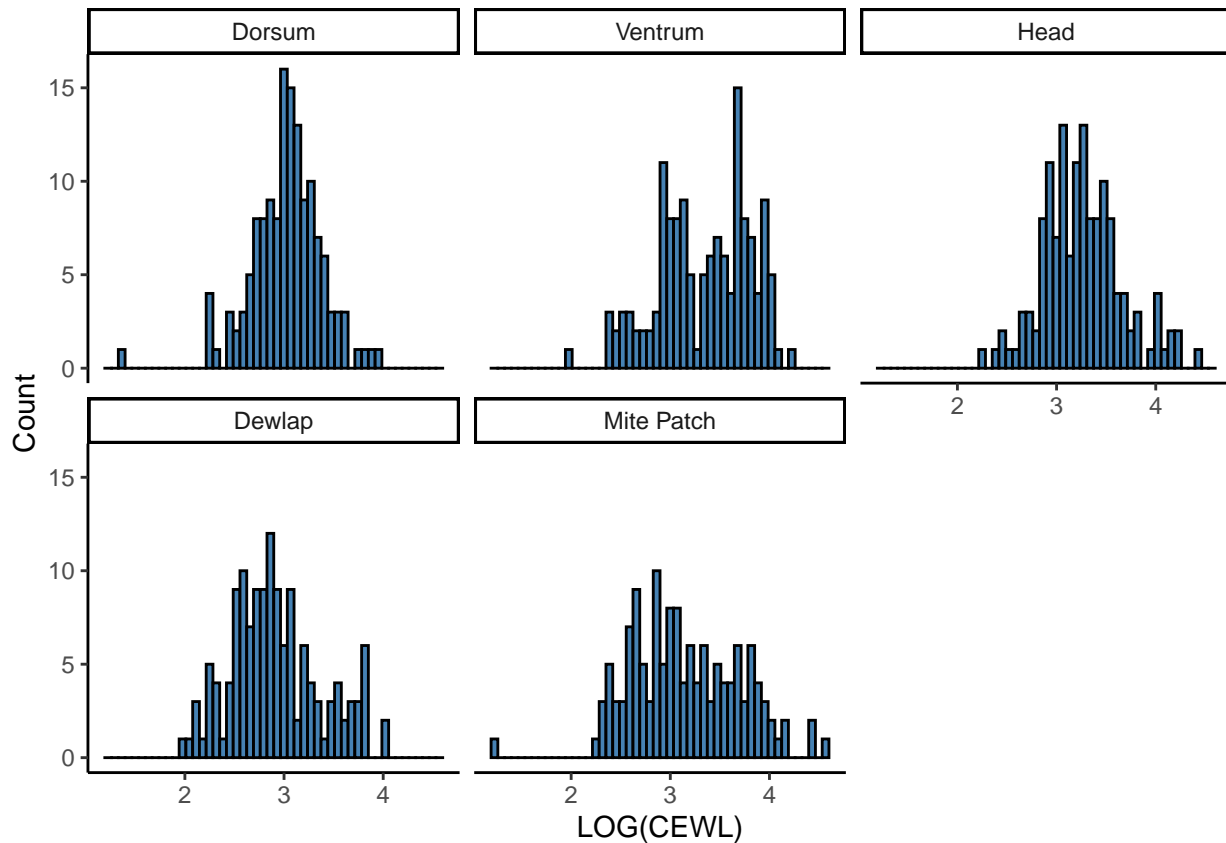


```
# sqrt(TEWL)
CEWL_data_full %>%
  ggplot(., aes(x = sqrt(TEWL_g_m2h))) +
  geom_histogram(color = "black", fill="steelblue", bins=50) +
  theme_classic() +
  xlab("sqrt(CEWL)") +
  ylab("Count") +
  facet_wrap(~region)
```





```
# 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)
```



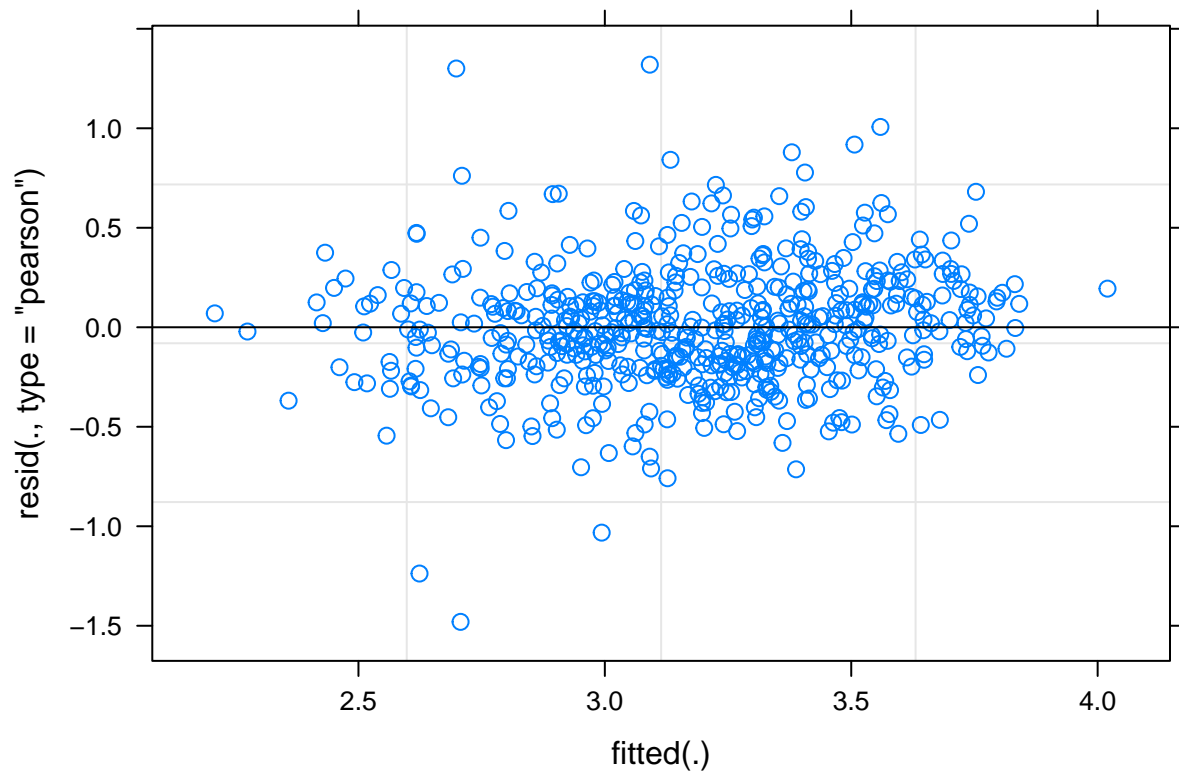
Log transforming seems to be pretty effective across body regions.

### 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:

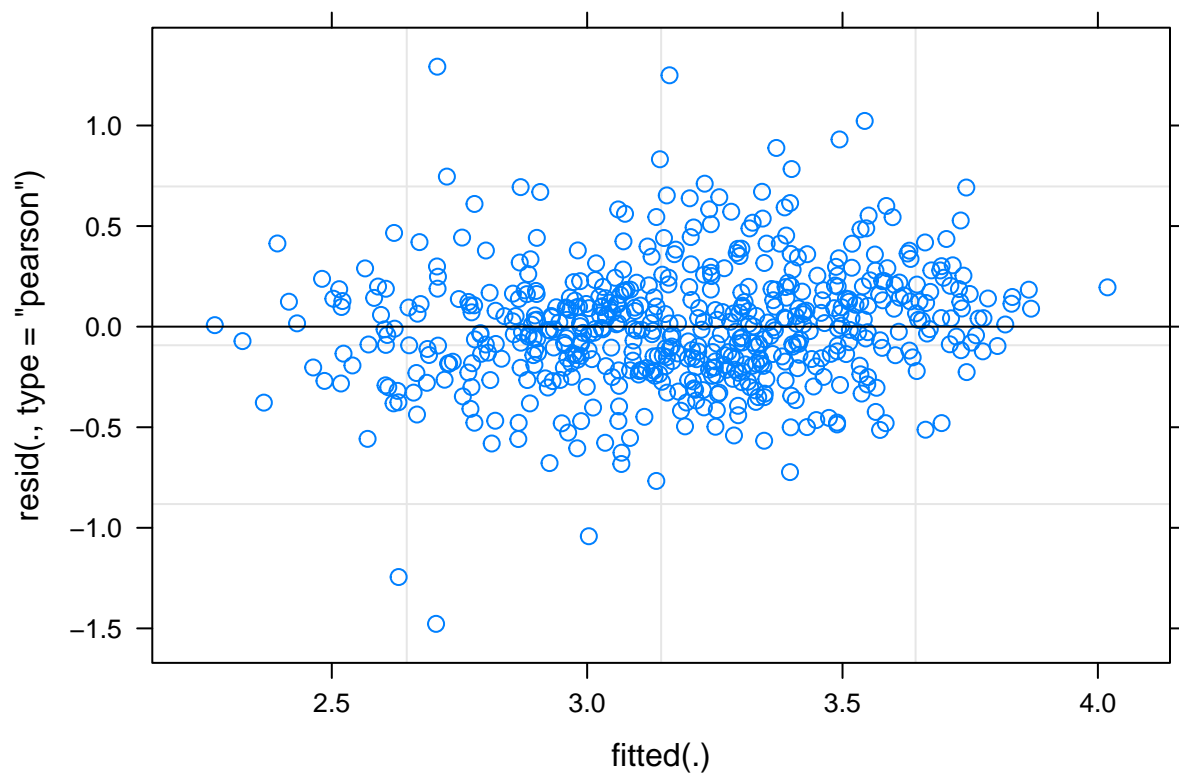
```
CEWL_mod16t <- lme4::lmer(data = CEWL_dat_sub1,
  # response variable
  log(TEWL_g_m2h) ~
  # potential predictors
  region * (VPD_kPa_int + mass_g) +
  Solar_rad_Wm2_interpol +
  cloacal_temp_C +
  ambient_temp_C + temp_C_interpol + VPD_kPa +
  # random effect
  (1|individual_ID))
plot(CEWL_mod16t)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



```
vif(CEWL_mod16t)
```

```
##              GVIF Df  GVIF^(1/(2*Df))
## region          2.643129e+05  4          4.761730
## VPD_kPa_int      8.785850e+01  1          9.373287
## mass_g           2.507115e+00  1          1.583387
## Solar_rad_Wm2_interpol 3.027354e+00  1          1.739929
## cloacal_temp_C    1.141428e+00  1          1.068376
## ambient_temp_C    2.414719e+00  1          1.553937
## temp_C_interpol   7.953116e+01  1          8.918025
## VPD_kPa           6.728539e+00  1          2.593943
## region:VPD_kPa_int 1.022920e+03  4          2.378100
## region:mass_g     1.449380e+05  4          4.417207
```

```
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)
```



```
vif(CEWL_mod17t)
```

```
##              GVIF Df  GVIF^(1/(2*Df))
## region          2.643837e+05  4      4.761890
## VPD_kPa_int      5.247587e+00  1      2.290761
## mass_g           2.435439e+00  1      1.560589
## Solar_rad_Wm2_interpol 2.535980e+00  1      1.592476
## cloacal_temp_C    1.136892e+00  1      1.066251
## ambient_temp_C    1.710211e+00  1      1.307750
## VPD_kPa           4.937485e+00  1      2.222045
## region:VPD_kPa_int 1.012540e+03  4      2.375071
## region:mass_g     1.445426e+05  4      4.415699
```

MUCH better! These models are good. VIF within tolerable limits.

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

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

```
CEWL_mod16tp <- lmerTest::lmer(data = CEWL_dat_sub2,
  # response variable
  log(TEWL_g_m2h) ~
  # potential predictors
  region * (VPD_kPa_int + mass_g) +
```

```

        Solar_rad_Wm2_interpol +
        cloacal_temp_C +
        ambient_temp_C + temp_C_interpol + VPD_kPa +
        # random effect
        (1|individual_ID))
summary(CEWL_mod16tp)

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula:
## log(TEWL_g_m2h) ~ region * (VPD_kPa_int + mass_g) + Solar_rad_Wm2_interpol +
##   cloacal_temp_C + ambient_temp_C + temp_C_interpol + VPD_kPa +
##   (1 | individual_ID)
##   Data: CEWL_dat_sub2
##
## REML criterion at convergence: 629.4
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -4.4784 -0.5927 -0.0390  0.4821  3.9107
##
## Random effects:
##   Groups             Name             Variance Std.Dev.
## individual_ID (Intercept) 0.03659   0.1913
## Residual                0.11350   0.3369
## Number of obs: 635, groups: individual_ID, 129
##
## Fixed effects:
##
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)    -4.043e-02  8.840e-01  1.357e+02  -0.046  0.963592
## regionVentrum   -2.050e-01  2.016e-01  4.969e+02  -1.017  0.309689
## regionHead       2.341e-01  2.018e-01  4.970e+02   1.160  0.246528
## regionDewlap    -1.018e+00  2.049e-01  5.011e+02  -4.965  9.42e-07
## regionMite Patch -8.023e-01  2.064e-01  4.976e+02  -3.888  0.000115
## VPD_kPa_int     -1.866e+00  4.352e-01  1.310e+02  -4.287  3.48e-05
## mass_g          1.819e-02  1.363e-02  4.918e+02   1.335  0.182545
## Solar_rad_Wm2_interpol  5.754e-04  2.041e-04  1.214e+02   2.819  0.005630
## cloacal_temp_C   8.684e-02  1.297e-02  1.209e+02   6.695  7.16e-10
## ambient_temp_C  -1.374e-01  4.475e-02  1.257e+02  -3.070  0.002622
## temp_C_interpol  1.914e-01  5.585e-02  1.222e+02   3.426  0.000834
## VPD_kPa         8.543e-01  3.541e-01  1.294e+02   2.413  0.017234
## regionVentrum:VPD_kPa_int  3.393e-01  1.153e-01  4.954e+02   2.943  0.003398
## regionHead:VPD_kPa_int    1.835e-01  1.152e-01  4.956e+02   1.593  0.111751
## regionDewlap:VPD_kPa_int  6.200e-01  1.154e-01  4.964e+02   5.372  1.20e-07
## regionMite Patch:VPD_kPa_int  5.235e-01  1.148e-01  4.946e+02   4.561  6.44e-06
## regionVentrum:mass_g      2.600e-02  1.658e-02  4.988e+02   1.568  0.117450
## regionHead:mass_g     -1.596e-02  1.646e-02  4.975e+02  -0.969  0.332780
## regionDewlap:mass_g      4.070e-02  1.681e-02  5.028e+02   2.421  0.015829
## regionMite Patch:mass_g    4.826e-02  1.702e-02  4.988e+02   2.836  0.004758
##
## (Intercept)
## regionVentrum
## regionHead
## regionDewlap
***

```

```

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

##
## Correlation matrix not shown by default, as p = 20 > 12.
## Use print(x, correlation=TRUE) or
##     vcov(x)           if you need it

CEWL_mod17tp <- lmerTest::lmer(data = CEWL_dat_sub2,
                               # response variable
                               log(TEWL_g_m2h) ~
                               # potential predictors
                               region * (VPD_kPa_int + mass_g) +
                               Solar_rad_Wm2_interpol +
                               cloacal_temp_C +
                               ambient_temp_C + VPD_kPa +
                               # random effect
                               (1|individual_ID))

summary(CEWL_mod17p)

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula:
## TEWL_g_m2h ~ region * (VPD_kPa_int + mass_g) + Solar_rad_Wm2_interpol +
##     cloacal_temp_C + ambient_temp_C + VPD_kPa + (1 | individual_ID)
## Data: CEWL_dat_sub1
##
## REML criterion at convergence: 4302.8
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.0661 -0.5956 -0.1231  0.3725  5.4784
##
## Random effects:
## Groups           Name             Variance Std.Dev.
## individual_ID (Intercept)  30.39      5.512
## Residual                100.17     10.009
## Number of obs: 570, groups: individual_ID, 116
##

```

```

## Fixed effects:
##
##               Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)      4.097965   22.870441  123.456940    0.179  0.858089
## regionVentrurn    -6.107394    6.245885  444.635136   -0.978  0.328692
## regionHead        7.471656    6.246290  444.668104    1.196  0.232266
## regionDewlap     -22.025097    6.357613  448.920268   -3.464  0.000583
## regionMite Patch  -19.424710    6.412131  445.398476   -3.029  0.002593
## VPD_kPa_int      -12.733030    4.057068  211.322355   -3.138  0.001941
## mass_g            0.291158    0.423411  447.687594    0.688  0.492030
## Solar_rad_Wm2_interpol  0.022793    0.006491  109.611562    3.511  0.000648
## cloacal_temp_C     2.343638    0.387322  108.290774    6.051  2.10e-08
## ambient_temp_C    -3.147068    1.129079  111.835533   -2.787  0.006247
## VPD_kPa           14.409836    8.940416  114.195750    1.612  0.109774
## regionVentrurn:VPD_kPa_int  7.476906    3.452851  442.783297    2.165  0.030888
## regionHead:VPD_kPa_int    2.939064    3.449868  442.902557    0.852  0.394710
## regionDewlap:VPD_kPa_int  13.660303    3.455489  443.552232    3.953  8.97e-05
## regionMite Patch:VPD_kPa_int 14.966590    3.437480  442.010751    4.354  1.66e-05
## regionVentrurn:mass_g     0.987961    0.518046  446.468204    1.907  0.057150
## regionHead:mass_g        -0.365361    0.514064  445.096592   -0.711  0.477623
## regionDewlap:mass_g      0.980463    0.525926  450.477002    1.864  0.062935
## regionMite Patch:mass_g   1.139601    0.533206  446.519281    2.137  0.033119
##
## (Intercept)
## regionVentrurn
## regionHead
## regionDewlap      ***
## regionMite Patch  **
## VPD_kPa_int       **
## mass_g
## Solar_rad_Wm2_interpol ***
## cloacal_temp_C    ***
## ambient_temp_C    **
## VPD_kPa
## regionVentrurn:VPD_kPa_int *
## regionHead:VPD_kPa_int
## regionDewlap:VPD_kPa_int ***
## regionMite Patch:VPD_kPa_int ***
## regionVentrurn:mass_g .
## regionHead:mass_g
## regionDewlap:mass_g .
## regionMite Patch:mass_g *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation matrix not shown by default, as p = 19 > 12.
## Use print(x, correlation=TRUE) or
##     vcov(x)         if you need it

```

## Export

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

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