Sceloporus Humidity Acclimation - Experimental Data Analysis

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Contents

Packages

Data

This data was collected in the Spring of 2021 in conjunction with a study carried out in Cal Poly's Herpetology class. Some lizards measured for that primary study were kept to observe physiological changes in response to different climate treatments. See (doi) for full details

Morphometrics & Hydration

Treatment Groups

variables: - individual lizard ID - temp_tmt_C = temperature treatment - humidity_tmt_percent = humidity treatment (high/low, not actually %) - trial_number = which set of lizards that individual was from - conclusion = how that individual's experiment ended (died, canceled, or complete)

```
tmts <- read.csv("./data/exp_tmt_assignment.csv")
```

Capture Data

variables: - date = date of capture & baseline measurements - individual lizard ID - mass_g = mass in grams
- hematocrit_percent = % of blood sample that's red blood cells - osmolality_mmol_kg = concentration of
solutes in blood plasma - type = when the measurements were taken along the course of the experiment (all
on capture day)

```
capture_hydration <- read.csv("./exported_data/capture_hydration.csv",
                              na.strings=c("","NA") # fix empty cells
                              ) %>%
  mutate(# correctly format date-only variable
         date = as.Date(date, format = "%Y-%m-%d")
         ) %>%
  # select only relevant variables
  dplyr::select(date, individual_ID,
                mass_g, hematocrit_percent, osmolality_mmol_kg
                ) %>%
  dplyr::filter(individual_ID %in% tmts$individual_ID) %>%
  mutate(type = as.factor("capture"))
summary(capture_hydration)
```

```
##       date              individual_ID       mass_g       hematocrit_percent
##  Min.   :2021-04-19   Min.   : 31.00   Min.   : 8.20   Min.   :16.00
##  1st Qu.:2021-04-26   1st Qu.: 57.00   1st Qu.:11.10   1st Qu.:32.75
##  Median :2021-04-26   Median : 78.00   Median :12.65   Median :36.00
##  Mean   :2021-04-29   Mean   : 77.46   Mean   :12.18   Mean   :36.08
##  3rd Qu.:2021-05-03   3rd Qu.: 98.25   3rd Qu.:13.32   3rd Qu.:39.00
##  Max.   :2021-05-10   Max.   :122.00   Max.   :15.00   Max.   :54.00
##  osmolality_mmol_kg       type
##  Min.   :319.0      capture:52
##  1st Qu.:354.2
##  Median :373.0
##  Mean   :373.7
##  3rd Qu.:392.2
##  Max.   :423.0
```

extract SVL data separately from capture data:

```
SVL <- read.csv("./exported_data/capture_hydration.csv",
                na.strings=c("","NA") # fix empty cells
                ) %>%
  dplyr::select(individual_ID, SVL_mm) %>%
  dplyr::filter(individual_ID %in% tmts$individual_ID)
summary(SVL)
```

```
##  individual_ID       SVL_mm
##  Min.   : 31.00   Min.   :59.00
##  1st Qu.: 57.00   1st Qu.:65.00
##  Median : 78.00   Median :68.00
##  Mean   : 77.46   Mean   :67.62
##  3rd Qu.: 98.25   3rd Qu.:70.00
##  Max.   :122.00   Max.   :73.00
```

extract capture CEWL cloacal temperature separately:

```
cap_CT <- read.csv("./exported_data/capture_hydration.csv",
                   na.strings=c("","NA") # fix empty cells
```

```
                             ) %>%
  dplyr::select(individual_ID, cloacal_temp_C) %>%
  dplyr::filter(individual_ID %in% tmts$individual_ID)
summary(cap_CT)
```

```
##  individual_ID   cloacal_temp_C
##  Min.   : 31.00  Min.   :20.00
##  1st Qu.: 57.00  1st Qu.:22.00
##  Median : 78.00  Median :24.00
##  Mean   : 77.46  Mean   :23.68
##  3rd Qu.: 98.25  3rd Qu.:25.00
##  Max.   :122.00  Max.   :28.00
##                  NA's   :2
```

Experiment Data

variables: - date = date of measurements - individual lizard ID - mass_g = mass in grams - hematocrit_percent = % of blood sample that's red blood cells - osmolality_mmol_kg = concentration of solutes in blood plasma (mean of 1-3 replicates) - type = when the measurements were taken along the course of the experiment (either during experimental treatment or after rehab)

```
exp_dat <- read.csv("./data/experimental_data.csv",
                         na.strings=c("","NA") # fix empty cells
                         ) %>%
             # format date
  dplyr::mutate(date = as.Date(date, format = "%m/%d/%y"),
                type = as.factor(type)
                ) %>%
  # select only variables to be analyzed
  dplyr::select(date, individual_ID, mass_g,
                hematocrit_percent, type,
                osmolality_mmol_kg = osmolality_mmol_kg_replicate_mean)
summary(exp_dat)
```

```
##       date             individual_ID      mass_g       hematocrit_percent
##  Min.   :2021-04-21   Min.   : 31.00   Min.   : 6.700   Min.   :12.0
##  1st Qu.:2021-04-28   1st Qu.: 51.25   1st Qu.: 9.875   1st Qu.:23.0
##  Median :2021-05-07   Median : 87.50   Median :11.250   Median :28.0
##  Mean   :2021-05-06   Mean   : 77.85   Mean   :11.076   Mean   :27.8
##  3rd Qu.:2021-05-14   3rd Qu.:101.25   3rd Qu.:12.225   3rd Qu.:33.0
##  Max.   :2021-05-20   Max.   :122.00   Max.   :14.700   Max.   :43.0
##                                                         NA's   :19
##     type     osmolality_mmol_kg
##  exp  :98   Min.   :298.0
##  rehab:34   1st Qu.:342.0
##             Median :355.0
##             Mean   :360.1
##             3rd Qu.:374.8
##             Max.   :441.0
##             NA's   :22
```

Join Dataframes

Now, attach all the dataframes, only use individuals whose treatment was completed, and add a "day" variable for what day of treatment each lizard/observation was on. I also calculate SMI using the equation created in

3

capture_analysis.

```r
all_dat <- exp_dat %>%
  # join data
  rbind(capture_hydration) %>%
  # add tmt group info
  left_join(tmts, by = "individual_ID") %>%
  dplyr::select(-notes) %>%
  # add SVL value for each obs of each indiv.
  # for computing BCI and scaled mass indices
  left_join(SVL, by = "individual_ID") %>%
  # only use completed experiment runs
  dplyr::filter(conclusion == "complete") %>%
  group_by(individual_ID) %>%
  # reformat a lot of variables
  mutate(capture_date = min(date),
         day = as.numeric(date - capture_date),
         humidity_tmt_percent = as.factor(humidity_tmt_percent),
         individual_ID = as.factor(individual_ID),
         temp_tmt_C = as.factor(temp_tmt_C),
         trial_number = as.factor(trial_number),
         conclusion = as.factor(conclusion),
         SMI = mass_g * ((65.02158/SVL_mm) ^ (3.09059/sqrt(0.8944)))
         ) %>%
  # in the first trial we took measurements every 2 days
  # exclude those obs to make consistent across trials
  dplyr::filter(day %nin% c(2,6))
```

```r
summary(all_dat)
```

```
##      date              individual_ID     mass_g       hematocrit_percent
##  Min.   :2021-04-19   37     :  4    Min.   : 6.70   Min.   :12.00
##  1st Qu.:2021-05-01   39     :  4    1st Qu.:10.20   1st Qu.:24.00
##  Median :2021-05-10   40     :  4    Median :11.50   Median :30.00
##  Mean   :2021-05-07   49     :  4    Mean   :11.35   Mean   :29.95
##  3rd Qu.:2021-05-14   52     :  4    3rd Qu.:12.70   3rd Qu.:35.00
##  Max.   :2021-05-20   54     :  4    Max.   :15.00   Max.   :54.00
##                       (Other):115                    NA's   :12
##      type     osmolality_mmol_kg temp_tmt_C humidity_tmt_percent trial_number
##  exp    :70   Min.   :298.0      25:139     dry  :68             1:23
##  rehab  :34   1st Qu.:342.0                 humid:71             2:24
##  capture:35   Median :358.5                                      3:44
##               Mean   :362.4                                      4:48
##               3rd Qu.:379.5
##               Max.   :441.0
##               NA's   :15
##     conclusion      SVL_mm        capture_date             day
##  complete:139   Min.   :59.00   Min.   :2021-04-19   Min.   : 0.000
##                 1st Qu.:66.00   1st Qu.:2021-04-26   1st Qu.: 2.000
##                 Median :68.00   Median :2021-05-03   Median : 4.000
##                 Mean   :67.66   Mean   :2021-05-01   Mean   : 5.547
##                 3rd Qu.:70.00   3rd Qu.:2021-05-10   3rd Qu.: 9.000
##                 Max.   :73.00   Max.   :2021-05-10   Max.   :11.000
##
##       SMI
```

```
##  Min.   : 7.343
##  1st Qu.: 8.976
##  Median : 9.977
##  Mean   : 9.958
##  3rd Qu.:10.751
##  Max.   :13.970
##
```

```r
unique(all_dat$individual_ID)
```

```
##  [1] 47  49  39  52  37  40  80  66  54  61  74  73  92  91  95  88  93  96  98
## [20] 89  99  81  97  104 108 122 118 109 113 105 114 101 117 102 103
## 35 Levels: 37 39 40 47 49 52 54 61 66 73 74 80 81 88 89 91 92 93 95 96 ... 122
```

re-order some factors:

```r
all_dat$humidity_tmt_percent <- factor(all_dat$humidity_tmt_percent,
                                       levels = c("humid", "dry"),
                                       labels = c("Humid", "Dry"))
```

```r
all_dat$day <- factor(all_dat$day,
                      levels = c("0", "4", "8", "9", "10", "11"),
                      labels = c("Before Acclimation",
                                 "Mid Acclimation",
                                 "After Acclimation",
                                 "After Acclimation",
                                 "After Rehydration",
                                 "After Rehydration"))
summary(all_dat)
```

```
##       date             individual_ID     mass_g        hematocrit_percent
##  Min.   :2021-04-19    37     :  4   Min.   : 6.70   Min.   :12.00
##  1st Qu.:2021-05-01    39     :  4   1st Qu.:10.20   1st Qu.:24.00
##  Median :2021-05-10    40     :  4   Median :11.50   Median :30.00
##  Mean   :2021-05-07    49     :  4   Mean   :11.35   Mean   :29.95
##  3rd Qu.:2021-05-14    52     :  4   3rd Qu.:12.70   3rd Qu.:35.00
##  Max.   :2021-05-20    54     :  4   Max.   :15.00   Max.   :54.00
##                        (Other):115                   NA's   :12
##      type    osmolality_mmol_kg temp_tmt_C humidity_tmt_percent trial_number
##  exp    :70   Min.   :298.0      25:139      Humid:71             1:23
##  rehab  :34   1st Qu.:342.0                  Dry  :68             2:24
##  capture:35   Median :358.5                                       3:44
##               Mean   :362.4                                       4:48
##               3rd Qu.:379.5
##               Max.   :441.0
##               NA's   :15
##    conclusion      SVL_mm       capture_date                    day
##  complete:139   Min.   :59.00   Min.   :2021-04-19   Before Acclimation:35
##                 1st Qu.:66.00   1st Qu.:2021-04-26   Mid Acclimation   :35
##                 Median :68.00   Median :2021-05-03   After Acclimation :35
##                 Mean   :67.66   Mean   :2021-05-01   After Rehydration :34
##                 3rd Qu.:70.00   3rd Qu.:2021-05-10
##                 Max.   :73.00   Max.   :2021-05-10
##
##       SMI
##  Min.   : 7.343
```

```
##  1st Qu.: 8.976
##  Median : 9.977
##  Mean   : 9.958
##  3rd Qu.:10.751
##  Max.   :13.970
##
```

make a sub-dataframe without rehab data to prevent any mix-ups:

```
all_dat_no_rehab <- all_dat %>%
  dplyr::filter(type != "rehab")
```

Checks

Dates:

```
# check that capture dates are valid
unique(all_dat$capture_date)
```

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

Check that each lizard has an accurate number of measurements.

```
all_dat %>%
  group_by(individual_ID, type) %>%
  summarise(n = n()) %>%
  arrange(type)
```

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

```
## # A tibble: 104 x 3
## # Groups:   individual_ID [35]
##    individual_ID type      n
##    <fct>         <fct> <int>
##  1 37            exp       2
##  2 39            exp       2
##  3 40            exp       2
##  4 47            exp       2
##  5 49            exp       2
##  6 52            exp       2
##  7 54            exp       2
##  8 61            exp       2
##  9 66            exp       2
## 10 73            exp       2
## # ... with 94 more rows
```

That all looks good, every lizard has 1 capture measurement, 2 experimental measurements, and 1 rehab measurement.

CEWL

Capture CEWL

variables: - date = date of capture & baseline measurements - individual lizard ID - region = which body area the measurement was taken from - TEWL_g_m2h = evaporative water loss - cloacal_temp_C = taken at measurement; influences CEWL

```
cap_CEWL <- read.csv("./exported_data/capture_CEWL.csv") %>%
  dplyr::select(date, individual_ID, region, TEWL_g_m2h) %>%
```

```r
  mutate(#individual_ID = as.factor(individual_ID), # do later
         date = as.Date(date, format = "%Y-%m-%d"),
         region = as.factor(region),
         day = as.factor("before"),
         n_day = 0
         ) %>%
  dplyr::filter(individual_ID %in% all_dat$individual_ID) %>%
  left_join(cap_CT, by = 'individual_ID')
summary(cap_CEWL)
```

```
##       date               individual_ID    region      TEWL_g_m2h          day
##  Min.   :2021-04-19   Min.   : 37.00   dewl:32   Min.   : 7.48   before:163
##  1st Qu.:2021-04-26   1st Qu.: 73.00   dors:33   1st Qu.:20.54
##  Median :2021-05-03   Median : 95.00   head:33   Median :27.43
##  Mean   :2021-05-02   Mean   : 87.46   mite:32   Mean   :29.30
##  3rd Qu.:2021-05-10   3rd Qu.:104.00   vent:33   3rd Qu.:36.91
##  Max.   :2021-05-10   Max.   :122.00             Max.   :62.94
##      n_day     cloacal_temp_C
##  Min.   :0   Min.   :20.00
##  1st Qu.:0   1st Qu.:22.00
##  Median :0   Median :24.00
##  Mean   :0   Mean   :23.84
##  3rd Qu.:0   3rd Qu.:25.00
##  Max.   :0   Max.   :28.00
```

Post-Experiment CEWL

Load in each of the post-rehab datafiles:

```r
# trial 1
CEWL_t1 <- read.csv("./data/post_exp_CEWL/4-28-21-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,
                Status,
                ID = Comments,
                TEWL_g_m2h = TEWL..g..m2h.. # rename
                )

# trial 2
CEWL_t2 <- read.csv("./data/post_exp_CEWL/5-4-21-CEWL.csv",
                    na.strings=c("","NA")) %>%
  dplyr::select(date = Date,
                Status,
                ID = Comments,
                TEWL_g_m2h = TEWL..g..m2h..
                )

# trial 3
CEWL_t3 <- read.csv("./data/post_exp_CEWL/5-11-21-CEWL.csv",
                    na.strings=c("","NA")) %>%
  dplyr::select(date = Date,
```

```
                  Status,
                  ID = Comments,
                  TEWL_g_m2h = TEWL..g..m2h..
                  )

# trial 4
CEWL_t4 <- read.csv("./data/post_exp_CEWL/5-18-21-CEWL.csv",
                    na.strings=c("","NA")) %>%
  dplyr::select(date = Date,
                Status,
                ID = Comments,
                TEWL_g_m2h = TEWL..g..m2h..
                )
```

Load in cloacal temperatures:

```
exp_CT <- read.csv("./data/post_exp_CEWL_cloacal_temps.csv") %>%
  mutate(date = as.Date(date, format = "%Y/%m/%d")) %>%
  dplyr::select(-time)
summary(exp_CT)
```

```
##       date            individual_ID    cloacal_temp_C
##  Min.   :2021-04-28   Min.   : 37.00   Min.   :19.0
##  1st Qu.:2021-05-04   1st Qu.: 69.50   1st Qu.:21.0
##  Median :2021-05-11   Median : 93.00   Median :23.0
##  Mean   :2021-05-09   Mean   : 85.91   Mean   :22.4
##  3rd Qu.:2021-05-18   3rd Qu.:103.50   3rd Qu.:23.0
##  Max.   :2021-05-18   Max.   :122.00   Max.   :26.0
```

Join Dataframes

Merge all post-experiment CEWL, add cloacal temperature, add capture CEWL:

```
# merge all CEWL datafiles & reformat
CEWL <- CEWL_t1 %>% # trial 1
  rbind(., CEWL_t2, # trial 2
        CEWL_t3, # trial 3
        CEWL_t4 # trial 4
        ) %>%
  # 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(# reformat date
                date = as.Date(date, format = "%m/%d/%y"),
                # format individual ID
                individual_ID = as.integer(individual_ID),
                # set body region as a factor variable after getting only the consistent characters due
                region = as.factor(substring(region, 1, 4)),
                # add when measurement taken
                day = as.factor("after"),
                n_day = 1 # technically day 8/9, just to help with figures
                ) %>%
  # remove cols not relevant to stats
```

```r
  dplyr::select(-Status) %>%
  # remove any rows with missing values
  # none actually needed to be removed
  dplyr::filter(complete.cases(.)) %>%
  # add cloacal temperatures
  left_join(exp_CT, by = c("date", "individual_ID")) %>%
  # now matching dataframes, add capture CEWL data
  rbind(cap_CEWL) %>%
  # add tmt assignments
  left_join(tmts, by = "individual_ID") %>%
  mutate(humidity_tmt_percent = as.factor(humidity_tmt_percent),
         individual_ID = as.factor(individual_ID),
         conclusion = as.factor(conclusion),
         trial_number = as.factor(trial_number)
         ) %>%
  # lizards 49 & 80 are missing pre-exp CEWL, so remove them
  dplyr::filter((individual_ID %nin% c('49', '80')))
# every lizard should have 10 measurements
summary(CEWL)
```

```
##      date             individual_ID  region     TEWL_g_m2h         day
##  Min.   :2021-04-19   37     : 10   dewl:65   Min.   :  4.60   after :163
##  1st Qu.:2021-05-03   39     : 10   dors:65   1st Qu.: 20.09   before:163
##  Median :2021-05-10   40     : 10   head:66   Median : 27.18
##  Mean   :2021-05-06   47     : 10   mite:64   Mean   : 30.69
##  3rd Qu.:2021-05-11   52     : 10   vent:66   3rd Qu.: 38.72
##  Max.   :2021-05-18   54     : 10             Max.   :106.38
##                       (Other):266
##      n_day       cloacal_temp_C   temp_tmt_C humidity_tmt_percent trial_number
##  Min.   :0.0   Min.   :19.00   Min.   :25   dry  :158            1: 50
##  1st Qu.:0.0   1st Qu.:21.00   1st Qu.:25   humid:168            2: 48
##  Median :0.5   Median :23.00   Median :25                       3:110
##  Mean   :0.5   Mean   :23.11   Mean   :25                       4:118
##  3rd Qu.:1.0   3rd Qu.:24.75   3rd Qu.:25
##  Max.   :1.0   Max.   :28.00   Max.   :25
##
##     conclusion       notes
##  complete:326    Length:326
##                  Class :character
##                  Mode  :character
##
##
##
##
```

Check that data looks correct:

```r
CEWL %>%
  group_by(individual_ID, day) %>%
  summarise(n = n()) %>%
  arrange(individual_ID, n)
```

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

```
## # A tibble: 66 x 3
```

```
## # Groups:   individual_ID [33]
##    individual_ID day          n
##    <fct>         <fct>  <int>
## 1 37            after      5
## 2 37            before     5
## 3 39            after      5
## 4 39            before     5
## 5 40            after      5
## 6 40            before     5
## 7 47            after      5
## 8 47            before     5
## 9 52            after      5
## 10 52           before     5
## # ... with 56 more rows
```

Everything looks great! (after removing the observations for the two lizards with missing pre-experiment CEWL measurements.)

Before/after aren't perfectly even because sometimes we were unable to get the AquaFlux to equilibrate and take a measurement.

Finally, make a small edit so the regions are spelled out completely. This requires reordering factor levels:

```r
CEWL$region <- factor(CEWL$region,
                      levels = c("dors", "vent", "head", "dewl", "mite"),
                      labels = c("Dorsum", "Ventrum", "Head",
                                 "Dewlap", "Mite Patch")
                )
CEWL$humidity_tmt_percent <- factor(CEWL$humidity_tmt_percent,
                                    levels = c("humid", "dry"),
                                    labels = c("Humid", "Dry"))
CEWL$day <- factor(CEWL$day,
                                    levels = c("before", "after"),
                                    labels = c("Before", "After"))
summary(CEWL)
```

```
##       date             individual_ID       region       TEWL_g_m2h
##  Min.   :2021-04-19   37     : 10   Dorsum    :65   Min.   :  4.60
##  1st Qu.:2021-05-03   39     : 10   Ventrum   :66   1st Qu.: 20.09
##  Median :2021-05-10   40     : 10   Head      :66   Median : 27.18
##  Mean   :2021-05-06   47     : 10   Dewlap    :65   Mean   : 30.69
##  3rd Qu.:2021-05-11   52     : 10   Mite Patch:64   3rd Qu.: 38.72
##  Max.   :2021-05-18   54     : 10                   Max.   :106.38
##                       (Other):266
##      day           n_day      cloacal_temp_C    temp_tmt_C  humidity_tmt_percent
##  Before:163   Min.   :0.0   Min.   :19.00   Min.   :25   Humid:168
##  After :163   1st Qu.:0.0   1st Qu.:21.00   1st Qu.:25   Dry  :158
##               Median :0.5   Median :23.00   Median :25
##               Mean   :0.5   Mean   :23.11   Mean   :25
##               3rd Qu.:1.0   3rd Qu.:24.75   3rd Qu.:25
##               Max.   :1.0   Max.   :28.00   Max.   :25
##
##   trial_number    conclusion        notes
##  1: 50         complete:326   Length:326
##  2: 48                        Class :character
##  3:110                        Mode  :character
```

10

```
##  4:118
##
##
##
```

Export Data Frames for Power Analyses

```
#write.csv(all_dat, "exported_data/exp_effects_hydration.csv")
#write.csv(CEWL, "exported_data/exp_effects_CEWL.csv")
```

Figures

Means to Overlay

```
all_dat_mean_SMI <- all_dat %>%
  group_by(humidity_tmt_percent, day) %>%
  summarise(SMI_mean = mean(SMI))
```

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

```
all_dat_mean_SMI
```

```
## # A tibble: 8 x 3
## # Groups:   humidity_tmt_percent [2]
##   humidity_tmt_percent day               SMI_mean
##   <fct>                <fct>                <dbl>
## 1 Humid                Before Acclimation   10.8
## 2 Humid                Mid Acclimation      10.2
## 3 Humid                After Acclimation     9.89
## 4 Humid                After Rehydration     9.94
## 5 Dry                  Before Acclimation   10.5
## 6 Dry                  Mid Acclimation       9.77
## 7 Dry                  After Acclimation     9.26
## 8 Dry                  After Rehydration     9.34
```

```
all_dat_mean_hct <- all_dat %>%
  dplyr::filter(complete.cases(hematocrit_percent)) %>%
  group_by(humidity_tmt_percent, day) %>%
  summarise(hct_mean = mean(hematocrit_percent))
```

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

```
all_dat_mean_hct
```

```
## # A tibble: 8 x 3
## # Groups:   humidity_tmt_percent [2]
##   humidity_tmt_percent day               hct_mean
##   <fct>                <fct>                <dbl>
## 1 Humid                Before Acclimation   36.4
## 2 Humid                Mid Acclimation      29.8
## 3 Humid                After Acclimation    28.2
## 4 Humid                After Rehydration    23.5
## 5 Dry                  Before Acclimation   35.5
## 6 Dry                  Mid Acclimation      30.6
## 7 Dry                  After Acclimation    27.6
```

```
## 8 Dry                    After Rehydration       22.7
```

```r
all_dat_mean_osml <- all_dat %>%
  dplyr::filter(complete.cases(osmolality_mmol_kg)) %>%
  group_by(humidity_tmt_percent, day) %>%
  summarise(osml_mean = mean(osmolality_mmol_kg))
```

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

```r
all_dat_mean_osml
```

```
## # A tibble: 8 x 3
## # Groups:   humidity_tmt_percent [2]
##   humidity_tmt_percent day                osml_mean
##   <fct>                <fct>                  <dbl>
## 1 Humid                Before Acclimation      375.
## 2 Humid                Mid Acclimation         346.
## 3 Humid                After Acclimation       362.
## 4 Humid                After Rehydration       367.
## 5 Dry                  Before Acclimation      365.
## 6 Dry                  Mid Acclimation         348.
## 7 Dry                  After Acclimation       371.
## 8 Dry                  After Rehydration       371.
```

```r
all_dat_mean_CEWL <- read.csv("./data/CEWL_predicted_exp_means.csv") %>%
  mutate(region = as.factor(region),
         humidity_tmt_percent = as.factor(humidity_tmt_percent))
all_dat_mean_CEWL
```

```
##     X      region humidity_tmt_percent n_day CEWL_mean
## 1   1      Dorsum                Humid     0  22.36294
## 2   2      Dorsum                Humid     1  37.14750
## 3   3      Dorsum                  Dry     0  24.71563
## 4   4      Dorsum                  Dry     1  18.95375
## 5   5      Ventrum               Humid     0  36.42765
## 6   6      Ventrum               Humid     1  54.91588
## 7   7      Ventrum                 Dry     0  38.43438
## 8   8      Ventrum                 Dry     1  35.11750
## 9   9        Head                Humid     0  27.56471
## 10 10        Head                Humid     1  34.06176
## 11 11        Head                  Dry     0  29.88344
## 12 12        Head                  Dry     1  22.23125
## 13 13      Dewlap                Humid     0  25.94750
## 14 14      Dewlap                Humid     1  34.87333
## 15 15      Dewlap                  Dry     0  28.39438
## 16 16      Dewlap                  Dry     1  24.54667
## 17 17  Mite Patch                Humid     0  27.38412
## 18 18  Mite Patch                Humid     1  34.30875
## 19 19  Mite Patch                  Dry     0  32.23400
## 20 20  Mite Patch                  Dry     1  22.31063
```

SMI ~ Time

```r
ggplot() +
  geom_point(data = all_dat,
             aes(x = day,
```

```r
                y = SMI,
                color = humidity_tmt_percent,
                shape = humidity_tmt_percent
                ),
            size = 1,
            alpha = 0.6) +
geom_line(data = all_dat,
          aes(x = day,
              y = SMI,
              group = individual_ID,
              color = humidity_tmt_percent,
              #linetype = humidity_tmt_percent
              ),
          alpha = 0.4) +
geom_line(data = all_dat_mean_SMI,
          aes(x = day,
              y = SMI_mean,
              group = humidity_tmt_percent,
              color = humidity_tmt_percent,
              #linetype = humidity_tmt_percent
              ),
          size = 1.5,
          alpha = 1) +
geom_point(data = all_dat_mean_SMI,
           aes(x = day,
               y = SMI_mean,
               color = humidity_tmt_percent,
               shape = humidity_tmt_percent),
           size = 5,
           alpha = 1) +
theme_classic() +
scale_color_brewer(palette = "Set2",
                   name = "") +
scale_shape_manual(values = c(17, 19), name = "") +
#scale_linetype_manual(values = c("solid", "dotdash"),
 #                  name = "") +
xlab("") +
ylab("Body Condition\n(g)") +
geom_vline(xintercept = 3.5,
           linetype = "dashed",
           color = "darkgrey") +
theme(text = element_text(color = "black",
                          family = "sans",
                          size = 26),
      axis.text = element_text(color = "black",
                               family = "sans",
                               size = 18),
      axis.text.x = element_blank(),
      legend.text = element_text(color = "black",
                                 family = "sans",
                                 size = 28),
      legend.text.align = 0,
      legend.position = "none",
```

```
        plot.margin = unit(c(0.1, #top
                             0.1, #right
                             0.1, #bottom
                             0.46 #left
                             ), "cm")
) -> tmt_effects_SMI
tmt_effects_SMI
```
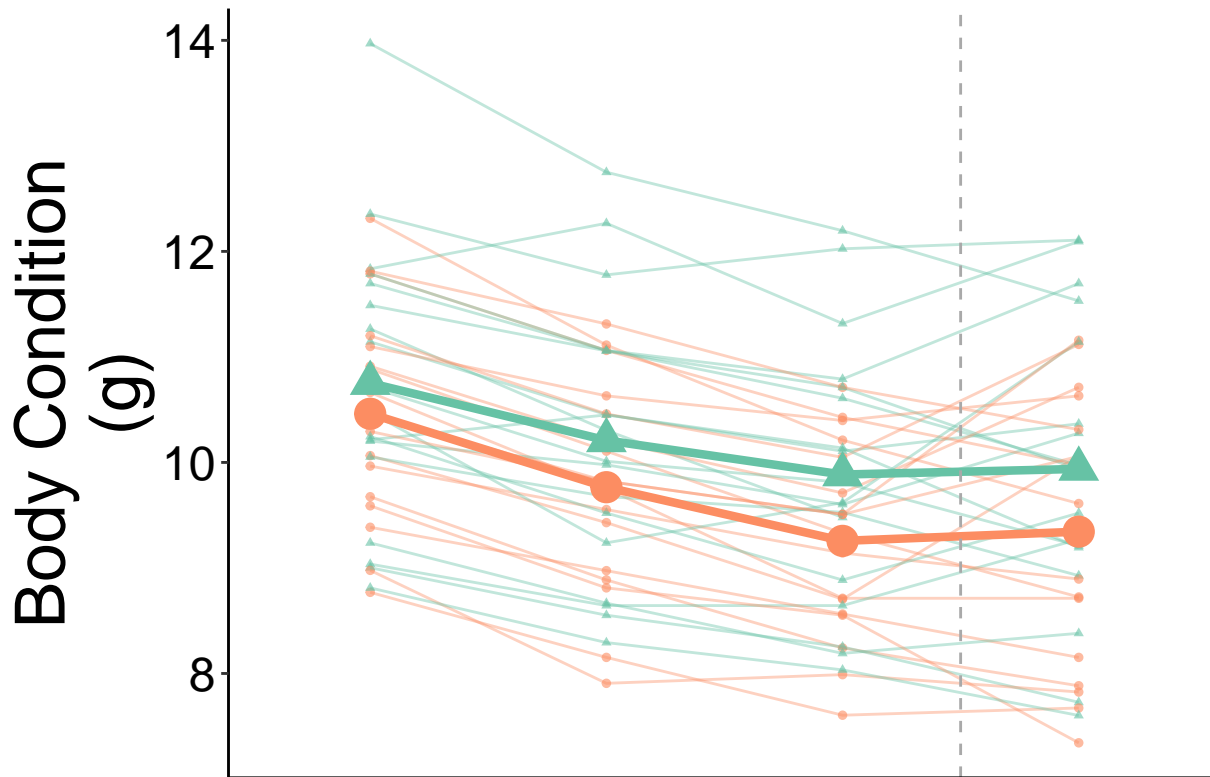


```
# export figure
#ggsave(filename = "tmt_effects_SMI.jpeg",
 #      plot = tmt_effects_SMI,
  #     path = "./final_figures",
   #    device = "jpeg",
    #   dpi = 1200,
     #  width = 5, height = 4)
```

Hct ~ Time

```
ggplot() +
  geom_point(data = all_dat,
             aes(x = day,
                 y = hematocrit_percent,
                 color = humidity_tmt_percent,
                 shape = humidity_tmt_percent
                 ),
             size = 1,
             alpha = 0.6) +
  geom_line(data = all_dat,
```

```
        aes(x = day,
            y = hematocrit_percent,
            group = individual_ID,
            color = humidity_tmt_percent,
            #linetype = humidity_tmt_percent
            ),
        alpha = 0.4) +
geom_line(data = all_dat_mean_hct,
        aes(x = day,
            y = hct_mean,
            group = humidity_tmt_percent,
            color = humidity_tmt_percent,
            #linetype = humidity_tmt_percent
            ),
        size = 1.5,
        alpha = 1) +
geom_point(data = all_dat_mean_hct,
         aes(x = day,
            y = hct_mean,
            color = humidity_tmt_percent,
            shape = humidity_tmt_percent),
        size = 5,
        alpha = 1) +
theme_classic() +
scale_color_brewer(palette = "Set2",
                 name = "") +
scale_shape_manual(values = c(17, 19), name = "") +
#scale_linetype_manual(values = c("solid", "dotdash"),
 #                 name = "") +
scale_x_discrete(labels = c("Before\nAcclimation",
                            "Mid\nAcclimation",
                            "After\nAcclimation",
                            "After\nRehydration")) +
xlab("") +
ylab("Hematocrit\n(%)") +
geom_vline(xintercept = 3.5,
         linetype = "dashed",
         color = "darkgrey") +
theme(text = element_text(color = "black",
                         family = "sans",
                         size = 26),
     axis.text = element_text(color = "black",
                             family = "sans",
                             size = 18),
     legend.text = element_text(color = "black",
                             family = "sans",
                             size = 28),
     legend.text.align = 0,
     legend.position = "none",
     plot.margin = unit(c(0.1, #top
                         0.1, #right
                         0.1, #bottom
                         0.46 #left
```
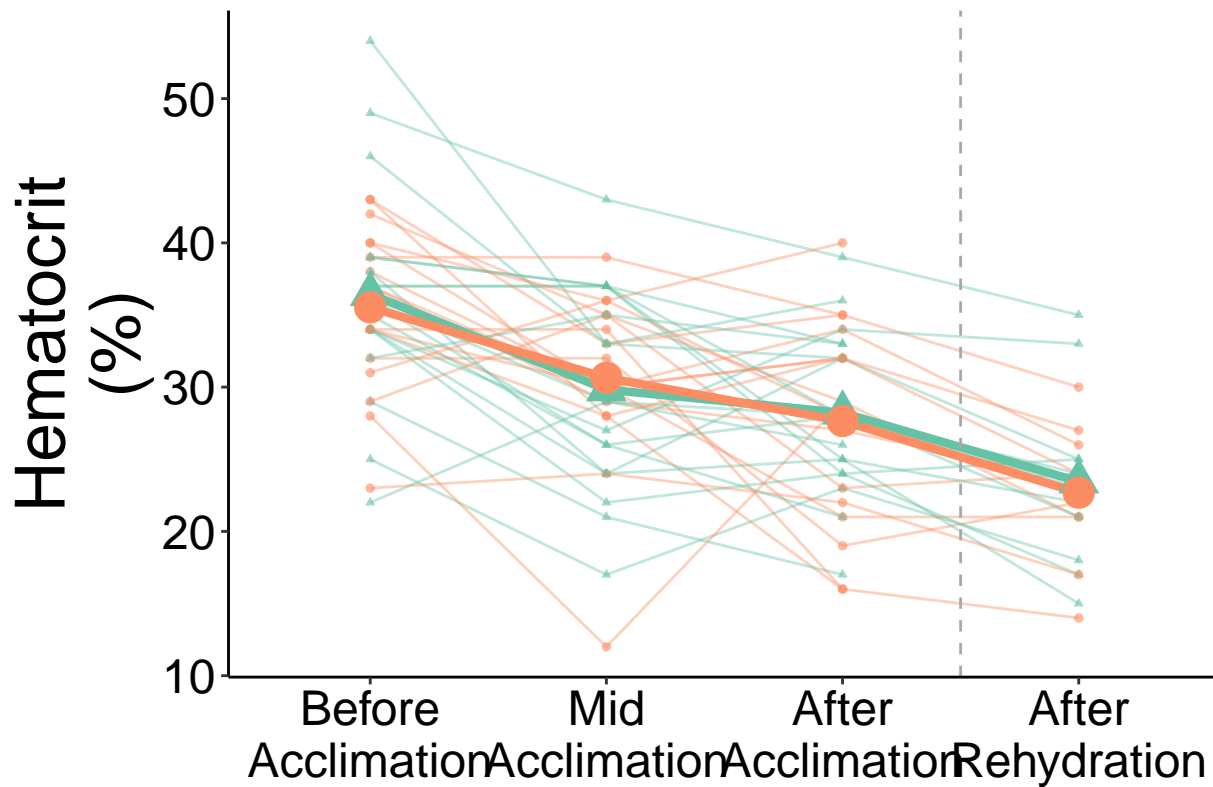
```
                          ), "cm")
        ) -> tmt_effects_hct
tmt_effects_hct
```

Warning: Removed 12 rows containing missing values (geom_point).

Warning: Removed 12 row(s) containing missing values (geom_path).


```
# export figure
#ggsave(filename = "tmt_effects_hct.jpeg",
 #      plot = tmt_effects_hct,
  #     path = "./final_figures",
   #    device = "jpeg",
    #   dpi = 1200,
     #  width = 5, height = 4)
```

Osml ~ Time

```
ggplot() +
  geom_point(data = all_dat,
            aes(x = day,
                y = osmolality_mmol_kg,
                color = humidity_tmt_percent,
                shape = humidity_tmt_percent
                ),
            size = 1,
            alpha = 0.6) +
  geom_line(data = all_dat,
            aes(x = day,
```

```r
                   y = osmolality_mmol_kg,
                   group = individual_ID,
                   color = humidity_tmt_percent,
                   #linetype = humidity_tmt_percent
                   ),
              alpha = 0.4) +
  geom_line(data = all_dat_mean_osml,
            aes(x = day,
                y = osml_mean,
                group = humidity_tmt_percent,
                color = humidity_tmt_percent,
                #linetype = humidity_tmt_percent
                ),
            size = 1.5,
            alpha = 1) +
  geom_point(data = all_dat_mean_osml,
             aes(x = day,
                 y = osml_mean,
                 color = humidity_tmt_percent,
                 shape = humidity_tmt_percent),
             size = 5,
             alpha = 1) +
  theme_classic() +
  scale_color_brewer(palette = "Set2",
                     name = "") +
  scale_shape_manual(values = c(17, 19), name = "") +
  #scale_linetype_manual(values = c("solid", "dotdash"),
  #                   name = "") +
  xlab("") +
  ylab("Plasma Osmolality\n(mmol/kg)") +
  geom_vline(xintercept = 3.5,
             linetype = "dashed",
             color = "darkgrey") +
  theme(text = element_text(color = "black",
                            family = "sans",
                            size = 26),
        axis.text = element_text(color = "black",
                                 family = "sans",
                                 size = 18),
        axis.text.x = element_blank(),
        legend.text = element_text(color = "black",
                                   family = "sans",
                                   size = 28),
        legend.text.align = 0,
        legend.position = "none",
        plot.margin = unit(c(0.1, #top
                             0.1, #right
                             0.1, #bottom
                             0.1 #left
                             ), "cm")
        ) -> tmt_effects_osml
tmt_effects_osml
```
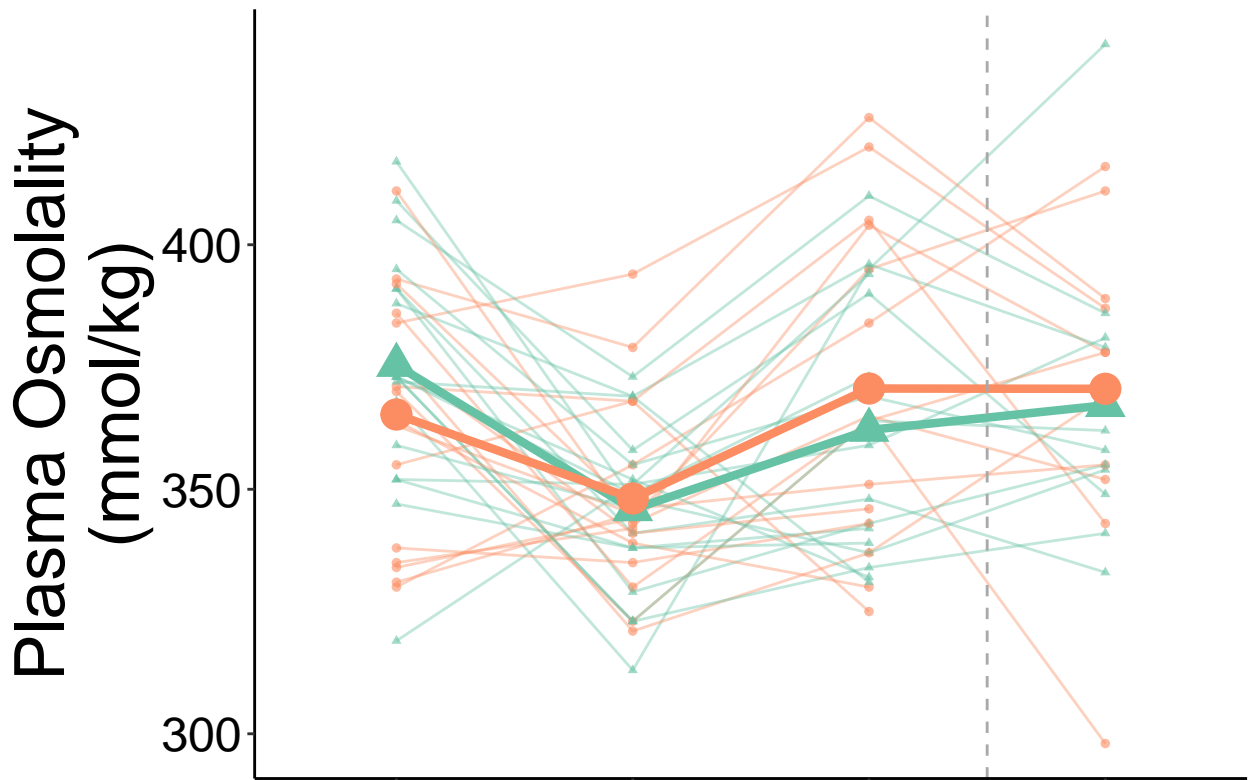
```
## Warning: Removed 15 rows containing missing values (geom_point).
```

```
# export figure
#ggsave(filename = "tmt_effects_osml.jpeg",
 #      plot = tmt_effects_osml,
  #     path = "./final_figures",
   #    device = "jpeg",
    #   dpi = 1200,
     #  width = 5, height = 4)
```

Multi-Figure

```
ggarrange(tmt_effects_SMI, tmt_effects_osml, tmt_effects_hct,
        ncol = 1, nrow = 3,
        labels = c("A", "B", "C"),
        font.label = list(size = 24, face = "bold", color ="black"),
        hjust = -2, vjust = 1.1,
        common.legend = TRUE,
        legend = "bottom"
        ) -> tmt_multi_fig
```

```
tmt_multi_fig
```

A

Humid ▲ Dry ●
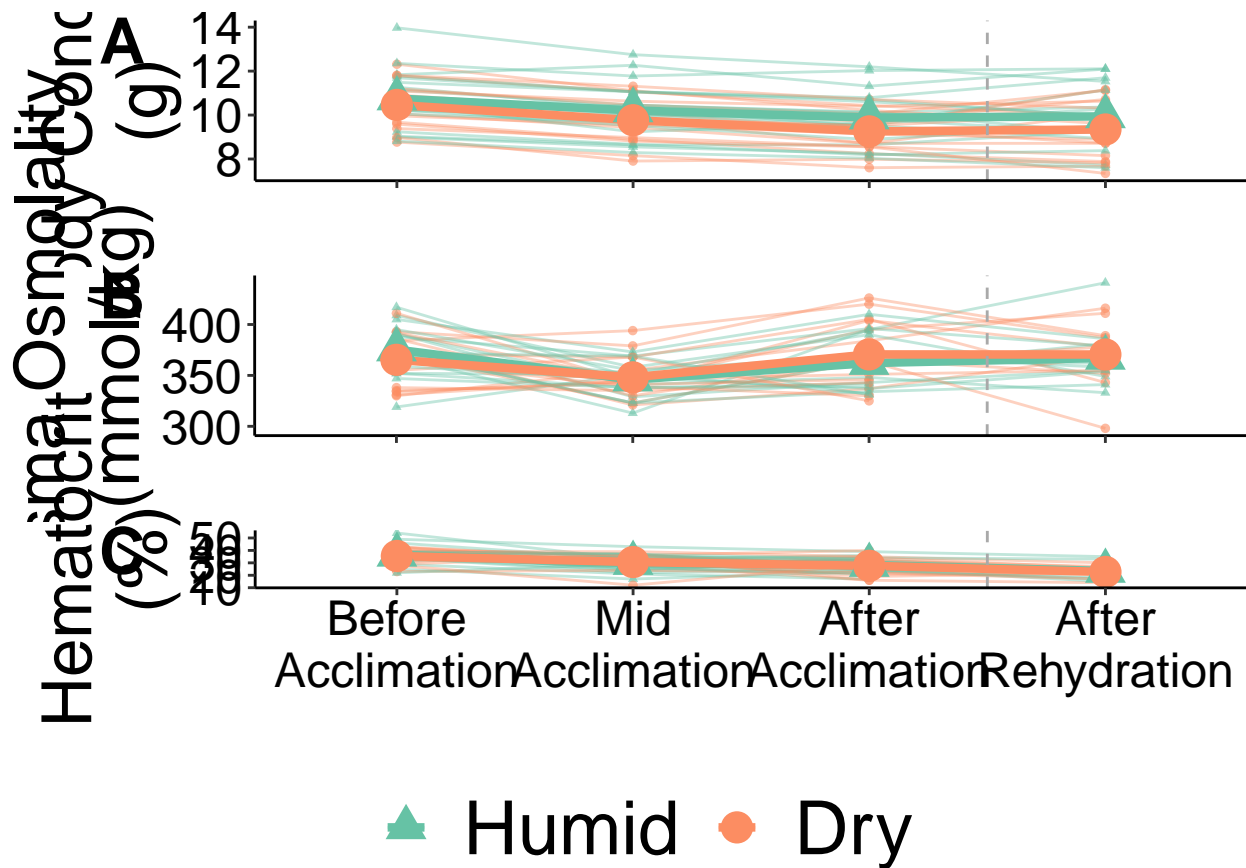
```
# export figure
ggsave(filename = "tmt_multi_fig2.jpeg",
       plot = tmt_multi_fig,
       path = "./final_figures",
       device = "jpeg",
       dpi = 1200,
       width = 8, height = 12)
```

CEWL

```
ggplot(data = CEWL) +
  geom_point(aes(x = n_day,
                 y = TEWL_g_m2h,
                 group = individual_ID,
                 color = humidity_tmt_percent,
                 shape = humidity_tmt_percent
                 ),
             size = 1,
             alpha = 0.6) +
  geom_line(aes(x = n_day,
                y = TEWL_g_m2h,
                group = individual_ID,
                color = humidity_tmt_percent,
                #linetype = humidity_tmt_percent
                ),
            alpha = 0.4) +
```

```r
    stat_smooth(aes(x = n_day,
                    y = TEWL_g_m2h,
                    color = humidity_tmt_percent,
                  #linetype = humidity_tmt_percent
                    ),
                formula = y ~ x,
                method = "lm",
                se = F,
                size = 1.5,
                alpha = 1) +
    geom_point(data = all_dat_mean_CEWL,
               aes(x = n_day,
                   y = CEWL_mean,
                   group = humidity_tmt_percent,
                   color = humidity_tmt_percent,
                   shape = humidity_tmt_percent
                   ),
               size = 5,
               alpha = 1) +
    theme_classic() +
    scale_color_brewer(palette = "Set2",
                       name = ""
                       #name = "Humidity\nTreatment"
                       ) +
    scale_shape_manual(values = c(17, 19), name = "") +
    #scale_linetype_manual(values = c("solid", "dotdash"),
     #                      name = "") +
    facet_wrap(~region, ncol = 2) +
    scale_x_continuous(breaks = c(0, 1),
                       labels = c("0" = "Before\nAcclimation",
                                  "1" = "After\nAcclimation")
                       ) +
    xlab("") +
    ylab(bquote('CEWL (g/'*m^2*'h)')) +
    theme(text = element_text(color = "black",
                              family = "sans",
                              size = 24),
          axis.text = element_text(color = "black",
                                   family = "sans",
                                   size = 18),
          axis.text.x = element_text(#angle = 90,
                                     hjust = c(0, 1),
                                     #vjust = 0.2
                                     ),
          legend.text = element_text(color = "black",
                                     family = "sans",
                                     size = 26),
          legend.text.align = 0,
          legend.position = c(0.75,0.12),
          #legend.justification = c(1, 1)
) -> CEWL_tmt_fig
```
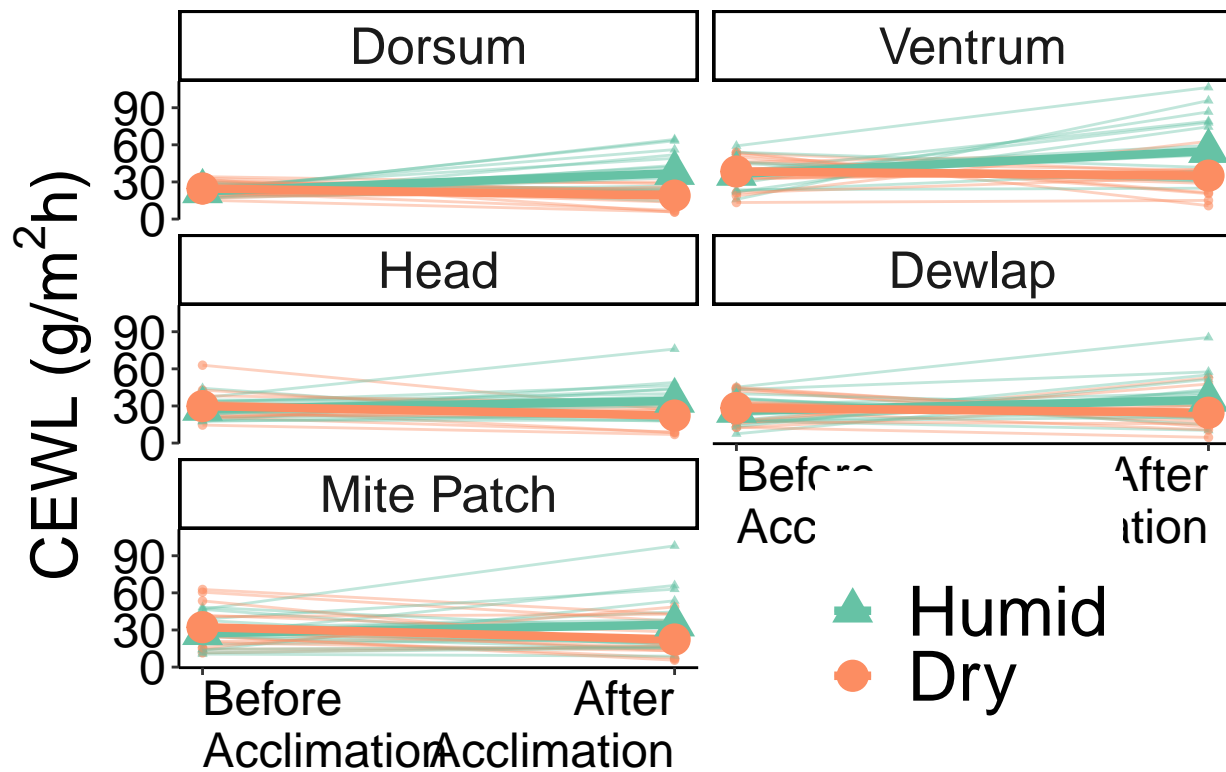
```
## Warning: Vectorized input to `element_text()` is not officially supported.
## Results may be unexpected or may change in future versions of ggplot2.
```

```r
# export figure
ggsave(filename = "tmt_effects_CEWL.jpeg",
       plot = CEWL_tmt_fig,
       path = "./final_figures",
       device = "jpeg",
       dpi = 1200,
       width = 8, height = 12)
```

Models

SMI

Check whether means started out different:

```r
SMI_diff_lm <- all_dat_no_rehab %>%
  dplyr::filter(day == "Before Acclimation") %>%
  lm(data = ., SMI ~ humidity_tmt_percent)
summary(SMI_diff_lm)
```

```
##
## Call:
## lm(formula = SMI ~ humidity_tmt_percent, data = .)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -1.9405 -0.7429 -0.0401  0.7385  3.2183
##
## Coefficients:
```

```
##                         Estimate Std. Error t value Pr(>|t|)
## (Intercept)               10.7517     0.2811   38.25   <2e-16 ***
## humidity_tmt_percentDry   -0.2904     0.4033   -0.72    0.476
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.192 on 33 degrees of freedom
## Multiple R-squared:  0.01547,    Adjusted R-squared:  -0.01436
## F-statistic: 0.5187 on 1 and 33 DF,  p-value: 0.4765
```

NOT significantly different, which is good.

Check whether means ended differently:

```
SMI_diff_lm_end <- all_dat_no_rehab %>%
  dplyr::filter(day == "After Acclimation") %>%
  lm(data = ., SMI ~ humidity_tmt_percent)
summary(SMI_diff_lm_end)
```

```
##
## Call:
## lm(formula = SMI ~ humidity_tmt_percent, data = .)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.85144 -0.69873 -0.07453  0.80895  2.31088
##
## Coefficients:
##                         Estimate Std. Error t value Pr(>|t|)
## (Intercept)                9.8852     0.2585  38.246   <2e-16 ***
## humidity_tmt_percentDry   -0.6287     0.3709  -1.695   0.0994 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.097 on 33 degrees of freedom
## Multiple R-squared:  0.08012,    Adjusted R-squared:  0.05224
## F-statistic: 2.874 on 1 and 33 DF,  p-value: 0.09943
```

Build Model

```
SMI_mod1 <- lme4::lmer(data = all_dat_no_rehab,
               SMI ~ day*humidity_tmt_percent +
               (1|trial_number/individual_ID))
drop1(SMI_mod1)
```

```
## boundary (singular) fit: see ?isSingular
```

```
## Single term deletions
##
## Model:
## SMI ~ day * humidity_tmt_percent + (1 | trial_number/individual_ID)
##                          npar    AIC
## <none>                        164.87
## day:humidity_tmt_percent    2 168.69
# drop interaction term
SMI_mod2 <- lme4::lmer(data = all_dat_no_rehab,
```

```
                 SMI ~ day + humidity_tmt_percent +
                 (1|trial_number/individual_ID))
```

```
## boundary (singular) fit: see ?isSingular
```

```
drop1(SMI_mod2)
```

```
## boundary (singular) fit: see ?isSingular
## boundary (singular) fit: see ?isSingular
```

```
## Single term deletions
##
## Model:
## SMI ~ day + humidity_tmt_percent + (1 | trial_number/individual_ID)
##                       npar    AIC
## <none>                     168.69
## day                     2 276.89
## humidity_tmt_percent    1 168.15
```

```
# drop humidity effect
SMI_mod3 <- lme4::lmer(data = all_dat_no_rehab,
                SMI ~ day +
                (1|trial_number/individual_ID))
```

```
## boundary (singular) fit: see ?isSingular
```

```
drop1(SMI_mod3)
```

```
## boundary (singular) fit: see ?isSingular
```

```
## Single term deletions
##
## Model:
## SMI ~ day + (1 | trial_number/individual_ID)
##         npar    AIC
## <none>       168.15
## day       2 276.35
```

```
# null model
SMI_mod_null <- lme4::lmer(data = all_dat_no_rehab,
                SMI ~ 1 +
                (1|trial_number/individual_ID))
```

```
## boundary (singular) fit: see ?isSingular
```

Selection

```
SMI_models <- list(SMI_mod1, SMI_mod2, SMI_mod3, SMI_mod_null)

#specify model names
SMI_mod_names <- c('(model 1) ~ day * humidity',
                   '(model 2) ~ day + humidity',
                   '(model 3) ~ day',
                   'null model')
#calculate AIC of each model
SMI_AICc <- data.frame(aictab(cand.set = SMI_models,
                               modnames = SMI_mod_names))
```

```
## Warning in aictab.AIClmerMod(cand.set = SMI_models, modnames = SMI_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
```

```
SMI_AICc
```

```
##                         Modnames K      AICc  Delta_AICc      ModelLik       AICcWt
## 3             (model 3) ~ day 6 178.1683   0.0000000 1.000000e+00 5.505278e-01
## 2 (model 2) ~ day + humidity 7 179.1421   0.9738317 6.145187e-01 3.383096e-01
## 1 (model 1) ~ day * humidity 9 181.3681   3.1997670 2.019200e-01 1.111626e-01
## 4                    null model 4 278.2215 100.0531912 1.878130e-22 1.033963e-22
##        Res.LL    Cum.Wt
## 3  -82.65558 0.5505278
## 2  -81.99375 0.8888374
## 1  -80.73666 1.0000000
## 4 -134.91075 1.0000000
```
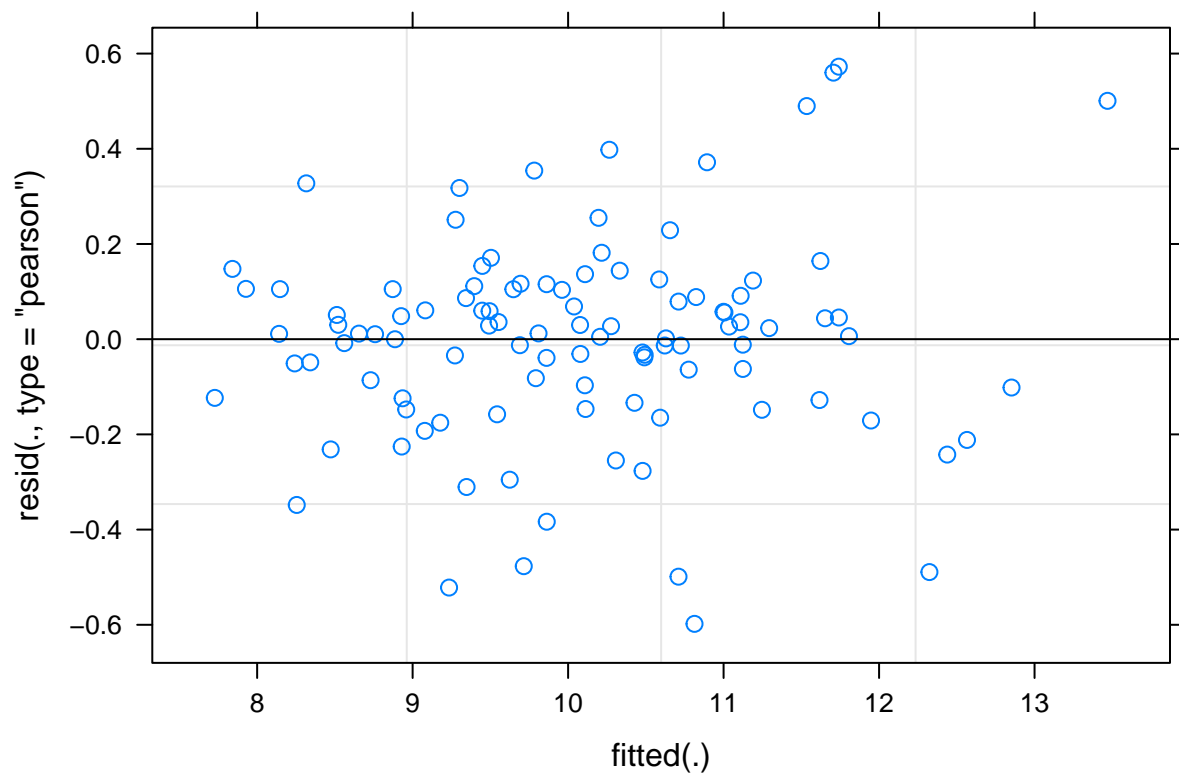
Check Conditions of Top Models

```
plot(SMI_mod2)
```
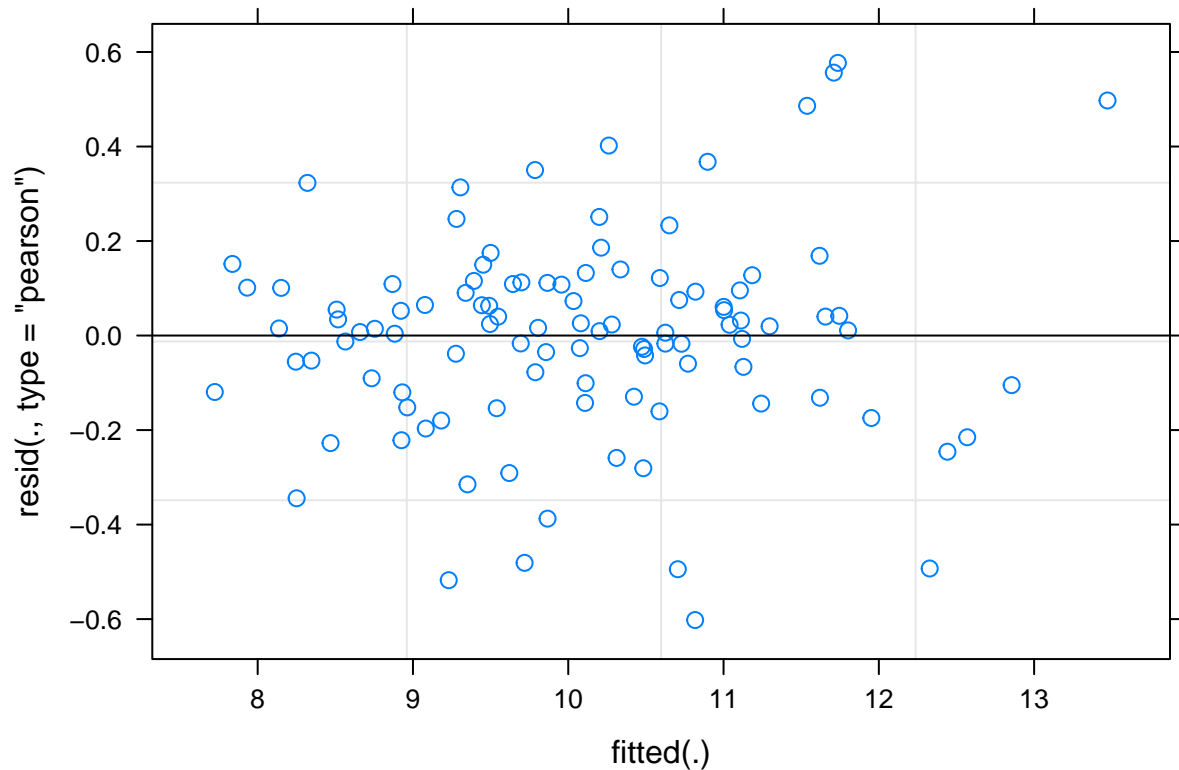


```
plot(SMI_mod3)
```
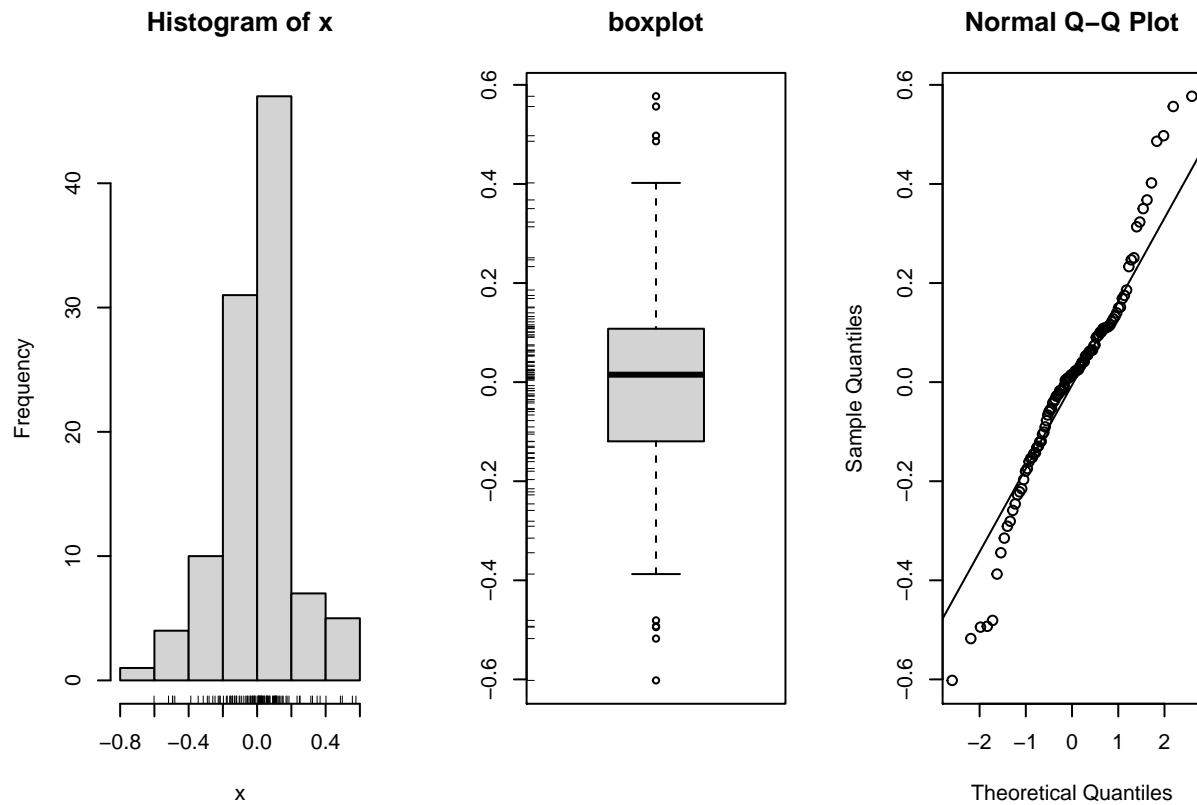
```
car::vif(SMI_mod2)
```

```
##                      GVIF Df GVIF^(1/(2*Df))
## day                    1  2               1
## humidity_tmt_percent   1  1               1
```

L & E both look good.

Is the distribution of residuals **normal**? use Shapiro-Wilk normality test: H0: data is NOT significantly different from normal distribution HA: data IS significantly different from normal distribution
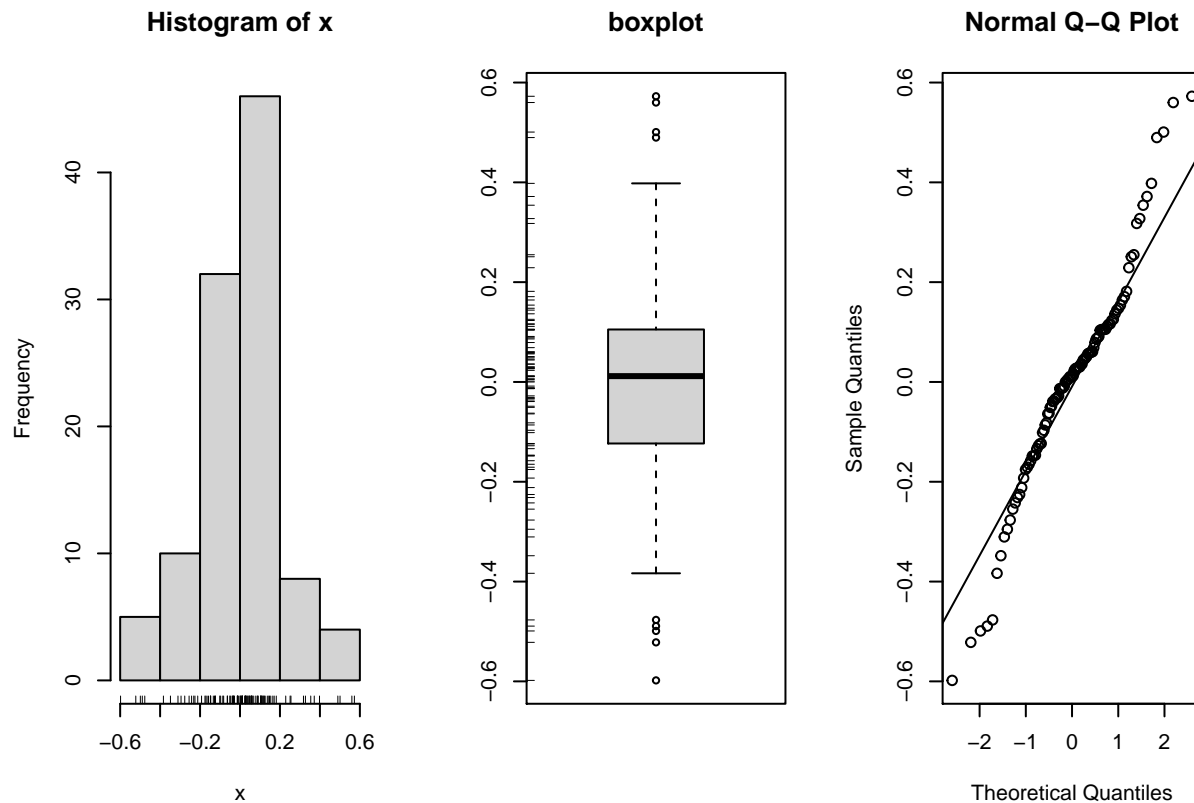
```
simple.eda(residuals(SMI_mod2))
```

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

```r
shapiro.test(residuals(SMI_mod2))
```

```
##
##  Shapiro-Wilk normality test
##
## data:  residuals(SMI_mod2)
## W = 0.96437, p-value = 0.006371
```

```r
simple.eda(residuals(SMI_mod3))
```

```r
shapiro.test(residuals(SMI_mod3))
```

```
##
##  Shapiro-Wilk normality test
##
## data:  residuals(SMI_mod3)
## W = 0.96359, p-value = 0.005557
```

Normality is fine.

Re-run top 2 models with lmerTest for p-values:

```r
SMI_mod2p <- lmerTest::lmer(data = all_dat_no_rehab,
                SMI ~ day + humidity_tmt_percent +
                (1|trial_number/individual_ID))
```

```
## boundary (singular) fit: see ?isSingular
```

```r
summary(SMI_mod2p)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: SMI ~ day + humidity_tmt_percent + (1 | trial_number/individual_ID)
##    Data: all_dat_no_rehab
##
## REML criterion at convergence: 164
##
## Scaled residuals:
##      Min      1Q   Median       3Q      Max
## -2.27820 -0.45209  0.05697  0.40778  2.18346
##
```

```
## Random effects:
##  Groups                      Name        Variance Std.Dev.
##  individual_ID:trial_number (Intercept) 1.25766  1.1215
##  trial_number               (Intercept) 0.00000  0.0000
##  Residual                               0.06983  0.2643
## Number of obs: 105, groups:  individual_ID:trial_number, 35; trial_number, 4
##
## Fixed effects:
##                          Estimate Std. Error       df t value Pr(>|t|)
## (Intercept)              10.83128    0.26925 34.23931  40.228  < 2e-16 ***
## dayMid Acclimation       -0.61729    0.06317 68.00000  -9.772 1.39e-14 ***
## dayAfter Acclimation     -1.03082    0.06317 68.00000 -16.319  < 2e-16 ***
## humidity_tmt_percentDry  -0.45433    0.38277 33.00001  -1.187    0.244
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) dyMdAc dyAftA
## dyMdAcclmtn -0.117
## dyAftrAcclm -0.117  0.500
## hmdty_tmt_D -0.691  0.000  0.000
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see ?isSingular
```

```r
SMI_mod3p <- lmerTest::lmer(data = all_dat_no_rehab,
            SMI ~ day +
            (1|trial_number/individual_ID))
```

```
## boundary (singular) fit: see ?isSingular
```

```r
summary(SMI_mod2p)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: SMI ~ day + humidity_tmt_percent + (1 | trial_number/individual_ID)
##    Data: all_dat_no_rehab
##
## REML criterion at convergence: 164
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.27820 -0.45209  0.05697  0.40778  2.18346
##
## Random effects:
##  Groups                      Name        Variance Std.Dev.
##  individual_ID:trial_number (Intercept) 1.25766  1.1215
##  trial_number               (Intercept) 0.00000  0.0000
##  Residual                               0.06983  0.2643
## Number of obs: 105, groups:  individual_ID:trial_number, 35; trial_number, 4
##
## Fixed effects:
##                          Estimate Std. Error       df t value Pr(>|t|)
## (Intercept)              10.83128    0.26925 34.23931  40.228  < 2e-16 ***
## dayMid Acclimation       -0.61729    0.06317 68.00000  -9.772 1.39e-14 ***
## dayAfter Acclimation     -1.03082    0.06317 68.00000 -16.319  < 2e-16 ***
```

```
## humidity_tmt_percentDry -0.45433     0.38277 33.00001  -1.187     0.244
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr) dyMdAc dyAftA
## dyMdAcclmtn -0.117
## dyAftrAcclm -0.117  0.500
## hmdty_tmt_D -0.691  0.000  0.000
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see ?isSingular
```

Export

Save information for the top models, as well as the table showing the rankings of the different models.

```
write.csv(SMI_AICc, "./best_models/exp_effects_SMI_mod_rankings.csv")
write.csv(broom.mixed::tidy(SMI_mod2p),
          "./best_models/exp_effects_SMI_best_mod1.csv")
write.csv(broom.mixed::tidy(SMI_mod3p),
          "./best_models/exp_effects_SMI_best_mod2.csv")
```

Hematocrit

Build Model

```
hct_mod1 <- all_dat_no_rehab %>%
  dplyr::filter(complete.cases(hematocrit_percent)) %>%
  lme4::lmer(data = .,
             hematocrit_percent ~ day * humidity_tmt_percent +
             (1|trial_number/individual_ID))
summary(hct_mod1)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula:
## hematocrit_percent ~ day * humidity_tmt_percent + (1 | trial_number/individual_ID)
##    Data: .
##
## REML criterion at convergence: 650.8
##
## Scaled residuals:
##     Min       1Q   Median       3Q      Max
## -2.74735 -0.45456  0.09102  0.58633  2.42394
##
## Random effects:
##  Groups                    Name        Variance Std.Dev.
##  individual_ID:trial_number (Intercept) 16.883   4.109
##  trial_number              (Intercept)  5.076   2.253
##  Residual                               23.269   4.824
## Number of obs: 105, groups:  individual_ID:trial_number, 35; trial_number, 4
##
## Fixed effects:
##                                     Estimate Std. Error t value
## (Intercept)                          36.1229     1.8851  19.163
## dayMid Acclimation                   -6.6111     1.6079  -4.112
```

```
## dayAfter Acclimation                                -8.2222    1.6079  -5.114
## humidity_tmt_percentDry                              -0.8893    2.1438  -0.415
## dayMid Acclimation:humidity_tmt_percentDry            1.7288    2.3071   0.749
## dayAfter Acclimation:humidity_tmt_percentDry          0.3399    2.3071   0.147
##
## Correlation of Fixed Effects:
##            (Intr) dyMdAc dyAftA hmd__D dMA:__
## dyMdAcclmtn -0.426
## dyAftrAcclm -0.426  0.500
## hmdty_tmt_D -0.554  0.375  0.375
## dyMAccl:__D  0.297 -0.697 -0.348 -0.538
## dyAAccl:__D  0.297 -0.348 -0.697 -0.538  0.500
```

```r
drop1(hct_mod1)
```

```
## Single term deletions
##
## Model:
## hematocrit_percent ~ day * humidity_tmt_percent + (1 | trial_number/individual_ID)
##                           npar    AIC
## <none>                         684.60
## day:humidity_tmt_percent    2 681.26
```

```r
# drop day*humidity interaction
hct_mod2 <- all_dat_no_rehab %>%
  dplyr::filter(complete.cases(hematocrit_percent)) %>%
  lme4::lmer(data = .,
             hematocrit_percent ~ day + humidity_tmt_percent +
             (1|trial_number/individual_ID))
summary(hct_mod2)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula:
## hematocrit_percent ~ day + humidity_tmt_percent + (1 | trial_number/individual_ID)
##    Data: .
##
## REML criterion at convergence: 658.2
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.65137 -0.49420  0.03089  0.55988  2.50915
##
## Random effects:
##  Groups                    Name        Variance Std.Dev.
##  individual_ID:trial_number (Intercept) 17.039   4.128
##  trial_number              (Intercept)  5.076   2.253
##  Residual                               22.800   4.775
## Number of obs: 105, groups:  individual_ID:trial_number, 35; trial_number, 4
##
## Fixed effects:
##                      Estimate Std. Error t value
## (Intercept)           35.7879     1.7680  20.242
## dayMid Acclimation    -5.7714     1.1414  -5.056
## dayAfter Acclimation  -8.0571     1.1414  -7.059
## humidity_tmt_percentDry -0.1997   1.6798  -0.119
```

```
## 
## Correlation of Fixed Effects:
##            (Intr) dyMdAc dyAftA
## dyMdAcclmtn -0.323
## dyAftrAcclm -0.323  0.500
## hmdty_tmt_D -0.463  0.000  0.000
```

```r
drop1(hct_mod2)
```

```
## Single term deletions
## 
## Model:
## hematocrit_percent ~ day + humidity_tmt_percent + (1 | trial_number/individual_ID)
##                      npar    AIC
## <none>                    681.26
## day                   2 717.56
## humidity_tmt_percent  1 679.28
```

```r
# drop humidity tmt
hct_mod3 <- all_dat_no_rehab %>%
  dplyr::filter(complete.cases(hematocrit_percent)) %>%
  lme4::lmer(data = .,
             hematocrit_percent ~ day +
             (1|trial_number/individual_ID))
summary(hct_mod3)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: hematocrit_percent ~ day + (1 | trial_number/individual_ID)
##    Data: .
## 
## REML criterion at convergence: 661
## 
## Scaled residuals:
##     Min       1Q   Median       3Q      Max
## -2.67914 -0.49106  0.02922  0.55515  2.53036
## 
## Random effects:
##  Groups                     Name        Variance Std.Dev.
##  individual_ID:trial_number (Intercept) 16.240   4.030
##  trial_number               (Intercept)  5.228   2.287
##  Residual                               22.800   4.775
## Number of obs: 105, groups:  individual_ID:trial_number, 35; trial_number, 4
## 
## Fixed effects:
##                     Estimate Std. Error t value
## (Intercept)           35.683      1.572  22.704
## dayMid Acclimation    -5.771      1.141  -5.056
## dayAfter Acclimation  -8.057      1.141  -7.059
## 
## Correlation of Fixed Effects:
##             (Intr) dyMdAc
## dyMdAcclmtn -0.363
## dyAftrAcclm -0.363  0.500
```
```

```
drop1(hct_mod3)
```

```
## Single term deletions
##
## Model:
## hematocrit_percent ~ day + (1 | trial_number/individual_ID)
##        npar    AIC
## <none>       679.28
## day       2 715.58
```

```
# null model
hct_mod_null <- all_dat_no_rehab %>%
  dplyr::filter(complete.cases(hematocrit_percent)) %>%
  lme4::lmer(data = .,
             hematocrit_percent ~ 1 +
             (1|trial_number/individual_ID))
summary(hct_mod_null)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: hematocrit_percent ~ 1 + (1 | trial_number/individual_ID)
##    Data: .
##
## REML criterion at convergence: 705.2
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.56598 -0.70089  0.04035  0.68616  2.93299
##
## Random effects:
##  Groups                    Name        Variance Std.Dev.
##  individual_ID:trial_number (Intercept) 10.710   3.273
##  trial_number              (Intercept)  5.229    2.287
##  Residual                               39.390   6.276
## Number of obs: 105, groups:  individual_ID:trial_number, 35; trial_number, 4
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)   31.074      1.427   21.78
```

Selection

```
hct_models <- list(hct_mod1, hct_mod2, hct_mod3, hct_mod_null)

#specify model names
hct_mod_names <- c('(model 1) ~ day * humidity',
                   '(model 2) ~ day + humidity',
                   '(model 3) ~ day',
                   'null model')
#calculate AIC of each model
hct_AICc <- data.frame(aictab(cand.set = hct_models,
                              modnames = hct_mod_names))
```

```
## Warning in aictab.AIClmerMod(cand.set = hct_models, modnames = hct_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
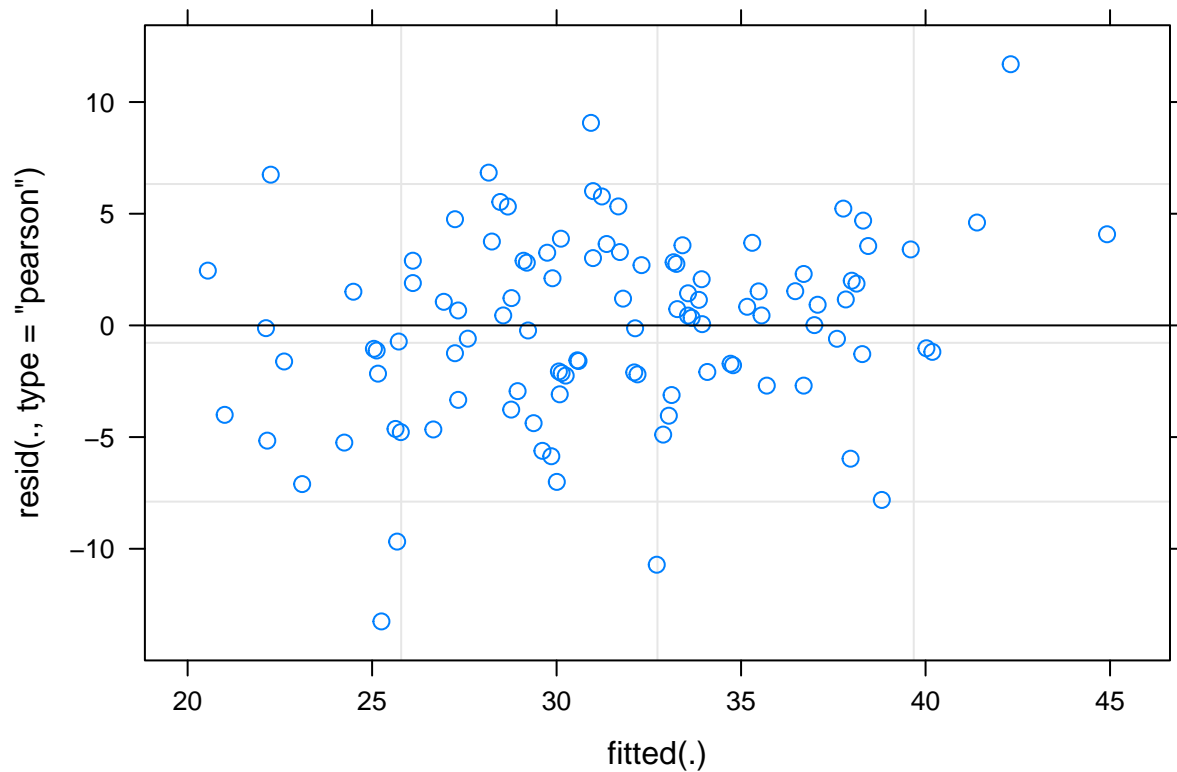```

```
hct_AICc
```

```
##                       Modnames K     AICc Delta_AICc     ModelLik       AICcWt
## 1 (model 1) ~ day * humidity 9 670.7040   0.000000 1.000000e+00 6.780023e-01
## 2 (model 2) ~ day + humidity 7 673.3124   2.608403 2.713891e-01 1.840024e-01
## 3            (model 3) ~ day 6 673.8879   3.183862 2.035322e-01 1.379953e-01
## 4                 null model 4 713.6214  42.917358 4.793074e-10 3.249715e-10
##      Res.LL    Cum.Wt
## 1 -325.4046 0.6780023
## 2 -329.0789 0.8620047
## 3 -330.5154 1.0000000
## 4 -352.6107 1.0000000
```

Check Conditions of Top Model

```
plot(hct_mod1)
```



```
car::vif(hct_mod1)
```

```
##                          GVIF Df GVIF^(1/(2*Df))
## day                  3.780864  2        1.394433
## humidity_tmt_percent 1.628820  1        1.276252
## day:humidity_tmt_percent 5.003569  2        1.495616
```

looks okay

Is the distribution of residuals **normal**? use Shapiro-Wilk normality test: H0: data is NOT significantly different from normal distribution HA: data IS significantly different from normal distribution

```
simple.eda(residuals(hct_mod1))
```

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

```r
shapiro.test(residuals(hct_mod1))
```
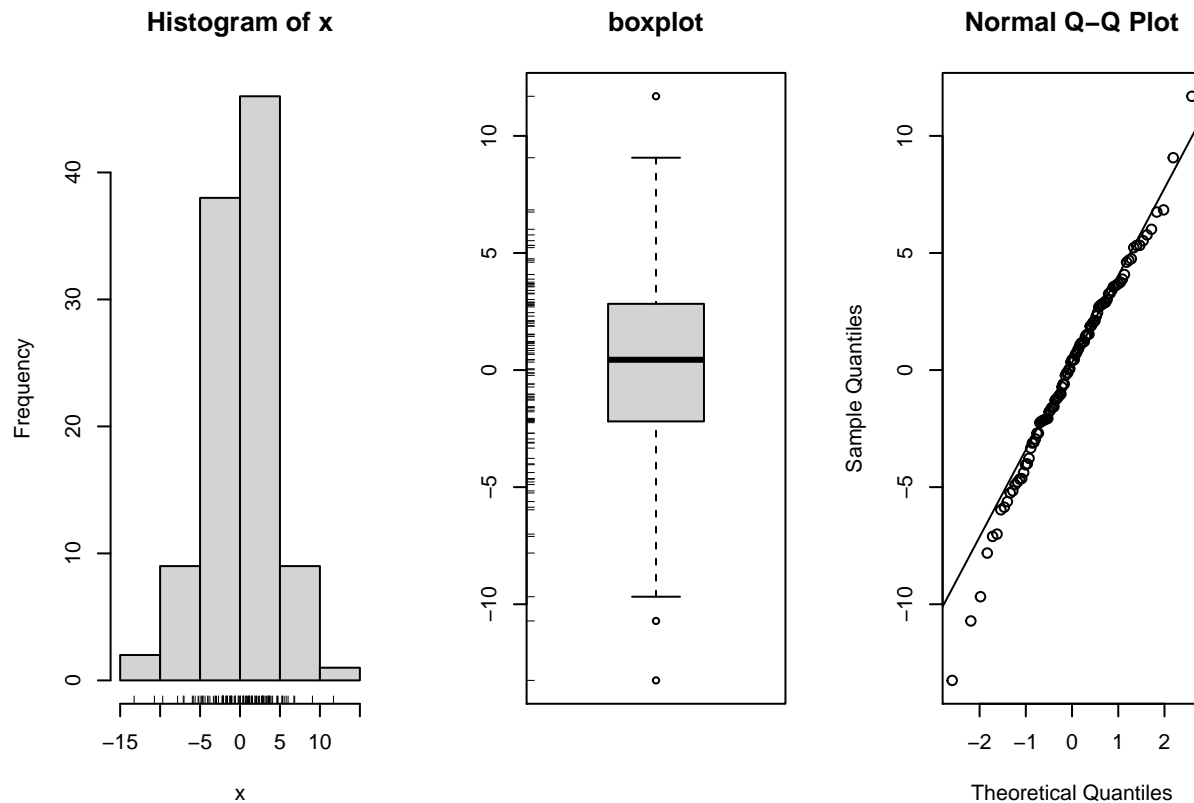
```
##
##  Shapiro-Wilk normality test
##
## data:  residuals(hct_mod1)
## W = 0.98775, p-value = 0.4539
```

residuals are normally distributed!

Re-run top model with lmerTest for p-values:

```r
hct_mod1p <- lmerTest::lmer(data = all_dat_no_rehab,
              hematocrit_percent ~ day * humidity_tmt_percent +
              (1|trial_number/individual_ID))
summary(hct_mod1p)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula:
## hematocrit_percent ~ day * humidity_tmt_percent + (1 | trial_number/individual_ID)
##    Data: all_dat_no_rehab
##
## REML criterion at convergence: 650.8
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.74735 -0.45456  0.09102  0.58633  2.42394
##
## Random effects:
```

```
##   Groups                     Name        Variance Std.Dev.
##   individual_ID:trial_number (Intercept) 16.883   4.109
##   trial_number               (Intercept)  5.076   2.253
##   Residual                               23.269   4.824
## Number of obs: 105, groups:  individual_ID:trial_number, 35; trial_number, 4
##
## Fixed effects:
##                                           Estimate Std. Error      df
## (Intercept)                                36.1229     1.8851  7.4887
## dayMid Acclimation                         -6.6111     1.6079 66.0000
## dayAfter Acclimation                       -8.2222     1.6079 66.0000
## humidity_tmt_percentDry                    -0.8893     2.1438 66.5297
## dayMid Acclimation:humidity_tmt_percentDry  1.7288     2.3071 66.0000
## dayAfter Acclimation:humidity_tmt_percentDry 0.3399    2.3071 66.0000
##                                           t value Pr(>|t|)
## (Intercept)                                19.163 1.23e-07 ***
## dayMid Acclimation                         -4.112 0.000111 ***
## dayAfter Acclimation                       -5.114 2.92e-06 ***
## humidity_tmt_percentDry                    -0.415 0.679610
## dayMid Acclimation:humidity_tmt_percentDry  0.749 0.456334
## dayAfter Acclimation:humidity_tmt_percentDry 0.147 0.883335
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) dyMdAc dyAftA hmd__D dMA:__
## dyMdAcclmtn -0.426
## dyAftrAcclm -0.426  0.500
## hmdty_tmt_D -0.554  0.375  0.375
## dyMAccl:__D  0.297 -0.697 -0.348 -0.538
## dyAAccl:__D  0.297 -0.348 -0.697 -0.538  0.500
```

Export

```
write.csv(hct_AICc, "./best_models/exp_effects_hct_mod_rankings.csv")
write.csv(broom.mixed::tidy(hct_mod1p),
          "./best_models/exp_effects_hct_best_mod1.csv")
```

Osmolality

Build Model

```
osml_mod1 <- all_dat_no_rehab %>%
  dplyr::filter(complete.cases(osmolality_mmol_kg)) %>%
  lme4::lmer(data = .,
             osmolality_mmol_kg ~ day * humidity_tmt_percent +
             (1|trial_number/individual_ID))
```

```
## boundary (singular) fit: see ?isSingular
```

```
summary(osml_mod1)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula:
## osmolality_mmol_kg ~ day * humidity_tmt_percent + (1 | trial_number/individual_ID)
```

```
##     Data: .
##
## REML criterion at convergence: 872.1
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.66849 -0.79364  0.00361  0.51469  2.41228
##
## Random effects:
##  Groups                     Name        Variance Std.Dev.
##  individual_ID:trial_number (Intercept)   0.0     0.00
##  trial_number               (Intercept) 313.5    17.71
##  Residual                               393.8    19.84
## Number of obs: 102, groups:  individual_ID:trial_number, 35; trial_number, 4
##
## Fixed effects:
##                                           Estimate Std. Error t value
## (Intercept)                                378.509     10.035  37.719
## dayMid Acclimation                         -29.500      6.615  -4.460
## dayAfter Acclimation                       -13.885      6.713  -2.068
## humidity_tmt_percentDry                    -10.215      6.713  -1.522
## dayMid Acclimation:humidity_tmt_percentDry  12.324      9.491   1.298
## dayAfter Acclimation:humidity_tmt_percentDry 17.783     9.721   1.829
##
## Correlation of Fixed Effects:
##            (Intr) dyMdAc dyAftA hmd__D dMA:__
## dyMdAcclmtn -0.330
## dyAftrAcclm -0.326  0.493
## hmdty_tmt_D -0.326  0.493  0.485
## dyMAccl:__D  0.230 -0.697 -0.343 -0.707
## dyAAccl:__D  0.224 -0.340 -0.690 -0.690  0.488
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see ?isSingular
```

```
drop1(osml_mod1)
```

```
## boundary (singular) fit: see ?isSingular

## Single term deletions
##
## Model:
## osmolality_mmol_kg ~ day * humidity_tmt_percent + (1 | trial_number/individual_ID)
##                          npar    AIC
## <none>                        922.78
## day:humidity_tmt_percent    2 922.47
```

```
# drop day*humidity interaction
osml_mod2 <- all_dat_no_rehab %>%
  dplyr::filter(complete.cases(osmolality_mmol_kg)) %>%
  lme4::lmer(data = .,
             osmolality_mmol_kg ~ day + humidity_tmt_percent +
             (1|trial_number/individual_ID))
```

```
## boundary (singular) fit: see ?isSingular
```

```r
summary(osml_mod2)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula:
## osmolality_mmol_kg ~ day + humidity_tmt_percent + (1 | trial_number/individual_ID)
##    Data: .
##
## REML criterion at convergence: 888.1
##
## Scaled residuals:
##     Min      1Q   Median      3Q      Max
## -2.41172 -0.73400  0.06196  0.58652  2.41801
##
## Random effects:
##  Groups                    Name         Variance Std.Dev.
##  individual_ID:trial_number (Intercept)   0.0     0.00
##  trial_number              (Intercept) 314.5    17.74
##  Residual                               400.2    20.01
## Number of obs: 102, groups:  individual_ID:trial_number, 35; trial_number, 4
##
## Fixed effects:
##                         Estimate Std. Error t value
## (Intercept)             373.7599     9.7086  38.498
## dayMid Acclimation      -23.5143     4.7822  -4.917
## dayAfter Acclimation     -5.3904     4.9001  -1.100
## humidity_tmt_percentDry  -0.4143     3.9679  -0.104
##
## Correlation of Fixed Effects:
##            (Intr) dyMdAc dyAftA
## dyMdAcclmtn -0.246
## dyAftrAcclm -0.245  0.488
## hmdty_tmt_D -0.200  0.000  0.013
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see ?isSingular
```

```r
drop1(osml_mod2)
```

```
## boundary (singular) fit: see ?isSingular
## boundary (singular) fit: see ?isSingular

## Single term deletions
##
## Model:
## osmolality_mmol_kg ~ day + humidity_tmt_percent + (1 | trial_number/individual_ID)
##                      npar    AIC
## <none>                    922.47
## day                    2 942.51
## humidity_tmt_percent   1 920.48
```

```r
# drop humidity tmt
osml_mod3 <- all_dat_no_rehab %>%
  dplyr::filter(complete.cases(osmolality_mmol_kg)) %>%
  lme4::lmer(data = .,
             osmolality_mmol_kg ~ day +
             (1|trial_number/individual_ID))
```

```
## boundary (singular) fit: see ?isSingular
```

```r
summary(osml_mod3)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: osmolality_mmol_kg ~ day + (1 | trial_number/individual_ID)
##     Data: .
##
## REML criterion at convergence: 892.7
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.41351 -0.74896  0.05141  0.57838  2.44024
##
## Random effects:
##  Groups                     Name        Variance Std.Dev.
##  individual_ID:trial_number (Intercept)   0.0     0.00
##  trial_number               (Intercept) 314.6    17.74
##  Residual                               396.1    19.90
## Number of obs: 102, groups:  individual_ID:trial_number, 35; trial_number, 4
##
## Fixed effects:
##                      Estimate Std. Error t value
## (Intercept)           373.559      9.507  39.294
## dayMid Acclimation    -23.514      4.757  -4.943
## dayAfter Acclimation   -5.384      4.874  -1.105
##
## Correlation of Fixed Effects:
##            (Intr) dyMdAc
## dyMdAcclmtn -0.250
## dyAftrAcclm -0.246  0.488
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see ?isSingular
```

```r
drop1(osml_mod3)
```

```
## boundary (singular) fit: see ?isSingular
```

```
## Single term deletions
##
## Model:
## osmolality_mmol_kg ~ day + (1 | trial_number/individual_ID)
##        npar    AIC
## <none>       920.48
## day       2 940.52
```

```r
# null model
osml_mod_null <- all_dat_no_rehab %>%
  dplyr::filter(complete.cases(osmolality_mmol_kg)) %>%
  lme4::lmer(data = .,
             osmolality_mmol_kg ~ 1 +
             (1|trial_number/individual_ID))
```

```
## boundary (singular) fit: see ?isSingular
```

```r
summary(osml_mod_null)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: osmolality_mmol_kg ~ 1 + (1 | trial_number/individual_ID)
##    Data: .
##
## REML criterion at convergence: 926.4
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.9986 -0.7111 -0.1767  0.7047  2.6120
##
## Random effects:
##  Groups                    Name        Variance Std.Dev.
##  individual_ID:trial_number (Intercept)   0.0     0.00
##  trial_number              (Intercept) 312.8    17.69
##  Residual                              495.7    22.26
## Number of obs: 102, groups:  individual_ID:trial_number, 35; trial_number, 4
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)  363.791      9.138   39.81
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see ?isSingular
```

Selection

```
osml_models <- list(osml_mod1, osml_mod2, osml_mod3, osml_mod_null)

#specify model names
osml_mod_names <- c('(model 1) ~ day * humidity',
                    '(model 2) ~ day + humidity',
                    '(model 3) ~ day',
                    'null model')
#calculate AIC of each model
osml_AICc <- data.frame(aictab(cand.set = osml_models,
                               modnames = osml_mod_names))
```

```
## Warning in aictab.AIClmerMod(cand.set = osml_models, modnames = osml_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
```

```
osml_AICc
```

```
##                    Modnames K     AICc Delta_AICc    ModelLik       AICcWt
## 1 (model 1) ~ day * humidity 9 892.0606    0.00000 1.000000e+00 9.952407e-01
## 2 (model 2) ~ day + humidity 7 903.2983   11.23765 3.628910e-03 3.611639e-03
## 3           (model 3) ~ day 6 905.5911   13.53048 1.153169e-03 1.147681e-03
## 4                null model 4 934.8224   42.76176 5.180853e-10 5.156196e-10
##      Res.LL   Cum.Wt
## 1 -436.0521 0.9952407
## 2 -444.0534 0.9988523
## 3 -446.3535 1.0000000
## 4 -463.2050 1.0000000
```

Check Conditions of Top Model

```
plot(osml_mod1)
```
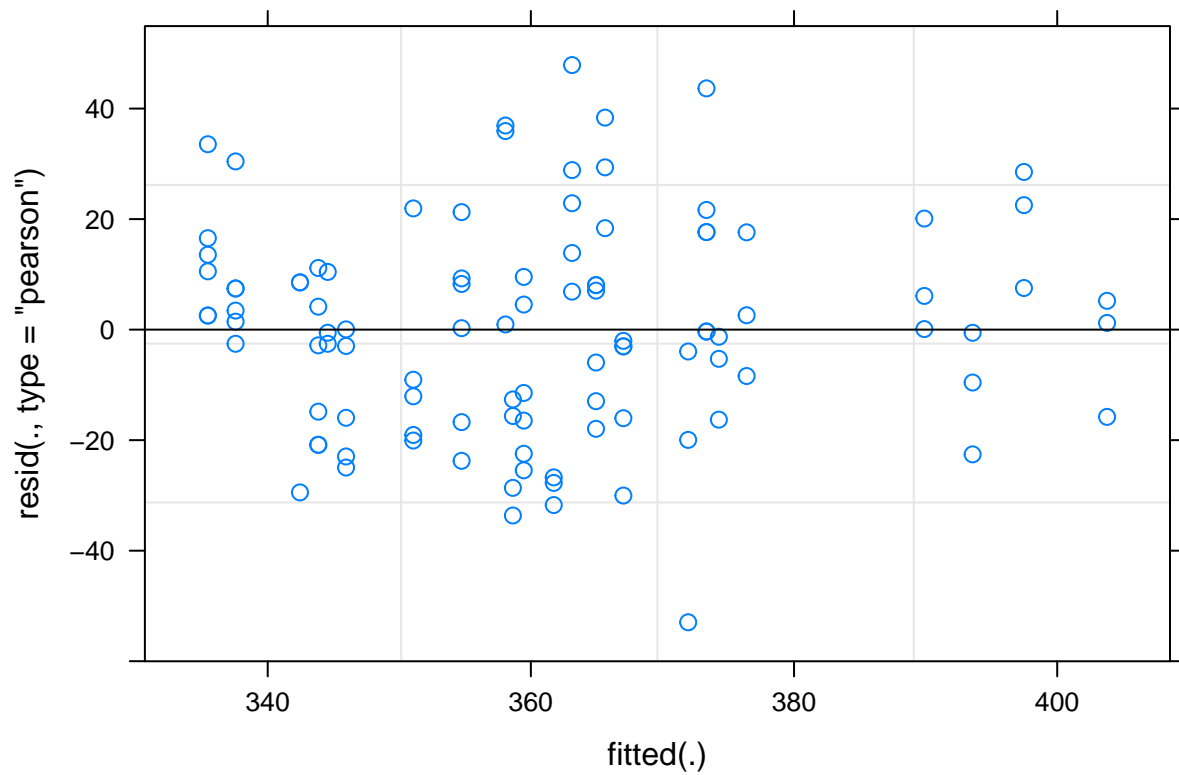


```
car::vif(osml_mod1)
```

```
##                              GVIF Df GVIF^(1/(2*Df))
## day                      3.687586  2        1.385752
## humidity_tmt_percent     2.909876  1        1.705836
## day:humidity_tmt_percent 7.291589  2        1.643257
```

looks pretty good

Is the distribution of residuals **normal**? use Shapiro-Wilk normality test: H0: data is NOT significantly different from normal distribution HA: data IS significantly different from normal distribution

```
simple.eda(residuals(osml_mod1))
```

Histogram of x	boxplot	Normal Q–Q Plot
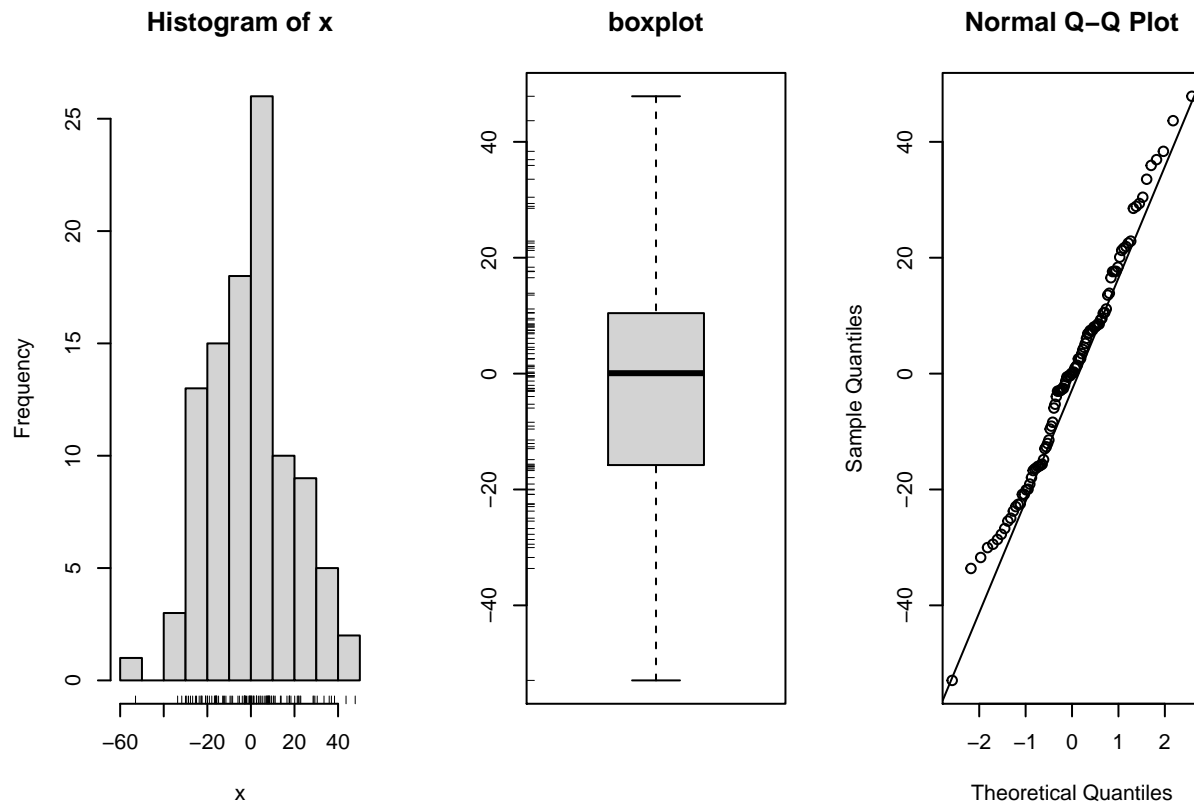

```r
shapiro.test(residuals(osml_mod1))
```

```
##
##  Shapiro-Wilk normality test
##
## data:  residuals(osml_mod1)
## W = 0.98957, p-value = 0.616
```

residuals are normally distributed!

Re-run top model with lmerTest for p-values:

```r
osml_mod1p <- lmerTest::lmer(data = all_dat_no_rehab,
              osmolality_mmol_kg ~ day * humidity_tmt_percent +
              (1|trial_number/individual_ID))
```

```
## boundary (singular) fit: see ?isSingular
```

```r
summary(osml_mod1p)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula:
## osmolality_mmol_kg ~ day * humidity_tmt_percent + (1 | trial_number/individual_ID)
##    Data: all_dat_no_rehab
##
## REML criterion at convergence: 872.1
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.66849 -0.79364  0.00361  0.51469  2.41228
```

```
##
## Random effects:
##  Groups                    Name          Variance Std.Dev.
##  individual_ID:trial_number (Intercept)   0.0      0.00
##  trial_number              (Intercept) 313.5     17.71
##  Residual                                393.8     19.84
## Number of obs: 102, groups:  individual_ID:trial_number, 35; trial_number, 4
##
## Fixed effects:
##                                          Estimate Std. Error      df
## (Intercept)                               378.509     10.035   4.379
## dayMid Acclimation                        -29.500      6.615  92.951
## dayAfter Acclimation                      -13.885      6.713  92.956
## humidity_tmt_percentDry                   -10.215      6.713  92.956
## dayMid Acclimation:humidity_tmt_percentDry 12.324      9.491  92.951
## dayAfter Acclimation:humidity_tmt_percentDry 17.783    9.721  92.954
##                                          t value Pr(>|t|)
## (Intercept)                               37.719 1.13e-06 ***
## dayMid Acclimation                        -4.460 2.29e-05 ***
## dayAfter Acclimation                      -2.068   0.0414 *
## humidity_tmt_percentDry                   -1.522   0.1315
## dayMid Acclimation:humidity_tmt_percentDry 1.298   0.1974
## dayAfter Acclimation:humidity_tmt_percentDry 1.829  0.0705 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr) dyMdAc dyAftA hmd__D dMA:__
## dyMdAcclmtn -0.330
## dyAftrAcclm -0.326  0.493
## hmdty_tmt_D -0.326  0.493  0.485
## dyMAccl:__D  0.230 -0.697 -0.343 -0.707
## dyAAccl:__D  0.224 -0.340 -0.690 -0.690  0.488
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see ?isSingular
```

Export

```
write.csv(osml_AICc, "./best_models/exp_effects_osml_mod_rankings.csv")
write.csv(broom.mixed::tidy(osml_mod1p),
          "./best_models/exp_effects_osml_best_mod1.csv")
```

CEWL

Build Model

```
# FULL model
CEWL_mod1 <- lme4::lmer(data = CEWL,
            TEWL_g_m2h ~ day * humidity_tmt_percent * region +
            cloacal_temp_C +
            (1|trial_number/individual_ID))
summary(CEWL_mod1)
```

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

```
## Formula: TEWL_g_m2h ~ day * humidity_tmt_percent * region + cloacal_temp_C +
##     (1 | trial_number/individual_ID)
##    Data: CEWL
##
## REML criterion at convergence: 2441.8
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.4361 -0.5707 -0.0822  0.4555  4.1852
##
## Random effects:
##  Groups                   Name        Variance Std.Dev.
##  individual_ID:trial_number (Intercept)  38.212   6.182
##  trial_number             (Intercept)   8.141   2.853
##  Residual                             123.274  11.103
## Number of obs: 326, groups:  individual_ID:trial_number, 33; trial_number, 4
##
## Fixed effects:
##                                                    Estimate Std. Error t value
## (Intercept)                                        -69.91895   11.98454  -5.834
## dayAfter                                            20.55665    3.96057   5.190
## humidity_tmt_percentDry                              0.09390    4.44521   0.021
## regionVentrum                                       14.06471    3.80826   3.693
## regionHead                                           5.20176    3.80826   1.366
## regionDewlap                                         2.76945    3.87231   0.715
## regionMite Patch                                     5.02118    3.80826   1.318
## cloacal_temp_C                                       3.90353    0.48902   7.982
## dayAfter:humidity_tmt_percentDry                   -22.17103    5.52280  -4.014
## dayAfter:regionVentrum                               4.82016    5.43126   0.887
## dayAfter:regionHead                                 -7.17102    5.43126  -1.320
## dayAfter:regionDewlap                               -2.93470    5.46212  -0.537
## dayAfter:regionMite Patch                           -6.04716    5.47797  -1.104
## humidity_tmt_percentDry:regionVentrum               -0.34596    5.46920  -0.063
## humidity_tmt_percentDry:regionHead                  -0.03395    5.46920  -0.006
## humidity_tmt_percentDry:regionDewlap                 0.90930    5.51399   0.165
## humidity_tmt_percentDry:regionMite Patch             2.90477    5.52066   0.526
## dayAfter:humidity_tmt_percentDry:regionVentrum      -2.37516    7.76641  -0.306
## dayAfter:humidity_tmt_percentDry:regionHead          5.28070    7.76641   0.680
## dayAfter:humidity_tmt_percentDry:regionDewlap        5.66684    7.82338   0.724
## dayAfter:humidity_tmt_percentDry:regionMite Patch    1.47809    7.83657   0.189
##
## Correlation matrix not shown by default, as p = 21 > 12.
## Use print(x, correlation=TRUE)  or
##     vcov(x)        if you need it
```

```
drop1(CEWL_mod1)
```

```
## Single term deletions
##
## Model:
## TEWL_g_m2h ~ day * humidity_tmt_percent * region + cloacal_temp_C +
##     (1 | trial_number/individual_ID)
##                                  npar    AIC
## <none>                                2570.1
```

```
## cloacal_temp_C                      1 2628.2
## day:humidity_tmt_percent:region     4 2563.8
# drop triple interaction
CEWL_mod2 <- lme4::lmer(data = CEWL,
              TEWL_g_m2h ~ day * (humidity_tmt_percent + region) +
                humidity_tmt_percent * region +
              cloacal_temp_C +
              (1|trial_number/individual_ID))
summary(CEWL_mod2)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula:
## TEWL_g_m2h ~ day * (humidity_tmt_percent + region) + humidity_tmt_percent *
##     region + cloacal_temp_C + (1 | trial_number/individual_ID)
##    Data: CEWL
##
## REML criterion at convergence: 2466
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.4329 -0.5884 -0.0677  0.4374  4.2096
##
## Random effects:
##  Groups                     Name        Variance Std.Dev.
##  individual_ID:trial_number (Intercept)  38.288   6.188
##  trial_number               (Intercept)   8.423   2.902
##  Residual                               122.185  11.054
## Number of obs: 326, groups:  individual_ID:trial_number, 33; trial_number, 4
##
## Fixed effects:
##                                           Estimate Std. Error t value
## (Intercept)                               -69.3812    11.8966  -5.832
## dayAfter                                   19.5581     3.1171   6.274
## humidity_tmt_percentDry                    -0.8763     3.7142  -0.236
## regionVentrum                              14.6508     3.3043   4.434
## regionHead                                  3.9319     3.3043   1.190
## regionDewlap                                1.3624     3.3442   0.407
## regionMite Patch                            4.6684     3.3136   1.409
## cloacal_temp_C                              3.9004     0.4871   8.007
## dayAfter:humidity_tmt_percentDry          -20.1657     2.4789  -8.135
## dayAfter:regionVentrum                      3.6904     3.8650   0.955
## dayAfter:regionHead                        -4.5888     3.8650  -1.187
## dayAfter:regionDewlap                      -0.1818     3.8935  -0.047
## dayAfter:regionMite Patch                  -5.3075     3.8986  -1.361
## humidity_tmt_percentDry:regionVentrum      -1.5548     3.8658  -0.402
## humidity_tmt_percentDry:regionHead          2.5852     3.8658   0.669
## humidity_tmt_percentDry:regionDewlap        3.7402     3.8849   0.963
## humidity_tmt_percentDry:regionMite Patch    3.6211     3.8995   0.929
##
## Correlation matrix not shown by default, as p = 17 > 12.
## Use print(x, correlation=TRUE)  or
##     vcov(x)         if you need it
```

```
drop1(CEWL_mod2)
```

```
## Single term deletions
##
## Model:
## TEWL_g_m2h ~ day * (humidity_tmt_percent + region) + humidity_tmt_percent *
##     region + cloacal_temp_C + (1 | trial_number/individual_ID)
##                              npar    AIC
## <none>                             2563.8
## cloacal_temp_C                  1 2621.6
## day:humidity_tmt_percent        1 2624.4
## day:region                      4 2563.5
## humidity_tmt_percent:region     4 2559.0
```

```
# drop humidity*region interaction
CEWL_mod3 <- lme4::lmer(data = CEWL,
            TEWL_g_m2h ~ day * (humidity_tmt_percent + region) +
            cloacal_temp_C +
            (1|trial_number/individual_ID))
summary(CEWL_mod3)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: TEWL_g_m2h ~ day * (humidity_tmt_percent + region) + cloacal_temp_C +
##     (1 | trial_number/individual_ID)
##    Data: CEWL
##
## REML criterion at convergence: 2485.9
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.3429 -0.5832 -0.0921  0.4654  4.1273
##
## Random effects:
##  Groups                    Name        Variance Std.Dev.
##  individual_ID:trial_number (Intercept)  38.280   6.187
##  trial_number              (Intercept)   8.625   2.937
##  Residual                              121.727  11.033
## Number of obs: 326, groups:  individual_ID:trial_number, 33; trial_number, 4
##
## Fixed effects:
##                                Estimate Std. Error t value
## (Intercept)                    -70.1518    11.8184  -5.936
## dayAfter                        19.5181     3.1111   6.274
## humidity_tmt_percentDry          0.7831     2.7920   0.280
## regionVentrum                   13.8970     2.7161   5.116
## regionHead                       5.1853     2.7161   1.909
## regionDewlap                     3.2049     2.7392   1.170
## regionMite Patch                 6.3894     2.7395   2.332
## cloacal_temp_C                   3.8988     0.4864   8.015
## dayAfter:humidity_tmt_percentDry -20.1455    2.4742  -8.142
## dayAfter:regionVentrum           3.7183     3.8575   0.964
## dayAfter:regionHead             -4.5610     3.8575  -1.182
## dayAfter:regionDewlap           -0.2458     3.8845  -0.063
## dayAfter:regionMite Patch       -5.2131     3.8900  -1.340
```

```
##
## Correlation matrix not shown by default, as p = 13 > 12.
## Use print(x, correlation=TRUE)  or
##     vcov(x)        if you need it
```

```r
drop1(CEWL_mod3)
```

```
## Single term deletions
##
## Model:
## TEWL_g_m2h ~ day * (humidity_tmt_percent + region) + cloacal_temp_C +
##     (1 | trial_number/individual_ID)
##                           npar    AIC
## <none>                         2559.0
## cloacal_temp_C            1 2616.1
## day:humidity_tmt_percent  1 2618.8
## day:region                4 2558.4
```

```r
# drop day*region interaction
CEWL_mod4 <- lme4::lmer(data = CEWL,
              TEWL_g_m2h ~ day * humidity_tmt_percent + region +
              cloacal_temp_C +
              (1|trial_number/individual_ID))
summary(CEWL_mod4)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: TEWL_g_m2h ~ day * humidity_tmt_percent + region + cloacal_temp_C +
##     (1 | trial_number/individual_ID)
##    Data: CEWL
##
## REML criterion at convergence: 2510.2
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.3478 -0.6058 -0.1117  0.4446  3.9319
##
## Random effects:
##  Groups                    Name        Variance Std.Dev.
##  individual_ID:trial_number (Intercept)  38.023   6.166
##  trial_number              (Intercept)   8.872   2.979
##  Residual                              123.111  11.096
## Number of obs: 326, groups:  individual_ID:trial_number, 33; trial_number, 4
##
## Fixed effects:
##                               Estimate Std. Error t value
## (Intercept)                   -69.3758    11.8197  -5.869
## dayAfter                       18.2632     1.9251   9.487
## humidity_tmt_percentDry         0.7605     2.7927   0.272
## regionVentrum                  15.7651     1.9396   8.128
## regionHead                      2.9138     1.9396   1.502
## regionDewlap                    3.0977     1.9483   1.590
## regionMite Patch                3.7912     1.9565   1.938
## cloacal_temp_C                  3.8920     0.4886   7.966
## dayAfter:humidity_tmt_percentDry -20.1375   2.4881  -8.094
##
```

```
## Correlation of Fixed Effects:
##            (Intr) dyAftr hmd__D rgnVnt regnHd rgnDwl rgnMtP clc__C
## dayAfter   -0.507
## hmdty_tmt_D  0.005  0.217
## regionVntrm -0.086 -0.004  0.000
## regionHead  -0.086 -0.004  0.000  0.504
## regionDewlp -0.098 -0.010 -0.006  0.502  0.502
## reginMtPtch -0.108  0.013  0.002  0.500  0.500  0.498
## clocl_tmp_C -0.972  0.456 -0.122  0.004  0.004  0.017  0.026
## dyAftr:h__D  0.191 -0.680 -0.418  0.004  0.004  0.017 -0.010 -0.146
```

```r
drop1(CEWL_mod4)
```

```
## Single term deletions
##
## Model:
## TEWL_g_m2h ~ day * humidity_tmt_percent + region + cloacal_temp_C +
##     (1 | trial_number/individual_ID)
##                          npar    AIC
## <none>                        2558.4
## region                    4 2622.8
## cloacal_temp_C            1 2614.1
## day:humidity_tmt_percent  1 2616.8
```

```r
# drop cloacal temp
CEWL_mod5 <- lme4::lmer(data = CEWL,
              TEWL_g_m2h ~ day * humidity_tmt_percent + region +
              (1|trial_number/individual_ID))
summary(CEWL_mod5)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula:
## TEWL_g_m2h ~ day * humidity_tmt_percent + region + (1 | trial_number/individual_ID)
##    Data: CEWL
##
## REML criterion at convergence: 2565.8
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.1498 -0.5992 -0.0657  0.4407  3.8101
##
## Random effects:
##  Groups                   Name        Variance Std.Dev.
##  individual_ID:trial_number (Intercept)  30.95    5.564
##  trial_number             (Intercept)  48.26    6.947
##  Residual                             148.18   12.173
## Number of obs: 326, groups:  individual_ID:trial_number, 33; trial_number, 4
##
## Fixed effects:
##                            Estimate Std. Error t value
## (Intercept)                  21.732      4.213   5.158
## dayAfter                     11.275      1.880   5.999
## humidity_tmt_percentDry       3.927      2.732   1.437
## regionVentrum                15.713      2.128   7.384
## regionHead                    2.862      2.128   1.345
```

```
## regionDewlap                                  2.843       2.137    1.330
## regionMite Patch                               3.364       2.145    1.568
## dayAfter:humidity_tmt_percentDry  -17.233      2.700   -6.382
##
## Correlation of Fixed Effects:
##             (Intr) dyAftr hmd__D rgnVnt regnHd rgnDwl rgnMtP
## dayAfter    -0.221
## hmdty_tmt_D -0.317  0.344
## regionVntrm -0.255 -0.006  0.001
## regionHead  -0.255 -0.006  0.001  0.504
## regionDewlp -0.252 -0.020 -0.004  0.502  0.502
## reginMtPtch -0.254  0.001  0.006  0.500  0.500  0.498
## dyAftr:h__D  0.153 -0.696 -0.494  0.004  0.004  0.019 -0.006
```

```r
drop1(CEWL_mod5)
```

```
## Single term deletions
##
## Model:
## TEWL_g_m2h ~ day * humidity_tmt_percent + region + (1 | trial_number/individual_ID)
##                          npar    AIC
## <none>                        2614.1
## region                     4 2667.8
## day:humidity_tmt_percent   1 2651.0
```

```r
# drop day*humidity interaction
CEWL_mod6 <- lme4::lmer(data = CEWL,
            TEWL_g_m2h ~ day + humidity_tmt_percent + region +
            (1|trial_number/individual_ID))
summary(CEWL_mod6)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula:
## TEWL_g_m2h ~ day + humidity_tmt_percent + region + (1 | trial_number/individual_ID)
##    Data: CEWL
##
## REML criterion at convergence: 2607.9
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.3435 -0.6517 -0.1429  0.5085  3.9211
##
## Random effects:
##  Groups                    Name        Variance Std.Dev.
##  individual_ID:trial_number (Intercept)  28.73    5.360
##  trial_number               (Intercept)  48.36    6.954
##  Residual                               168.67   12.987
## Number of obs: 326, groups:  individual_ID:trial_number, 33; trial_number, 4
##
## Fixed effects:
##                          Estimate Std. Error t value
## (Intercept)               25.855      4.203   6.152
## dayAfter                   2.919      1.439   2.028
## humidity_tmt_percentDry   -4.690      2.372  -1.977
## regionVentrum             15.768      2.270   6.946
```

48

```
## regionHead                 2.917      2.270    1.285
## regionDewlap               3.095      2.280    1.358
## regionMite Patch           3.270      2.289    1.429
##
## Correlation of Fixed Effects:
##             (Intr) dyAftr hmd__D rgnVnt regnHd rgnDwl
## dayAfter    -0.170
## hmdty_tmt_D -0.278  0.001
## regionVntrm -0.273 -0.004  0.004
## regionHead  -0.273 -0.004  0.004  0.504
## regionDewlp -0.272 -0.009  0.007  0.502  0.502
## reginMtPtch -0.270 -0.004  0.003  0.500  0.500  0.498
```

drop1(CEWL_mod6)

```
## Single term deletions
##
## Model:
## TEWL_g_m2h ~ day + humidity_tmt_percent + region + (1 | trial_number/individual_ID)
##                       npar    AIC
## <none>                     2651.0
## day                      1 2653.2
## humidity_tmt_percent     1 2652.9
## region                   4 2697.8
```

 # drop humidity
```
CEWL_mod7 <- lme4::lmer(data = CEWL,
             TEWL_g_m2h ~ day + region +
             (1|trial_number/individual_ID))
```
summary(CEWL_mod7)

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: TEWL_g_m2h ~ day + region + (1 | trial_number/individual_ID)
##    Data: CEWL
##
## REML criterion at convergence: 2615.2
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.2889 -0.6743 -0.1261  0.5013  3.9525
##
## Random effects:
##  Groups                    Name        Variance Std.Dev.
##  individual_ID:trial_number (Intercept) 32.89    5.735
##  trial_number               (Intercept) 53.60    7.322
##  Residual                               168.64   12.986
## Number of obs: 326, groups:  individual_ID:trial_number, 33; trial_number, 4
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)    23.542      4.214   5.586
## dayAfter        2.923      1.439   2.031
## regionVentrum  15.787      2.270   6.955
## regionHead      2.935      2.270   1.293
## regionDewlap    3.130      2.279   1.373
```

49

```
## regionMite Patch    3.289      2.289    1.437
##
## Correlation of Fixed Effects:
##            (Intr) dyAftr rgnVnt regnHd rgnDwl
## dayAfter    -0.169
## regionVntrm -0.271 -0.004
## regionHead  -0.271 -0.004  0.504
## regionDewlp -0.270 -0.009  0.502  0.502
## reginMtPtch -0.269 -0.004  0.500  0.500  0.498
```

```r
drop1(CEWL_mod7)
```

```
## Single term deletions
##
## Model:
## TEWL_g_m2h ~ day + region + (1 | trial_number/individual_ID)
##        npar    AIC
## <none>      2652.9
## day      1 2655.1
## region   4 2699.7
```

```r
# drop day
CEWL_mod8 <- lme4::lmer(data = CEWL,
             TEWL_g_m2h ~ region +
             (1|trial_number/individual_ID))
summary(CEWL_mod8)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: TEWL_g_m2h ~ region + (1 | trial_number/individual_ID)
##    Data: CEWL
##
## REML criterion at convergence: 2621.9
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.3881 -0.6550 -0.1507  0.4282  4.0461
##
## Random effects:
##  Groups                    Name        Variance Std.Dev.
##  individual_ID:trial_number (Intercept)  32.63    5.713
##  trial_number              (Intercept)  53.17    7.291
##  Residual                               170.50   13.058
## Number of obs: 326, groups:  individual_ID:trial_number, 33; trial_number, 4
##
## Fixed effects:
##                 Estimate Std. Error t value
## (Intercept)       24.992      4.143   6.033
## regionVentrum     15.807      2.282   6.925
## regionHead         2.956      2.282   1.295
## regionDewlap       3.171      2.292   1.383
## regionMite Patch   3.309      2.301   1.438
##
## Correlation of Fixed Effects:
##            (Intr) rgnVnt regnHd rgnDwl
## regionVntrm -0.278
```

```
## regionHead  -0.278  0.504
## regionDewlp -0.277  0.502  0.502
## reginMtPtch -0.276  0.500  0.500  0.498
```

```r
drop1(CEWL_mod8)
```

```
## Single term deletions
##
## Model:
## TEWL_g_m2h ~ region + (1 | trial_number/individual_ID)
##        npar    AIC
## <none>       2655.1
## region    4 2701.2
```

```r
# NULL model
CEWL_mod_null <- lme4::lmer(data = CEWL,
               TEWL_g_m2h ~ 1 +
               (1|trial_number/individual_ID))
```

Selection

```r
CEWL_models <- list(CEWL_mod1, CEWL_mod2, CEWL_mod3, CEWL_mod4,
                    CEWL_mod5, CEWL_mod6, CEWL_mod7, CEWL_mod8,
                    CEWL_mod_null)

#specify model names
CEWL_mod_names <- c('(model 1) ~ day * humidity * region + cloacal temp',
                    '(model 2) ~ day * humidity + day * region + humidity * region + cloacal temp',
                    '(model 3) ~ day * humidity + day * region + cloacal temp',
                    '(model 4) ~ day * humidity + region + cloacal temp',
                    '(model 5) ~ day * humidity + region',
                    '(model 6) ~ day + humidity + region',
                    '(model 7) ~ day + region',
                    '(model 8) ~ region',
                    '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
```

```r
CEWL_AICc
```

```
##                                                                      Modnames
## 1                         (model 1) ~ day * humidity * region + cloacal temp
## 2 (model 2) ~ day * humidity + day * region + humidity * region + cloacal temp
## 3                 (model 3) ~ day * humidity + day * region + cloacal temp
## 4                         (model 4) ~ day * humidity + region + cloacal temp
## 5                                       (model 5) ~ day * humidity + region
## 6                                       (model 6) ~ day + humidity + region
## 7                                              (model 7) ~ day + region
## 8                                                     (model 8) ~ region
## 9                                                            null model
##     K    AICc Delta_AICc    ModelLik     AICcWt    Res.LL    Cum.Wt
```

```
## 1 24 2493.777     0.00000 1.000000e+00 9.994309e-01 -1220.895 0.9994309
## 2 20 2508.727    14.95000 5.670846e-04 5.667619e-04 -1232.986 0.9999977
## 3 16 2519.710    25.93355 2.336689e-06 2.335359e-06 -1242.975 1.0000000
## 4 12 2535.175    41.39888 1.024111e-09 1.023528e-09 -1255.089 1.0000000
## 5 11 2588.687    94.91003 2.457815e-21 2.456416e-21 -1282.923 1.0000000
## 6 10 2628.577  134.80036 5.351474e-30 5.348428e-30 -1303.939 1.0000000
## 7  9 2633.794  140.01781 3.940207e-31 3.937965e-31 -1307.612 1.0000000
## 8  8 2638.351  144.57453 4.036827e-32 4.034530e-32 -1310.948 1.0000000
## 9  4 2696.967  203.18999 7.548388e-45 7.544092e-45 -1344.421 1.0000000
```

The FULL model is the best model.

Predict

Use the model to get the predicted means, which I will go back and use in the tmt_effects_CEWL figure.

```
CEWL_predicts <- CEWL %>%
  mutate(pred = predict(CEWL_mod1)) %>%
  group_by(region, humidity_tmt_percent, n_day) %>%
  summarise(CEWL_mean = mean(pred))
```

```
## `summarise()` regrouping output by 'region', 'humidity_tmt_percent' (override with `.groups` argument
```

```
CEWL_predicts
```

```
## # A tibble: 20 x 4
## # Groups:   region, humidity_tmt_percent [10]
##     region      humidity_tmt_percent n_day CEWL_mean
##     <fct>       <fct>                <dbl>     <dbl>
##  1 Dorsum      Humid                    0      22.4
##  2 Dorsum      Humid                    1      37.1
##  3 Dorsum      Dry                      0      24.7
##  4 Dorsum      Dry                      1      19.0
##  5 Ventrum     Humid                    0      36.4
##  6 Ventrum     Humid                    1      54.9
##  7 Ventrum     Dry                      0      38.4
##  8 Ventrum     Dry                      1      35.1
##  9 Head        Humid                    0      27.6
## 10 Head        Humid                    1      34.1
## 11 Head        Dry                      0      29.9
## 12 Head        Dry                      1      22.2
## 13 Dewlap      Humid                    0      25.9
## 14 Dewlap      Humid                    1      34.9
## 15 Dewlap      Dry                      0      28.4
## 16 Dewlap      Dry                      1      24.5
## 17 Mite Patch  Humid                    0      27.4
## 18 Mite Patch  Humid                    1      34.3
## 19 Mite Patch  Dry                      0      32.2
## 20 Mite Patch  Dry                      1      22.3
```

```
#write.csv(CEWL_predicts, "./data/CEWL_predicted_exp_means.csv")
```

Check Conditions

Is the function **linear**? Is there **equal** variance of the residuals? The residuals should be homoskedactic relative to y_hat (or x). Plotting residuals shows us whether the data meets linearity and equal variance assumptions:

```
plot(CEWL_mod1)
```
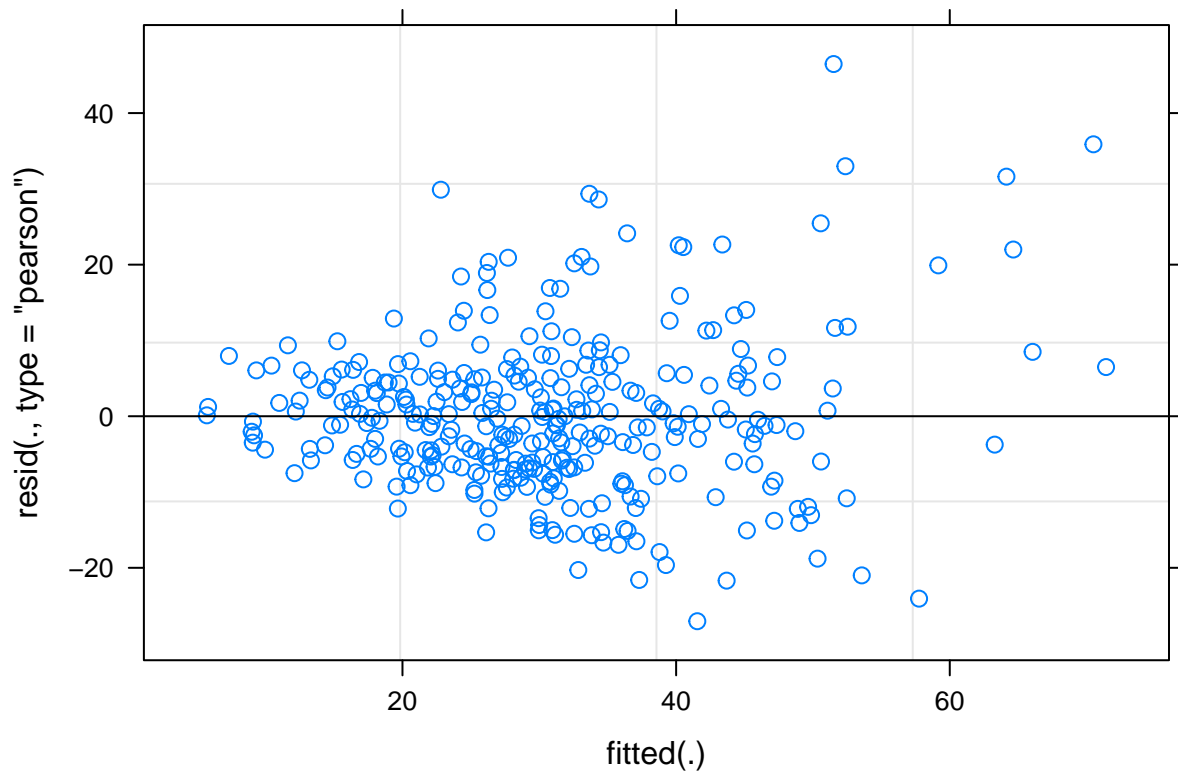


```
car::vif(CEWL_mod1)
```

```
##                                       GVIF Df GVIF^(1/(2*Df))
## day                               10.359562  1        3.218627
## humidity_tmt_percent               3.191166  1        1.786384
## region                           227.122403  4        1.970301
## cloacal_temp_C                     1.393922  1        1.180645
## day:humidity_tmt_percent          10.993060  1        3.315578
## day:region                       697.771225  4        2.267066
## humidity_tmt_percent:region      340.167300  4        2.072343
## day:humidity_tmt_percent:region  734.646278  4        2.281707
```

clear fanning shape... L & E are not satisfied.

Transform CEWL

Log-transformation worked well in the capture analysis, so try that here.

```
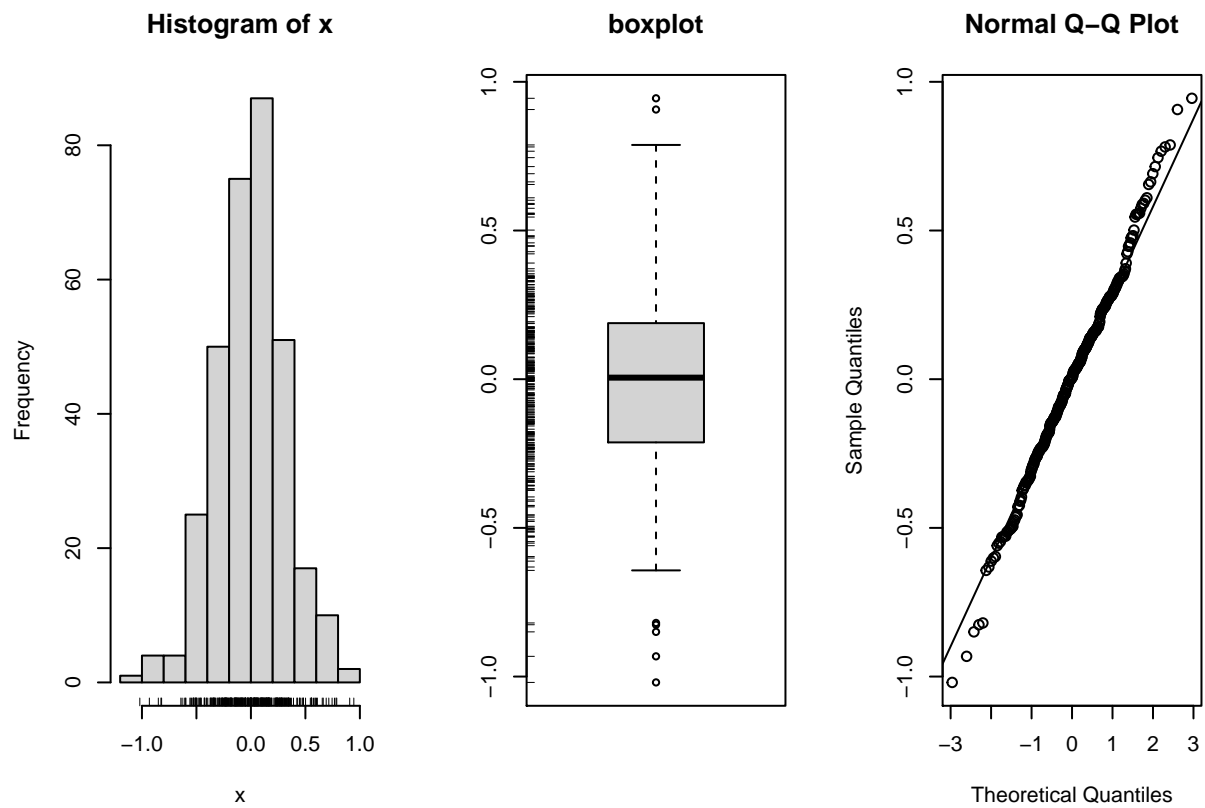CEWL_mod1t <- lme4::lmer(data = CEWL,
              log(TEWL_g_m2h) ~ day * humidity_tmt_percent * region +
              cloacal_temp_C +
              (1|trial_number/individual_ID))
plot(CEWL_mod1t)
```
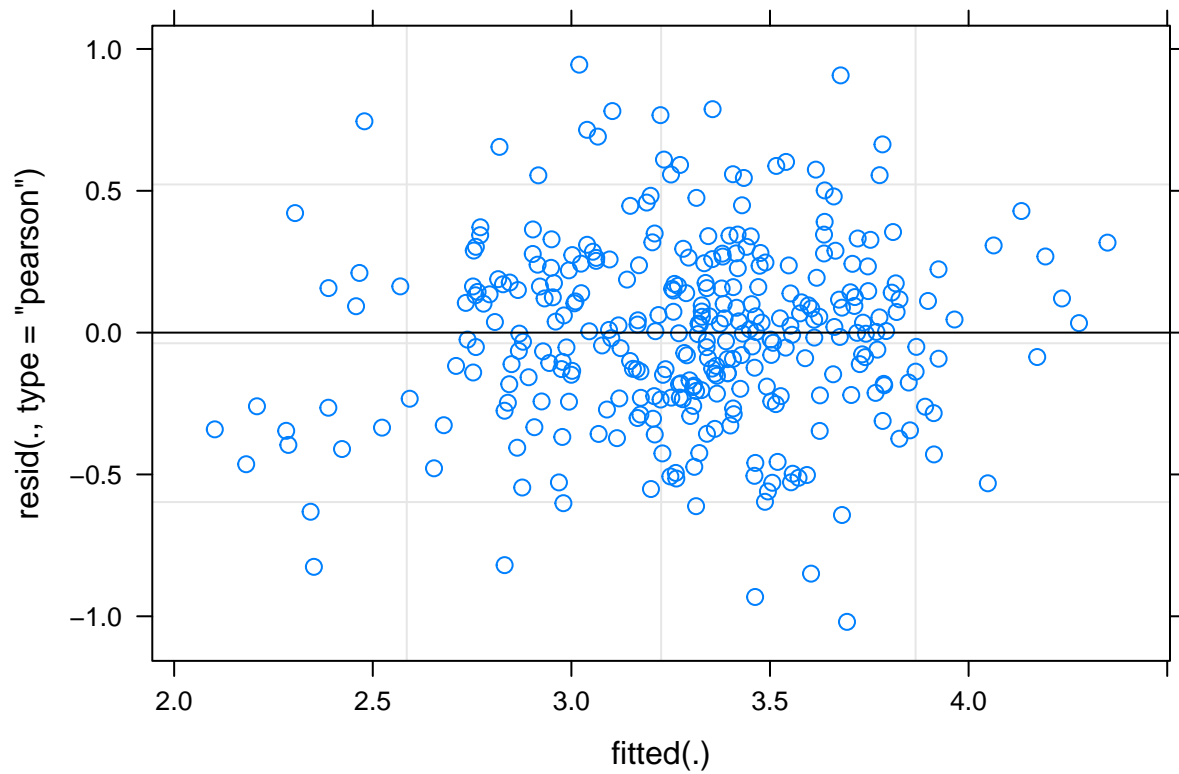
```r
simple.eda(residuals(CEWL_mod1t))
```

```
shapiro.test(residuals(CEWL_mod1t))
```

```
##
##  Shapiro-Wilk normality test
##
## data:  residuals(CEWL_mod1t)
## W = 0.99487, p-value = 0.35
```

L, E, and N are all satisfied now. :)

Re-run top model with lmerTest for p-values:

```
CEWL_mod1tp <- lmerTest::lmer(data = CEWL,
            log(TEWL_g_m2h) ~ day * humidity_tmt_percent * region +
            cloacal_temp_C +
            (1|trial_number/individual_ID))
summary(CEWL_mod1tp)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula:
## log(TEWL_g_m2h) ~ day * humidity_tmt_percent * region + cloacal_temp_C +
##     (1 | trial_number/individual_ID)
##    Data: CEWL
##
## REML criterion at convergence: 319
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.97137 -0.61425  0.01531  0.54828  2.75262
##
## Random effects:
##  Groups                   Name        Variance Std.Dev.
##  individual_ID:trial_number (Intercept) 0.02803  0.1674
##  trial_number             (Intercept) 0.03894  0.1973
##  Residual                             0.11777  0.3432
## Number of obs: 326, groups:  individual_ID:trial_number, 33; trial_number, 4
##
## Fixed effects:
##                                          Estimate Std. Error
## (Intercept)                              -0.17643    0.37743
## dayAfter                                  0.62673    0.12238
## humidity_tmt_percentDry                   0.02522    0.13373
## regionVentrum                             0.45536    0.11771
## regionHead                                0.19454    0.11771
## regionDewlap                              0.02448    0.11968
## regionMite Patch                          0.10936    0.11771
## cloacal_temp_C                            0.13669    0.01501
## dayAfter:humidity_tmt_percentDry         -0.82882    0.17069
## dayAfter:regionVentrum                   -0.02994    0.16787
## dayAfter:regionHead                      -0.22825    0.16787
## dayAfter:regionDewlap                    -0.05098    0.16879
## dayAfter:regionMite Patch                -0.24118    0.16930
## humidity_tmt_percentDry:regionVentrum    -0.05006    0.16904
## humidity_tmt_percentDry:regionHead       -0.03247    0.16904
```

```
## humidity_tmt_percentDry:regionDewlap                        0.05969   0.17042
## humidity_tmt_percentDry:regionMite Patch                    0.06529   0.17063
## dayAfter:humidity_tmt_percentDry:regionVentrum              0.26103   0.24004
## dayAfter:humidity_tmt_percentDry:regionHead                 0.24592   0.24004
## dayAfter:humidity_tmt_percentDry:regionDewlap               0.21627   0.24178
## dayAfter:humidity_tmt_percentDry:regionMite Patch           0.14559   0.24220
##                                                        df t value Pr(>|t|)
## (Intercept)                                      173.23775  -0.467 0.640762
## dayAfter                                         279.57165   5.121 5.66e-07
## humidity_tmt_percentDry                          211.50009   0.189 0.850623
## regionVentrum                                    273.43987   3.869 0.000137
## regionHead                                       273.43987   1.653 0.099524
## regionDewlap                                     273.94809   0.205 0.838091
## regionMite Patch                                 273.43987   0.929 0.353650
## cloacal_temp_C                                   265.46375   9.107  < 2e-16
## dayAfter:humidity_tmt_percentDry                 274.19820  -4.856 2.02e-06
## dayAfter:regionVentrum                           273.68460  -0.178 0.858566
## dayAfter:regionHead                              273.68460  -1.360 0.175037
## dayAfter:regionDewlap                            275.46822  -0.302 0.762859
## dayAfter:regionMite Patch                        273.95495  -1.425 0.155428
## humidity_tmt_percentDry:regionVentrum            273.43987  -0.296 0.767347
## humidity_tmt_percentDry:regionHead               273.43987  -0.192 0.847838
## humidity_tmt_percentDry:regionDewlap             273.69087   0.350 0.726414
## humidity_tmt_percentDry:regionMite Patch         273.72770   0.383 0.702305
## dayAfter:humidity_tmt_percentDry:regionVentrum   273.55964   1.087 0.277812
## dayAfter:humidity_tmt_percentDry:regionHead      273.55964   1.024 0.306507
## dayAfter:humidity_tmt_percentDry:regionDewlap    274.65325   0.895 0.371833
## dayAfter:humidity_tmt_percentDry:regionMite Patch 273.87346   0.601 0.548266
##
## (Intercept)
## dayAfter                                         ***
## humidity_tmt_percentDry
## regionVentrum                                    ***
## regionHead                                       .
## regionDewlap
## regionMite Patch
## cloacal_temp_C                                   ***
## dayAfter:humidity_tmt_percentDry                 ***
## dayAfter:regionVentrum
## dayAfter:regionHead
## dayAfter:regionDewlap
## dayAfter:regionMite Patch
## humidity_tmt_percentDry:regionVentrum
## humidity_tmt_percentDry:regionHead
## humidity_tmt_percentDry:regionDewlap
## humidity_tmt_percentDry:regionMite Patch
## dayAfter:humidity_tmt_percentDry:regionVentrum
## dayAfter:humidity_tmt_percentDry:regionHead
## dayAfter:humidity_tmt_percentDry:regionDewlap
## dayAfter:humidity_tmt_percentDry:regionMite Patch
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```
## Correlation matrix not shown by default, as p = 21 > 12.
## Use print(x, correlation=TRUE)   or
##      vcov(x)            if you need it
```

Export

```r
write.csv(CEWL_AICc, "./best_models/exp_effects_CEWL_mod_rankings.csv")
write.csv(broom.mixed::tidy(CEWL_mod1tp),
          "./best_models/exp_effects_CEWL_best_mod1.csv")
```