Cal Poly Herpetology CURE - Capture Data Analyses

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Contents

Packages

Background and Goals

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

Data

Morphometrics and Blood Data

This data was collected upon capture of each lizard.

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

processing time for each lizard, when all measurements were finished - hemolyzed = whether or not red blood cells burst and contaminated plasma

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

```
# 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.   :2022-03-08 10:17:00   1      :  1
##  1st Qu.:2021-04-19   1st Qu.:2022-03-08 12:36:00   2      :  1
##  Median :2021-04-26   Median :2022-03-08 12:48:00   3      :  1
##  Mean   :2021-04-27   Mean   :2022-03-08 12:51:12   4      :  1
##  3rd Qu.:2021-05-10   3rd Qu.:2022-03-08 13:03:00   5      :  1
##  Max.   :2021-05-17   Max.   :2022-03-08 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.   :2022-03-08 12:44:00   N   :85   Min.   :2021-04-05 10:17:00
##  1st Qu.:2022-03-08 14:09:00   Y   :39   1st Qu.:2021-04-19 12:49:00
##  Median :2022-03-08 15:17:30   NA's:24   Median :2021-04-26 15:34:00
##  Mean   :2022-03-08 15:12:09             Mean   :2021-04-28 20:28:01
##  3rd Qu.:2022-03-08 16:15:15             3rd Qu.:2021-05-10 12:44:00
##  Max.   :2022-03-08 17:38:00             Max.   :2021-05-17 13:01:00
##  NA's   :8                               NA's   :3
##    hold_time
##  Min.   : 21.0
##  1st Qu.: 95.0
##  Median :141.5
##  Mean   :143.8
##  3rd Qu.:197.5
##  Max.   :268.0
##  NA's   :10
```

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

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

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

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

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

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

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

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

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

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

Stats for CDFW Permit Report

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

```r
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
```

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

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

```r
# 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)

```r
# week 1
CEWL_April_05 <- read.csv("./data/capture_CEWL/4-5-21-CEWL.csv", # filename
                          na.strings=c("","NA")) %>% # fix empty cells
  # rename and select the pertinent variables/cols
  # I have to do this for each one
  # so they all have the same number of columns for joining
  dplyr::select(date = Date,
                Time, Status,
                ID = Comments,
```

```
                TEWL_g_m2h = TEWL..g..m2h.., # rename
                ambient_temp_C = AmbT..C., # rename
                ambient_RH_percent = AmbRH....
                )

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

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

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

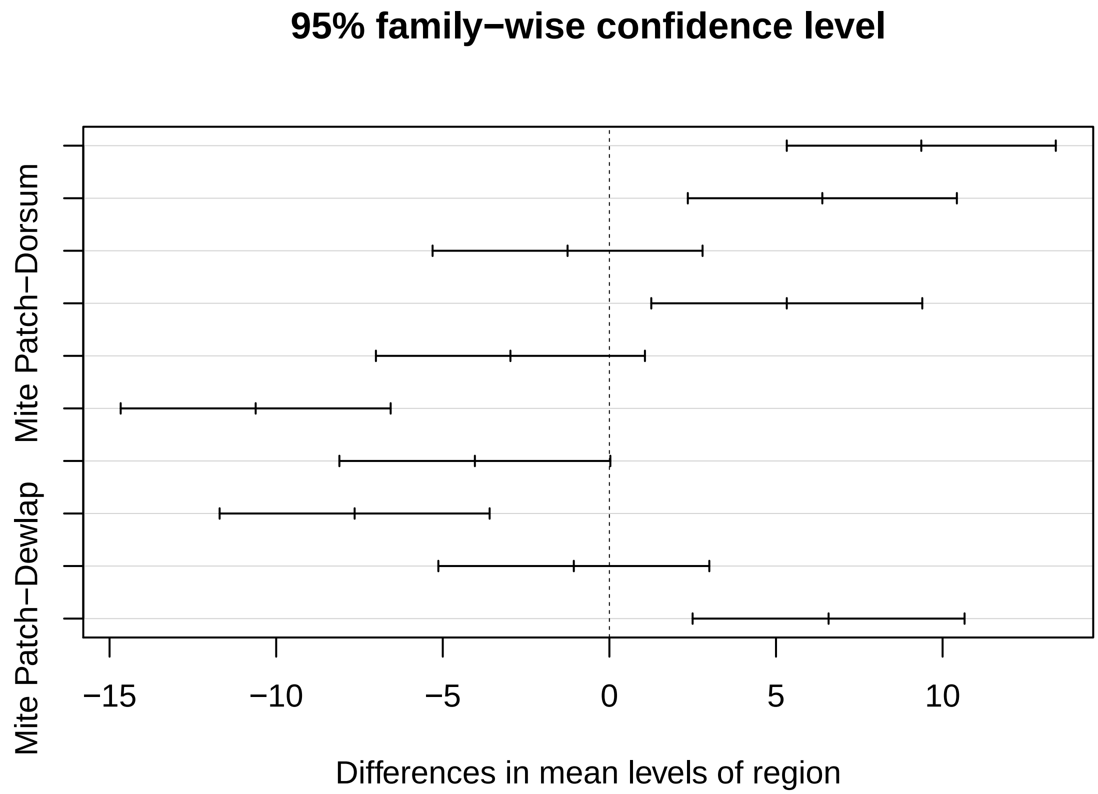
```
            SD_CEWL = sd(TEWL_g_m2h),
            SEM_CEWL = SD_CEWL/sqrt(n_obs)
            ) %>%
  dplyr::select(region, mean_CEWL, SEM_CEWL)
```

```
## `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)
```




```
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)
```

```r
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
```

```r
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.

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

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

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

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

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

```r
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.

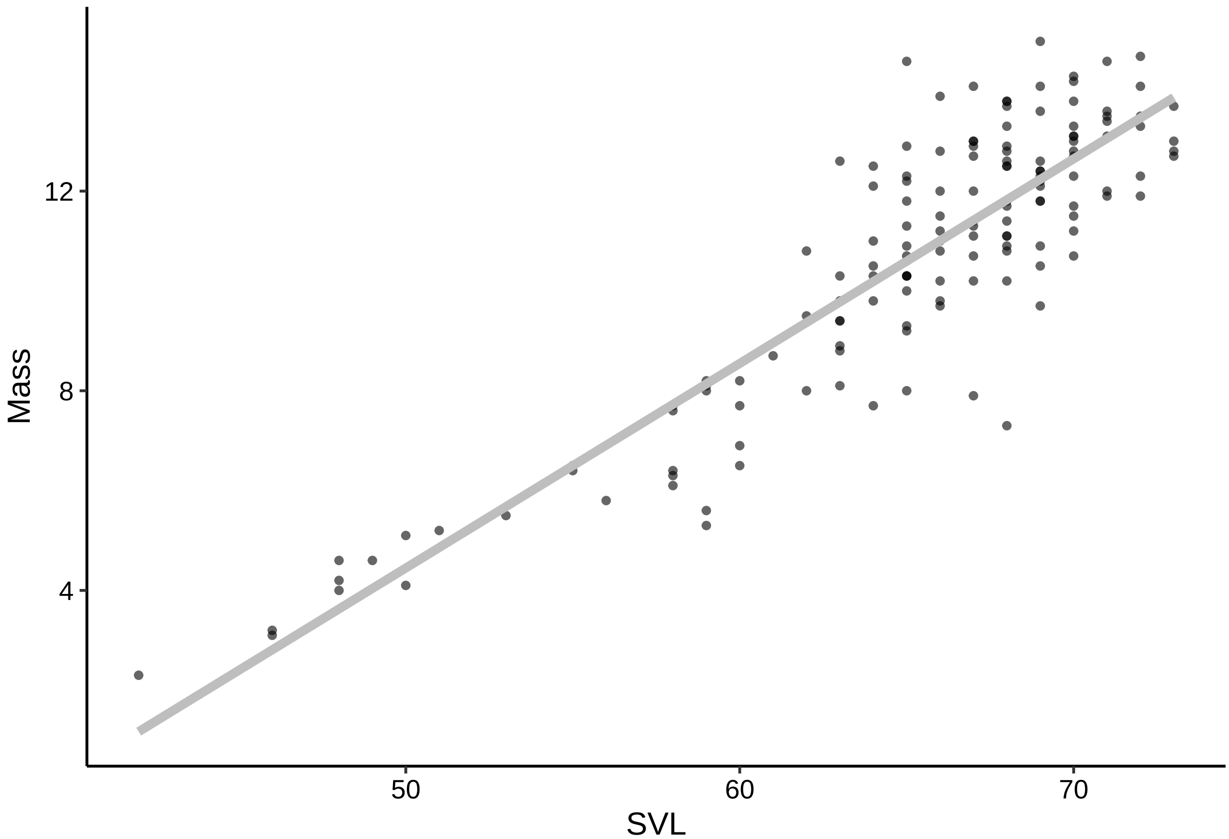
I calculate as described by: Peig, J., & Green, A. J. (2009). New perspectives for estimating body condition from mass/length data: The scaled mass index as an alternative method. Oikos, 118(12), 1883–1891. https://doi.org/10.1111/j.1600-0706.2009.17643.x

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
```

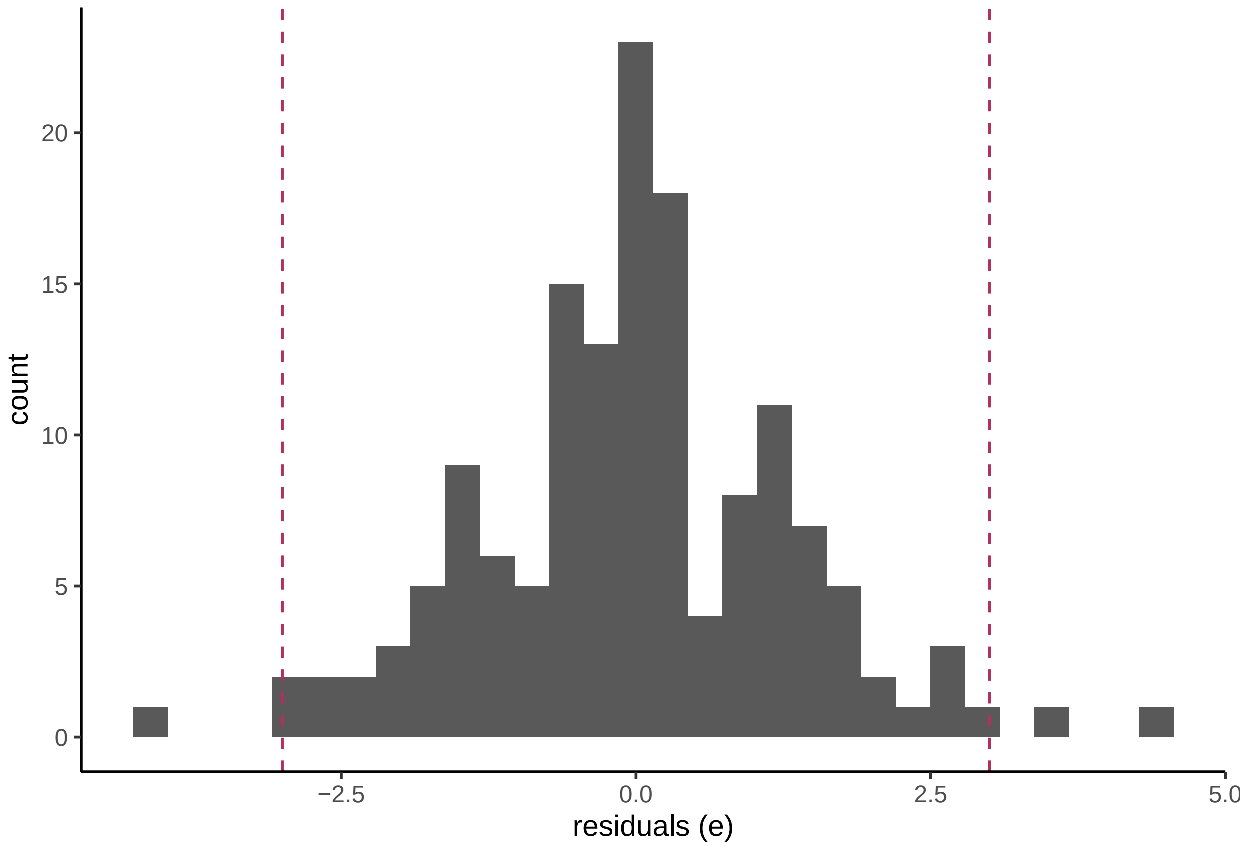
look for outliers by calculating residuals

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

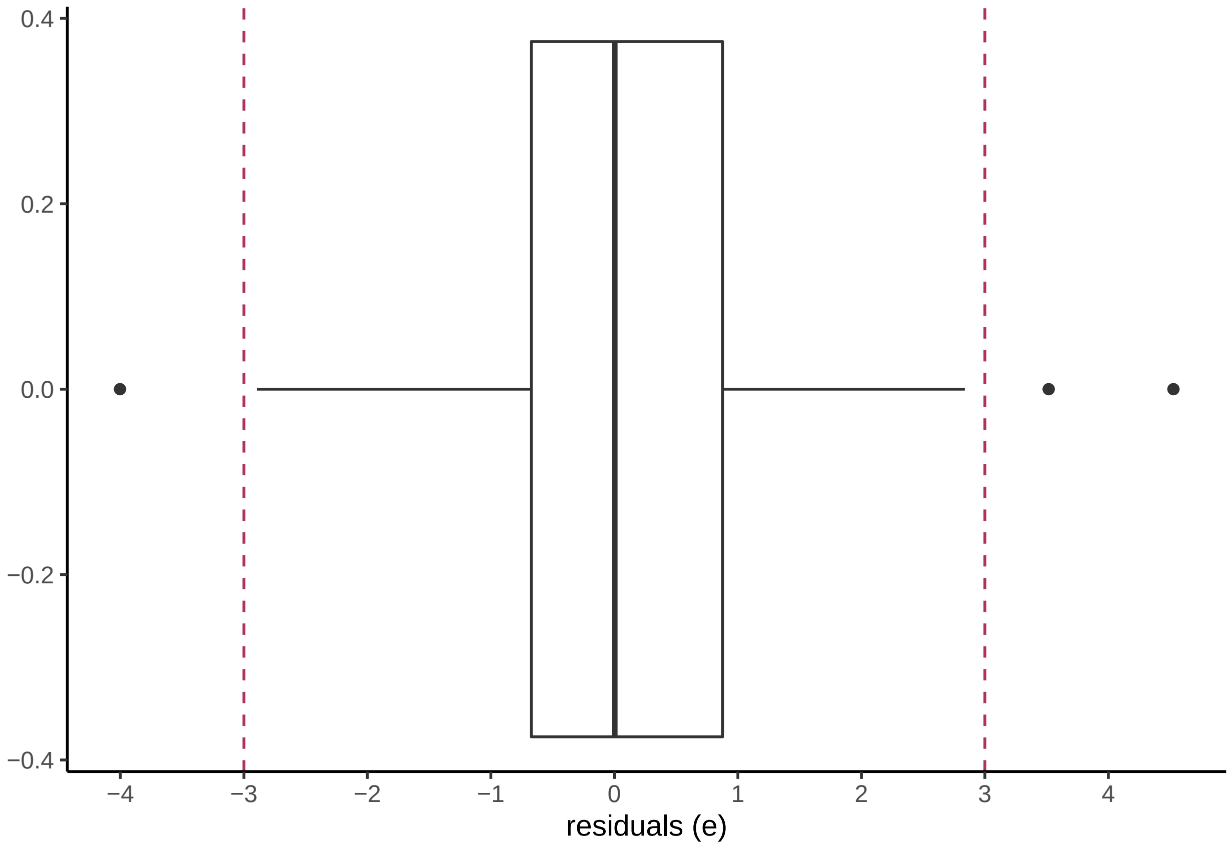
plot residuals

```
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.

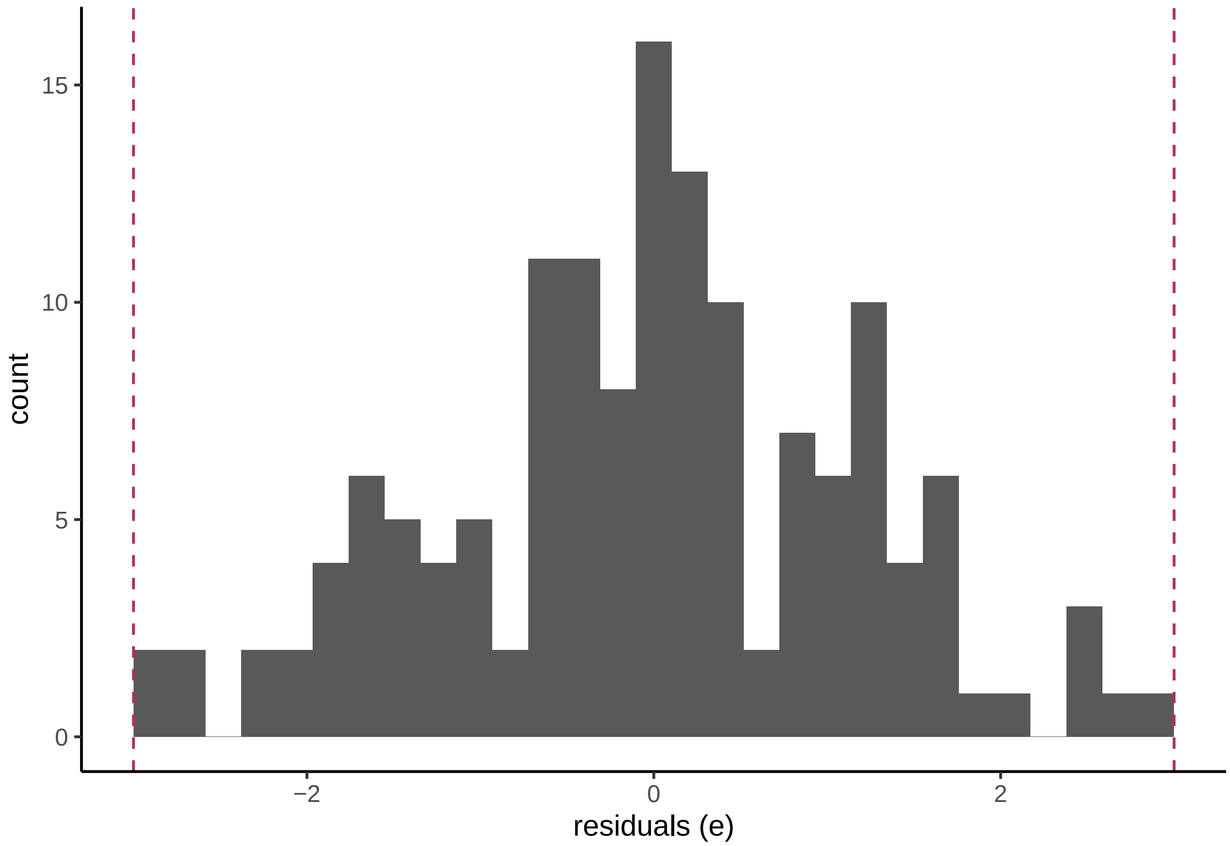
calculating residuals with outliers excluded

```
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)
```

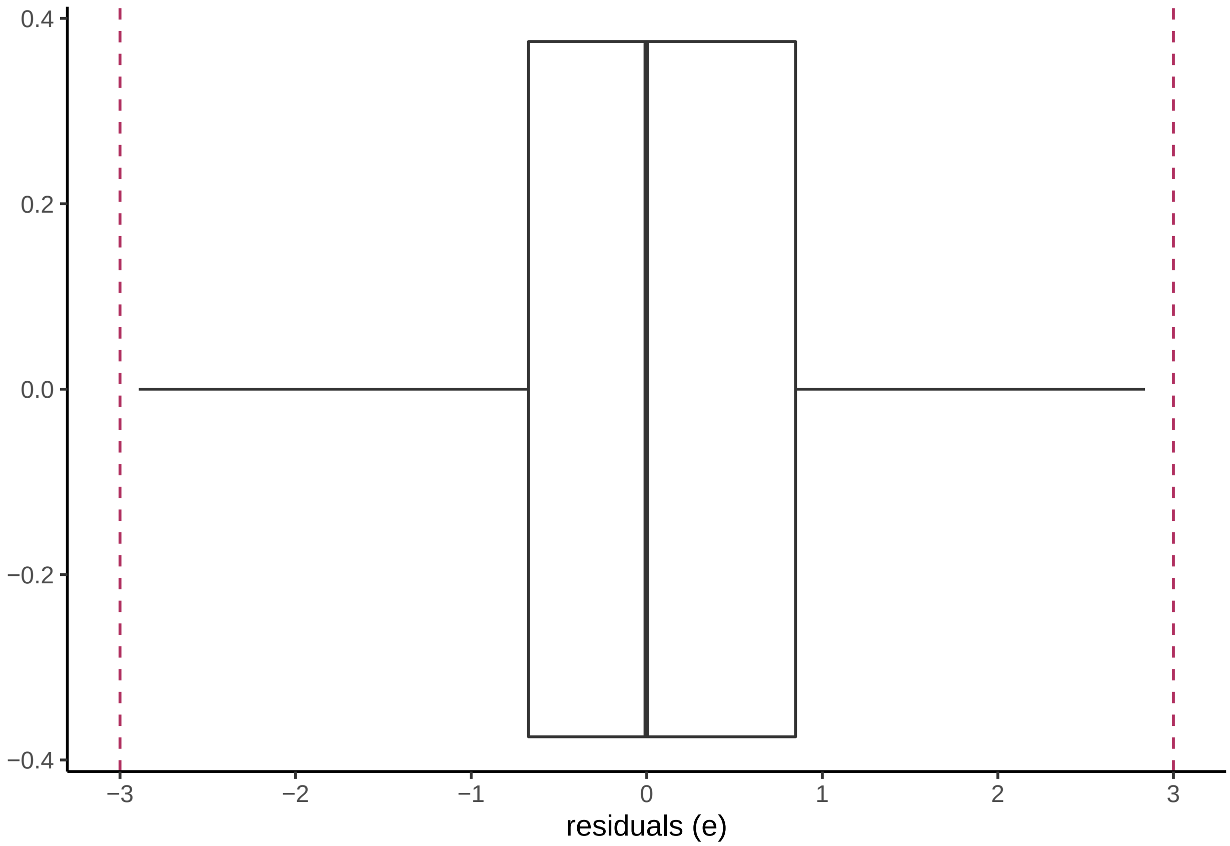
plot new residuals

```
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`.
```




```r
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 2022-03-08 10:38:00             4     48    4.2       M
```

```
## 2  2021-04-05 2022-03-08 10:17:00           5     50    4.1       M
## 3  2021-04-05 2022-03-08 10:47:00           6     48    4.6       M
## 4  2021-04-05 2022-03-08 10:42:00           8     42    2.3       M
## 5  2021-04-05 2022-03-08 13:27:00           9     46    3.1       F
## 6  2021-04-26 2022-03-08 12:32:00          55     46    3.2       F
## 7  2021-04-26 2022-03-08 12:47:00          62     51    5.2       M
## 8  2021-04-26 2022-03-08 12:40:00          65     48    4.0       M
## 9  2021-05-03 2022-03-08 12:36:00          85     49    4.6       M
## 10 2021-05-10 2022-03-08 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 2022-03-08 14:02:00         Y 2021-04-05 10:38:00       204
## 2              25 2022-03-08 13:59:00         Y 2021-04-05 10:17:00       222
## 3              24 2022-03-08 14:06:00         N 2021-04-05 10:47:00       199
## 4              23 2022-03-08 14:20:00         N 2021-04-05 10:42:00       218
## 5              23 2022-03-08 14:43:00      <NA> 2021-04-05 13:27:00        76
## 6              27 2022-03-08 13:16:00         N 2021-04-26 12:32:00        44
## 7              26 2022-03-08 14:28:00         N 2021-04-26 12:47:00       101
## 8              25 2022-03-08 15:26:00      <NA> 2021-04-26 12:40:00       166
## 9              24 2022-03-08 14:13:00         Y 2021-05-03 12:36:00        97
## 10             21 2022-03-08 17:15:00         Y 2021-05-10 13:10:00       245
##      y_hat        e row          H
## 1  3.62910 -0.57090   4 0.05776372
## 2  4.44886  0.34886   5 0.04645120
## 3  3.62910 -0.97090   6 0.05776372
## 4  1.16982 -1.13018   8 0.10020003
## 5  2.80934 -0.29066   9 0.07049270
## 6  2.80934 -0.39066  54 0.07049270
## 7  4.85874 -0.34126  60 0.04132611
## 8  3.62910 -0.37090  63 0.05776372
## 9  4.03898 -0.56102  83 0.05193040
## 10 4.44886 -0.65114 118 0.04645120
```

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

Check for influential points based on Cook's distance:

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

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

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

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

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

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

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

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

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

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

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

# check residuals values
```

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

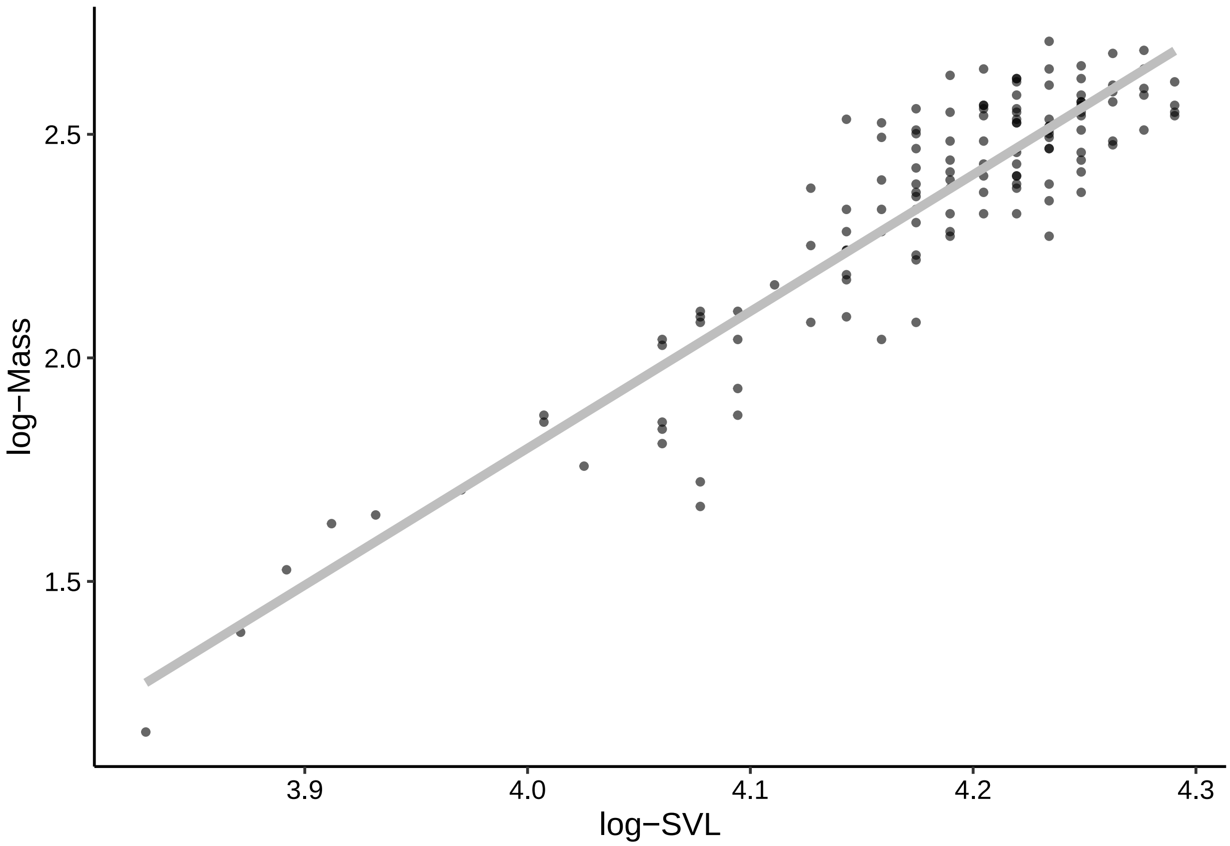
```
##       mean_res         med
## 1 4.654038e-17 0.001458016
```

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

Step 2: make log-log relationship

plot and calculate SLR for filtered data

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



SLR

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

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

compute standardized major axis using this regression equation:

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

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

also get a value for L0:

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

Step 3: calculate scaled mass index

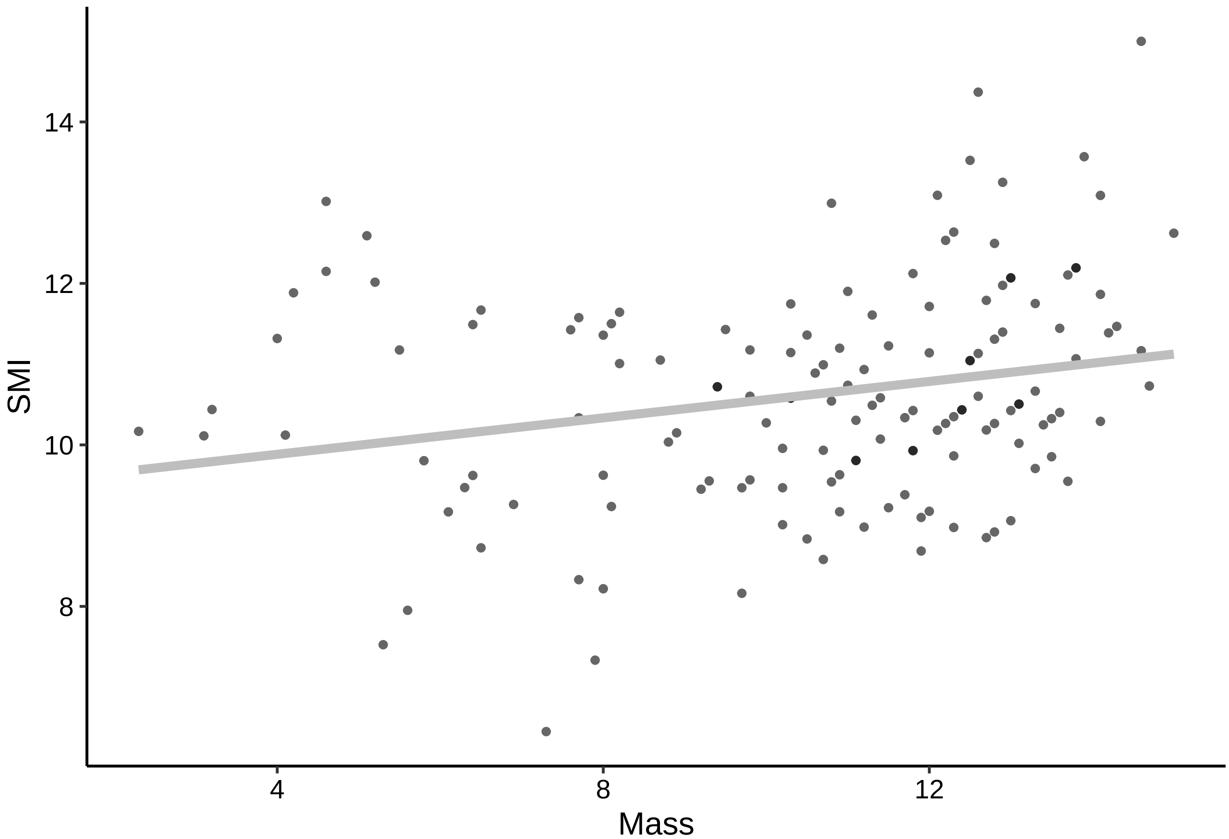
(And join weather data.)

```
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.   :2022-03-08 11:29:00   Min.   :46.00   Min.   : 3.20
##  1st Qu.:1.541   1st Qu.:2022-03-08 12:37:00   1st Qu.:64.00   1st Qu.: 9.70
##  Median :1.683   Median :2022-03-08 12:48:00   Median :67.00   Median :11.40
##  Mean   :1.673   Mean   :2022-03-08 12:55:48   Mean   :65.81   Mean   :10.88
##  3rd Qu.:1.779   3rd Qu.:2022-03-08 13:02:15   3rd Qu.:69.00   3rd Qu.:12.80
##  Max.   :2.055   Max.   :2022-03-08 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.   :2022-03-08 12:44:00   N   :368
##  1st Qu.:22.0   1st Qu.:2022-03-08 14:14:00   Y   :179
##  Median :23.0   Median :2022-03-08 15:25:00   NA's:152
##  Mean   :23.4   Mean   :2022-03-08 15:16:48
##  3rd Qu.:25.0   3rd Qu.:2022-03-08 16:18:00
##  Max.   :28.0   Max.   :2022-03-08 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
```

Figures

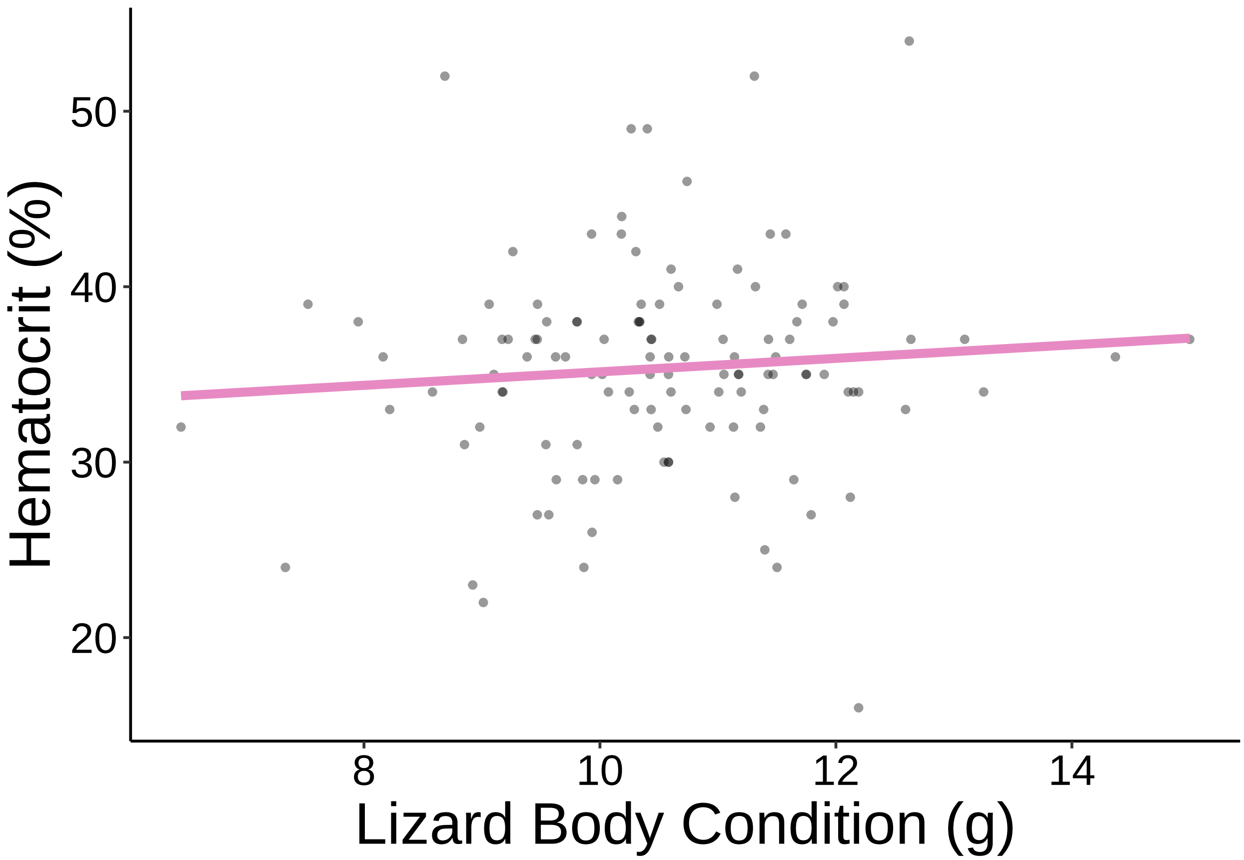
osmolality & hematocrit

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).
```



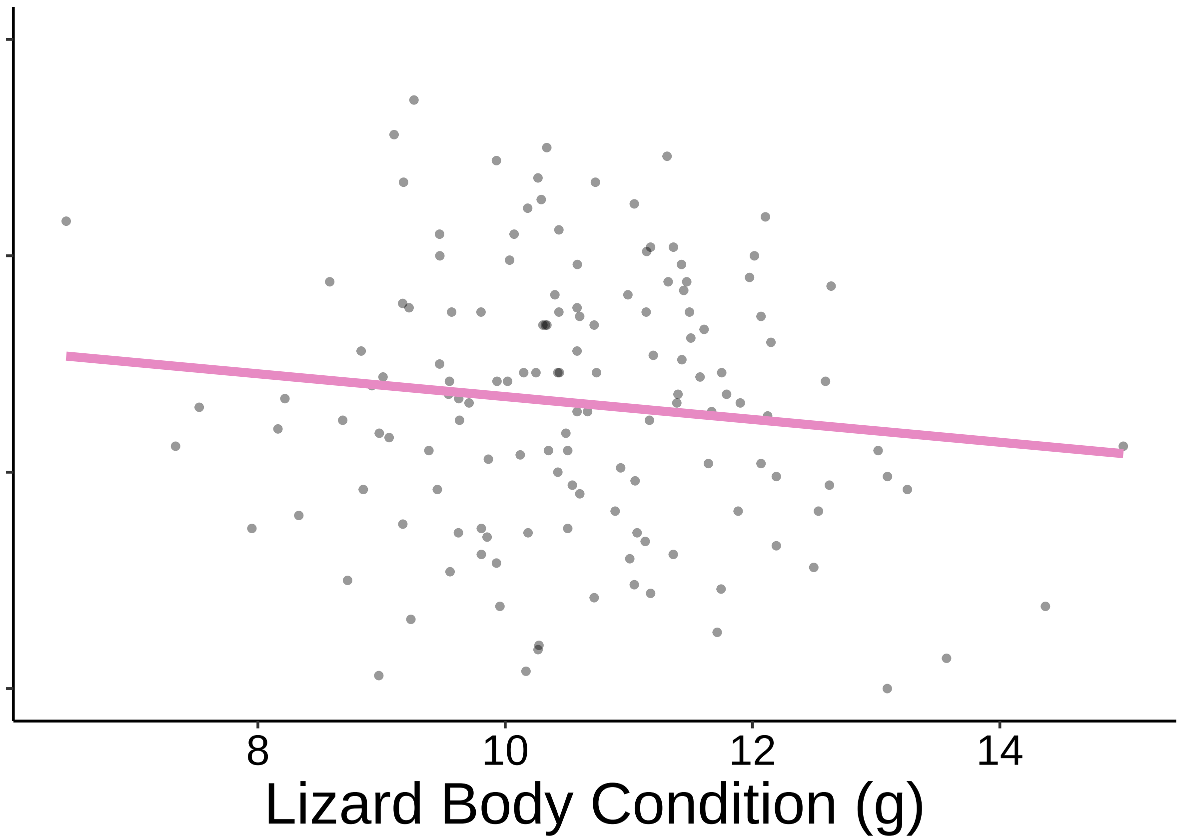
Osml ~ SMI

```
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),
```

```r
        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

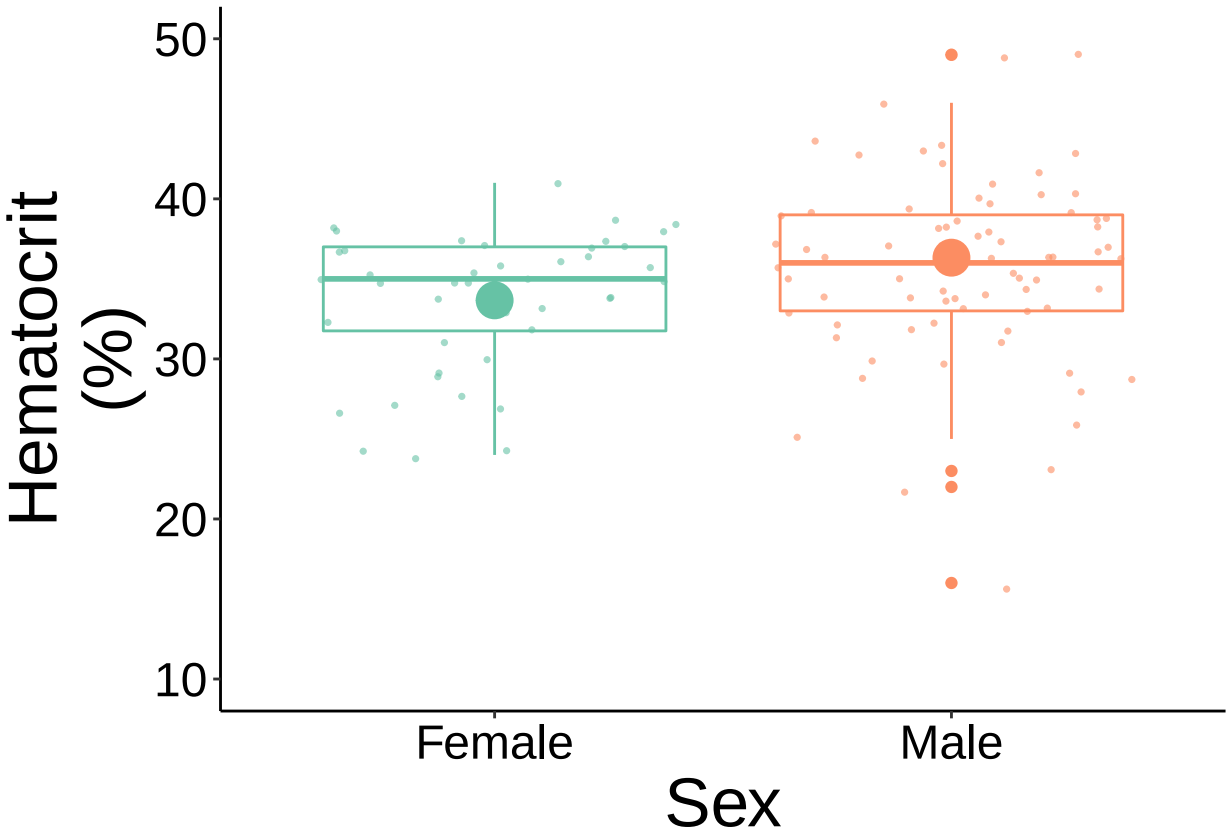
males have significantly higher hematocrit %

```r
# 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)
```

```r
# 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))
```

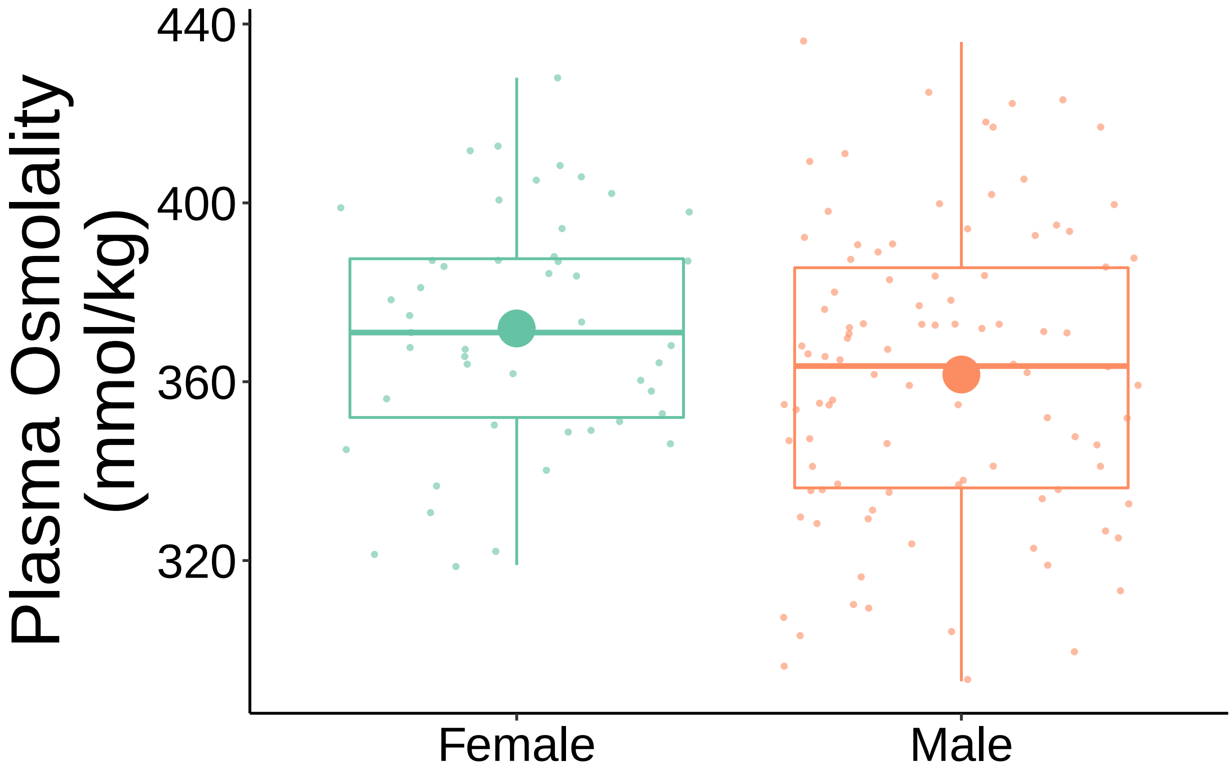
```
## `summarise()` ungrouping output (override with `.groups` argument)
```

```
# 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).
```

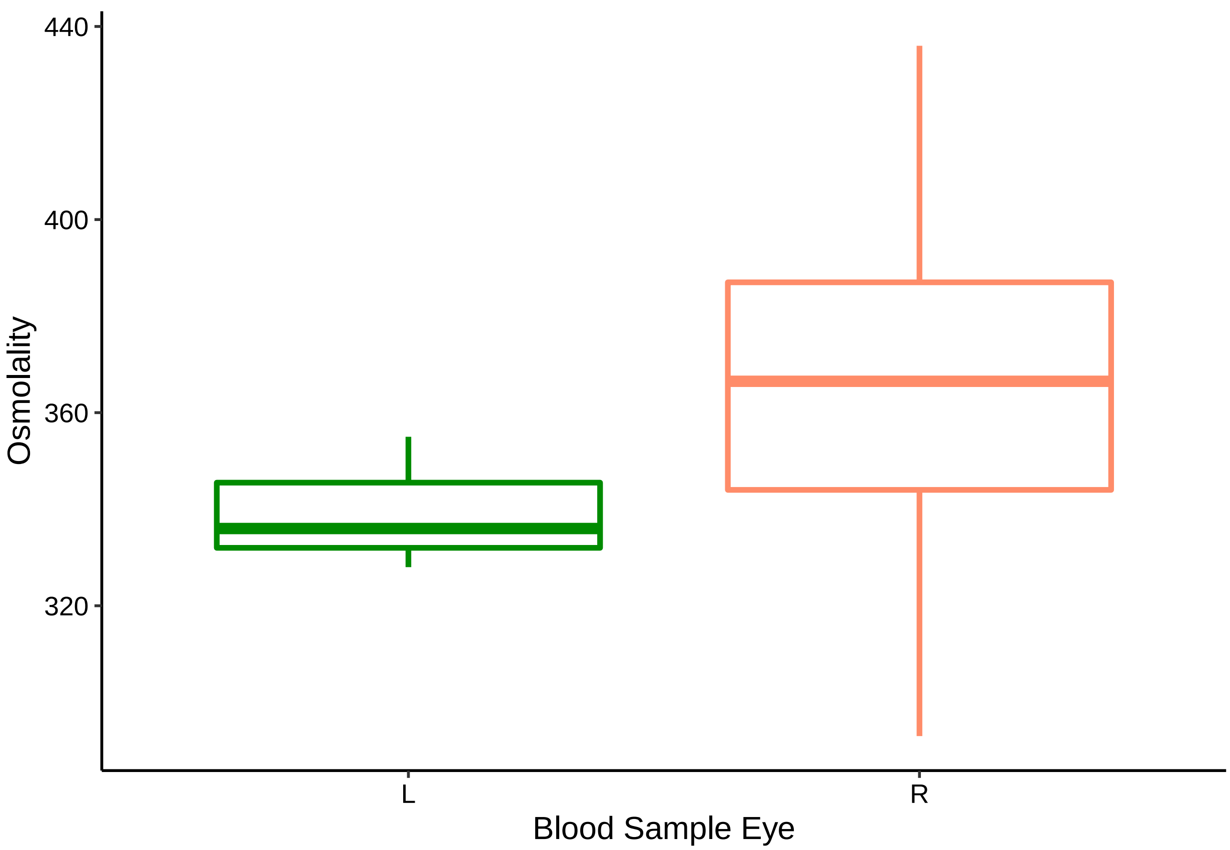
```
## Warning: Removed 3 rows containing missing values (geom_point).
```



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).
```

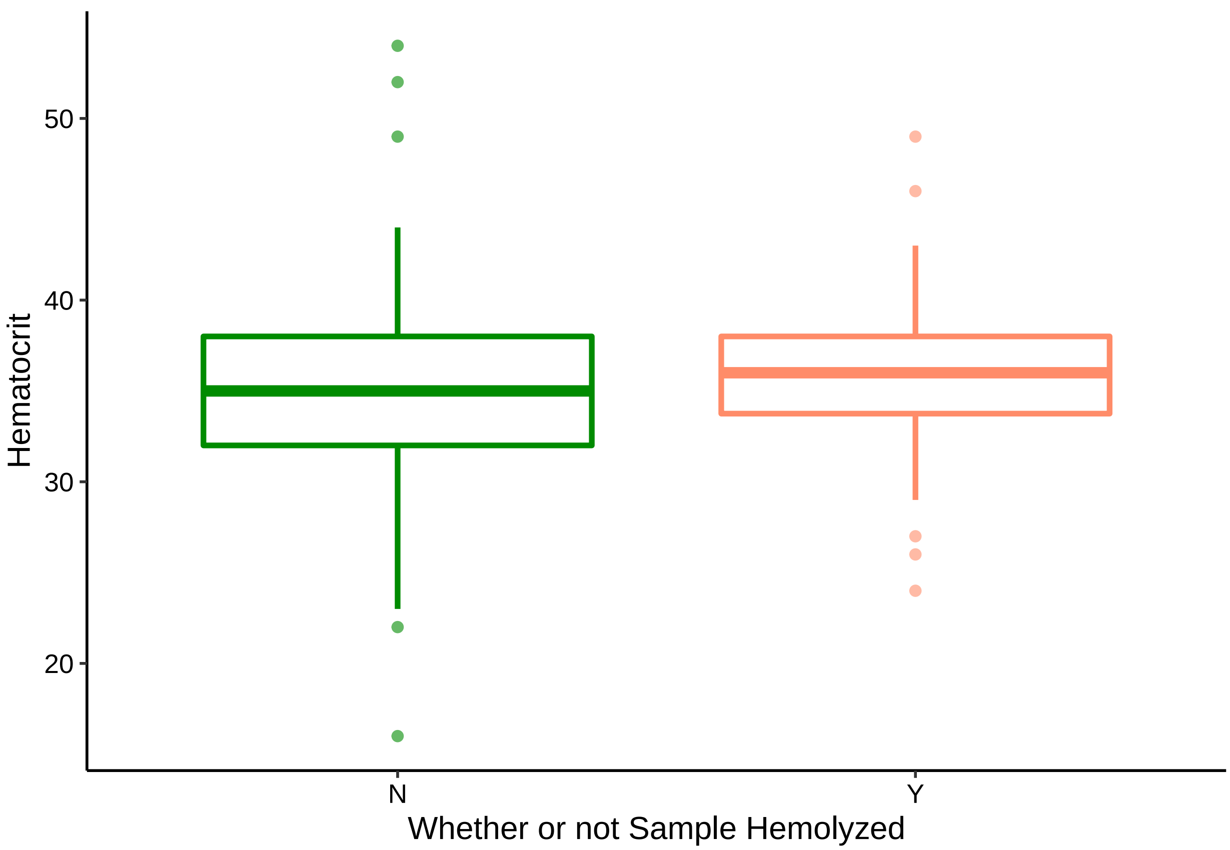


There IS a significant difference, but upon further inspection, the number of blood draws taken from the right postorbital sinus vs left or both is so uneven, this would be unhelpful in the actual model.

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).
```

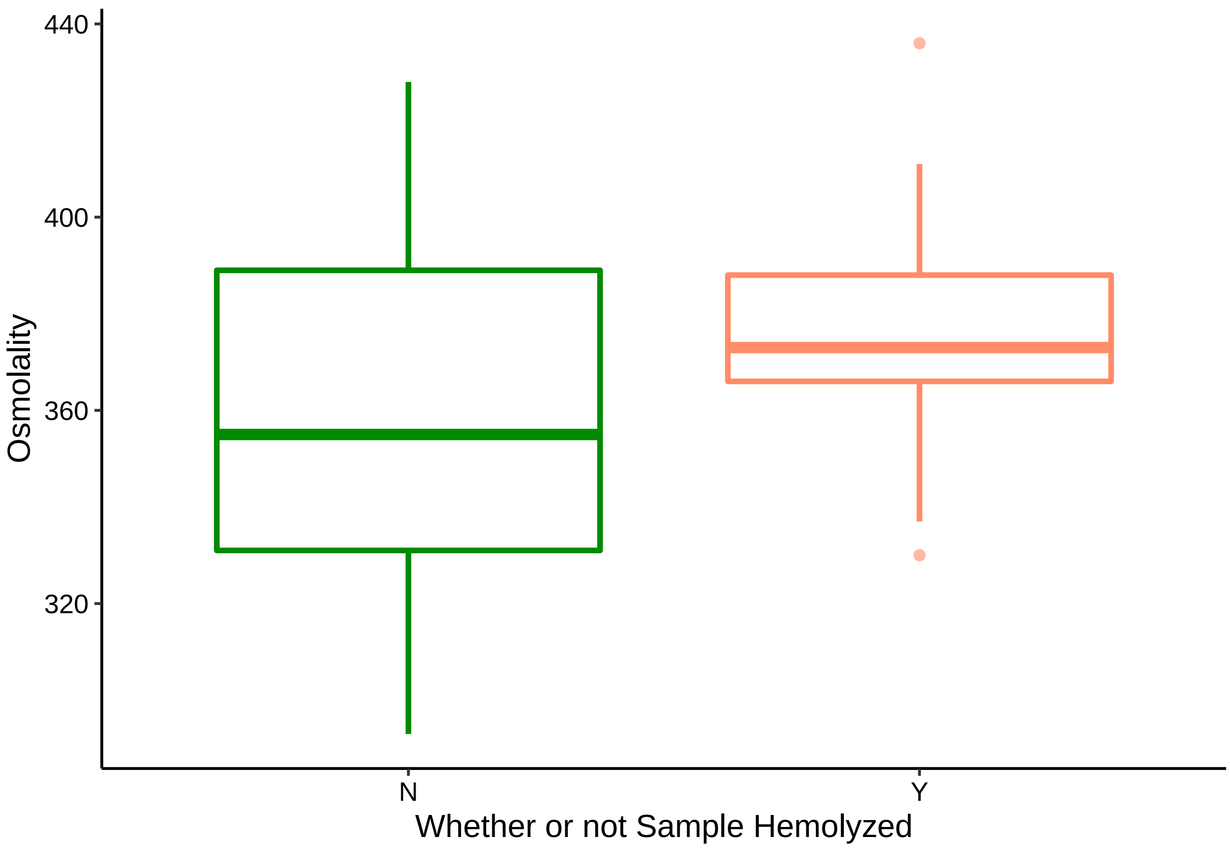


Osml ~ Hemolyzed/Not

```
morpho_blood_SMI %>%
  dplyr::filter(hemolyzed %in% c("Y", "N")) %>%
```

```r
  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).
```



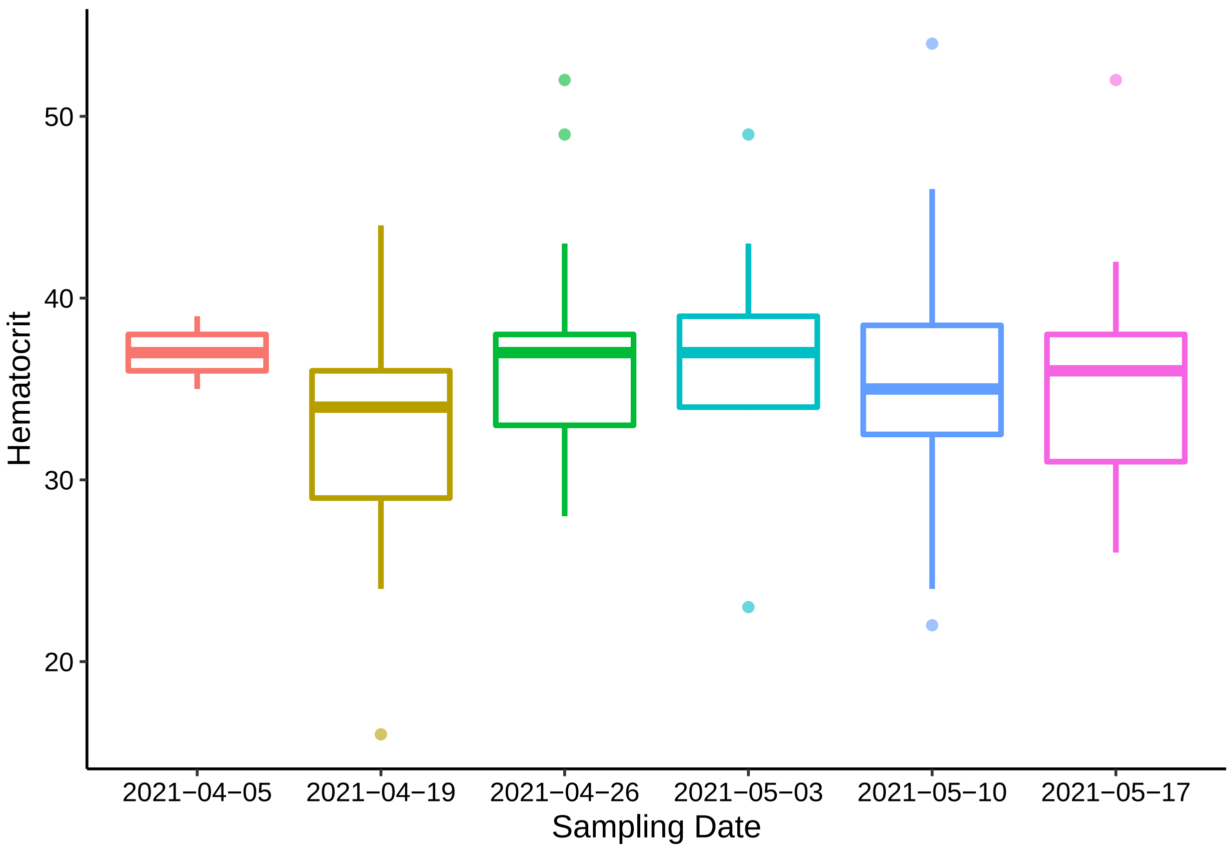
Osmolality in hemolyzed samples versus not are significantly different! This is an unfortunate trait of the dataset, and not something we are specifically interested in testing, so we will include it as a random factor in the LMM.

Hct ~ Week

```r
morpho_blood_SMI %>%
  ggplot(data = .) +
```

```r
  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

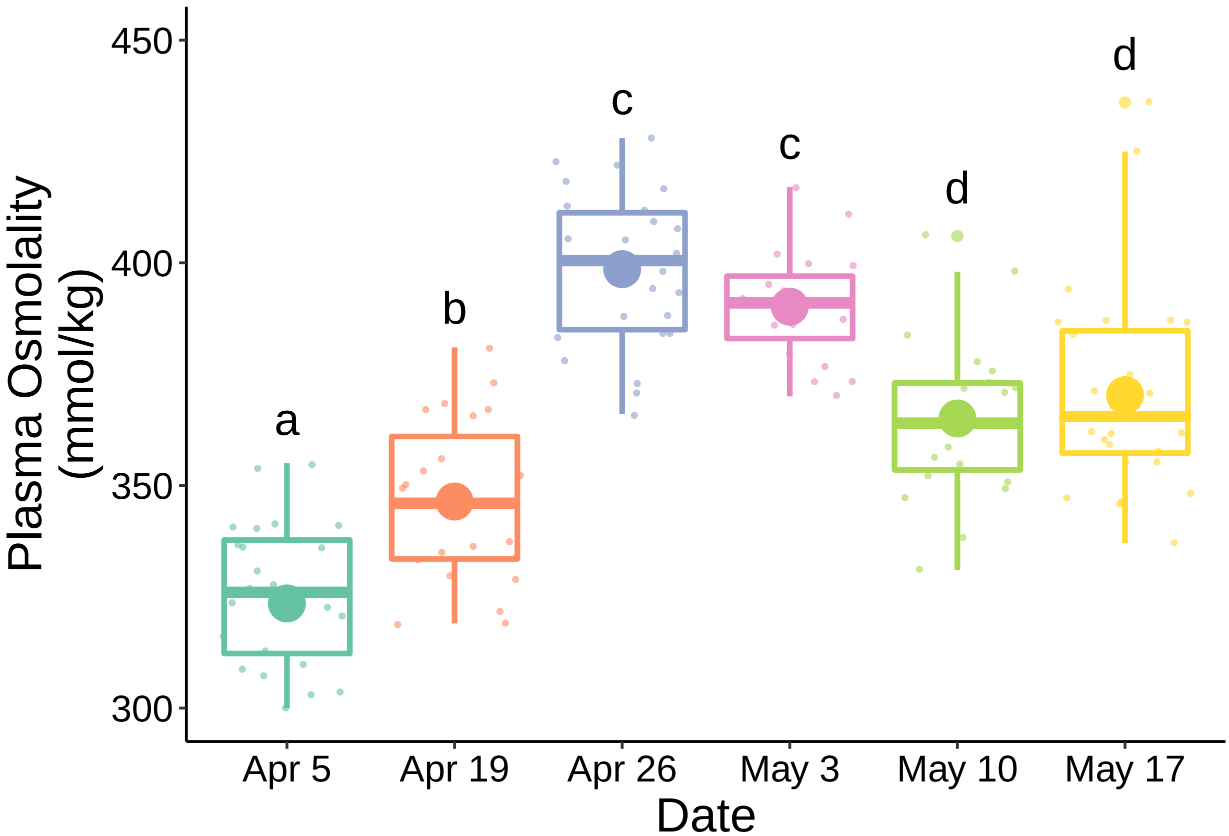
```r
# calculate means to overlay
weekly_means <- morpho_blood_SMI %>%
  dplyr::filter(complete.cases(osmolality_mmol_kg)) %>%
  group_by(d = as.factor(date)) %>%
  summarise(mean_osml = mean(osmolality_mmol_kg))
```

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

```r
# 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).
```




```r
# 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 6 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:

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

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = osmolality_mmol_kg ~ as.factor(date), data = morpho_blood_SMI)
##
## $`as.factor(date)`
##                              diff        lwr        upr     p adj
## 2021-04-19-2021-04-05   22.891304   7.979417  37.803191 0.0002634
```

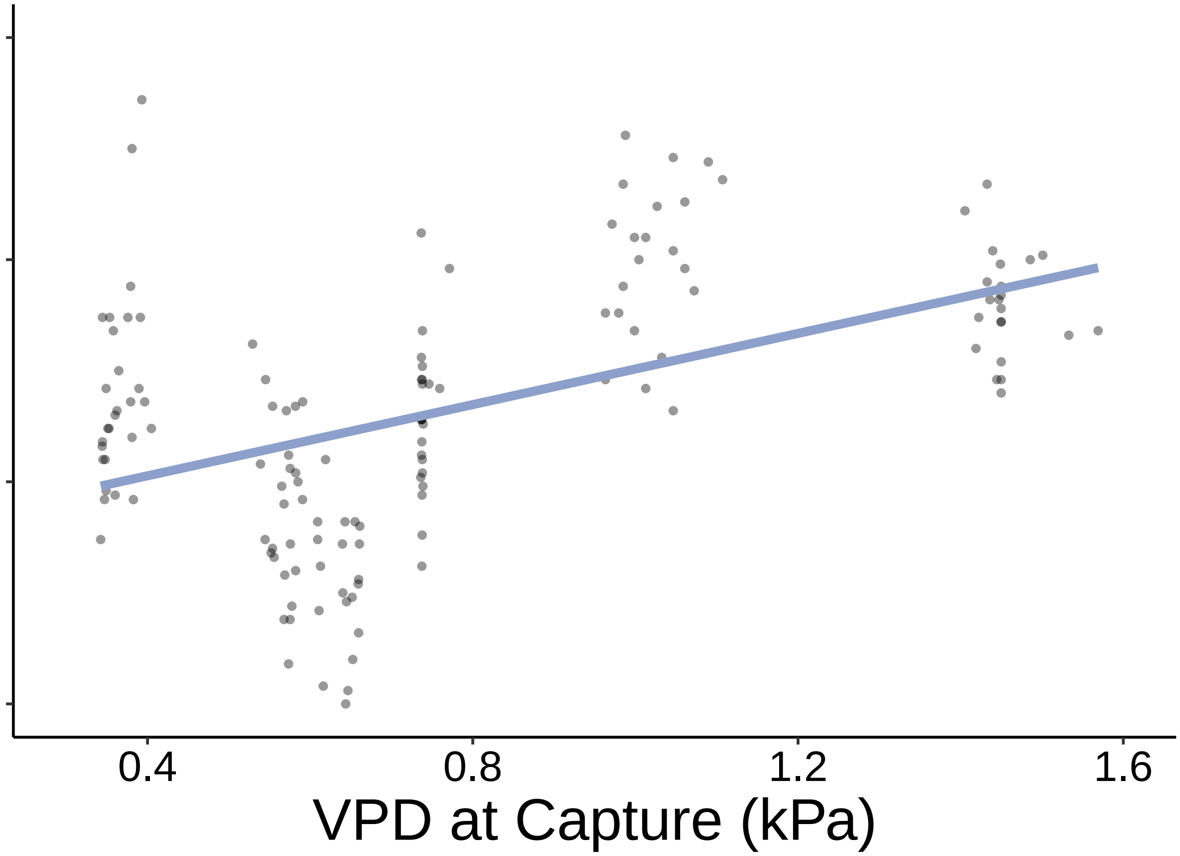
```
## 2021-04-26-2021-04-05  75.076923  60.628732  89.525114 0.0000000
## 2021-05-03-2021-04-05  66.657895  50.935165  82.380624 0.0000000
## 2021-05-10-2021-04-05  41.543478  26.631591  56.455365 0.0000000
## 2021-05-17-2021-04-05  46.785714  32.597872  60.973557 0.0000000
## 2021-04-26-2021-04-19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

Osml ~ VPD

```r
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).
```



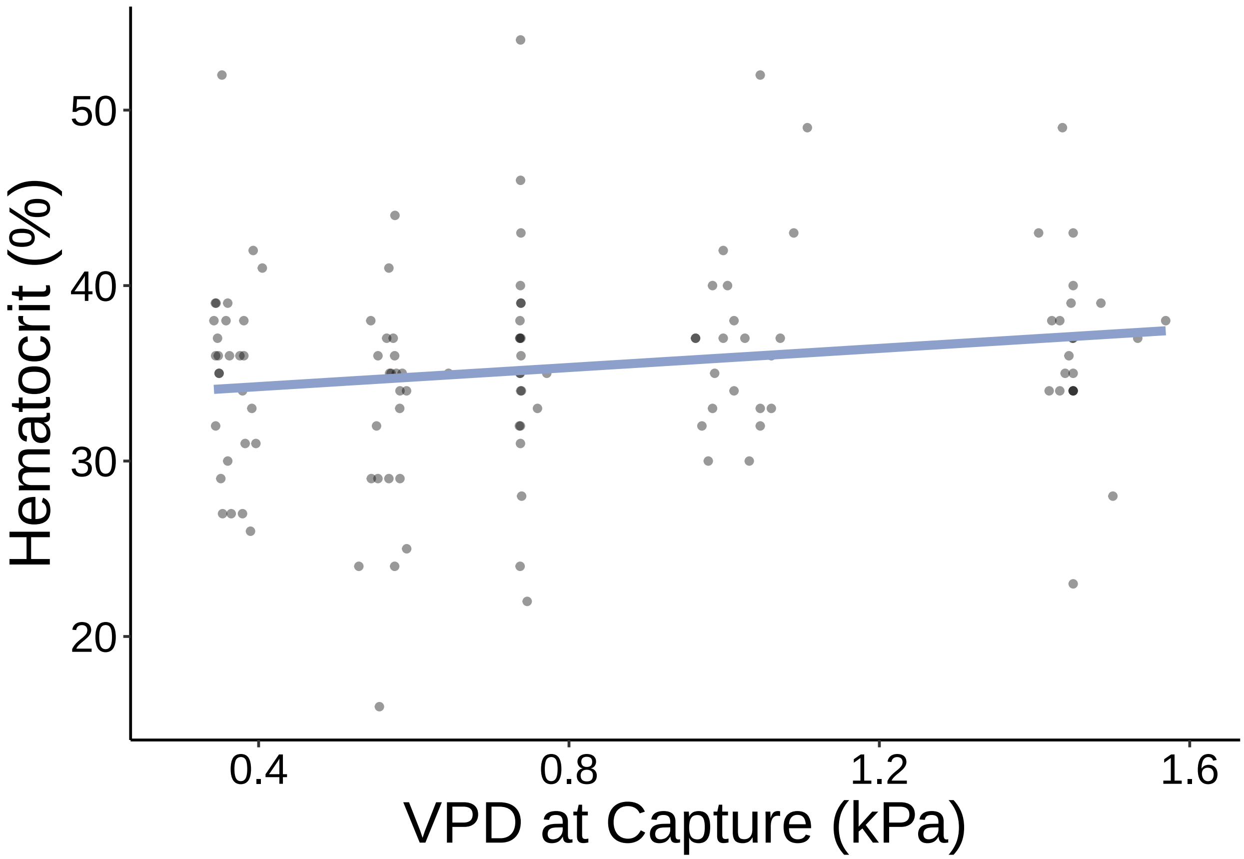
Hct ~ VPD

```
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).
```



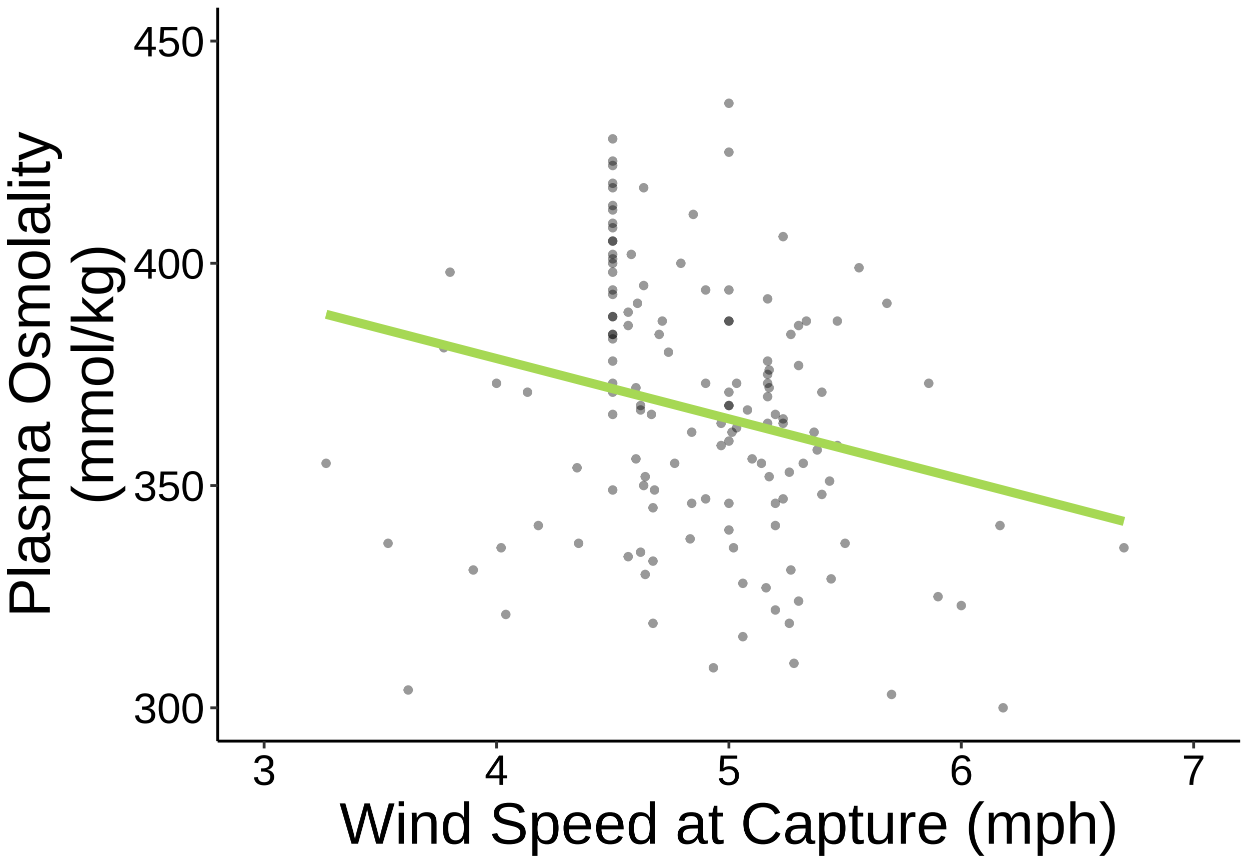
Osml ~ Wind

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

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

```r
  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)
```

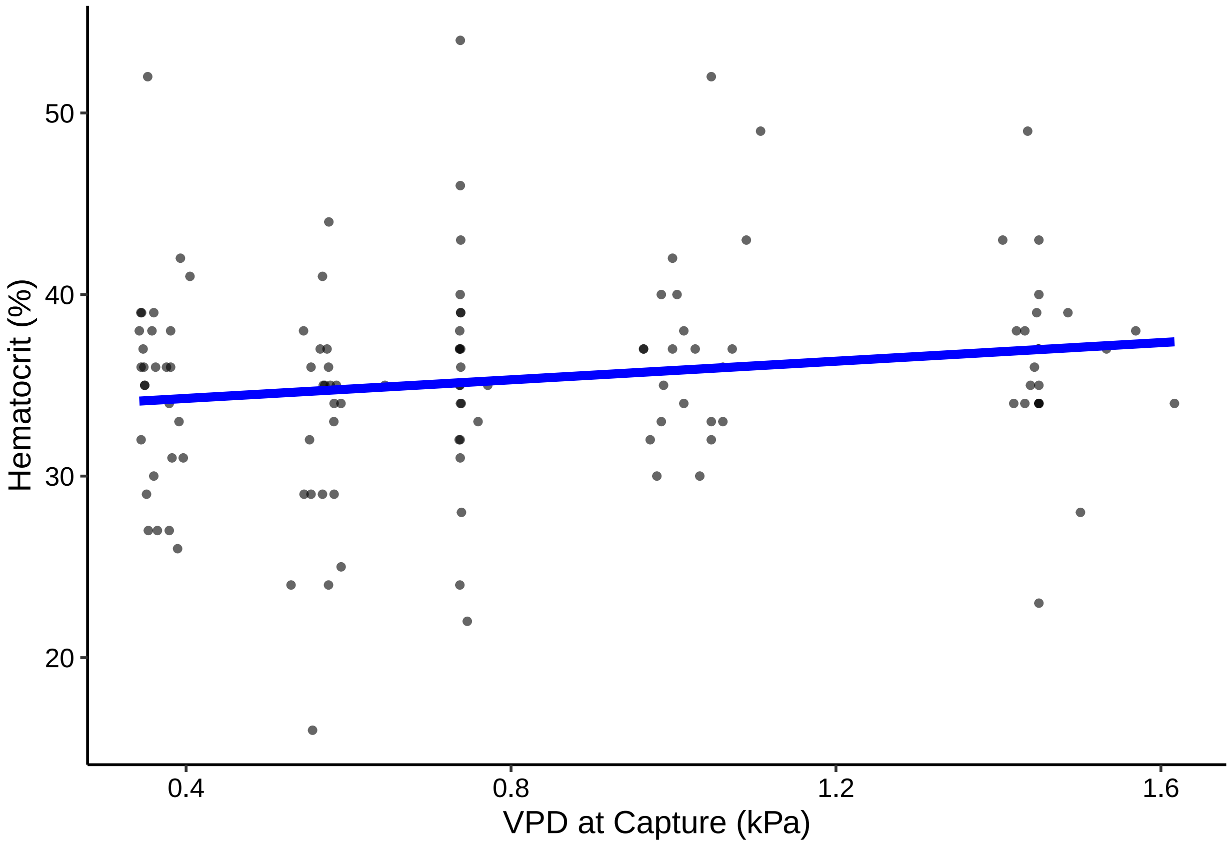
Hct ~ VPD

```
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() +
```

```r
  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).
```



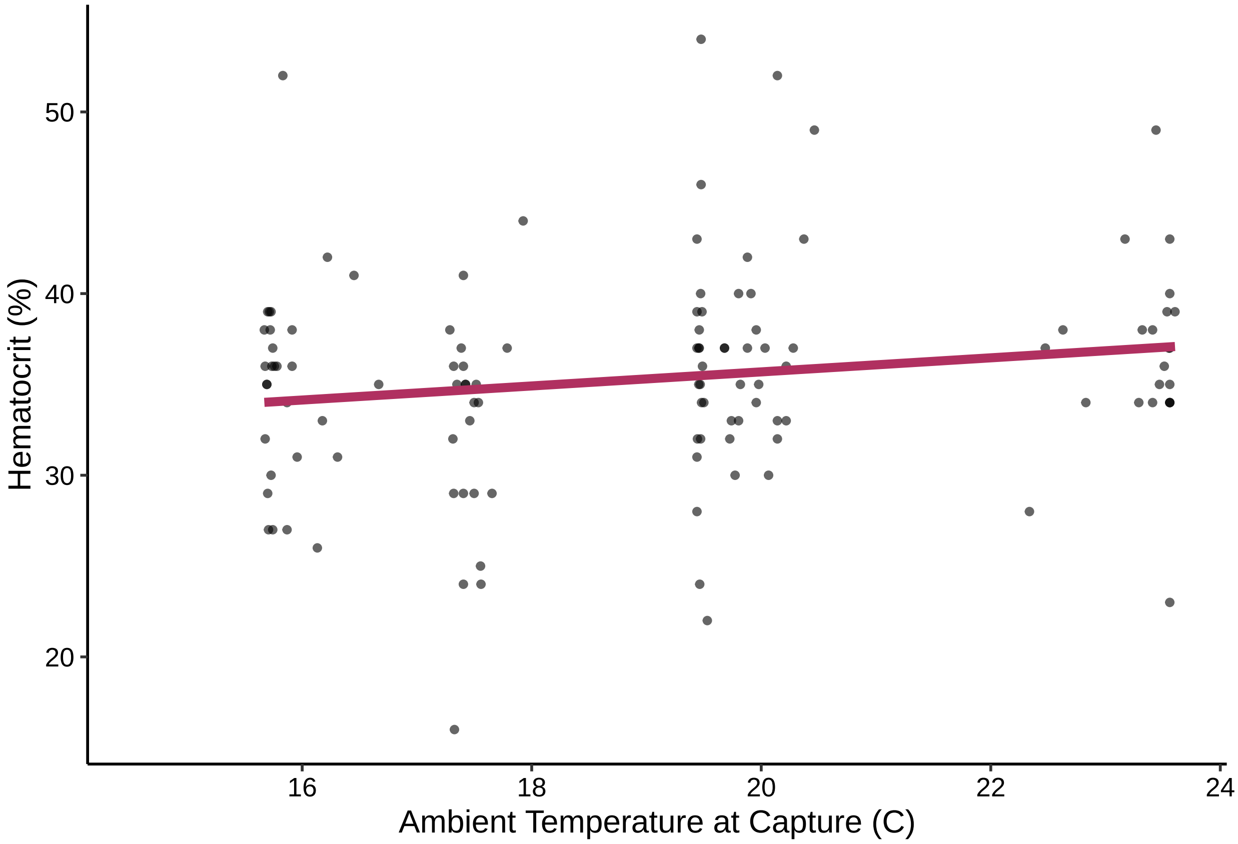
Hct ~ Temperature

```r
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",
```

```r
              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).
```



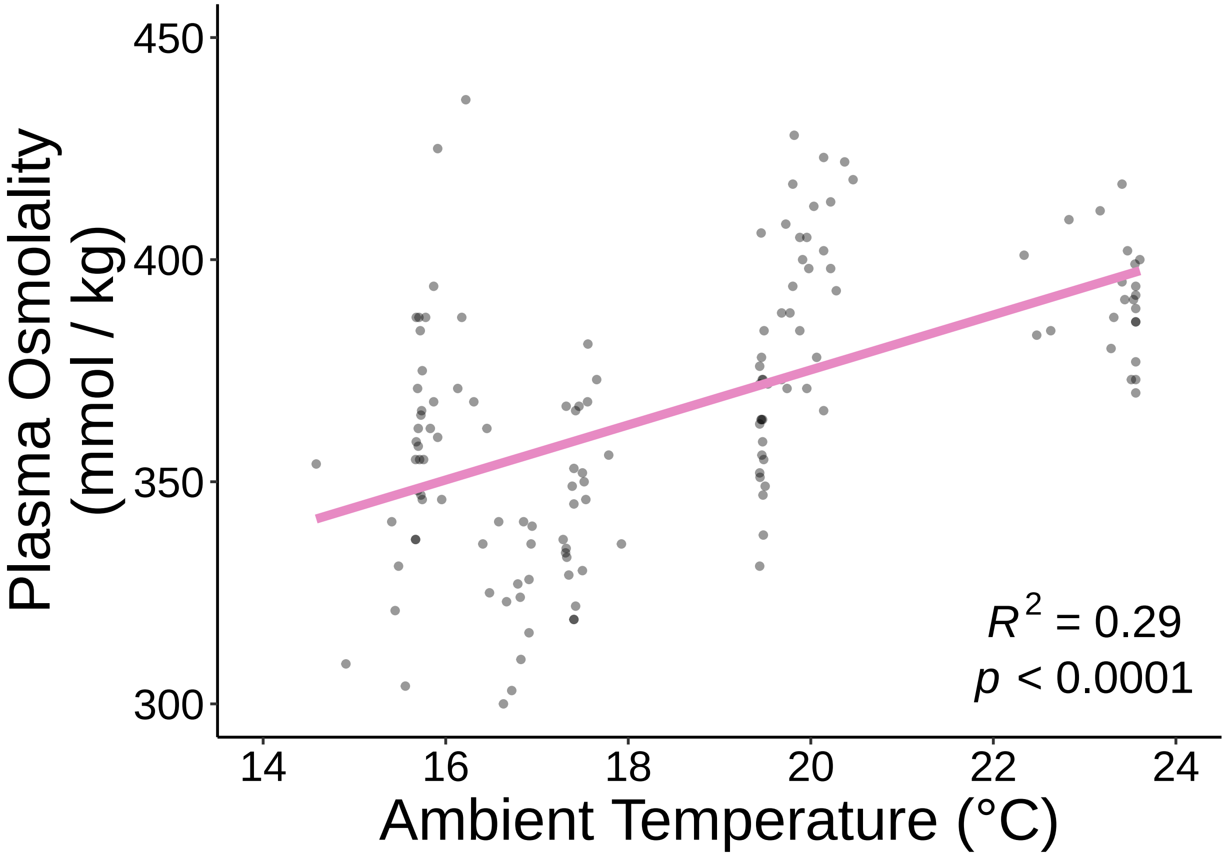
Osml ~ Temperature

```r
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)
```

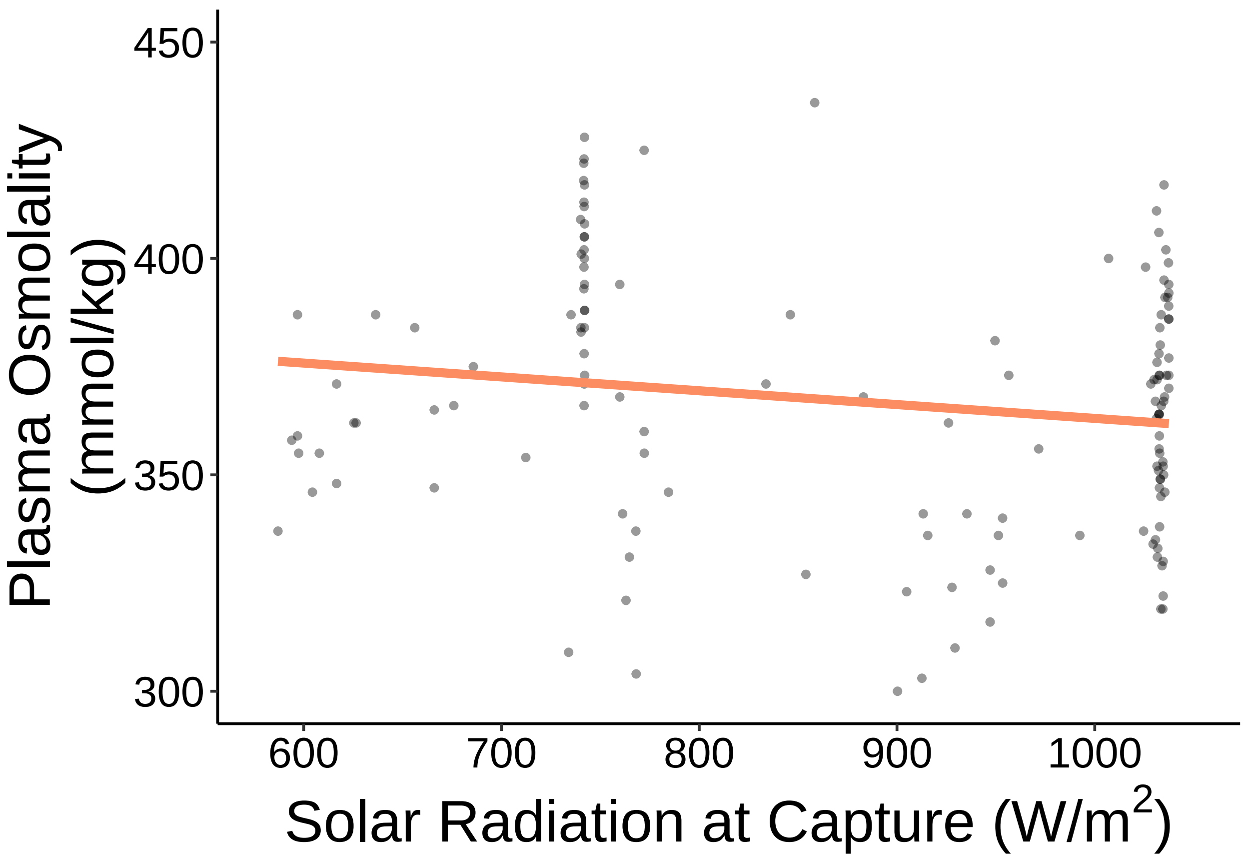
Osml ~ Solar Radiation

```
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).
```

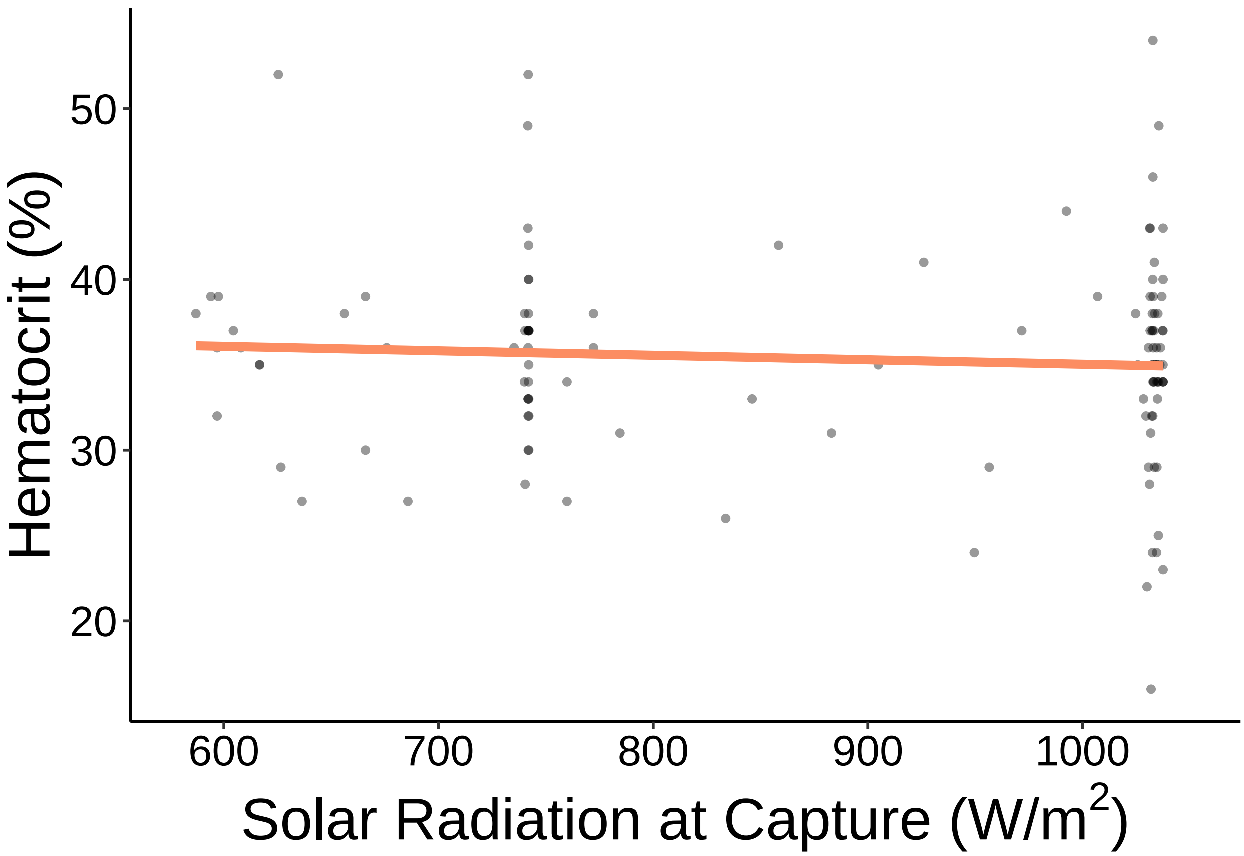
```
## Warning: Removed 7 rows containing missing values (geom_point).
```



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).
```

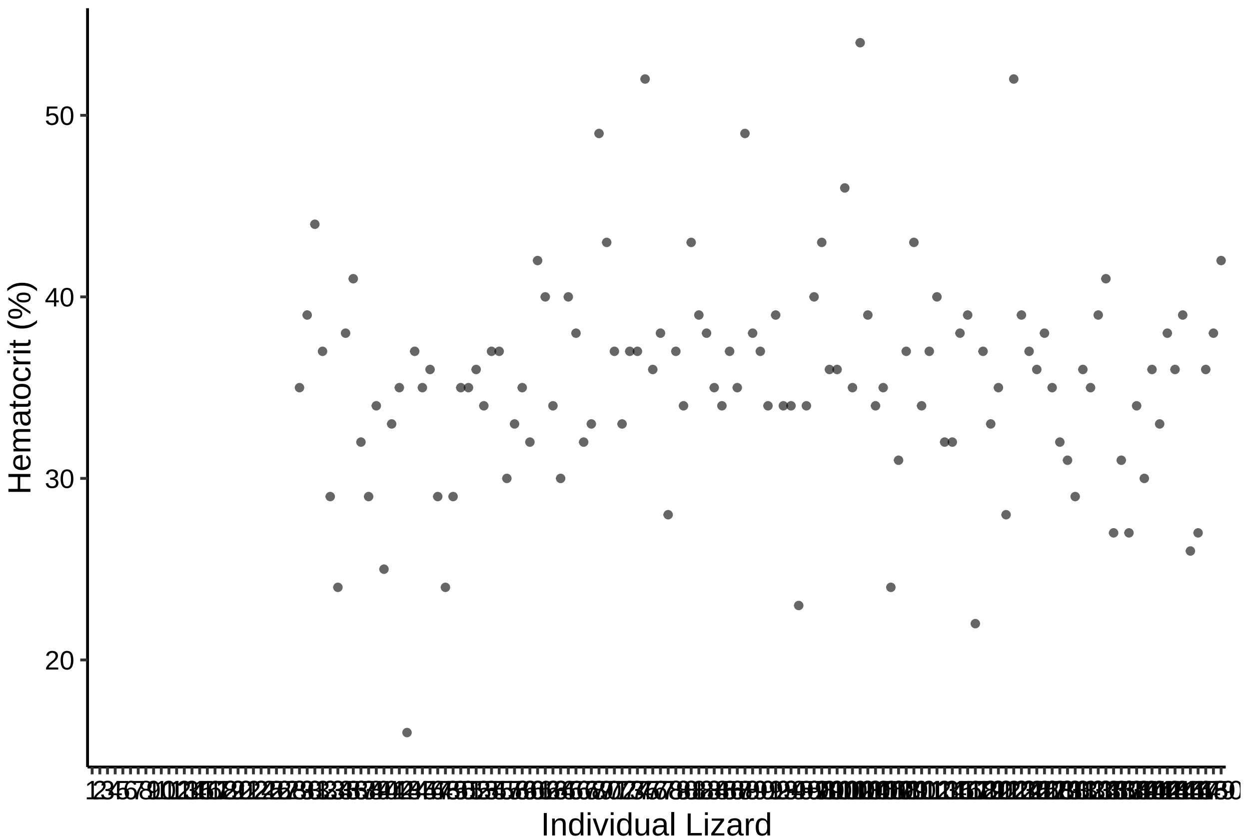


Hct ~ Individual

```
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).
```

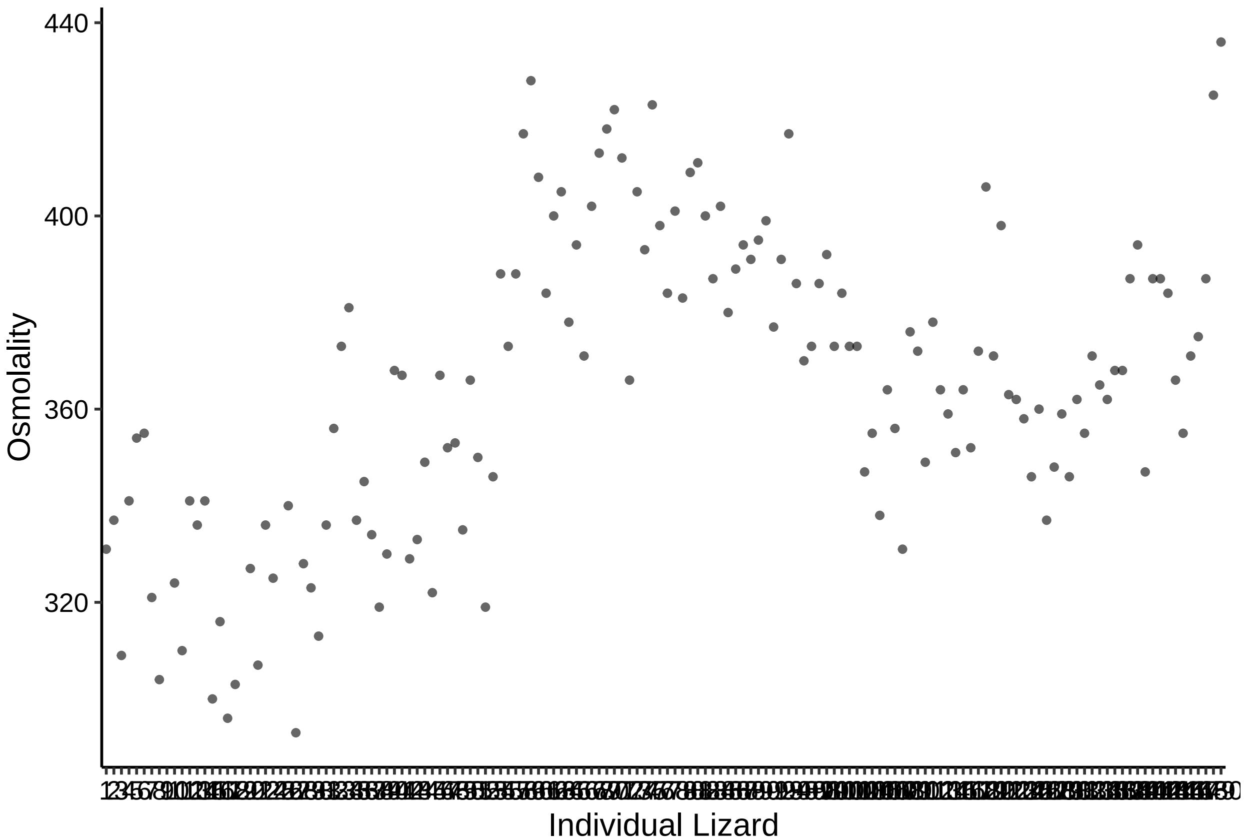


Osml ~ Individual

```
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") +
```

```r
  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

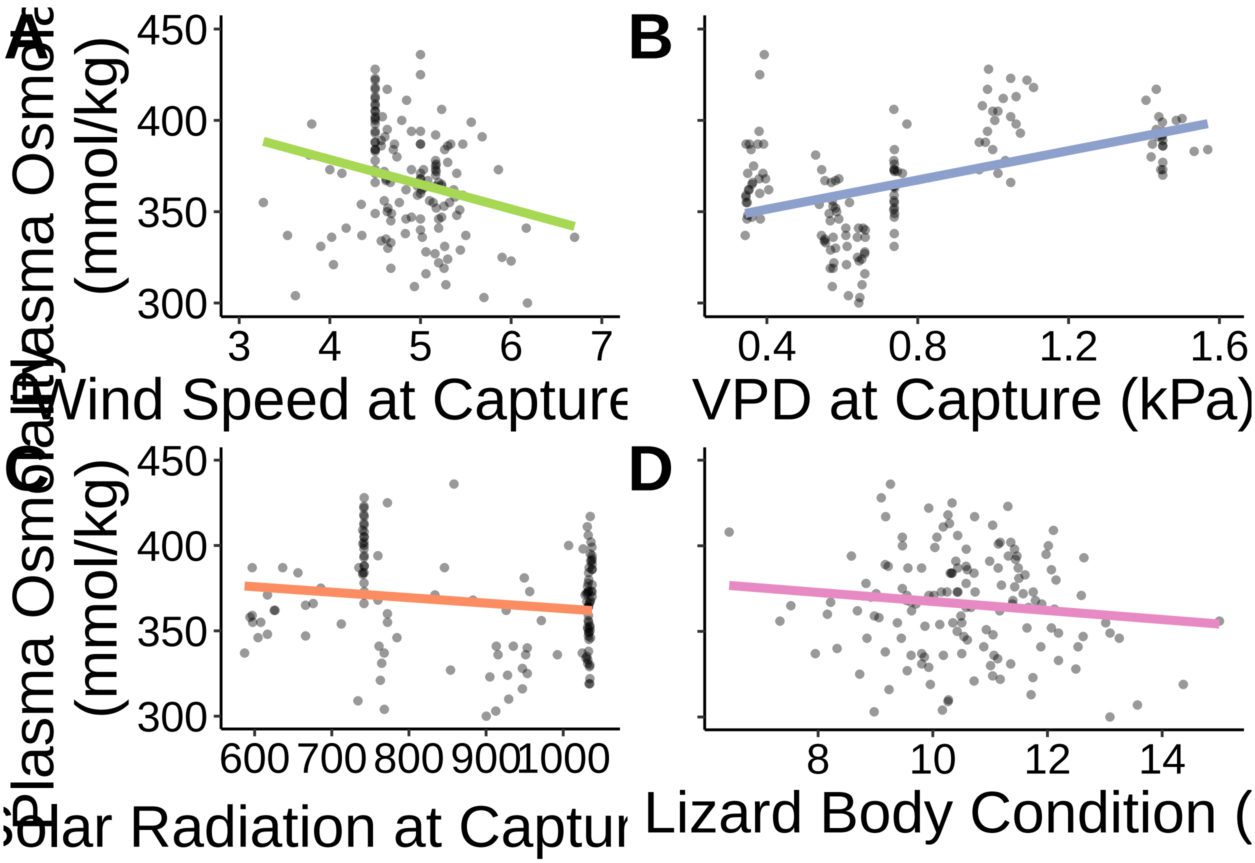
Based on reviewer comments & model revisions, this should include: VPD, wind, and sorad at capture, body condition, and sex. I'll do the 4 continuous variables in one multi-fig, then do the fig for sex separately bc its categorical.

```r
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

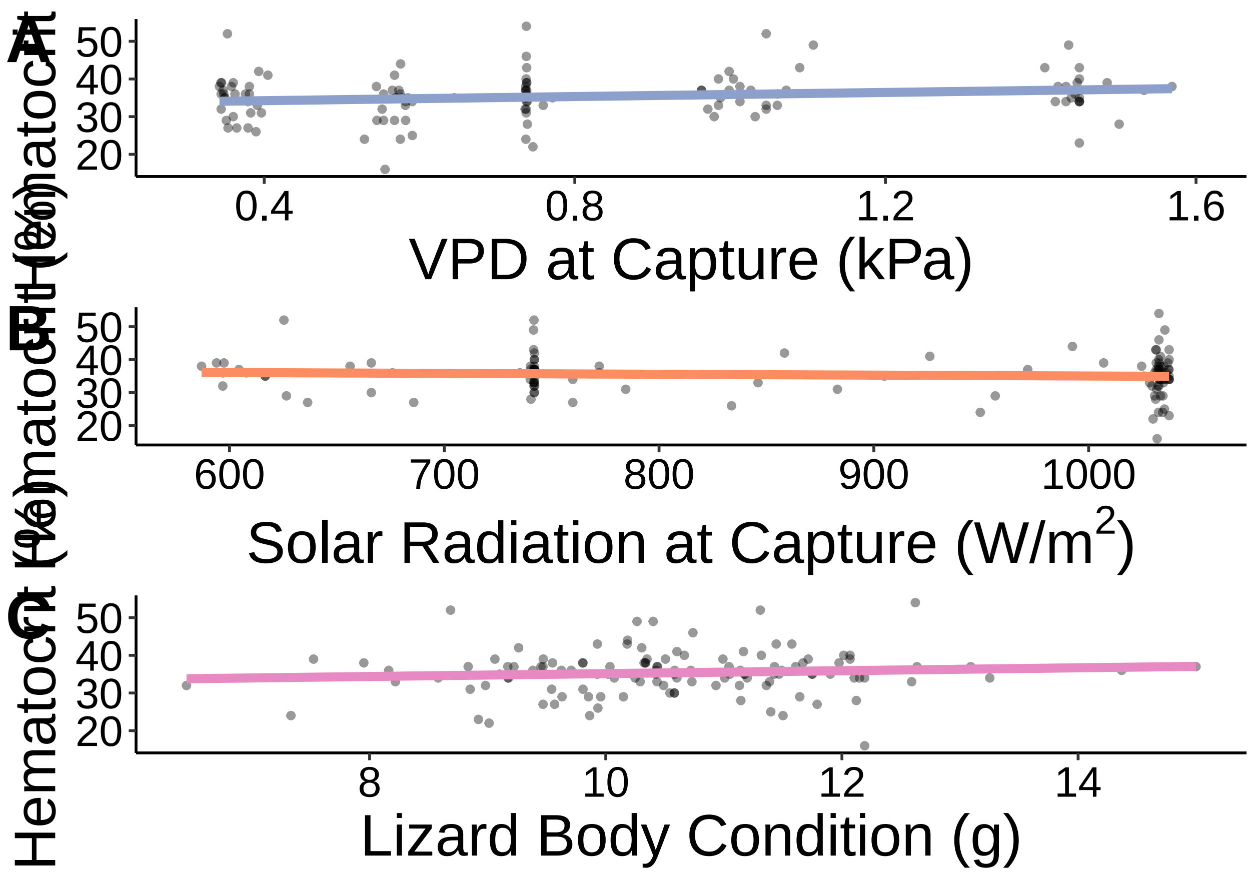
VPD, sorad, body condition, and sex should be plotted. I'm doing ~sex jointly with osmolality, which leaves the 3 continuous variables. hct_vpd_fig

```
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
```



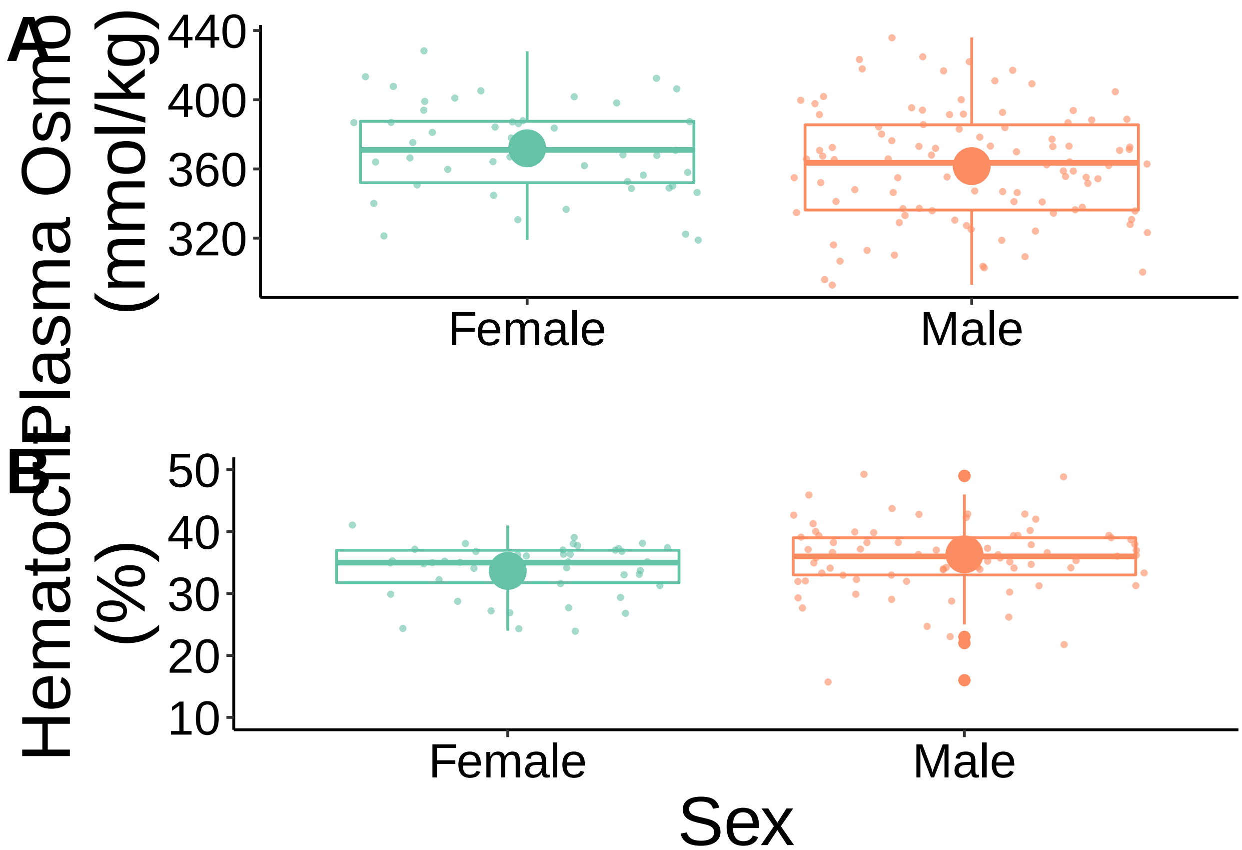

```
# export figure
ggsave(filename = "hct_multi_fig.jpeg",
       plot = hct_multi_fig,
       path = "./final_figures",
       device = "jpeg",
       dpi = 1200,
       width = 6, height = 12)
```

Hct-Osml ~ Sex

```r
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).
```

```r
sex_multi_fig
```

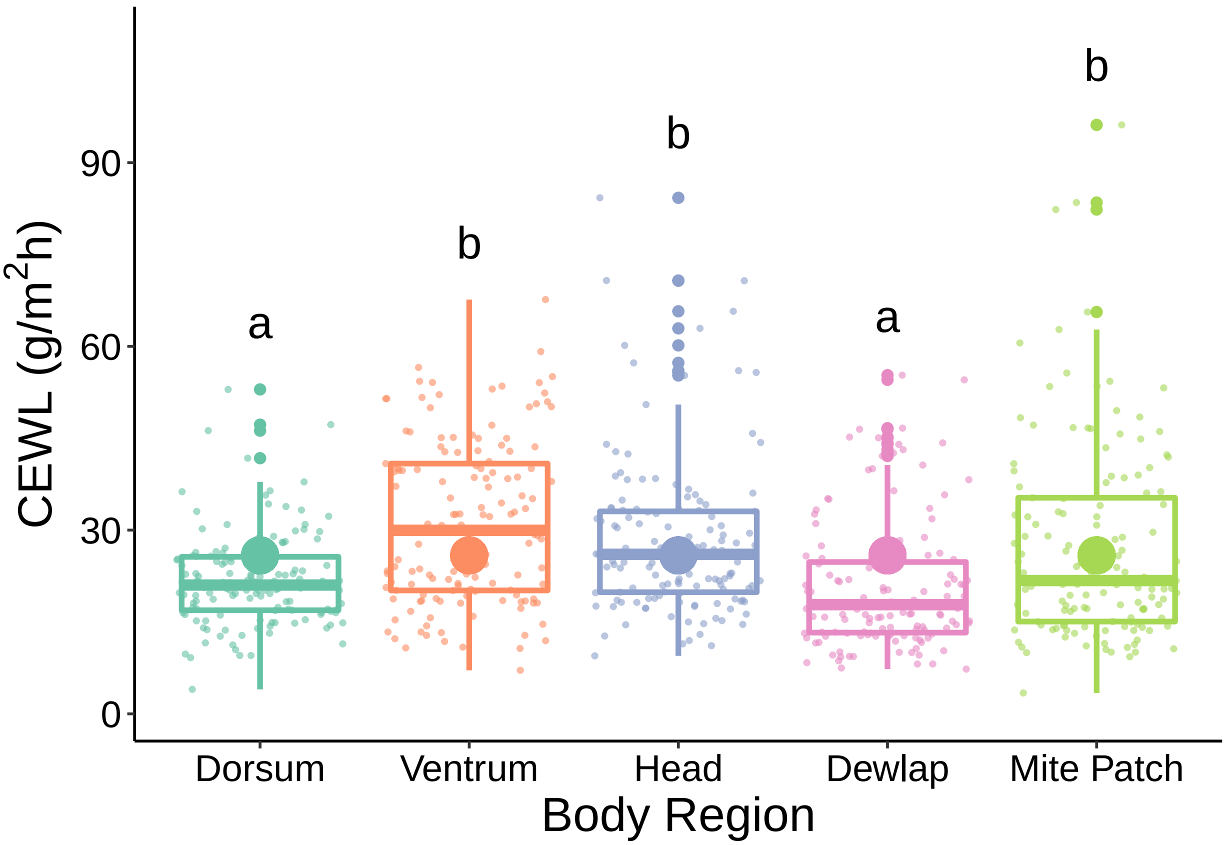



```r
# export figure
ggsave(filename = "sex_multi_fig.jpeg",
       plot = sex_multi_fig,
       path = "./final_figures",
       device = "jpeg",
       dpi = 1200,
       width = 5, height = 9)
```

evaporative water loss

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)
```

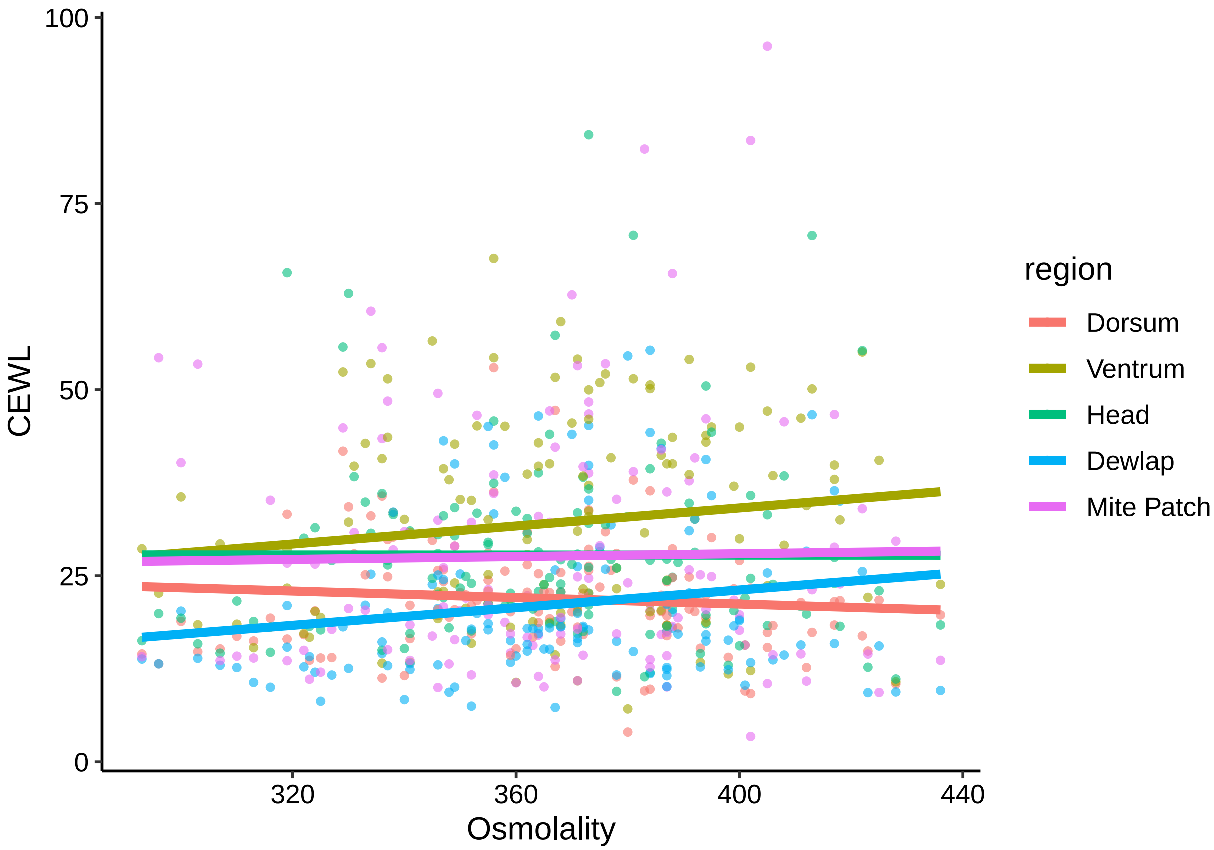
CEWL ~ Osmolality

```
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).
```

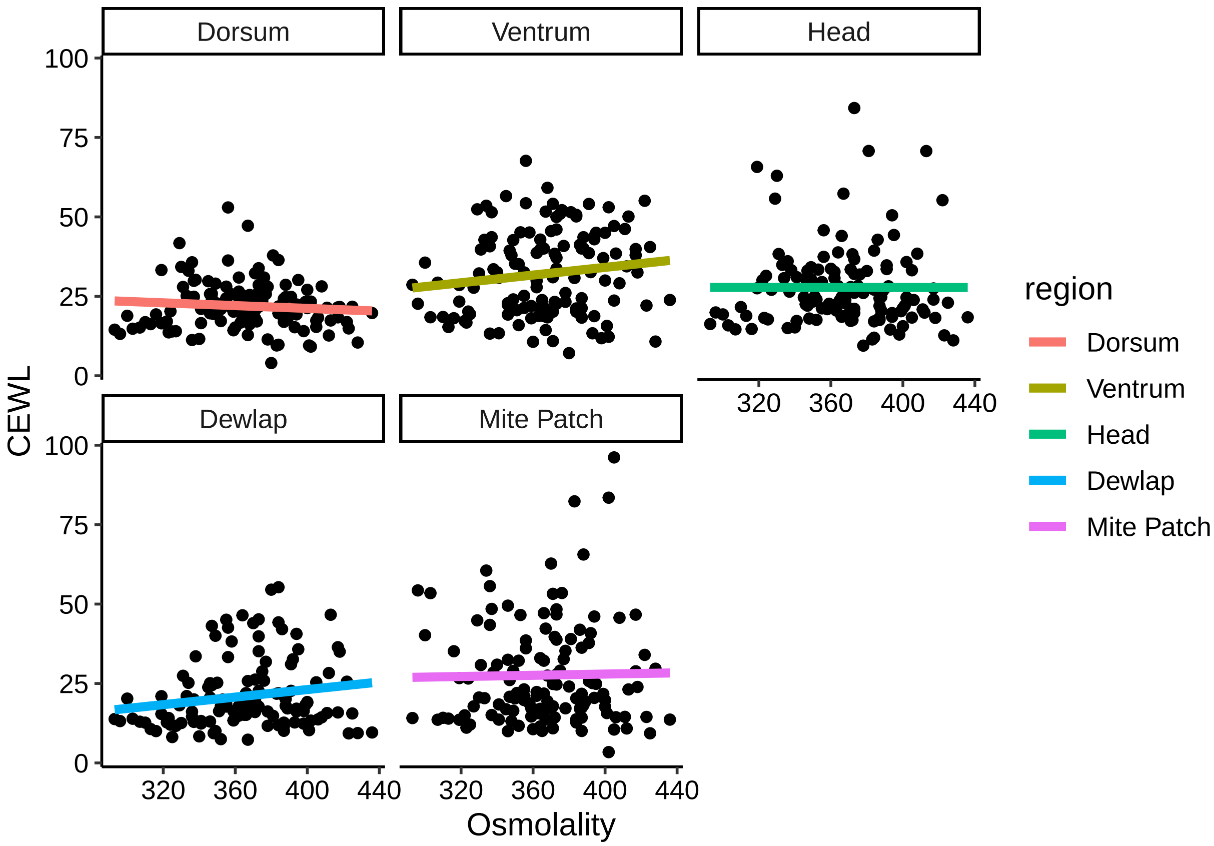



```
# Facet ggplot
ggplot(aes(osmolality_mmol_kg, TEWL_g_m2h), data = CEWL_data_full) +
  geom_point() +
  stat_smooth(aes(x = osmolality_mmol_kg,
                  y = TEWL_g_m2h,
                  color = region
                  ),
              formula = y ~ x,
              method = "lm",
              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).
```



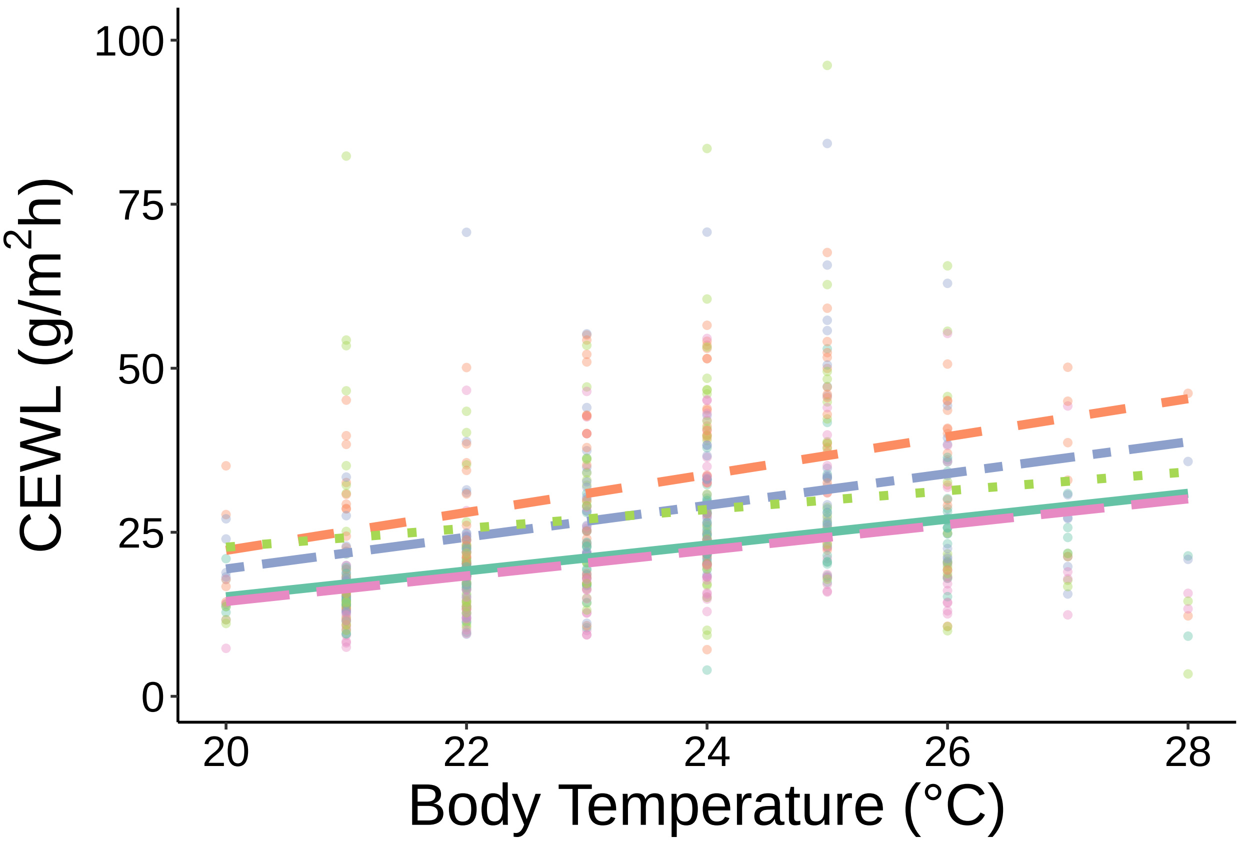
CEWL ~ Cloacal Temperature

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

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

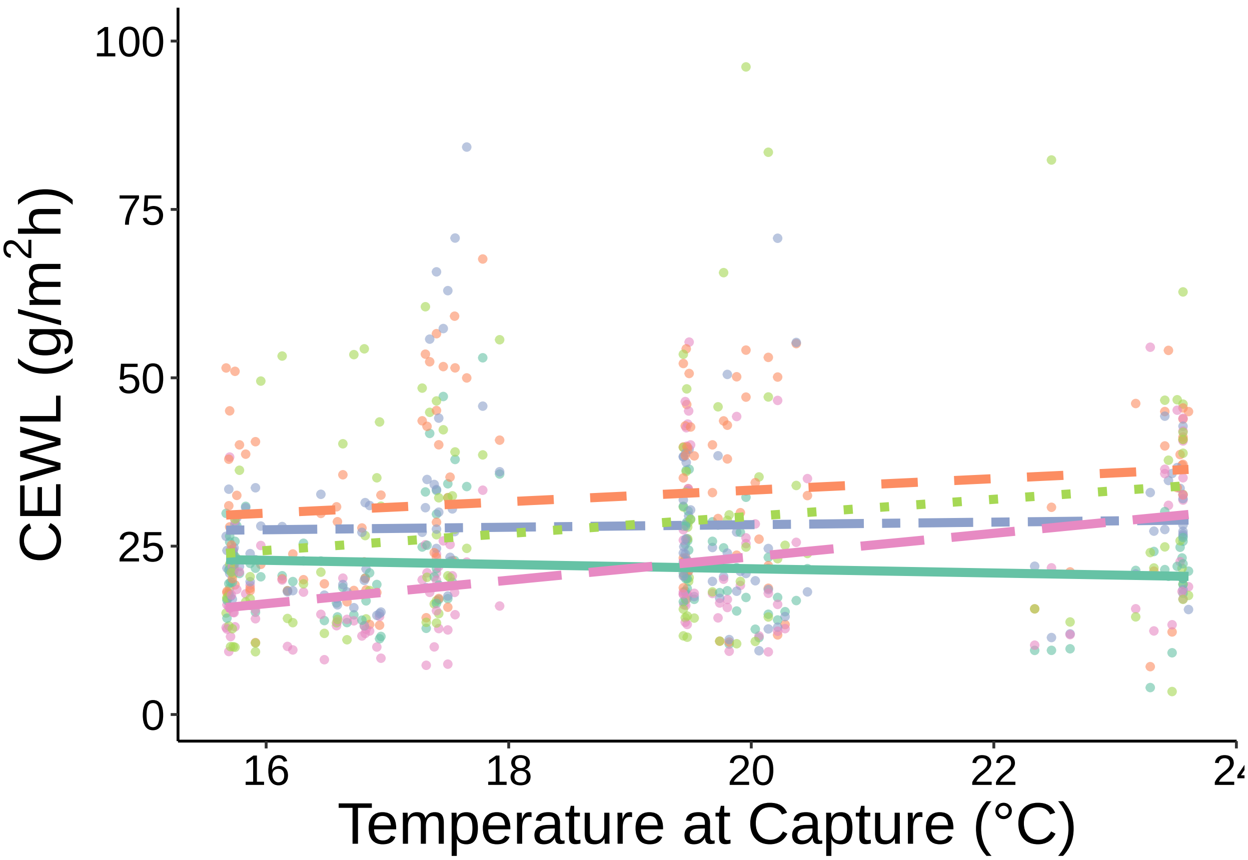
CEWL ~ Capture Temperature

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

```r
              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/'*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"
) -> 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).
```



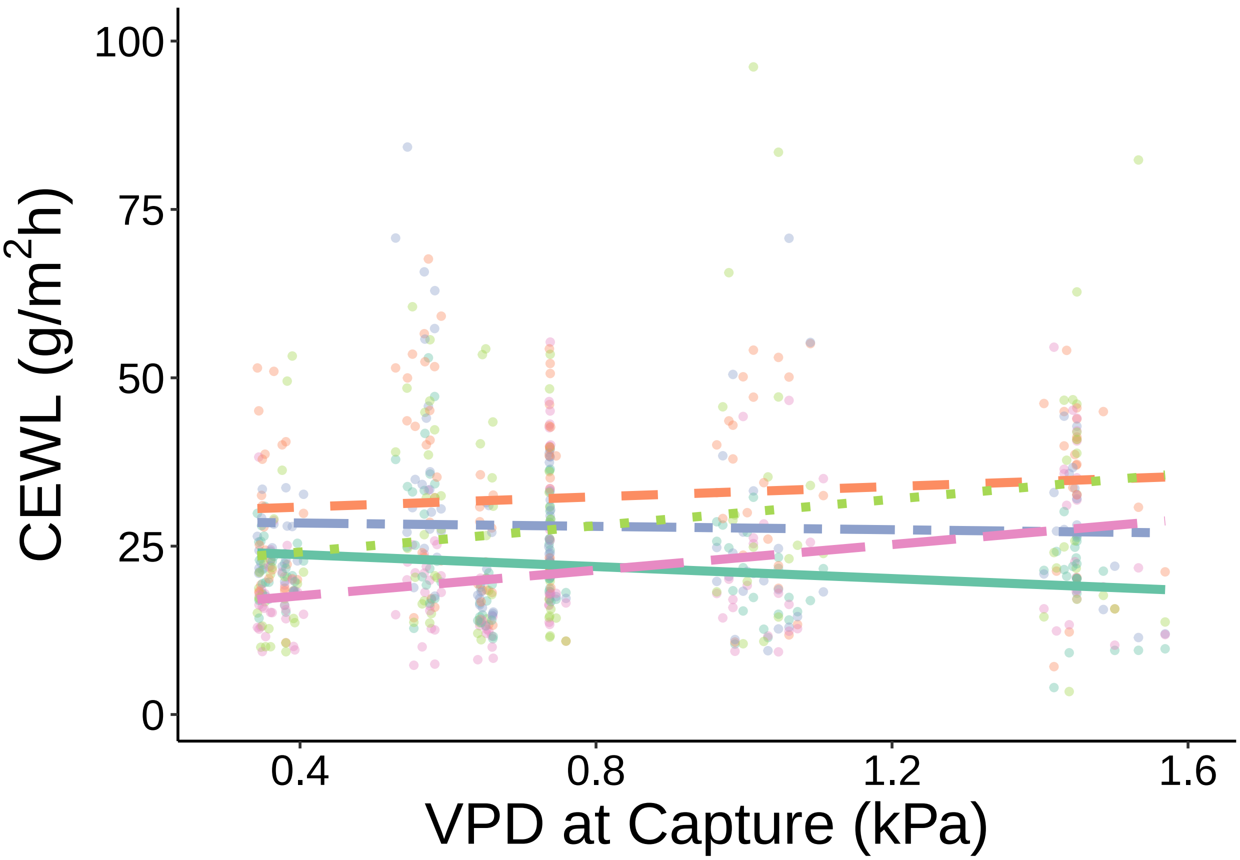
CEWL ~ Capture VPD

```
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/'*m^2*'h)')) +
  #ylab("") +
  scale_color_brewer(palette = "Set2",
                     name = "") +
```

```r
  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).
```



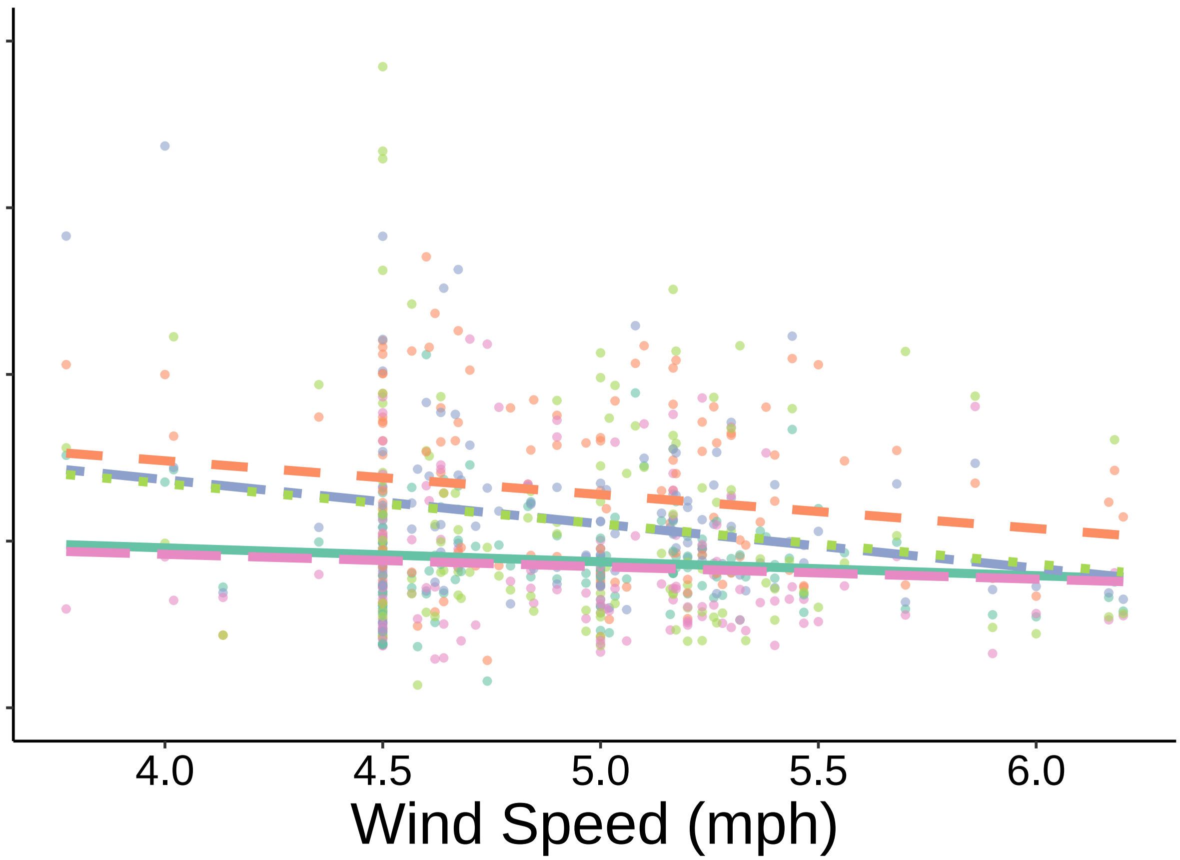

```
# export figure
#ggsave(filename = "CEWL_vpd_fig.tiff",
 #      plot = CEWL_vpd_fig,
  #     path = "./final_figures",
   #    device = "tiff",
    #   dpi = 1200,
     #  width = 6, height = 4)
```

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).
```



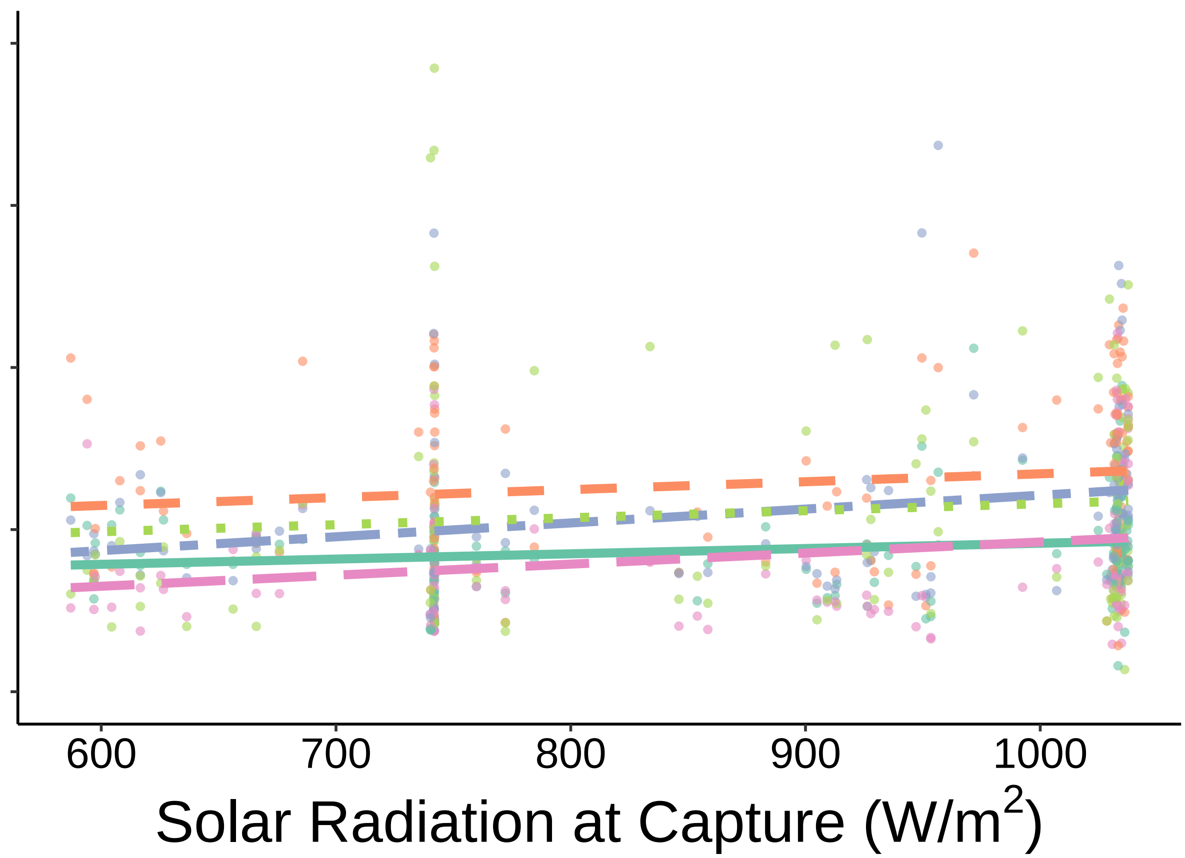
CEWL ~ Solar Rad

```
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
```

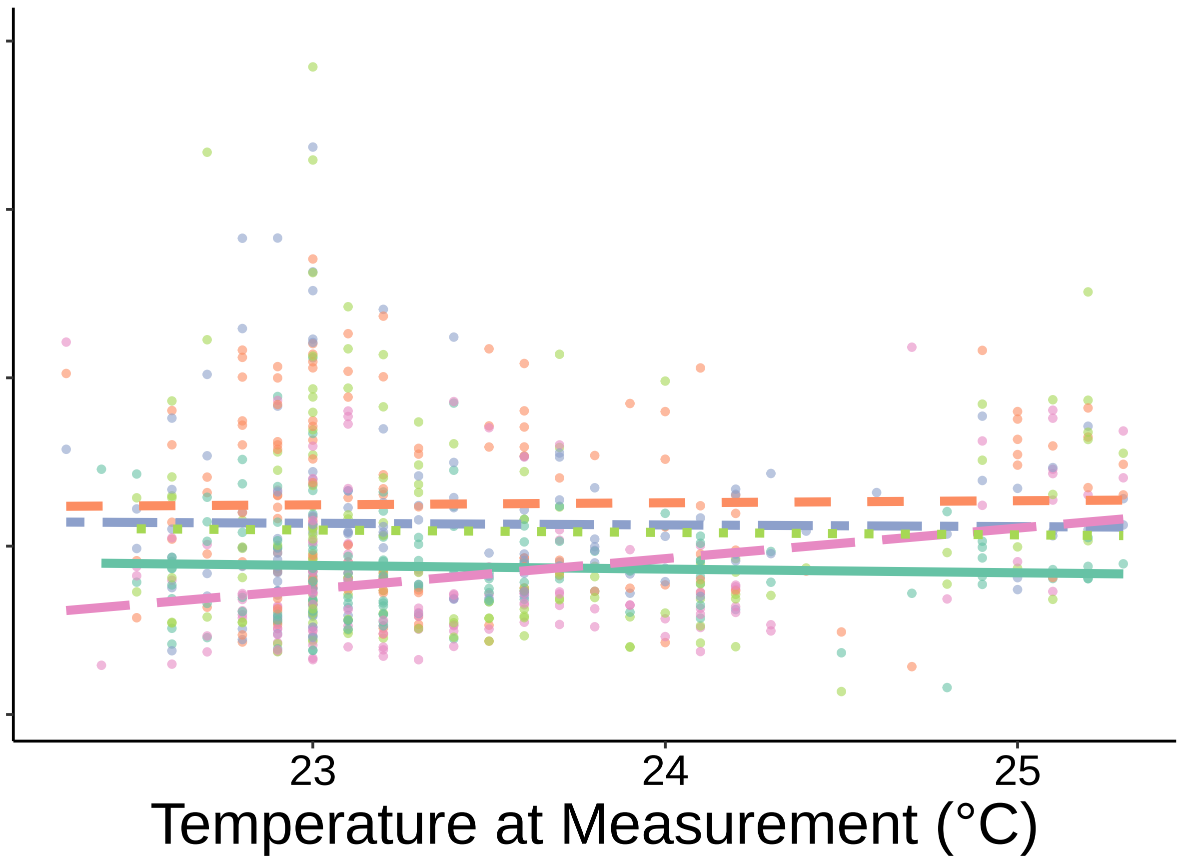
```
## Warning: Removed 59 rows containing non-finite values (stat_smooth).
```

```
## 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

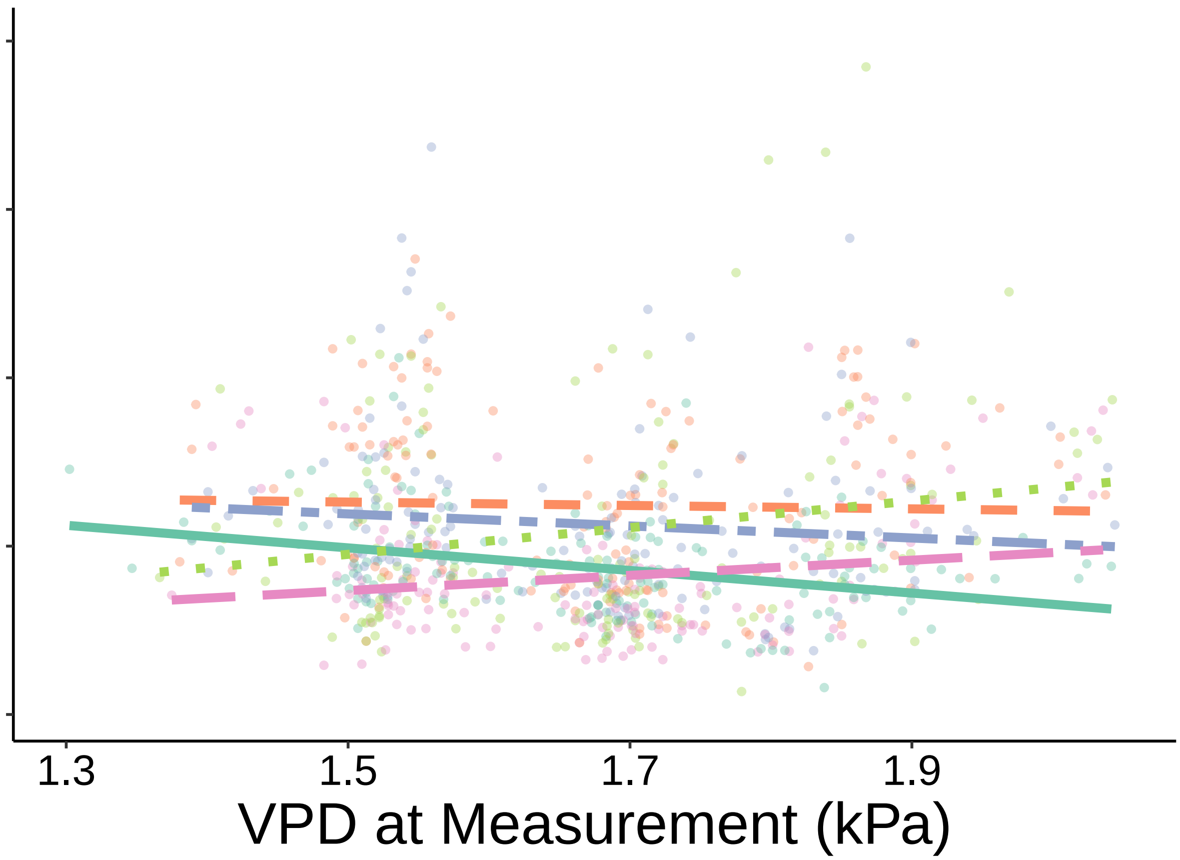
Very interesting relationship! Mite patch CEWL decreases as VPD increases, but every other location appears to increase. In this case, an interaction term is warranted.

```
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("") +
```

```r
  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).
```

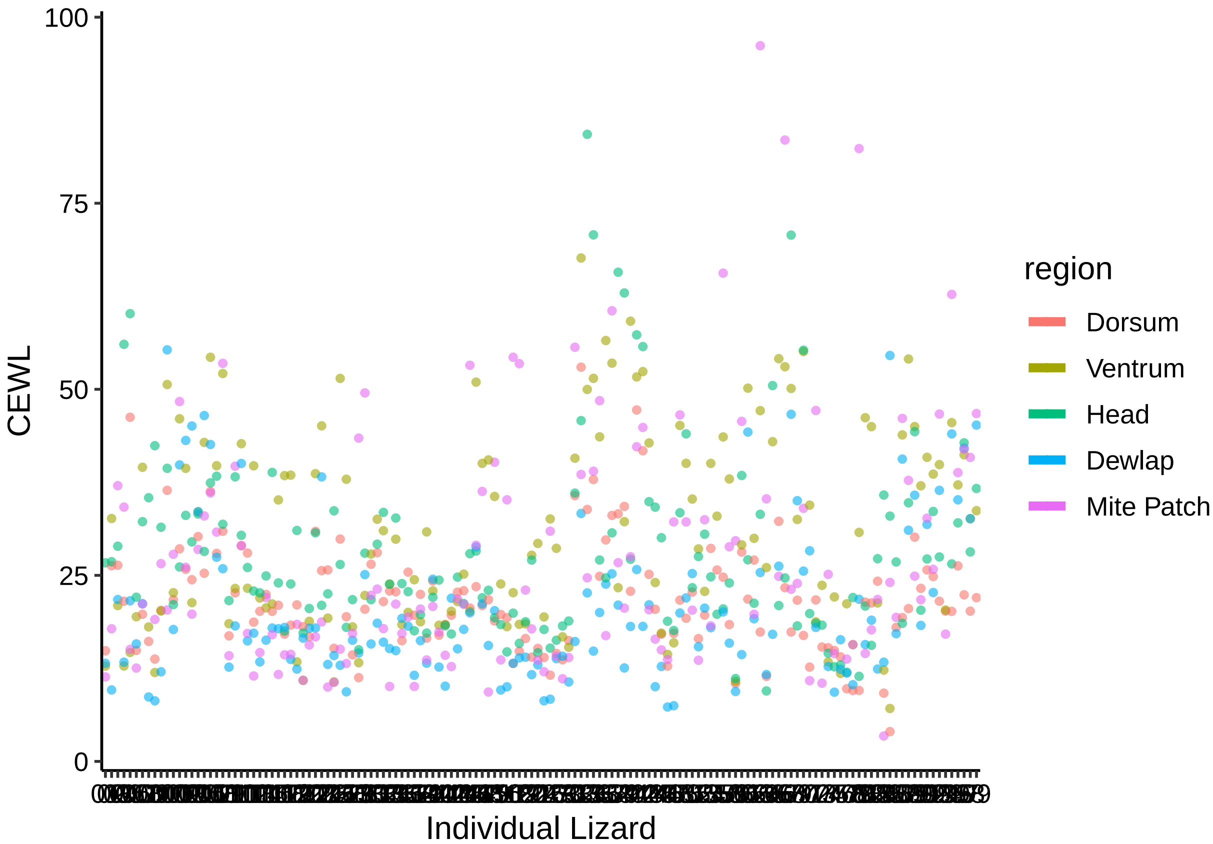
```
## Warning: Removed 4 rows containing missing values (geom_point).
```



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) +
```

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



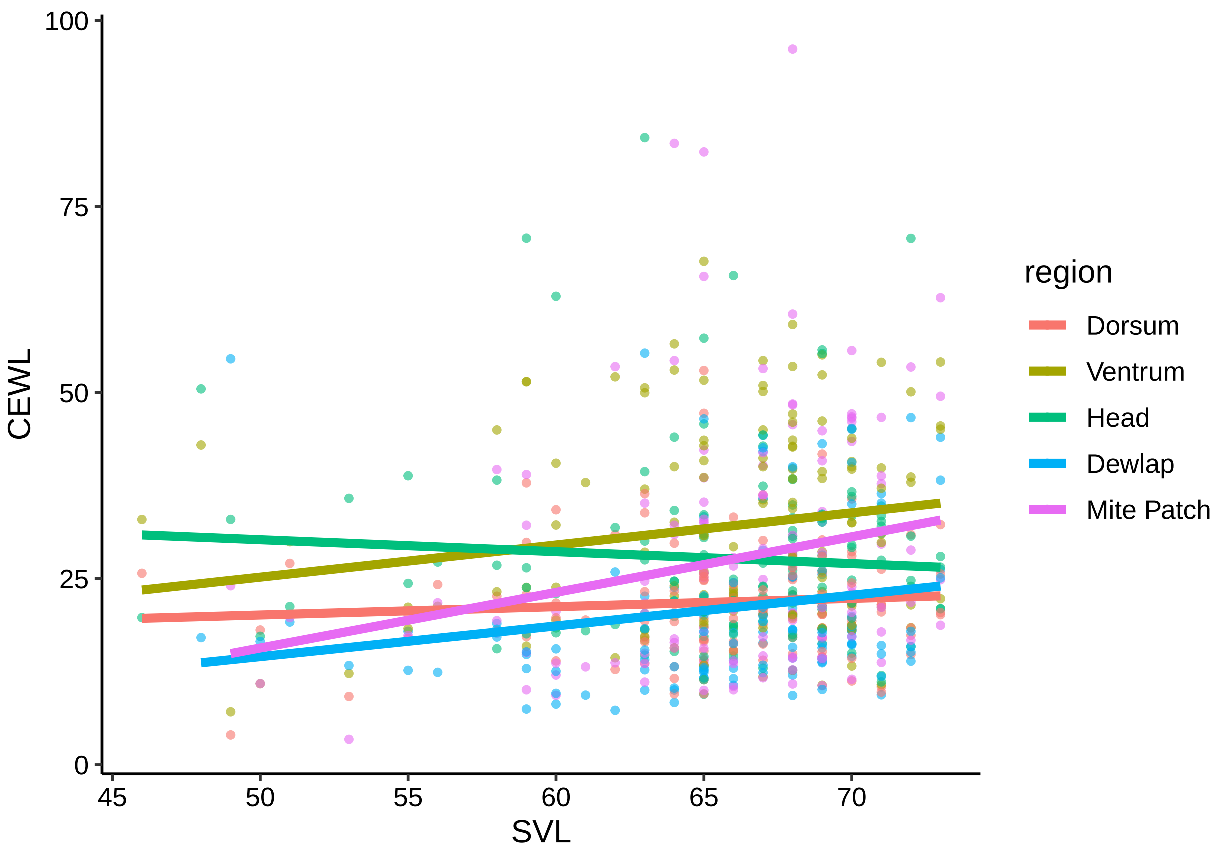
CEWL ~ SVL

```r
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

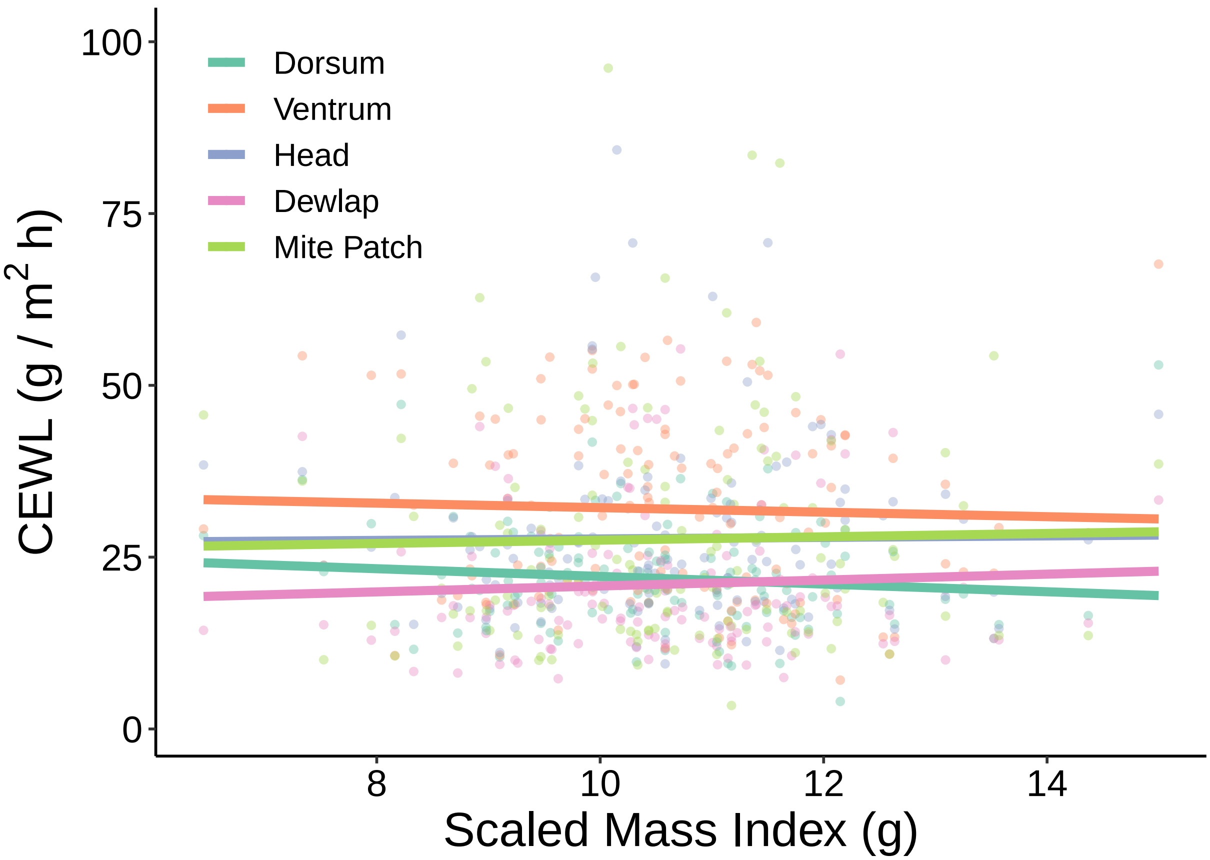
```
CEWL_data_full %>%
  ggplot(data = .) +
  geom_point(aes(x = SMI,
                 y = TEWL_g_m2h,
                 color = region
                 ),
             size = 1,
             alpha = 0.4) +
  stat_smooth(aes(x = SMI,
```

```
                  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

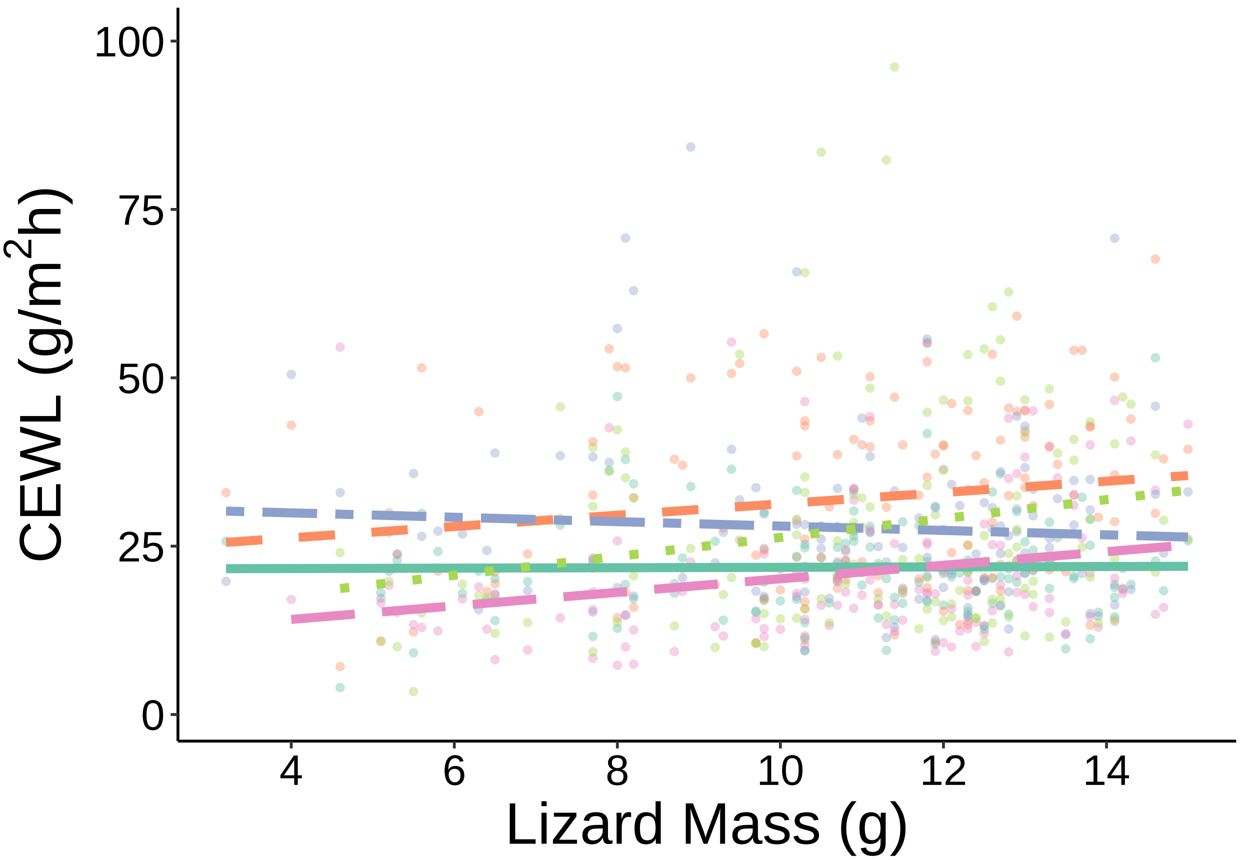
Head has an opposite trend from all the other body regions, so we need an interaction term.

```
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",
```

```r
              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).
```

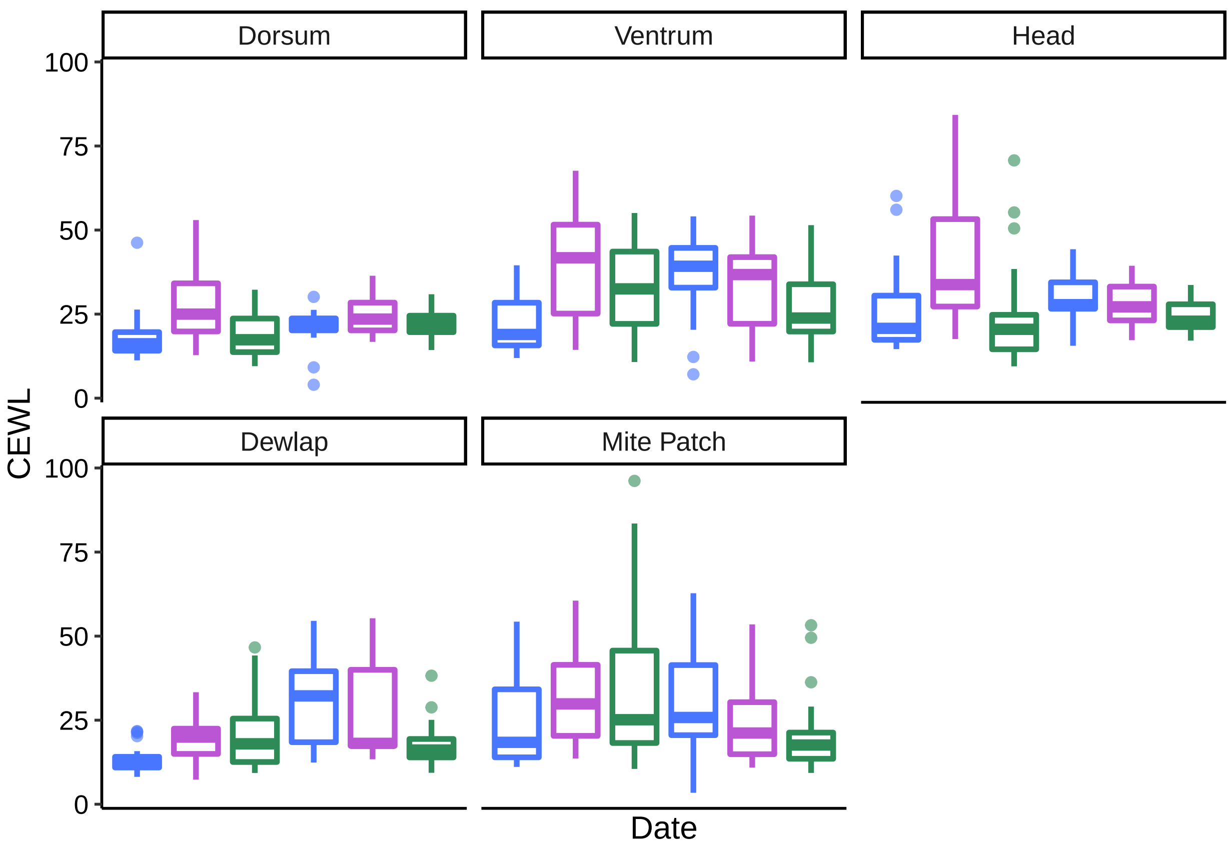



```
# MUST CHANGE COMMENTS ABOVE to produce this
CEWL_legend <- as_ggplot(get_legend(mass_CEWL_fig))

## 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 ~ 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")
```

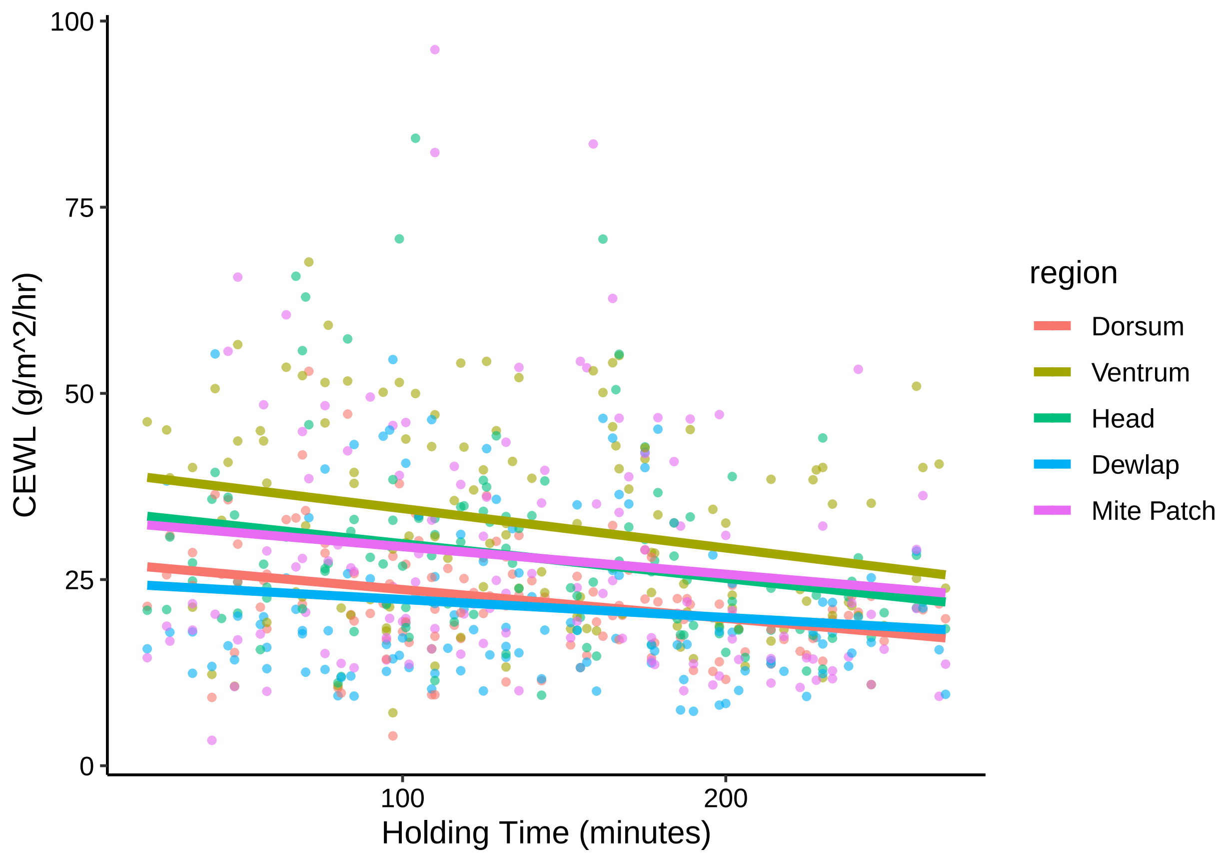


CEWL ~ holding time

```
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).
```



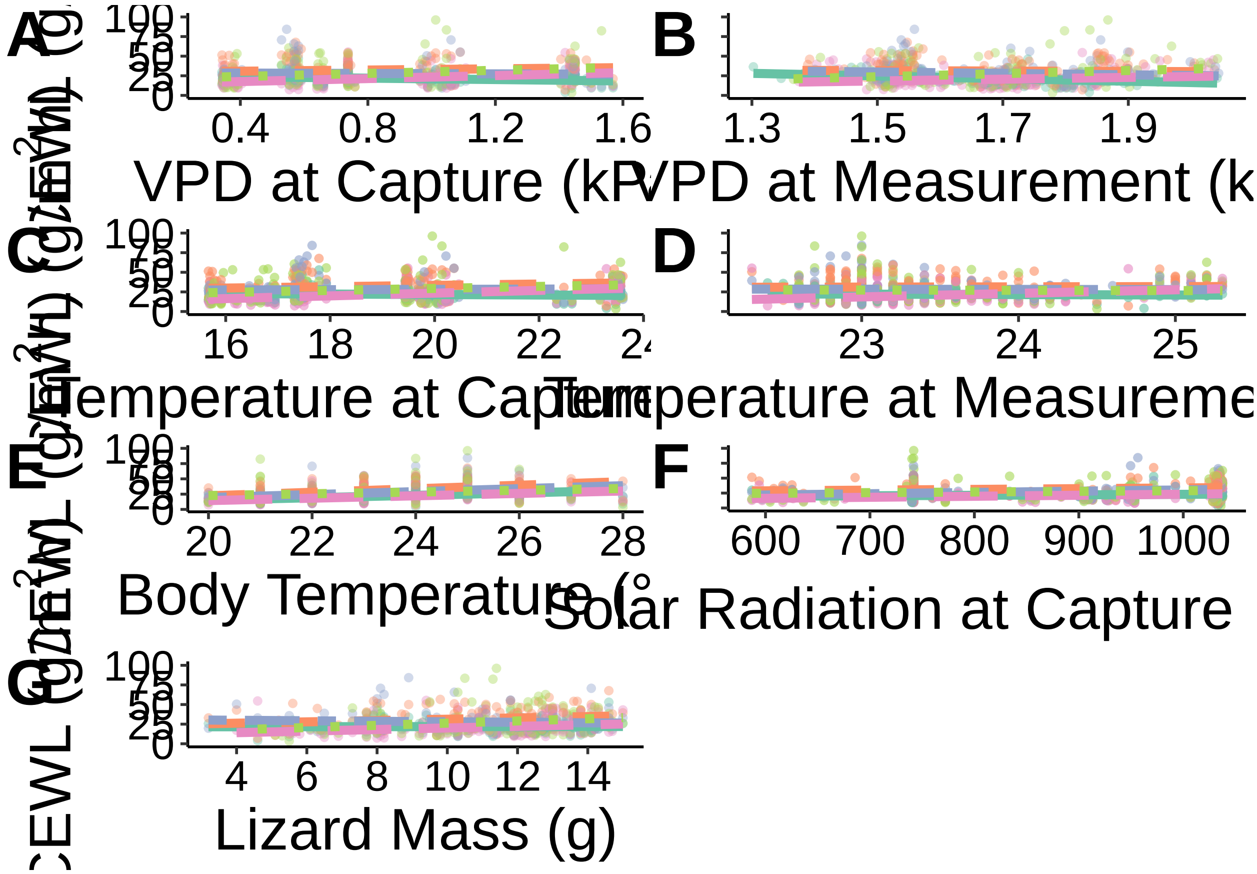
CEWL Multi-Figure

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
```




```r
# 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:

```r
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:

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

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

drop VPD*temp interaction:

```r
hct_mod2 <- lm(data = morpho_blood_SMI,
                          # response variable
                          hematocrit_percent ~
                          # predictor variables
                          VPD_kPa_int + temp_C_interpol +
                          Wind_mph_interpol + Solar_rad_Wm2_interpol +
                          SMI + SVL_mm + mass_g + sex_M_F)
```

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

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

drop SVL:

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

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

drop temperature:

```r
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.

```r
summary(hct_mod4)
```

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

```r
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:

```r
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
```

```r
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:

```r
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
```

```r
drop1(hct_mod8)
```

```
## Single term deletions
##
## Model:
## hematocrit_percent ~ VPD_kPa_int + sex_M_F
##             Df Sum of Sq    RSS    AIC
```

```
## <none>                   3946.0 425.16
## VPD_kPa_int  1    67.486 4013.5 425.19
## sex_M_F      1   142.923 4089.0 427.43
```

drop VPD:

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

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

finally, test the null model

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

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

Selection

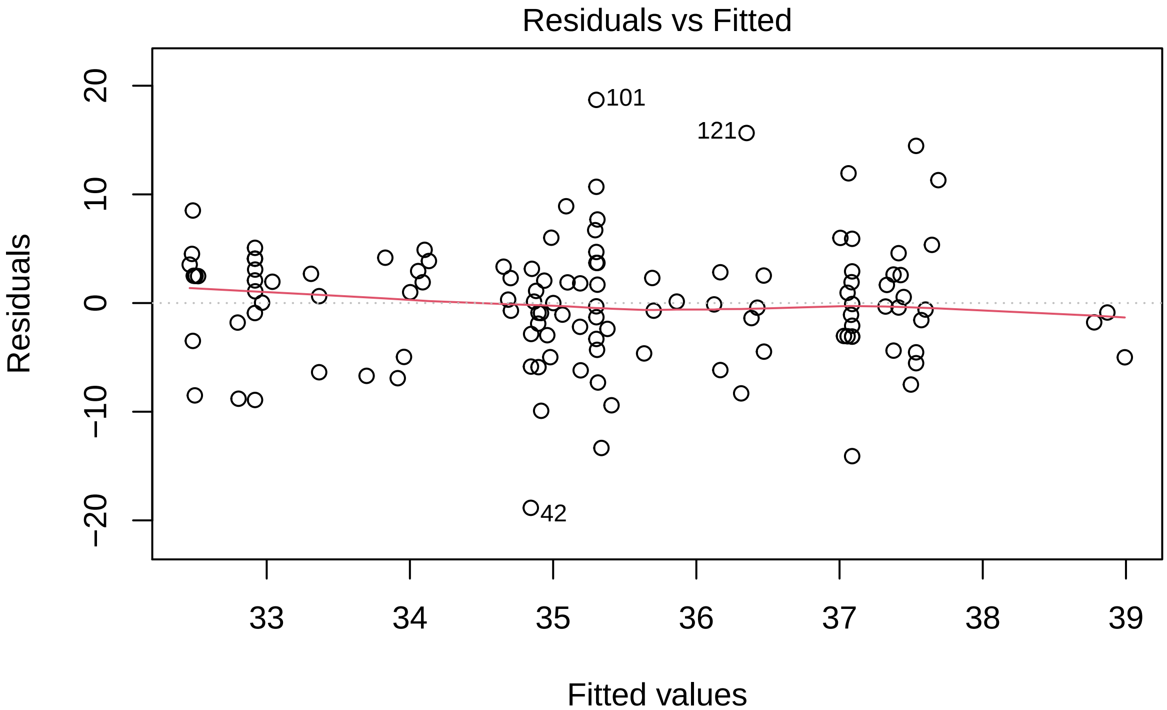
models 4-11 and the null model are the ones we should compare. models 1-3 had serious multicollinearity thus are not trustworthy models.

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

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

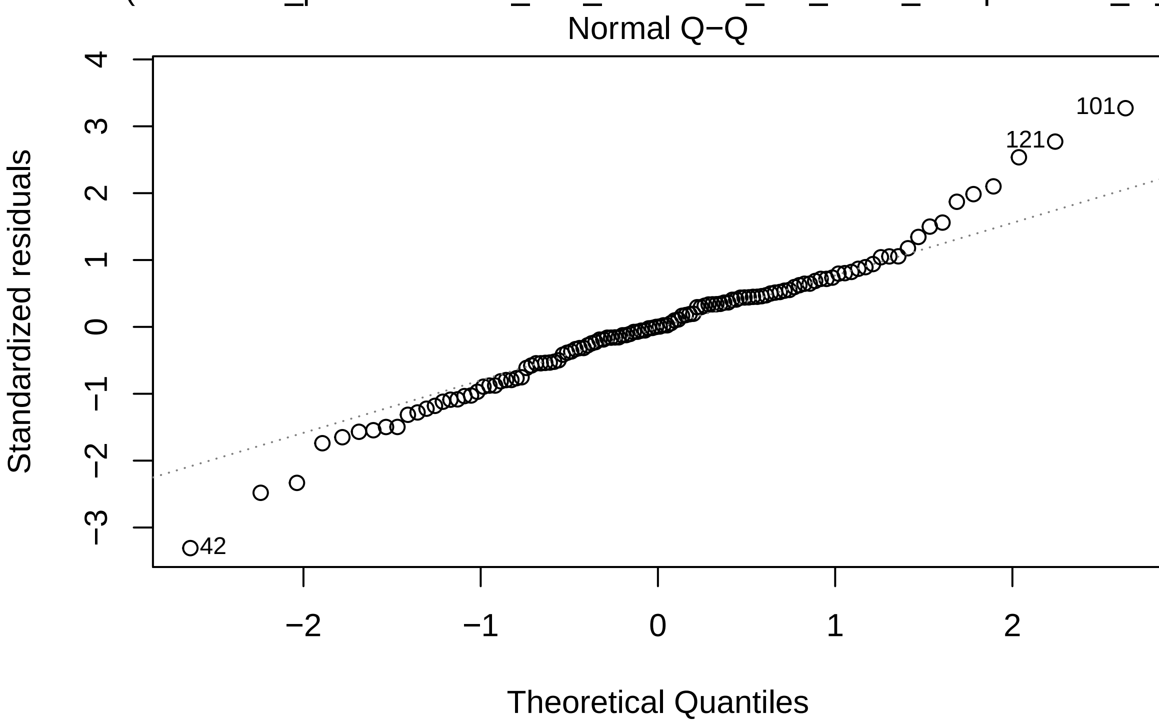
```
##                                                                                      Modnames
## 4                                   (model 7) ~ sex, VPD at capture, solar radiation at capture
## 5                                                               (model 8) ~ sex, VPD at capture
## 3                              (model 6) ~ sex, VPD at capture, solar radiation at capture, SMI
## 2       (model 5) ~ sex, VPD at capture, solar radiation at capture, SMI, wind speed at capture
## 6                                                                              (model 9) ~ sex
## 1 (model 4) ~ sex, VPD at capture, solar radiation at capture, SMI, wind speed at capture, mass
## 7                                                                                   null model
##   K     AICc Delta_AICc    ModelLik      AICcWt        LL    Cum.Wt
## 4 5 768.0253 0.00000000 1.000000000 0.369737267 -378.7495 0.3697373
## 5 4 768.0500 0.02461668 0.987767098 0.365214308 -379.8511 0.7349516
## 3 6 769.7022 1.67689258 0.432381797 0.159867664 -378.4794 0.8948192
## 2 7 771.7042 3.67884825 0.158908911 0.058754547 -378.3521 0.9535738
## 6 3 773.5043 5.47892148 0.064605177 0.023886941 -383.6496 0.9774607
## 1 8 773.9770 5.95168270 0.051004503 0.018858266 -378.3399 0.9963190
## 7 2 777.2445 9.21921256 0.009955737 0.003681007 -386.5714 1.0000000
```

Check LM Assumptions

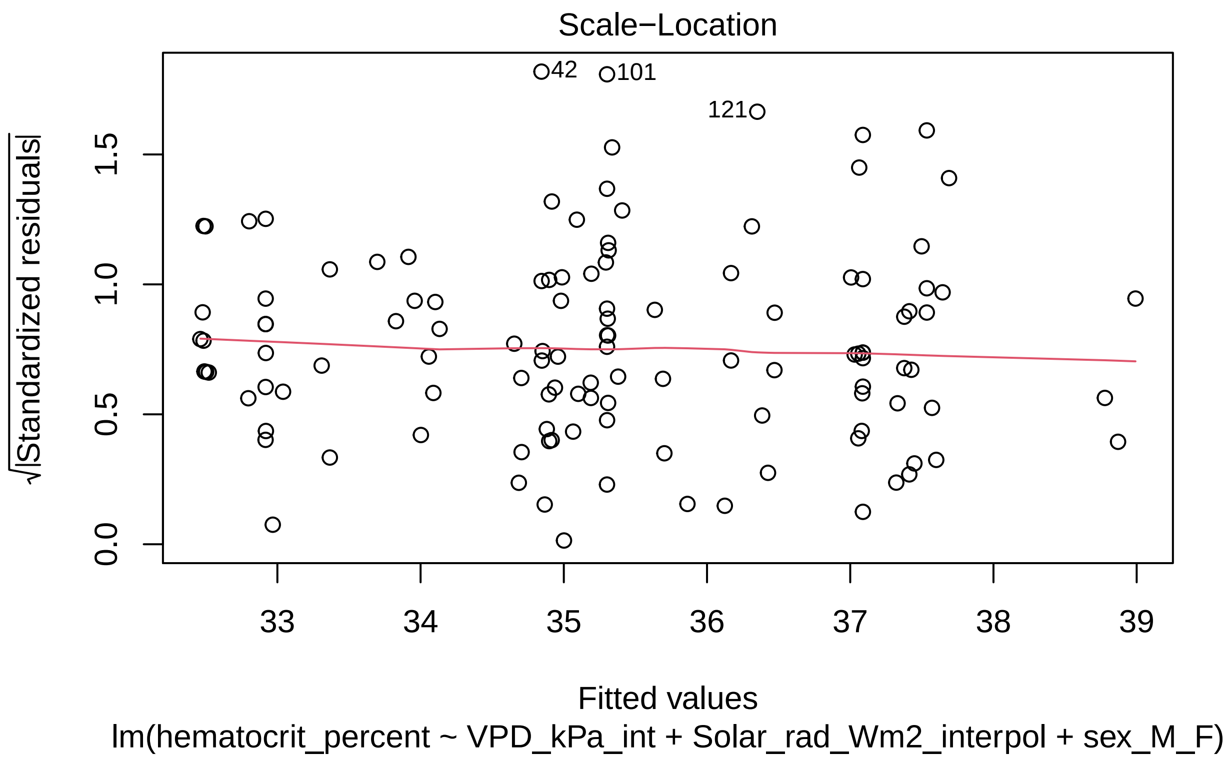
```
plot(hct_mod7)
```

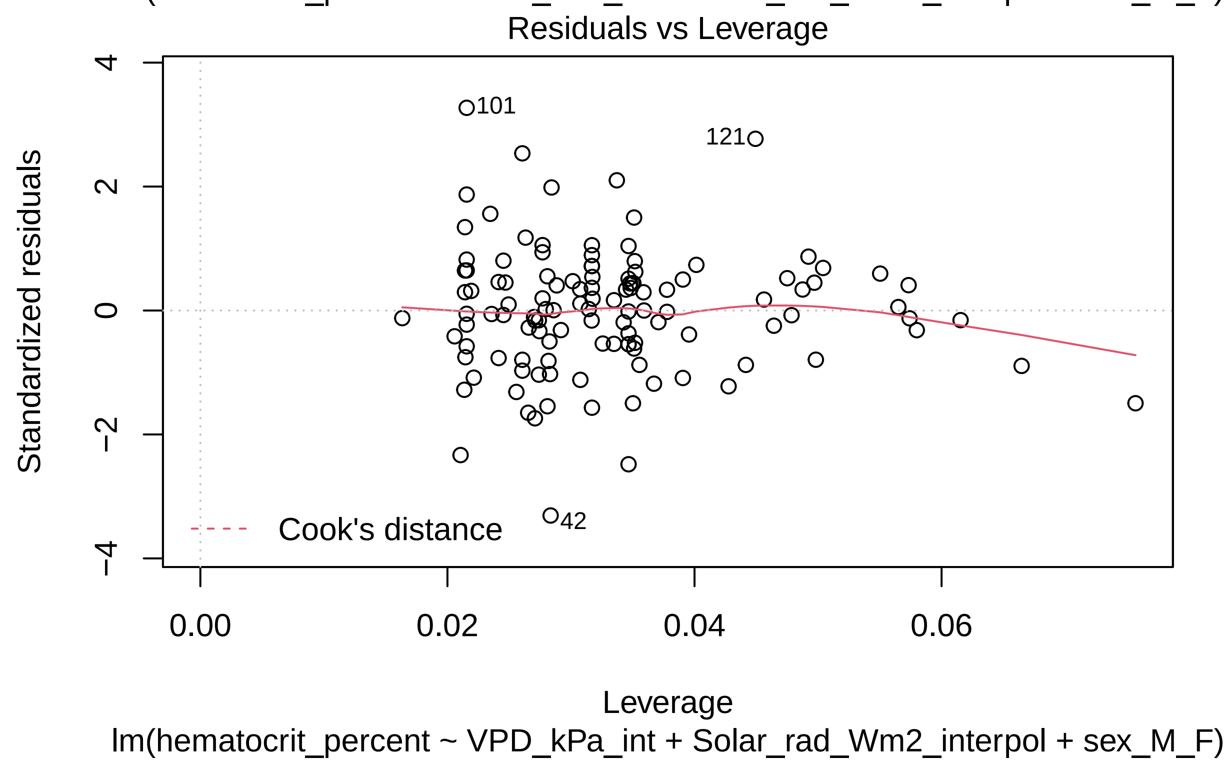


lm(hematocrit_percent ~ VPD_kPa_int + Solar_rad_Wm2_interpol + sex_M_F)

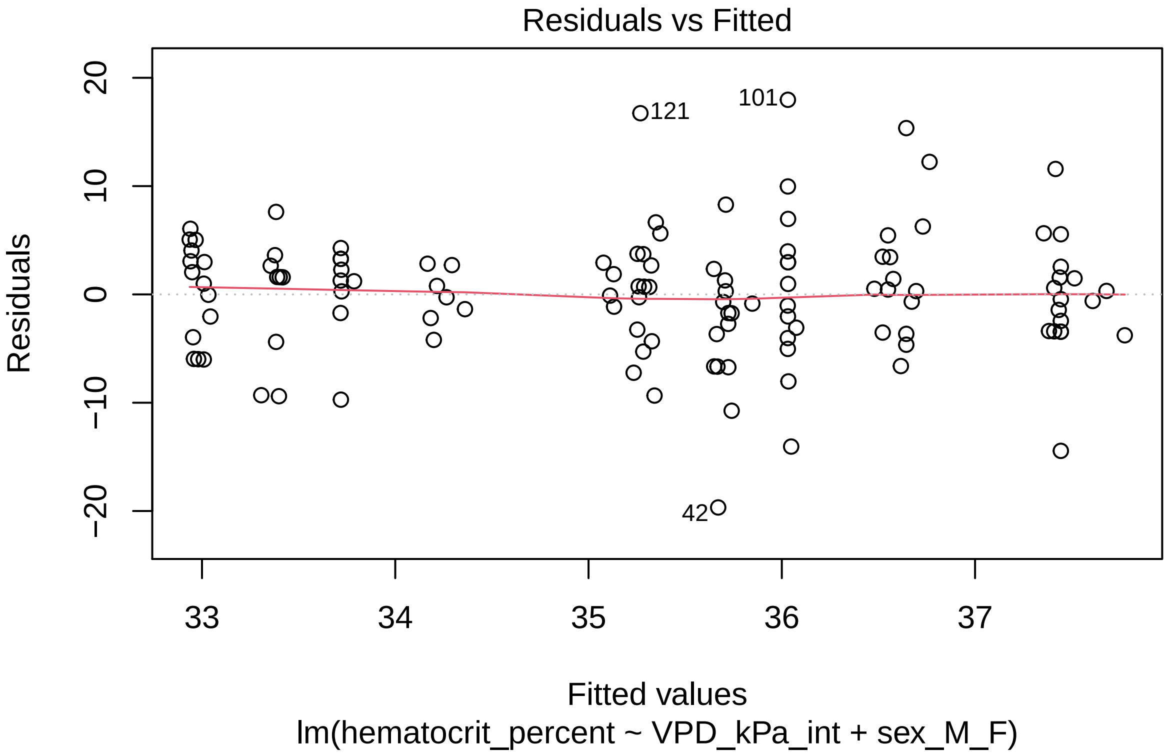


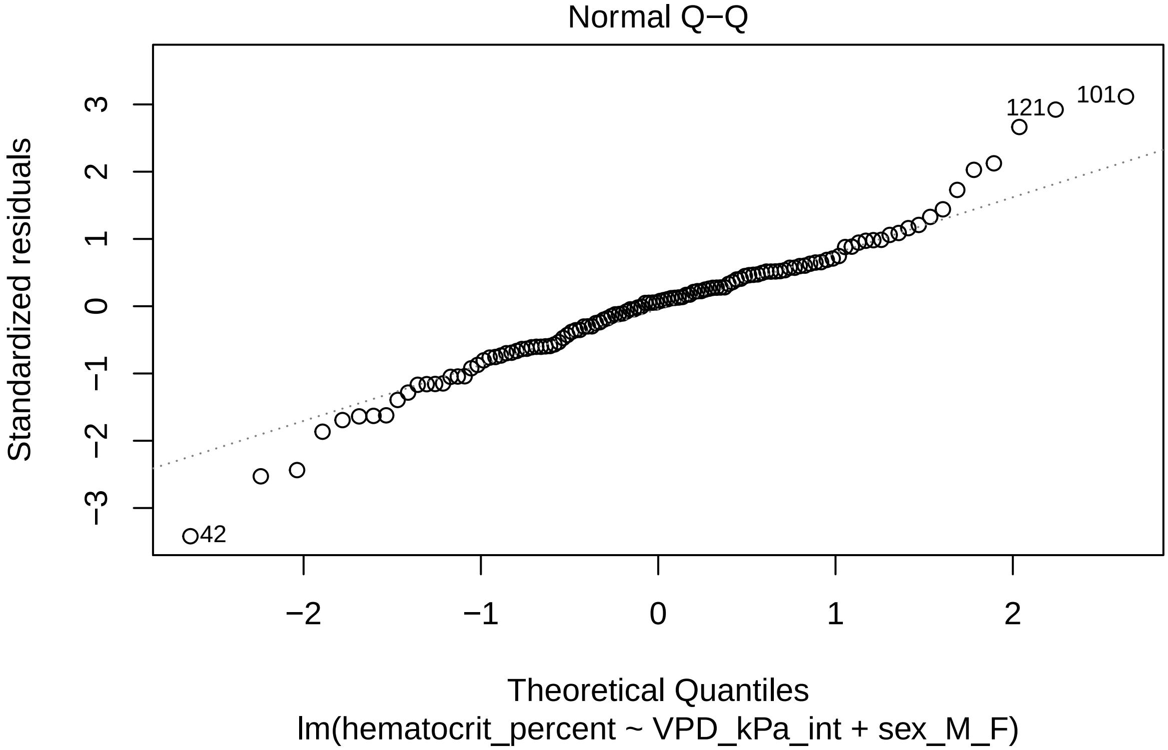
lm(hematocrit_percent ~ VPD_kPa_int + Solar_rad_Wm2_interpol + sex_M_F)

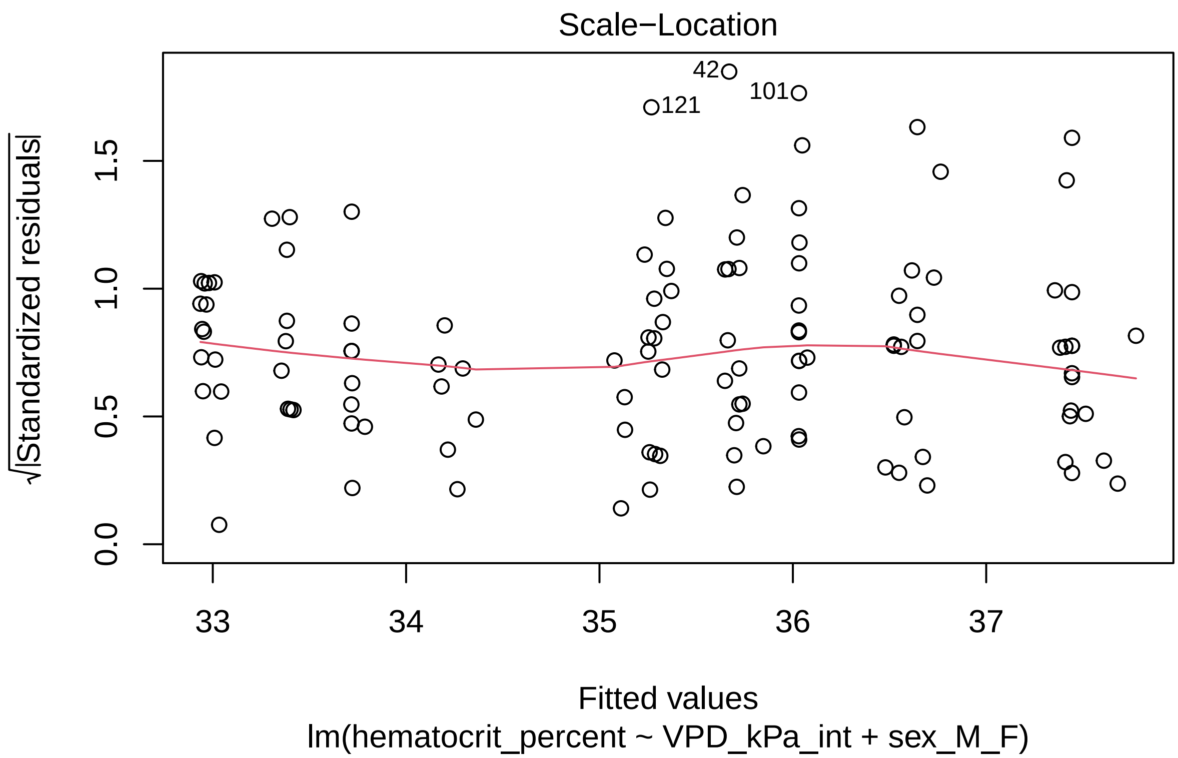


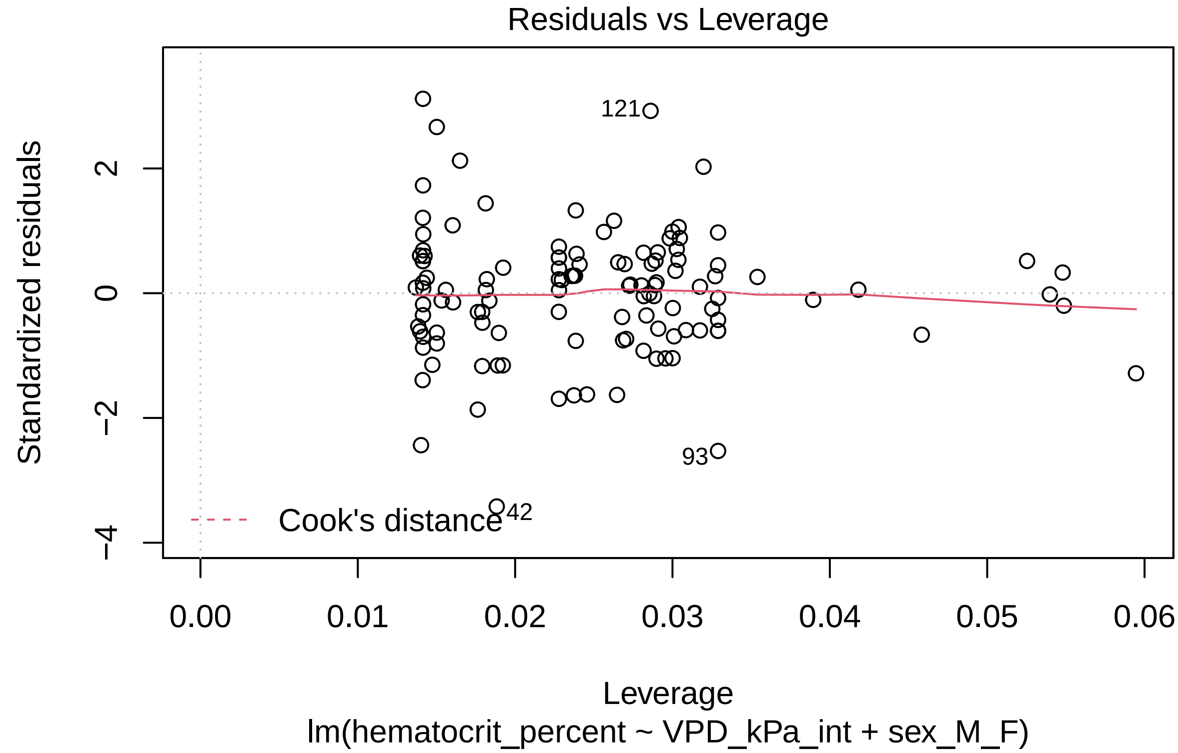



```
plot(hct_mod8)
```

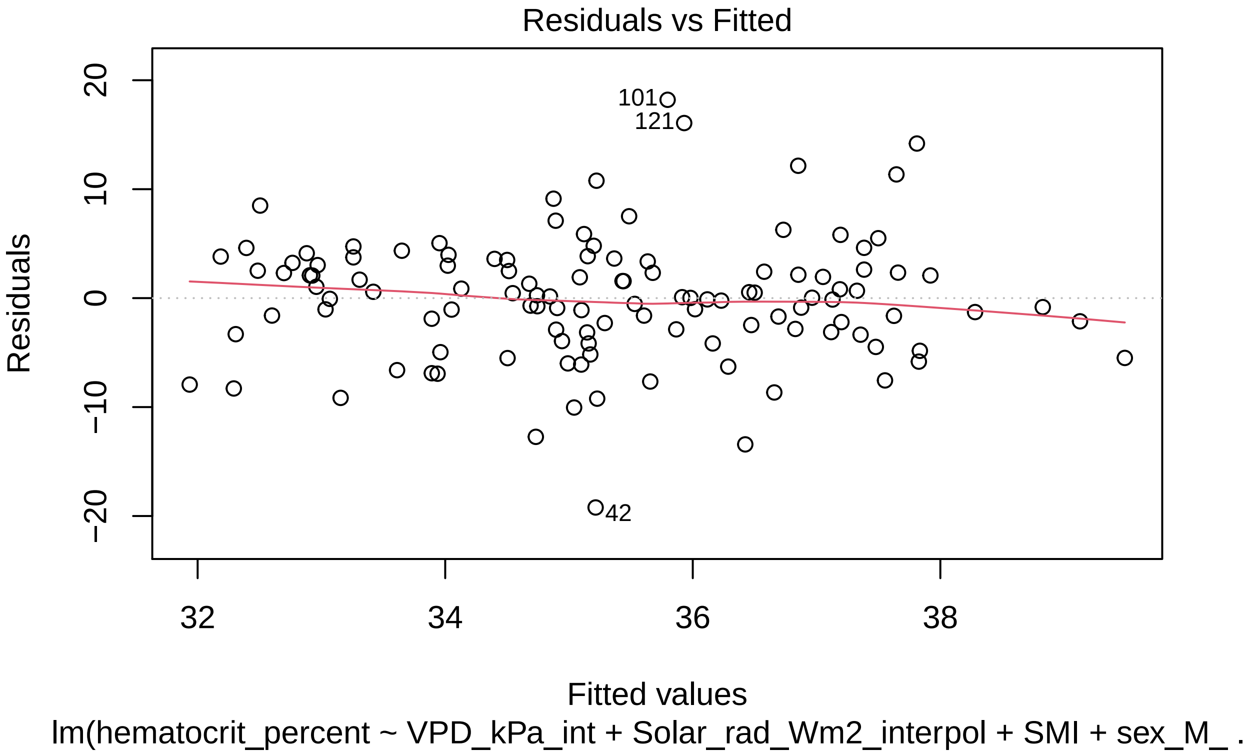

Residuals vs Fitted
Residuals
20
10
0
−10
−20
121
101
42
33
34
35
36
37
Fitted values
lm(hematocrit_percent ~ VPD_kPa_int + sex_M_F)

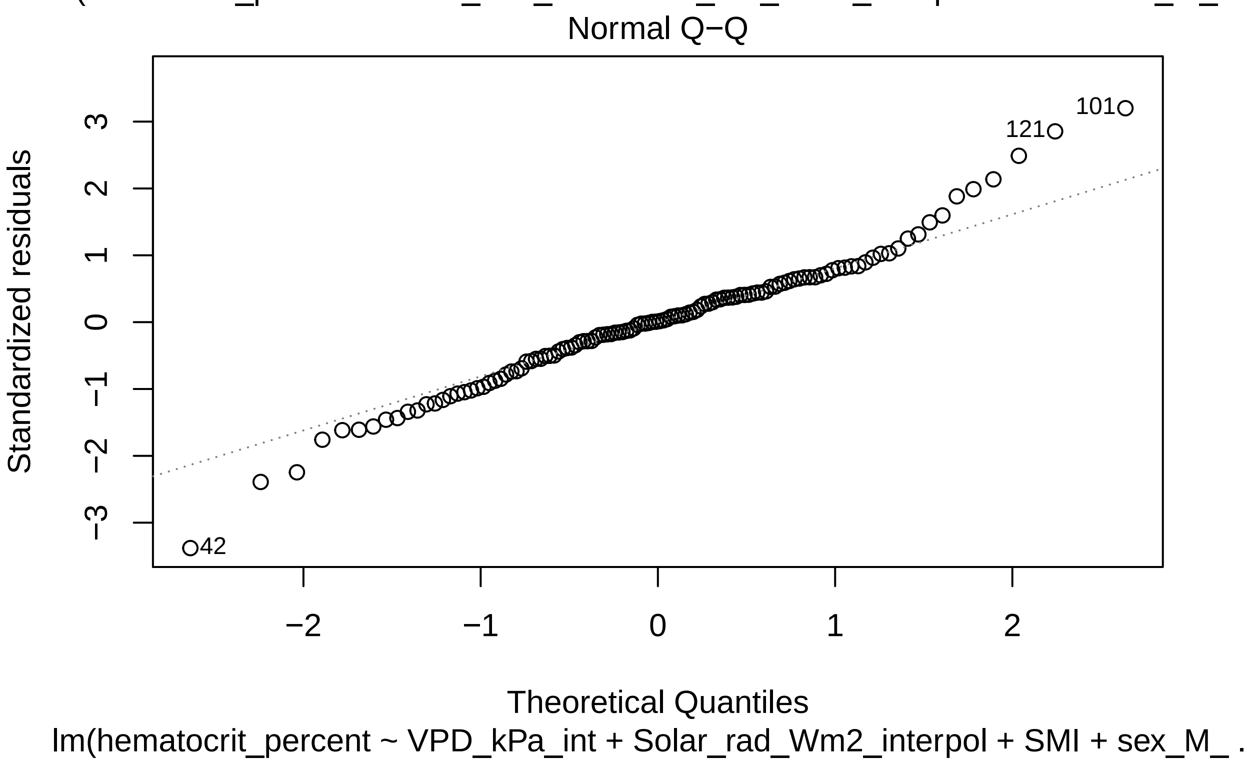

Normal Q−Q
Standardized residuals
3
2
1
0
−1
−2
−3
121
101
42
−2
−1
0
1
2
Theoretical Quantiles
lm(hematocrit_percent ~ VPD_kPa_int + sex_M_F)

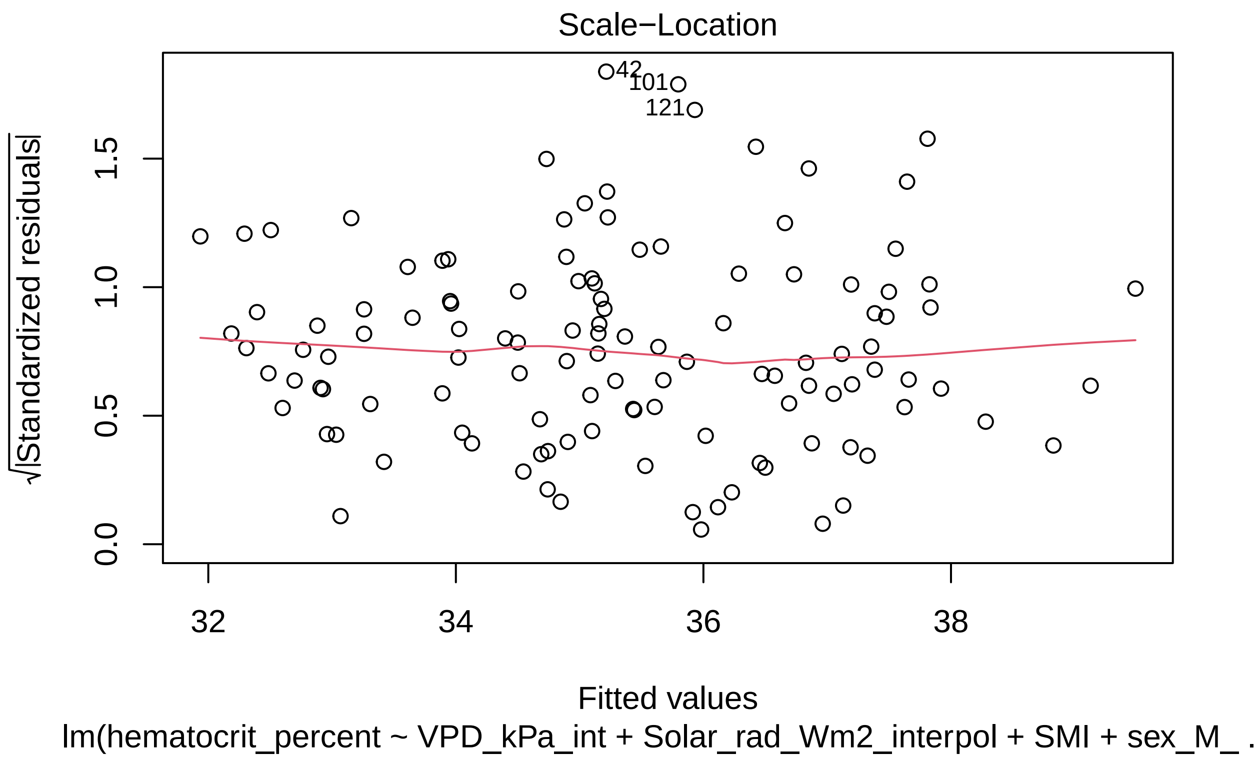


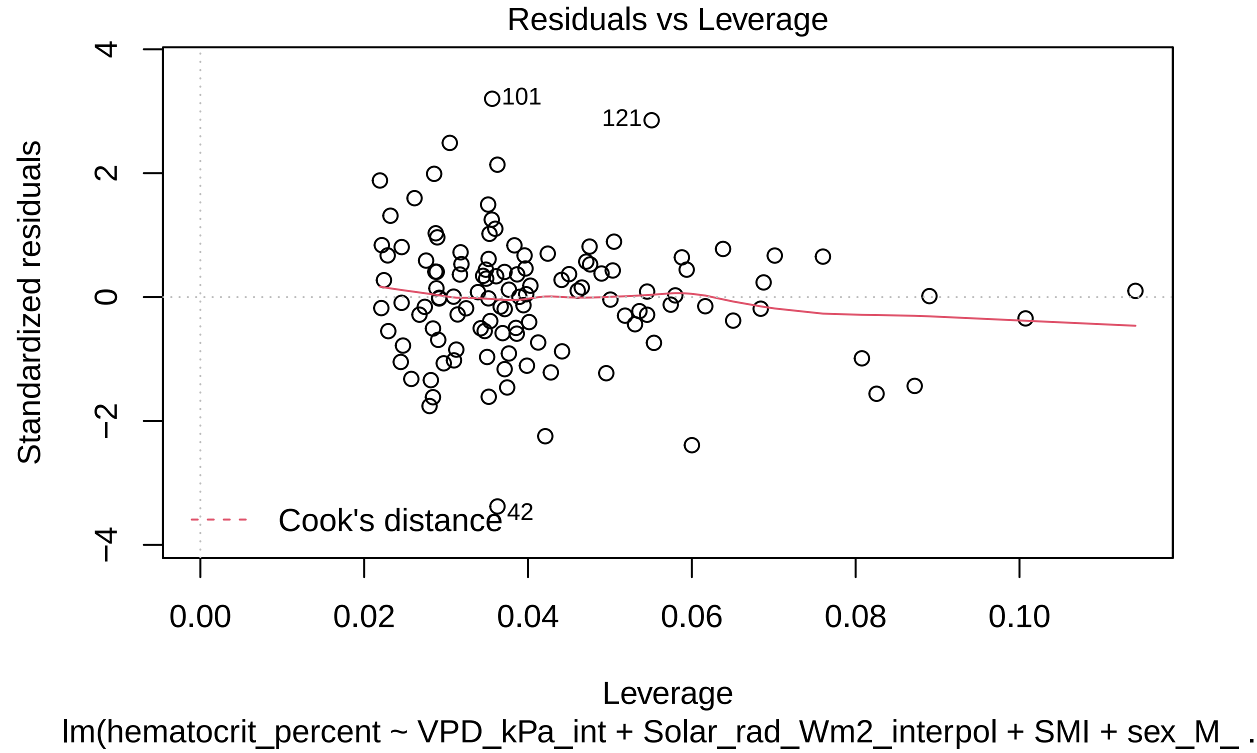



```
plot(hct_mod6)
```


Residuals vs Fitted
Residuals
Fitted values
lm(hematocrit_percent ~ VPD_kPa_int + Solar_rad_Wm2_interpol + SMI + sex_M_ .
101
121
42
20
10
0
−10
−20
32
34
36
38


Normal Q−Q
Standardized residuals
Theoretical Quantiles
lm(hematocrit_percent ~ VPD_kPa_int + Solar_rad_Wm2_interpol + SMI + sex_M_ .
101
121
42
3
2
1
0
−1
−2
−3
−2
−1
0
1
2






```r
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_kP_ tmp_C_ Wnd_m_ S__W2_ SMI    SVL_mm mass_g s_M_FM
## VPD_kPa_int -0.529
## tmp_C_ntrpl -0.631  0.305
## Wnd_mph_ntr -0.024  0.152   0.047
## Slr_rd_Wm2_  0.387 -0.201  -0.669 -0.313
## SMI         -0.550 -0.041  -0.148 -0.095  0.009
## SVL_mm      -0.574 -0.020  -0.132 -0.123 -0.029  0.944
## mass_g       0.576  0.025   0.120  0.091  0.023 -0.944 -0.987
## sex_M_FM    -0.081 -0.043   0.020 -0.016 -0.106  0.108  0.163 -0.190
## VPD_kP_:_C_  0.598 -0.986  -0.448 -0.148  0.291  0.059  0.039 -0.042  0.035
```

use VIF to look for multicollinearity:

```r
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.

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

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

drop mass.

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

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

drop temperature

```r
# 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 +
```

```r
                              # random effects
                              (1|date) + (1|hemolyzed))
hydrat_mod4_VIFs <- data.frame(VIF = car::vif(hydrat_mod4)) %>%
  arrange(VIF)
hydrat_mod4_VIFs
```

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

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

```r
summary(hydrat_mod4)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula:
## osmolality_mmol_kg ~ VPD_kPa_int + Wind_mph_interpol + Solar_rad_Wm2_interpol +
##     SMI + SVL_mm + sex_M_F + (1 | date) + (1 | hemolyzed)
##    Data: morpho_blood_SMI
##
## REML criterion at convergence: 1026.9
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.22452 -0.63811  0.06486  0.65425  2.72400
##
## Random effects:
##  Groups    Name        Variance Std.Dev.
##  date      (Intercept) 930.06   30.497
##  hemolyzed (Intercept)  19.33    4.397
##  Residual              284.66   16.872
## Number of obs: 121, groups:  date, 6; hemolyzed, 2
##
## Fixed effects:
##                         Estimate Std. Error t value
## (Intercept)            385.41079   37.34722  10.320
## VPD_kPa_int              4.10087   15.42376   0.266
## Wind_mph_interpol      -11.58238    3.56118  -3.252
## Solar_rad_Wm2_interpol   0.05656    0.03674   1.540
## SMI                     -0.63969    1.24862  -0.512
## SVL_mm                  -0.07346    0.29247  -0.251
## sex_M_FM                -4.92854    3.61752  -1.362
##
## Correlation of Fixed Effects:
##             (Intr) VPD_P_ Wnd_m_ S__W2_ SMI    SVL_mm
## VPD_kPa_int -0.141
## Wnd_mph_ntr -0.005  0.039
## Slr_rd_Wm2_ -0.591 -0.135 -0.404
## SMI         -0.420 -0.153 -0.024  0.030
## SVL_mm      -0.335 -0.072 -0.213 -0.133  0.229
```

```
## sex_M_FM     0.182 -0.034  0.007 -0.100 -0.216 -0.141
```

```r
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:

```r
# 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
```

```r
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:

```r
# 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
```

```r
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:

```r
# 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
```

```r
drop1(hydrat_mod8)
```

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

drop solar radiation:

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

finally, test the null model

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

Selection

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

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

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

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

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

```
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
```

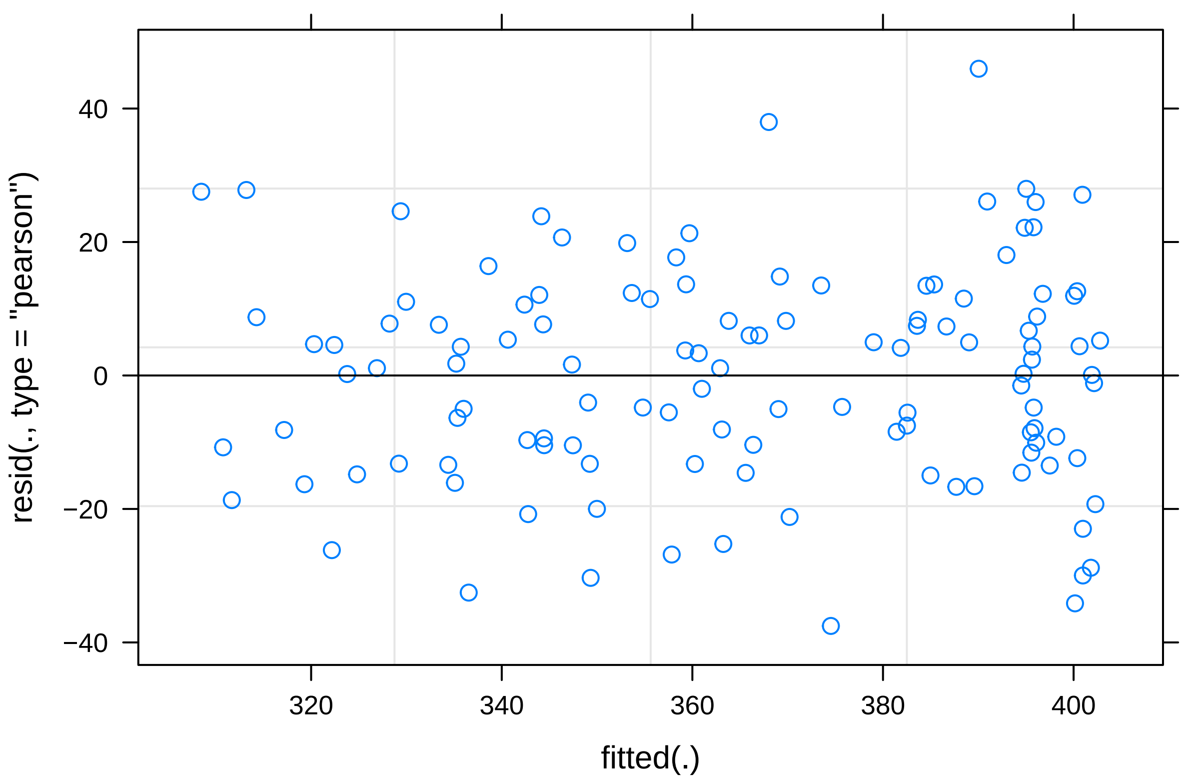
```
hydrat_mod4p <- lmerTest::lmer(data = morpho_blood_SMI,
                          # response variable
                          osmolality_mmol_kg ~
                           VPD_kPa_int +
                            Wind_mph_interpol + Solar_rad_Wm2_interpol +
                            SMI + 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|)
```

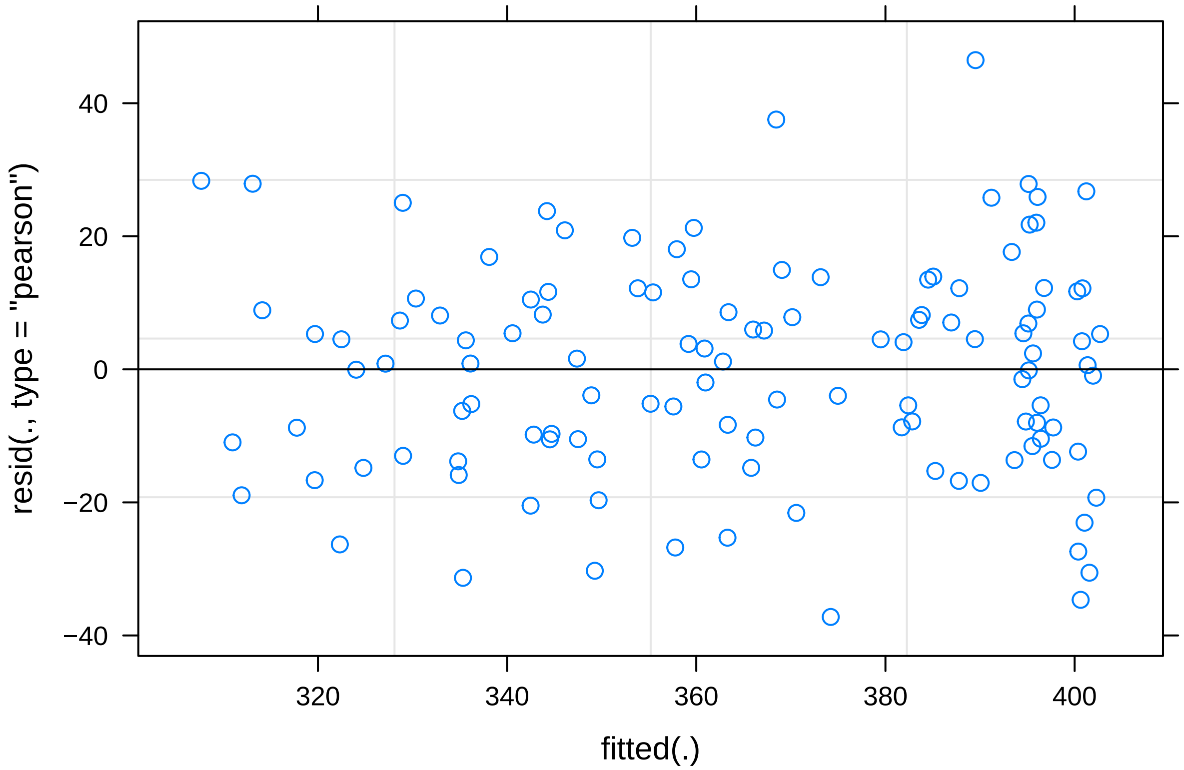
```
## (Intercept)             385.41079   37.34722  71.15211  10.320  8.8e-16 ***
## VPD_kPa_int               4.10087   15.42376  72.07437   0.266  0.79109
## Wind_mph_interpol       -11.58238    3.56118 112.70287  -3.252  0.00151 **
## Solar_rad_Wm2_interpol    0.05656    0.03674  85.31715   1.540  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

```r
plot(hydrat_mod4)
```




```r
plot(hydrat_mod5)
```




```r
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
```

```r
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.

```r
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
```

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

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

```r
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:

```r
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
```

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

```
##                                     VIF
## region                        25.258239
## region:VPD_kPa                19.963109
## region:Wind_mph_interpol      13.124017
## VPD_kPa_int                   10.400445
## temp_C_interpol                9.708892
## region:SMI                     8.806453
## mass_g                         8.729644
## SVL_mm                         8.724491
## region:Solar_rad_Wm2_interpol  8.270208
## region:VPD_kPa_int             4.833504
## region:mass_g                  4.656277
## SMI                            4.647721
## VPD_kPa                        3.779206
## Solar_rad_Wm2_interpol         2.749008
## ambient_temp_C                 1.952601
## Wind_mph_interpol              1.948642
## region:sex_M_F                 1.833544
## sex_M_F                        1.725410
## hold_time                      1.725326
## cloacal_temp_C                 1.665317
## osmolality_mmol_kg             1.568108
## hematocrit_percent             1.144285
```

remove region interaction with ambient VPD at msmt:

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

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

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

```
##                                     VIF
## region                        16.466551
## region:Wind_mph_interpol      12.882602
## VPD_kPa_int                   10.138740
## temp_C_interpol                9.706791
## region:SMI                     8.787887
## mass_g                         8.731534
## SVL_mm                         8.724861
## region:Solar_rad_Wm2_interpol  6.138976
## SMI                            4.651252
```

```
## region:mass_g                    4.614621
## VPD_kPa                          2.838801
## region:VPD_kPa_int               2.622438
## Solar_rad_Wm2_interpol           2.446258
## ambient_temp_C                   1.951671
## Wind_mph_interpol                1.940963
## region:sex_M_F                   1.834019
## sex_M_F                          1.731281
## hold_time                        1.725295
## cloacal_temp_C                   1.665036
## osmolality_mmol_kg               1.568036
## hematocrit_percent               1.144262
```

remove region interaction with wind at capture:

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

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

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

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

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

Need dataset without NAs first.

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

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

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

```
summary(CEWL_mod6a)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: TEWL_g_m2h ~ region * (VPD_kPa_int + Solar_rad_Wm2_interpol +
##     SMI + mass_g + sex_M_F) + SVL_mm + hematocrit_percent + osmolality_mmol_kg +
##     cloacal_temp_C + hold_time + ambient_temp_C + temp_C_interpol +
##     VPD_kPa + Wind_mph_interpol + (1 | individual_ID)
##    Data: CEWL_dat_sub1
##
## REML criterion at convergence: 4290.1
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.0037 -0.5475 -0.1039  0.4156  5.3855
##
## Random effects:
##  Groups        Name        Variance Std.Dev.
##  individual_ID (Intercept) 28.82    5.368
##  Residual                  99.93    9.996
## Number of obs: 570, groups:  individual_ID, 116
##
## Fixed effects:
##                                       Estimate Std. Error t value
## (Intercept)                         -5.050e+01  7.980e+01  -0.633
## regionVentrum                       -3.554e+00  1.198e+01  -0.297
## regionHead                          -7.150e+00  1.196e+01  -0.598
```

```
## regionDewlap                             -2.436e+01  1.205e+01  -2.022
## regionMite Patch                         -9.044e+00  1.204e+01  -0.751
## VPD_kPa_int                              -5.157e+01  1.719e+01  -3.000
## Solar_rad_Wm2_interpol                    1.337e-02  9.815e-03   1.362
## SMI                                       5.601e-01  2.303e+00   0.243
## mass_g                                   -5.258e-01  2.208e+00  -0.238
## sex_M_FM                                  1.792e+00  2.343e+00   0.765
## SVL_mm                                    3.885e-01  1.051e+00   0.369
## hematocrit_percent                       -2.839e-01  1.241e-01  -2.288
## osmolality_mmol_kg                       -1.076e-02  3.969e-02  -0.271
## cloacal_temp_C                            2.313e+00  5.952e-01   3.887
## hold_time                                -7.909e-03  1.694e-02  -0.467
## ambient_temp_C                           -5.550e+00  1.661e+00  -3.341
## temp_C_interpol                           5.925e+00  2.438e+00   2.431
## VPD_kPa                                   2.766e+01  1.123e+01   2.464
## Wind_mph_interpol                         1.632e+00  2.342e+00   0.697
## regionVentrum:VPD_kPa_int                 7.429e+00  3.678e+00   2.020
## regionHead:VPD_kPa_int                    1.830e+00  3.690e+00   0.496
## regionDewlap:VPD_kPa_int                  1.431e+01  3.704e+00   3.863
## regionMite Patch:VPD_kPa_int              1.627e+01  3.686e+00   4.414
## regionVentrum:Solar_rad_Wm2_interpol     -3.674e-04  8.894e-03  -0.041
## regionHead:Solar_rad_Wm2_interpol         1.173e-02  8.888e-03   1.320
## regionDewlap:Solar_rad_Wm2_interpol      -3.166e-03  8.957e-03  -0.354
## regionMite Patch:Solar_rad_Wm2_interpol -1.293e-02  9.020e-03  -1.434
## regionVentrum:SMI                        -2.672e-01  1.091e+00  -0.245
## regionHead:SMI                            6.388e-01  1.087e+00   0.588
## regionDewlap:SMI                          5.436e-01  1.093e+00   0.497
## regionMite Patch:SMI                     -3.879e-02  1.095e+00  -0.035
## regionVentrum:mass_g                      9.784e-01  5.385e-01   1.817
## regionHead:mass_g                        -3.732e-01  5.357e-01  -0.697
## regionDewlap:mass_g                       9.755e-01  5.476e-01   1.781
## regionMite Patch:mass_g                   1.046e+00  5.573e-01   1.877
## regionVentrum:sex_M_FM                    1.102e+00  2.864e+00   0.385
## regionHead:sex_M_FM                      -2.433e+00  2.883e+00  -0.844
## regionDewlap:sex_M_FM                    -1.666e+00  2.897e+00  -0.575
## regionMite Patch:sex_M_FM                 2.398e+00  2.877e+00   0.833
##
## Correlation matrix not shown by default, as p = 39 > 12.
## Use print(x, correlation=TRUE)  or
##     vcov(x)        if you need it
## fit warnings:
## Some predictor variables are on very different scales: consider rescaling
```

```
drop1(CEWL_mod6a)
```

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

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

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

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

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

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

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

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

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

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

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

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

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

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

drop region*SMI interaction:

```r
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
```

```r
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
```

```r
drop1(CEWL_mod7)
```

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

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

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

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

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

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

```
## rescaling

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

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

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

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

## 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
```

```r
summary(CEWL_mod8)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: TEWL_g_m2h ~ region * (VPD_kPa_int + Solar_rad_Wm2_interpol +
##     mass_g) + SVL_mm + SMI + sex_M_F + hematocrit_percent + osmolality_mmol_kg +
##     cloacal_temp_C + hold_time + ambient_temp_C + temp_C_interpol +
##     VPD_kPa + Wind_mph_interpol + (1 | individual_ID)
##    Data: CEWL_dat_sub1
##
## REML criterion at convergence: 4315.9
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.9570 -0.5539 -0.1066  0.4054  5.2381
##
## Random effects:
##  Groups        Name        Variance Std.Dev.
##  individual_ID (Intercept) 29.08    5.393
##  Residual                  99.06    9.953
## Number of obs: 570, groups:  individual_ID, 116
##
## Fixed effects:
##                                           Estimate Std. Error t value
## (Intercept)                              -5.068e+01  7.966e+01  -0.636
## regionVentrum                            -5.585e+00  8.987e+00  -0.621
## regionHead                               -2.329e+00  9.008e+00  -0.259
## regionDewlap                             -2.037e+01  9.193e+00  -2.216
## regionMite Patch                         -9.422e+00  9.276e+00  -1.016
## VPD_kPa_int                              -5.145e+01  1.720e+01  -2.992
## Solar_rad_Wm2_interpol                    1.290e-02  9.670e-03   1.334
## mass_g                                   -5.332e-01  2.206e+00  -0.242
## SVL_mm                                    3.852e-01  1.051e+00   0.366
## SMI                                       7.293e-01  2.197e+00   0.332
## sex_M_FM                                  1.696e+00  1.495e+00   1.134
## hematocrit_percent                       -2.858e-01  1.242e-01  -2.301
## osmolality_mmol_kg                       -1.015e-02  3.972e-02  -0.255
## cloacal_temp_C                            2.316e+00  5.957e-01   3.889
## hold_time                                -8.048e-03  1.696e-02  -0.475
## ambient_temp_C                           -5.601e+00  1.662e+00  -3.370
## temp_C_interpol                           5.924e+00  2.440e+00   2.428
## VPD_kPa                                   2.743e+01  1.123e+01   2.443
## Wind_mph_interpol                         1.725e+00  2.343e+00   0.736
## regionVentrum:VPD_kPa_int                 7.597e+00  3.610e+00   2.105
## regionHead:VPD_kPa_int                    1.278e+00  3.608e+00   0.354
## regionDewlap:VPD_kPa_int                  1.394e+01  3.623e+00   3.848
## regionMite Patch:VPD_kPa_int              1.678e+01  3.618e+00   4.637
## regionVentrum:Solar_rad_Wm2_interpol     -8.488e-04  8.503e-03  -0.100
## regionHead:Solar_rad_Wm2_interpol         1.284e-02  8.502e-03   1.511
## regionDewlap:Solar_rad_Wm2_interpol      -2.171e-03  8.556e-03  -0.254
## regionMite Patch:Solar_rad_Wm2_interpol -1.262e-02  8.601e-03  -1.468
## regionVentrum:mass_g                      9.970e-01  5.155e-01   1.934
## regionHead:mass_g                        -3.925e-01  5.114e-01  -0.767
## regionDewlap:mass_g                       9.816e-01  5.232e-01   1.876
## regionMite Patch:mass_g                   1.119e+00  5.311e-01   2.107
```

```
##
## Correlation matrix not shown by default, as p = 31 > 12.
## Use print(x, correlation=TRUE)  or
##     vcov(x)        if you need it
## fit warnings:
## Some predictor variables are on very different scales: consider rescaling
```

```
drop1(CEWL_mod8)
```

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

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

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

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

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

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

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

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

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

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

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

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

## 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
```

```r
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 +
```

```r
                          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
```

```r
summary(CEWL_mod10)
```

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

```
## regionHead:Solar_rad_Wm2_interpol        1.287e-02  8.501e-03   1.514
## regionDewlap:Solar_rad_Wm2_interpol     -2.184e-03  8.554e-03  -0.255
## regionMite Patch:Solar_rad_Wm2_interpol -1.267e-02  8.599e-03  -1.473
## regionVentrum:mass_g                     9.994e-01  5.153e-01   1.939
## regionHead:mass_g                       -3.898e-01  5.113e-01  -0.762
## regionDewlap:mass_g                      9.757e-01  5.229e-01   1.866
## regionMite Patch:mass_g                  1.108e+00  5.303e-01   2.090
```

```
##
## Correlation matrix not shown by default, as p = 29 > 12.
## Use print(x, correlation=TRUE)  or
##     vcov(x)        if you need it
```

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

```
drop1(CEWL_mod10)
```

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

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

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

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

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

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

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

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

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

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

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

```
## Single term deletions
##
## Model:
## TEWL_g_m2h ~ region * (VPD_kPa_int + Solar_rad_Wm2_interpol +
##     mass_g) + sex_M_F + hematocrit_percent + osmolality_mmol_kg +
```

```
##     cloacal_temp_C + hold_time + ambient_temp_C + temp_C_interpol +
##     VPD_kPa + Wind_mph_interpol + (1 | individual_ID)
##                               npar    AIC
## <none>                             4370.4
## sex_M_F                          1 4369.9
## hematocrit_percent               1 4375.1
## osmolality_mmol_kg               1 4368.5
## cloacal_temp_C                   1 4384.8
## hold_time                        1 4368.7
## ambient_temp_C                   1 4381.0
## temp_C_interpol                  1 4374.9
## VPD_kPa                          1 4375.1
## Wind_mph_interpol                1 4369.2
## region:VPD_kPa_int               4 4396.2
## region:Solar_rad_Wm2_interpol    4 4371.7
## region:mass_g                    4 4376.8
```

drop osmolality:

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

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

```
summary(CEWL_mod11)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: TEWL_g_m2h ~ region * (VPD_kPa_int + Solar_rad_Wm2_interpol +
##     mass_g) + sex_M_F + hematocrit_percent + cloacal_temp_C +
##     hold_time + ambient_temp_C + temp_C_interpol + VPD_kPa +
##     Wind_mph_interpol + (1 | individual_ID)
##    Data: CEWL_dat_sub1
##
## REML criterion at convergence: 4314.1
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.9682 -0.5511 -0.1043  0.4021  5.2537
##
## Random effects:
##  Groups        Name        Variance Std.Dev.
##  individual_ID (Intercept) 27.80    5.272
##  Residual                  99.04    9.952
## Number of obs: 570, groups:  individual_ID, 116
##
```

```
## Fixed effects:
##                                          Estimate Std. Error t value
## (Intercept)                            -2.803e+01  2.959e+01  -0.947
## regionVentrum                          -5.615e+00  8.984e+00  -0.625
## regionHead                             -2.361e+00  9.005e+00  -0.262
## regionDewlap                           -2.029e+01  9.189e+00  -2.208
## regionMite Patch                       -9.299e+00  9.266e+00  -1.004
## VPD_kPa_int                            -5.125e+01  1.693e+01  -3.027
## Solar_rad_Wm2_interpol                  1.390e-02  8.933e-03   1.556
## mass_g                                  2.622e-01  4.224e-01   0.621
## sex_M_FM                                1.747e+00  1.431e+00   1.221
## hematocrit_percent                     -3.000e-01  1.170e-01  -2.564
## cloacal_temp_C                          2.278e+00  5.700e-01   3.996
## hold_time                              -9.884e-03  1.530e-02  -0.646
## ambient_temp_C                         -5.619e+00  1.636e+00  -3.434
## temp_C_interpol                         5.816e+00  2.384e+00   2.439
## VPD_kPa                                 2.734e+01  1.108e+01   2.467
## Wind_mph_interpol                       1.972e+00  2.202e+00   0.895
## regionVentrum:VPD_kPa_int               7.595e+00  3.609e+00   2.104
## regionHead:VPD_kPa_int                  1.274e+00  3.608e+00   0.353
## regionDewlap:VPD_kPa_int                1.395e+01  3.622e+00   3.850
## regionMite Patch:VPD_kPa_int            1.679e+01  3.617e+00   4.643
## regionVentrum:Solar_rad_Wm2_interpol   -8.316e-04  8.502e-03  -0.098
## regionHead:Solar_rad_Wm2_interpol       1.286e-02  8.501e-03   1.513
## regionDewlap:Solar_rad_Wm2_interpol    -2.185e-03  8.554e-03  -0.255
## regionMite Patch:Solar_rad_Wm2_interpol -1.266e-02  8.599e-03  -1.472
## regionVentrum:mass_g                    9.985e-01  5.153e-01   1.938
## regionHead:mass_g                      -3.907e-01  5.113e-01  -0.764
## regionDewlap:mass_g                     9.757e-01  5.229e-01   1.866
## regionMite Patch:mass_g                 1.110e+00  5.303e-01   2.093
```

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

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

```r
drop1(CEWL_mod11)
```

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

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

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

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

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

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

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

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

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

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

## Single term deletions
##
## Model:
## TEWL_g_m2h ~ region * (VPD_kPa_int + Solar_rad_Wm2_interpol +
##     mass_g) + sex_M_F + hematocrit_percent + cloacal_temp_C +
##     hold_time + ambient_temp_C + temp_C_interpol + VPD_kPa +
##     Wind_mph_interpol + (1 | individual_ID)
##                                npar    AIC
## <none>                              4368.5
## sex_M_F                           1 4368.1
## hematocrit_percent                1 4373.6
## cloacal_temp_C                    1 4383.1
## hold_time                         1 4367.0
## ambient_temp_C                    1 4379.0
## temp_C_interpol                   1 4373.0
## VPD_kPa                           1 4373.1
## Wind_mph_interpol                 1 4367.4
## region:VPD_kPa_int                4 4394.3
## region:Solar_rad_Wm2_interpol     4 4369.7
## region:mass_g                     4 4374.9
```

drop hold time:

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

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

```
summary(CEWL_mod12)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: TEWL_g_m2h ~ region * (VPD_kPa_int + Solar_rad_Wm2_interpol +
##     mass_g) + sex_M_F + hematocrit_percent + cloacal_temp_C +
##     ambient_temp_C + temp_C_interpol + VPD_kPa + Wind_mph_interpol +
##     (1 | individual_ID)
##    Data: CEWL_dat_sub1
##
## REML criterion at convergence: 4308
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.9776 -0.5654 -0.1071  0.4025  5.2559
##
## Random effects:
##  Groups        Name        Variance Std.Dev.
##  individual_ID (Intercept) 27.58    5.252
##  Residual                  99.01    9.951
## Number of obs: 570, groups:  individual_ID, 116
##
## Fixed effects:
##                                          Estimate Std. Error t value
## (Intercept)                            -2.819e+01  2.952e+01  -0.955
## regionVentrum                          -5.645e+00  8.983e+00  -0.628
## regionHead                             -2.415e+00  9.004e+00  -0.268
## regionDewlap                           -2.033e+01  9.188e+00  -2.212
## regionMite Patch                       -9.308e+00  9.265e+00  -1.005
## VPD_kPa_int                            -4.766e+01  1.596e+01  -2.987
## Solar_rad_Wm2_interpol                  1.393e-02  8.919e-03   1.561
## mass_g                                  2.821e-01  4.208e-01   0.670
## sex_M_FM                                1.621e+00  1.415e+00   1.146
## hematocrit_percent                     -2.990e-01  1.168e-01  -2.561
## cloacal_temp_C                          2.543e+00  3.939e-01   6.456
## ambient_temp_C                         -5.485e+00  1.620e+00  -3.387
## temp_C_interpol                         5.350e+00  2.267e+00   2.360
## VPD_kPa                                 2.500e+01  1.045e+01   2.393
## Wind_mph_interpol                       1.767e+00  2.174e+00   0.813
## regionVentrum:VPD_kPa_int               7.596e+00  3.609e+00   2.105
## regionHead:VPD_kPa_int                  1.276e+00  3.607e+00   0.354
## regionDewlap:VPD_kPa_int                1.395e+01  3.622e+00   3.853
## regionMite Patch:VPD_kPa_int            1.681e+01  3.617e+00   4.647
## regionVentrum:Solar_rad_Wm2_interpol   -7.923e-04  8.501e-03  -0.093
## regionHead:Solar_rad_Wm2_interpol       1.291e-02  8.499e-03   1.519
## regionDewlap:Solar_rad_Wm2_interpol    -2.153e-03  8.553e-03  -0.252
## regionMite Patch:Solar_rad_Wm2_interpol -1.263e-02  8.598e-03  -1.469
## regionVentrum:mass_g                    9.989e-01  5.152e-01   1.939
## regionHead:mass_g                      -3.892e-01  5.112e-01  -0.761
## regionDewlap:mass_g                     9.772e-01  5.228e-01   1.869
## regionMite Patch:mass_g                 1.109e+00  5.302e-01   2.092

##
## Correlation matrix not shown by default, as p = 27 > 12.
## Use print(x, correlation=TRUE)  or
##     vcov(x)        if you need it

## fit warnings:
```

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

```r
drop1(CEWL_mod12)
```

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

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

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

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

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

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

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

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

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

```
## Single term deletions
##
## Model:
## TEWL_g_m2h ~ region * (VPD_kPa_int + Solar_rad_Wm2_interpol +
##     mass_g) + sex_M_F + hematocrit_percent + cloacal_temp_C +
##     ambient_temp_C + temp_C_interpol + VPD_kPa + Wind_mph_interpol +
##     (1 | individual_ID)
##                              npar    AIC
## <none>                            4367.0
## sex_M_F                         1 4366.4
## hematocrit_percent              1 4372.0
## cloacal_temp_C                  1 4403.9
## ambient_temp_C                  1 4377.0
## temp_C_interpol                 1 4371.0
## VPD_kPa                         1 4371.1
## Wind_mph_interpol               1 4365.7
## region:VPD_kPa_int              4 4392.8
## region:Solar_rad_Wm2_interpol   4 4368.2
## region:mass_g                   4 4373.4
```

drop wind:

```r
CEWL_mod13 <- lme4::lmer(data = CEWL_dat_sub1,
                          # response variable
                          TEWL_g_m2h ~
```

```r
                           # 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
```

```r
summary(CEWL_mod13)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: TEWL_g_m2h ~ region * (VPD_kPa_int + Solar_rad_Wm2_interpol +
##     mass_g) + sex_M_F + hematocrit_percent + cloacal_temp_C +
##     ambient_temp_C + temp_C_interpol + VPD_kPa + (1 | individual_ID)
##    Data: CEWL_dat_sub1
##
## REML criterion at convergence: 4312.1
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.9675 -0.5520 -0.1066  0.4046  5.2659
##
## Random effects:
##  Groups        Name        Variance Std.Dev.
##  individual_ID (Intercept) 27.35    5.230
##  Residual                  99.05    9.952
## Number of obs: 570, groups:  individual_ID, 116
##
## Fixed effects:
##                                         Estimate Std. Error t value
## (Intercept)                           -2.789e+01  2.945e+01  -0.947
## regionVentrum                         -5.577e+00  8.984e+00  -0.621
## regionHead                            -2.397e+00  9.005e+00  -0.266
## regionDewlap                          -2.037e+01  9.189e+00  -2.217
## regionMite Patch                      -9.365e+00  9.266e+00  -1.011
## VPD_kPa_int                           -4.567e+01  1.573e+01  -2.904
## Solar_rad_Wm2_interpol                 1.375e-02  8.903e-03   1.544
## mass_g                                 2.888e-01  4.204e-01   0.687
## sex_M_FM                               1.597e+00  1.411e+00   1.131
## hematocrit_percent                    -2.880e-01  1.157e-01  -2.489
## cloacal_temp_C                         2.467e+00  3.817e-01   6.463
## ambient_temp_C                        -4.707e+00  1.303e+00  -3.611
## temp_C_interpol                        4.994e+00  2.219e+00   2.251
## VPD_kPa                                2.304e+01  1.014e+01   2.273
## regionVentrum:VPD_kPa_int              7.597e+00  3.610e+00   2.105
## regionHead:VPD_kPa_int                 1.283e+00  3.608e+00   0.356
## regionDewlap:VPD_kPa_int               1.396e+01  3.622e+00   3.853
## regionMite Patch:VPD_kPa_int           1.678e+01  3.617e+00   4.638
## regionVentrum:Solar_rad_Wm2_interpol  -8.341e-04  8.502e-03  -0.098
## regionHead:Solar_rad_Wm2_interpol      1.288e-02  8.501e-03   1.515
```

```
## regionDewlap:Solar_rad_Wm2_interpol     -2.131e-03  8.554e-03  -0.249
## regionMite Patch:Solar_rad_Wm2_interpol -1.264e-02  8.599e-03  -1.470
## regionVentrum:mass_g                     9.961e-01  5.153e-01   1.933
## regionHead:mass_g                       -3.879e-01  5.113e-01  -0.759
## regionDewlap:mass_g                      9.790e-01  5.229e-01   1.872
## regionMite Patch:mass_g                  1.117e+00  5.302e-01   2.106
```

```
##
## Correlation matrix not shown by default, as p = 26 > 12.
## Use print(x, correlation=TRUE)  or
##     vcov(x)        if you need it
```

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

```
drop1(CEWL_mod13)
```

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

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

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

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

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

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

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

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

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

```
## region:Solar_rad_Wm2_interpol    4 4366.9
## region:mass_g                    4 4372.1
```

drop sex:

```r
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
```

```r
summary(CEWL_mod14)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: TEWL_g_m2h ~ region * (VPD_kPa_int + Solar_rad_Wm2_interpol +
##     mass_g) + hematocrit_percent + cloacal_temp_C + ambient_temp_C +
##     temp_C_interpol + VPD_kPa + (1 | individual_ID)
##    Data: CEWL_dat_sub1
##
## REML criterion at convergence: 4315.9
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.9876 -0.5559 -0.1019  0.3960  5.2201
##
## Random effects:
##  Groups        Name        Variance Std.Dev.
##  individual_ID (Intercept) 27.39    5.233
##  Residual                  99.09    9.955
## Number of obs: 570, groups:  individual_ID, 116
##
## Fixed effects:
##                                      Estimate Std. Error t value
## (Intercept)                        -2.845e+01  2.946e+01  -0.966
## regionVentrum                      -5.527e+00  8.986e+00  -0.615
## regionHead                         -2.383e+00  9.007e+00  -0.265
## regionDewlap                       -2.032e+01  9.191e+00  -2.211
## regionMite Patch                   -9.317e+00  9.268e+00  -1.005
## VPD_kPa_int                        -4.566e+01  1.574e+01  -2.902
## Solar_rad_Wm2_interpol              1.430e-02  8.893e-03   1.608
## mass_g                              3.394e-01  4.182e-01   0.812
## hematocrit_percent                 -2.620e-01  1.135e-01  -2.310
## cloacal_temp_C                      2.462e+00  3.818e-01   6.449
## ambient_temp_C                     -4.772e+00  1.303e+00  -3.663
## temp_C_interpol                     5.016e+00  2.220e+00   2.259
## VPD_kPa                             2.354e+01  1.013e+01   2.323
## regionVentrum:VPD_kPa_int           7.595e+00  3.610e+00   2.104
```

```
## regionHead:VPD_kPa_int                     1.318e+00  3.609e+00   0.365
## regionDewlap:VPD_kPa_int                   1.399e+01  3.623e+00   3.862
## regionMite Patch:VPD_kPa_int               1.678e+01  3.618e+00   4.637
## regionVentrum:Solar_rad_Wm2_interpol      -8.686e-04  8.504e-03  -0.102
## regionHead:Solar_rad_Wm2_interpol          1.287e-02  8.503e-03   1.513
## regionDewlap:Solar_rad_Wm2_interpol       -2.145e-03  8.556e-03  -0.251
## regionMite Patch:Solar_rad_Wm2_interpol -1.264e-02  8.601e-03  -1.470
## regionVentrum:mass_g                       9.944e-01  5.154e-01   1.929
## regionHead:mass_g                         -3.901e-01  5.114e-01  -0.763
## regionDewlap:mass_g                        9.735e-01  5.230e-01   1.862
## regionMite Patch:mass_g                    1.112e+00  5.303e-01   2.097
```

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

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

```r
drop1(CEWL_mod14)
```

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

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

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

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

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

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

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

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

```
## region:VPD_kPa_int              4 4390.8
## region:Solar_rad_Wm2_interpol    4 4366.3
## region:mass_g                    4 4371.4
```

drop hematocrit:

```r
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
```

```r
summary(CEWL_mod15)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: TEWL_g_m2h ~ region * (VPD_kPa_int + Solar_rad_Wm2_interpol +
##     mass_g) + cloacal_temp_C + ambient_temp_C + temp_C_interpol +
##     VPD_kPa + (1 | individual_ID)
##    Data: CEWL_dat_sub1
##
## REML criterion at convergence: 4318.6
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.9727 -0.5678 -0.1167  0.3925  5.2412
##
## Random effects:
##  Groups        Name        Variance Std.Dev.
##  individual_ID (Intercept) 29.27    5.410
##  Residual                  99.10    9.955
## Number of obs: 570, groups:  individual_ID, 116
##
## Fixed effects:
##                                          Estimate Std. Error t value
## (Intercept)                            -3.296e+01  2.994e+01  -1.101
## regionVentrum                          -5.605e+00  8.987e+00  -0.624
## regionHead                             -2.427e+00  9.008e+00  -0.269
## regionDewlap                           -2.044e+01  9.193e+00  -2.224
## regionMite Patch                       -9.316e+00  9.269e+00  -1.005
## VPD_kPa_int                            -4.300e+01  1.600e+01  -2.688
## Solar_rad_Wm2_interpol                  1.788e-02  8.862e-03   2.017
## mass_g                                  2.651e-01  4.201e-01   0.631
## cloacal_temp_C                          2.305e+00  3.830e-01   6.017
## ambient_temp_C                         -4.598e+00  1.326e+00  -3.468
## temp_C_interpol                         4.384e+00  2.247e+00   1.951
## VPD_kPa                                 2.498e+01  1.030e+01   2.424
## regionVentrum:VPD_kPa_int               7.574e+00  3.611e+00   2.098
## regionHead:VPD_kPa_int                  1.283e+00  3.609e+00   0.355
```

```
## regionDewlap:VPD_kPa_int                 1.394e+01  3.623e+00   3.848
## regionMite Patch:VPD_kPa_int             1.677e+01  3.618e+00   4.633
## regionVentrum:Solar_rad_Wm2_interpol    -8.689e-04  8.504e-03  -0.102
## regionHead:Solar_rad_Wm2_interpol        1.285e-02  8.503e-03   1.511
## regionDewlap:Solar_rad_Wm2_interpol     -2.101e-03  8.557e-03  -0.246
## regionMite Patch:Solar_rad_Wm2_interpol -1.270e-02  8.602e-03  -1.477
## regionVentrum:mass_g                     1.002e+00  5.155e-01   1.943
## regionHead:mass_g                       -3.836e-01  5.115e-01  -0.750
## regionDewlap:mass_g                      9.819e-01  5.231e-01   1.877
## regionMite Patch:mass_g                  1.116e+00  5.304e-01   2.105
```

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

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

```r
drop1(CEWL_mod15)
```

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

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

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

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

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

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

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

drop region*sorad interaction:

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

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

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

```
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
```

```r
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:

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

```
## Linear mixed model fit by REML ['lmerMod']
## Formula:
## TEWL_g_m2h ~ region * (VPD_kPa_int + mass_g) + Solar_rad_Wm2_interpol +
##     cloacal_temp_C + ambient_temp_C + (1 | individual_ID)
##    Data: CEWL_dat_sub1
##
## REML criterion at convergence: 4311.6
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.1109 -0.5796 -0.1096  0.3721  5.5173
##
## Random effects:
##  Groups        Name        Variance Std.Dev.
##  individual_ID (Intercept)  31.36    5.6
##  Residual                  100.07   10.0
## Number of obs: 570, groups:  individual_ID, 116
##
## Fixed effects:
##                               Estimate Std. Error t value
## (Intercept)                   8.787318  22.888471   0.384
## regionVentrum                -5.968820   6.242171  -0.956
## regionHead                    7.613204   6.242608   1.220
## regionDewlap                -21.887146   6.354175  -3.445
## regionMite Patch            -19.374143   6.409004  -3.023
## VPD_kPa_int                  -8.185200   2.928817  -2.795
## mass_g                        0.355432   0.422858   0.841
## Solar_rad_Wm2_interpol        0.014955   0.004342   3.444
## cloacal_temp_C                2.320429   0.390650   5.940
## ambient_temp_C               -2.191820   0.968373  -2.263
## regionVentrum:VPD_kPa_int     7.513621   3.451025   2.177
## regionHead:VPD_kPa_int        2.957280   3.448109   0.858
## regionDewlap:VPD_kPa_int     13.677128   3.453759   3.960
## regionMite Patch:VPD_kPa_int  15.031802   3.435475   4.375
## regionVentrum:mass_g          0.978204   0.517761   1.889
## regionHead:mass_g            -0.373426   0.513790  -0.727
## regionDewlap:mass_g           0.974520   0.525688   1.854
## regionMite Patch:mass_g       1.138635   0.532959   2.136

##
## Correlation matrix not shown by default, as p = 18 > 12.
## Use print(x, correlation=TRUE)  or
##     vcov(x)        if you need it
```

```
drop1(CEWL_mod18)
```

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

```
## ambient_temp_C            1 4375.9
## region:VPD_kPa_int        4 4393.3
## region:mass_g             4 4378.6
```

drop ambient temp at msmt:

```
CEWL_mod19 <- lme4::lmer(data = CEWL_dat_sub1,
                          # response variable
                          TEWL_g_m2h ~
                          # potential predictors
                          region * (VPD_kPa_int + mass_g) +
                          Solar_rad_Wm2_interpol +
                          cloacal_temp_C +
                          # random effect
                          (1|individual_ID))
summary(CEWL_mod19)
```

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

##
```

```
## Correlation matrix not shown by default, as p = 17 > 12.
## Use print(x, correlation=TRUE)  or
##     vcov(x)        if you need it
```

```
drop1(CEWL_mod19)
```

```
## Single term deletions
##
## Model:
## TEWL_g_m2h ~ region * (VPD_kPa_int + mass_g) + Solar_rad_Wm2_interpol +
##     cloacal_temp_C + (1 | individual_ID)
##                        npar    AIC
## <none>                      4375.9
## Solar_rad_Wm2_interpol    1 4384.3
## cloacal_temp_C            1 4402.0
## region:VPD_kPa_int        4 4396.1
## region:mass_g             4 4382.2
```

finally, test the null model

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

Selection

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

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

#specify model names
CEWL_mod_names <- c('(model 6a) ~ region*VPD_kPa_int + region*Solar_rad_Wm2_interpol + region*SMI + reg
                     '(model 7) ~ region*VPD_kPa_int + region*Solar_rad_Wm2_interpol + SMI + region*ma
                     '(model 8) ~ region*VPD_kPa_int + region*Solar_rad_Wm2_interpol + SMI + region*ma
                     '(model 9) ~ region*VPD_kPa_int + region*Solar_rad_Wm2_interpol + region*mass_g +
                     '(model 10) ~ region*VPD_kPa_int + region*Solar_rad_Wm2_interpol + region*mass_g
                     '(model 11) ~ region*VPD_kPa_int + region*Solar_rad_Wm2_interpol + region*mass_g
                    '(model 12) ~ region*VPD_kPa_int + region*Solar_rad_Wm2_interpol + region*mass_g +
                    '(model 13) ~ region*VPD_kPa_int + region*Solar_rad_Wm2_interpol + region*mass_g +
                    '(model 14) ~ region*VPD_kPa_int + region*Solar_rad_Wm2_interpol + region*mass_g +
                    '(model 15) ~ region*VPD_kPa_int + region*Solar_rad_Wm2_interpol + region*mass_g +
                    '(model 16) ~ region*VPD_kPa_int + Solar_rad_Wm2_interpol + region*mass_g + cloaca
                    '(model 17) ~ region*VPD_kPa_int + Solar_rad_Wm2_interpol + region*mass_g + cloaca
                    '(model 18) ~ region*VPD_kPa_int + Solar_rad_Wm2_interpol + region*mass_g + cloaca
                    '(model 19) ~ region*VPD_kPa_int + Solar_rad_Wm2_interpol + region*mass_g + cloaca
                     'null model')
#calculate AIC of each model
CEWL_AICc <- data.frame(aictab(cand.set = CEWL_models,
                               modnames = CEWL_mod_names))
```

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

```
CEWL_AICc
```

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

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

```
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
```

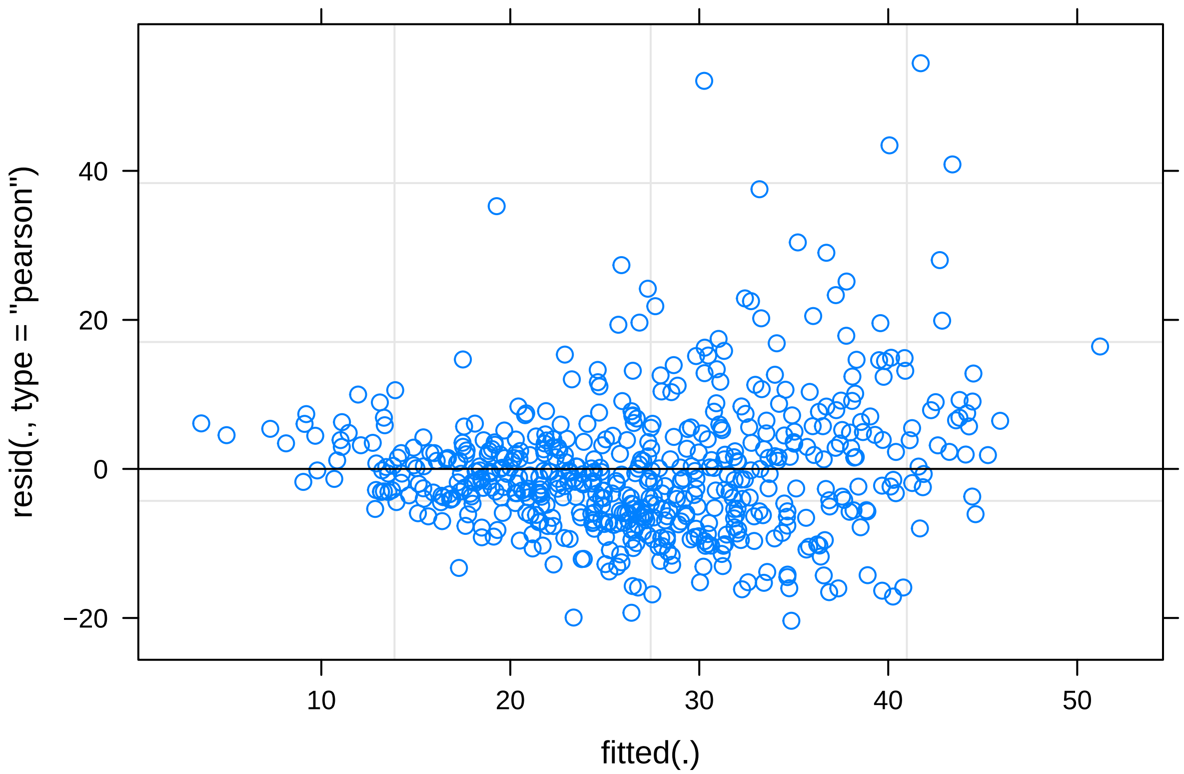
```
CEWL_mod17p <- lmerTest::lmer(data = CEWL_dat_sub1,
                          # response variable
                          TEWL_g_m2h ~
                          # potential predictors
                          region * (VPD_kPa_int + mass_g) +
                          Solar_rad_Wm2_interpol +
                          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
```

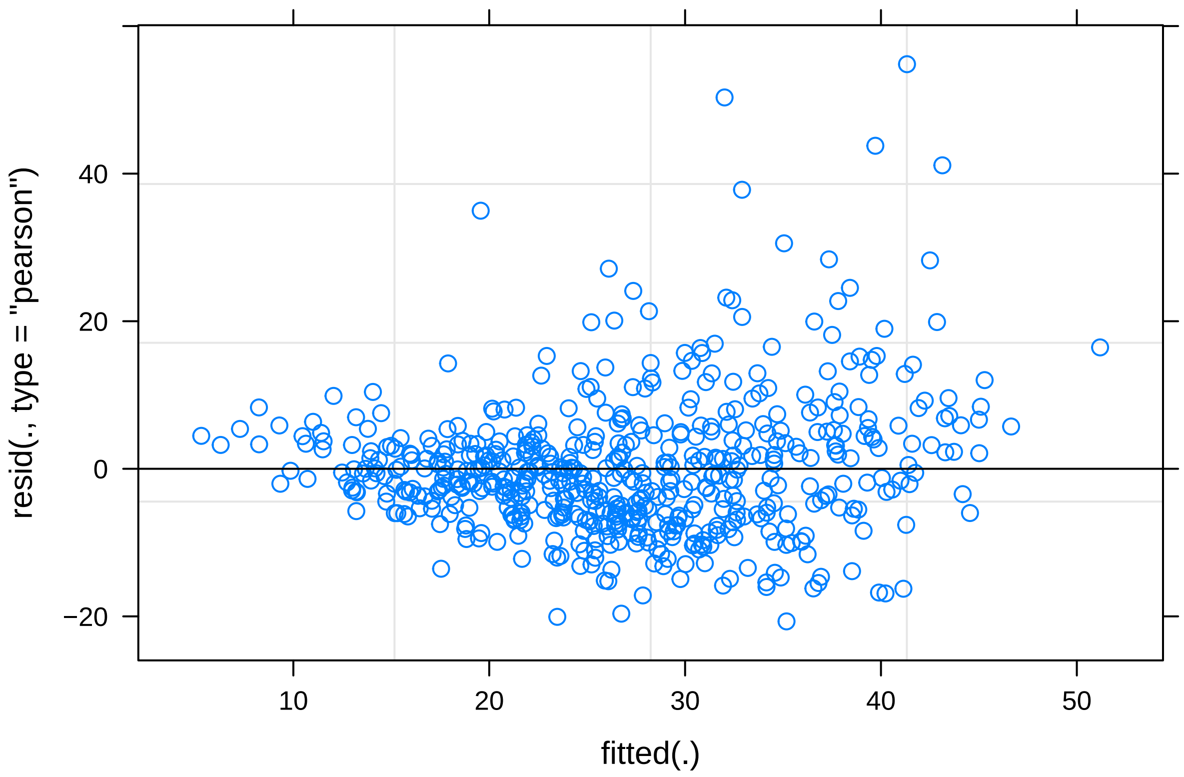
```
## regionVentrum:VPD_kPa_int      7.476906   3.452851 442.783297   2.165 0.030888
## regionHead:VPD_kPa_int         2.939064   3.449868 442.902557   0.852 0.394710
## regionDewlap:VPD_kPa_int      13.660303   3.455489 443.552232   3.953 8.97e-05
## regionMite Patch:VPD_kPa_int  14.966590   3.437480 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)
```




```r
plot(CEWL_mod17)
```

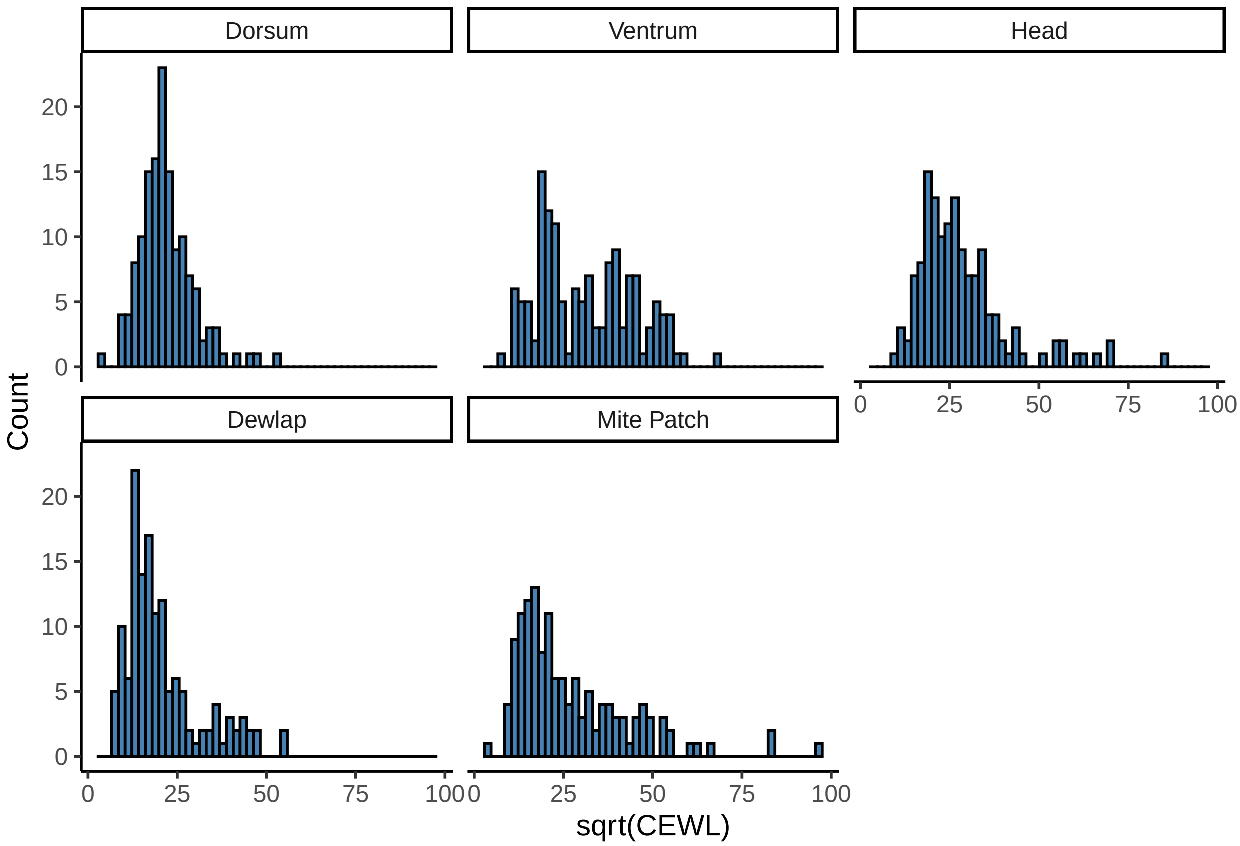


Both have fanning, which indicates that linearity and equal error variance are not satisfied.

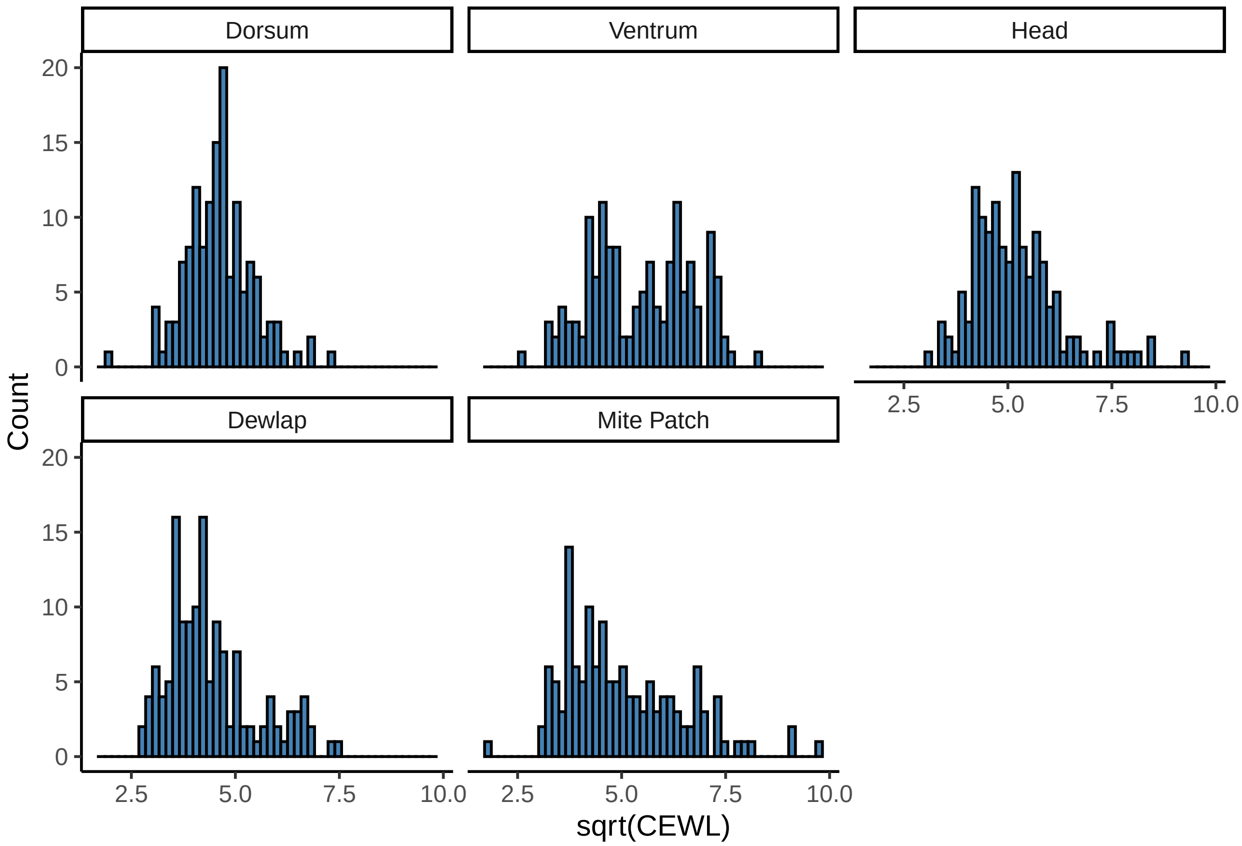
Test Transformations

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

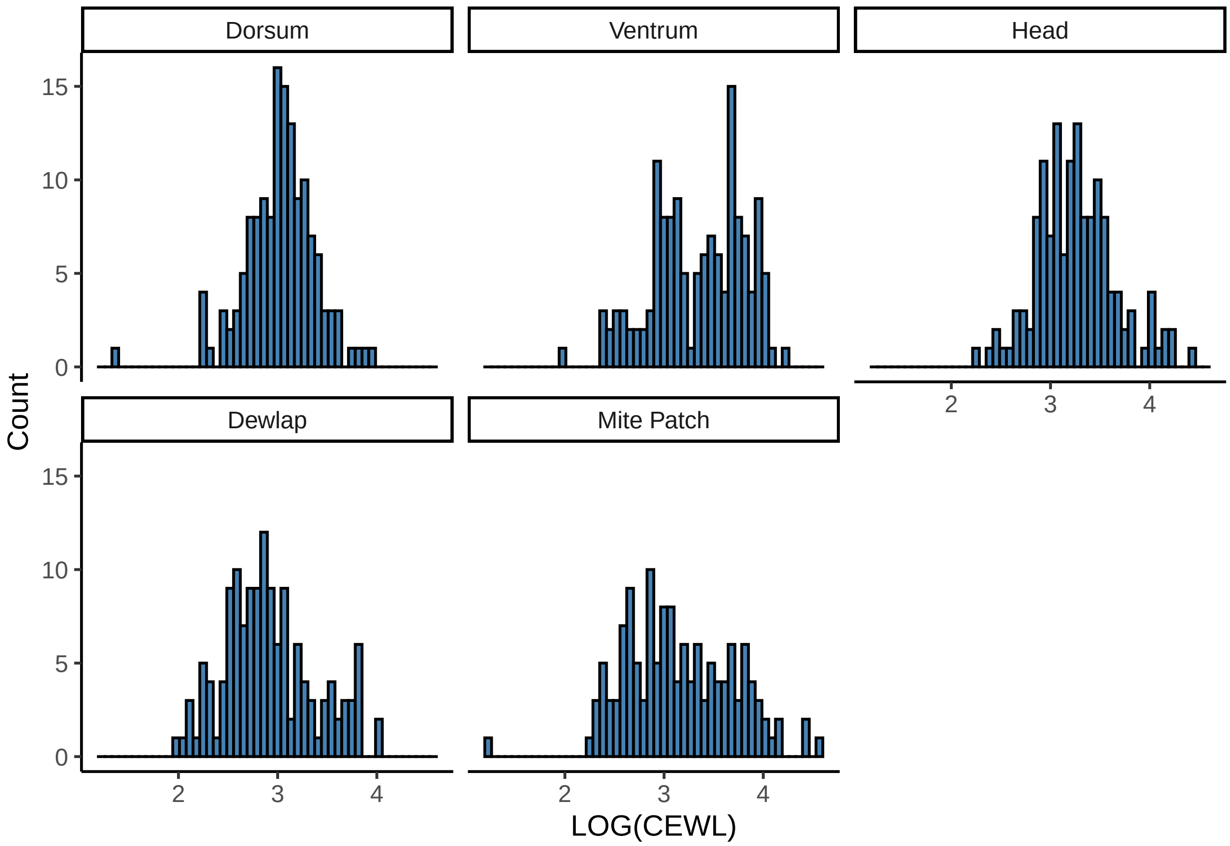
```
# normal TEWL
CEWL_data_full %>%
  ggplot(., aes(x = (TEWL_g_m2h))) +
  geom_histogram(color = "black", fill="steelblue", bins=50) +
  theme_classic() +
  xlab("sqrt(CEWL)") +
  ylab("Count") +
  facet_wrap(~region)
```




```
# 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)
```




```r
# 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)
```



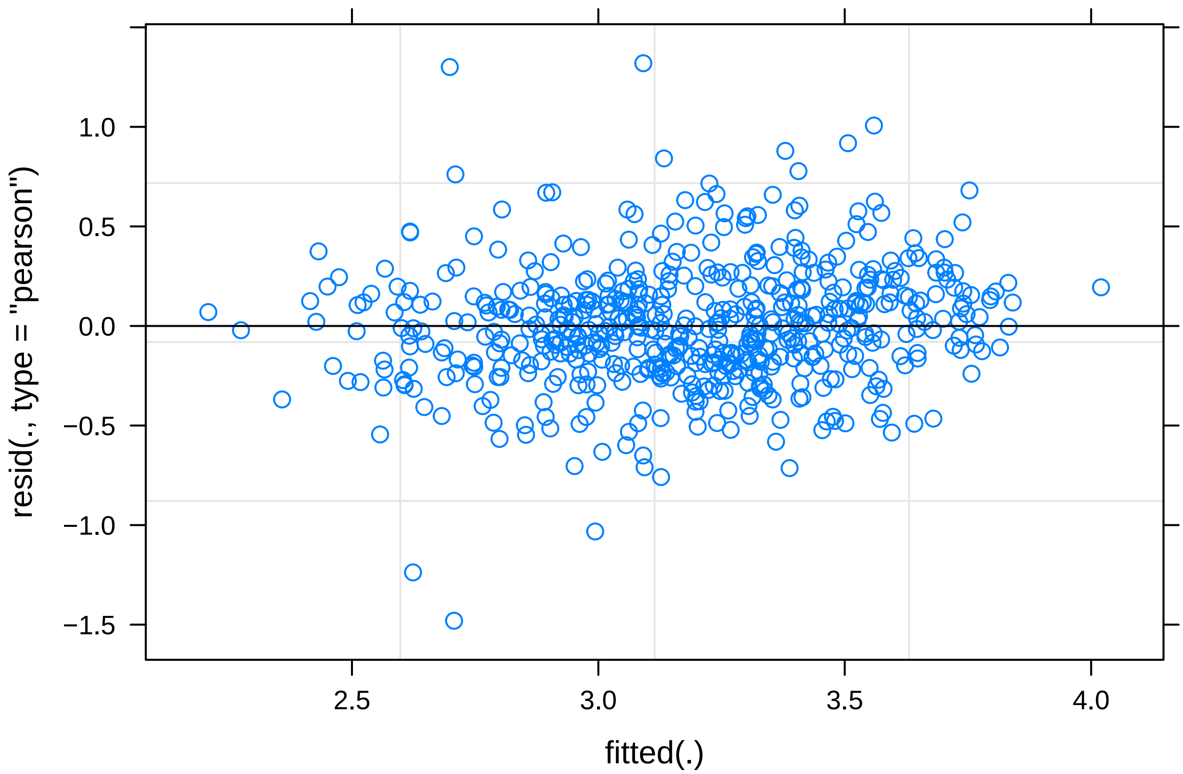
Log transforming seems to be pretty effective across body regions.

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:

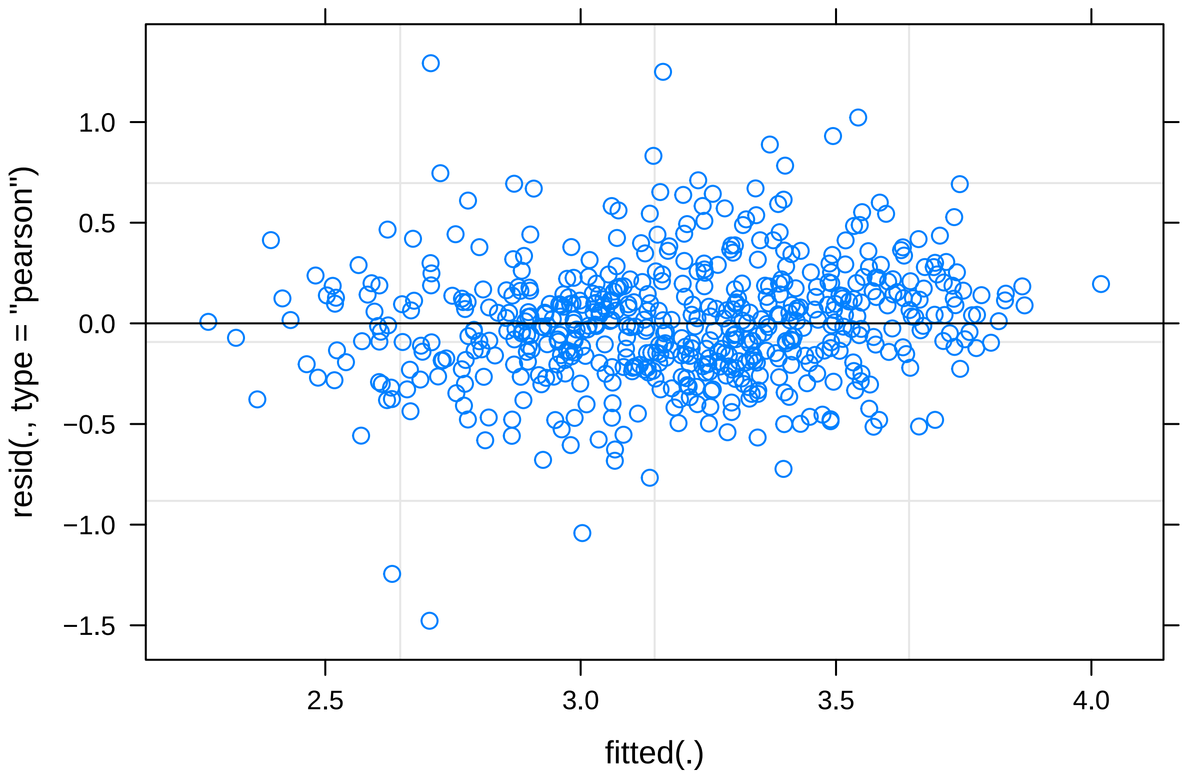
```
CEWL_mod16t <- lme4::lmer(data = CEWL_dat_sub1,
                          # response variable
                          log(TEWL_g_m2h) ~
                          # potential predictors
                          region * (VPD_kPa_int + mass_g) +
                          Solar_rad_Wm2_interpol +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




```r
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
```

```r
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)
```




```r
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:

```r
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))
```

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

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

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

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

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

```r
CEWL_mod17tp <- lmerTest::lmer(data = CEWL_dat_sub2,
                          # response variable
                          log(TEWL_g_m2h) ~
                          # potential predictors
                          region * (VPD_kPa_int + mass_g) +
                          Solar_rad_Wm2_interpol +
                          cloacal_temp_C +
                          ambient_temp_C + VPD_kPa +
                          # random effect
                          (1|individual_ID))
summary(CEWL_mod17p)
```

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

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

Export

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

```
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")
```