

Experimental Data Analysis

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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 capture_analysis.

```
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))

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
##
```

```
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:

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

```
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) %>%
  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

In the future, I could automate this like I did for the HOBO data.

Load in each of the post-rehab datafiles:

```
# 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
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
## 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
##
##      conclusion      notes
## complete:326      Length:326
##                  Class :character
##                  Mode  :character
##
##
##
##

```

Check that data looks correct:

```
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:

```
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           :65   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
## 4:118
##
##
##
```

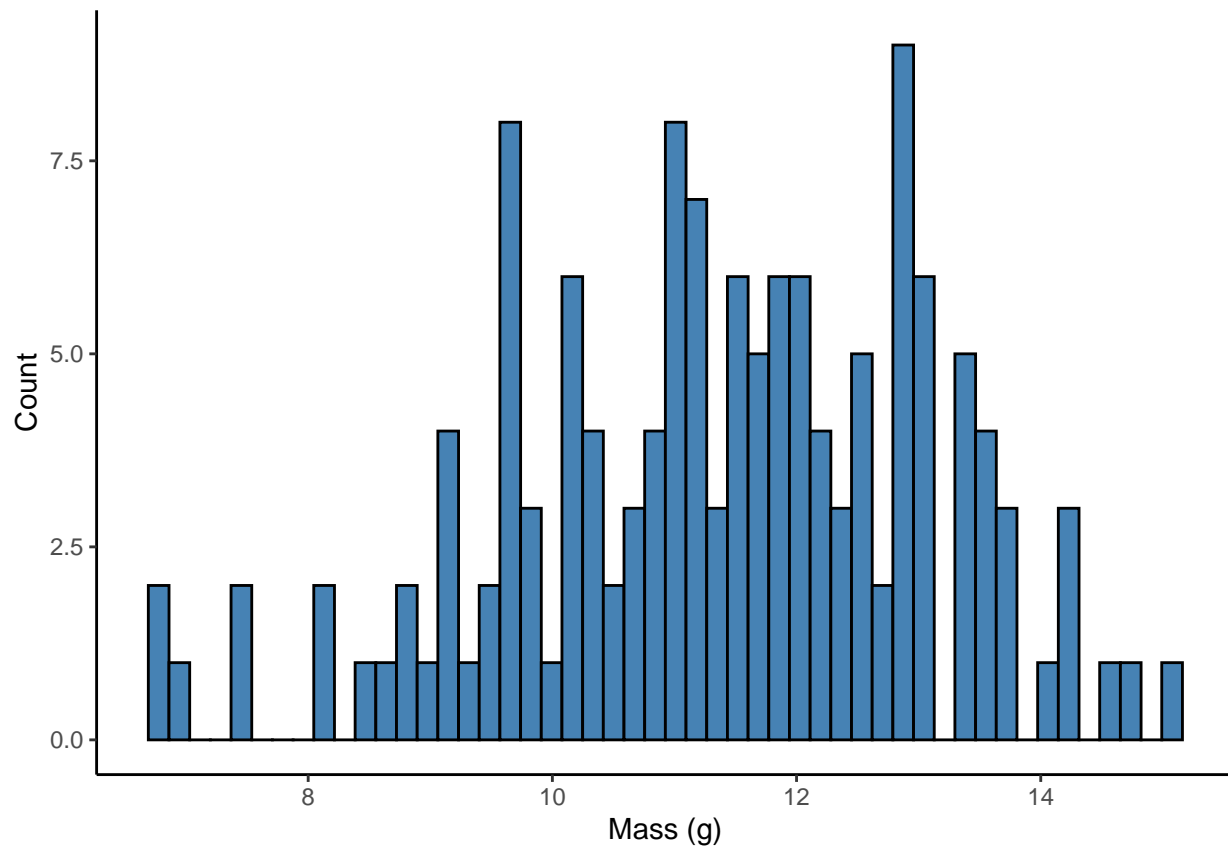
Export Data Frames for Power Analyses

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

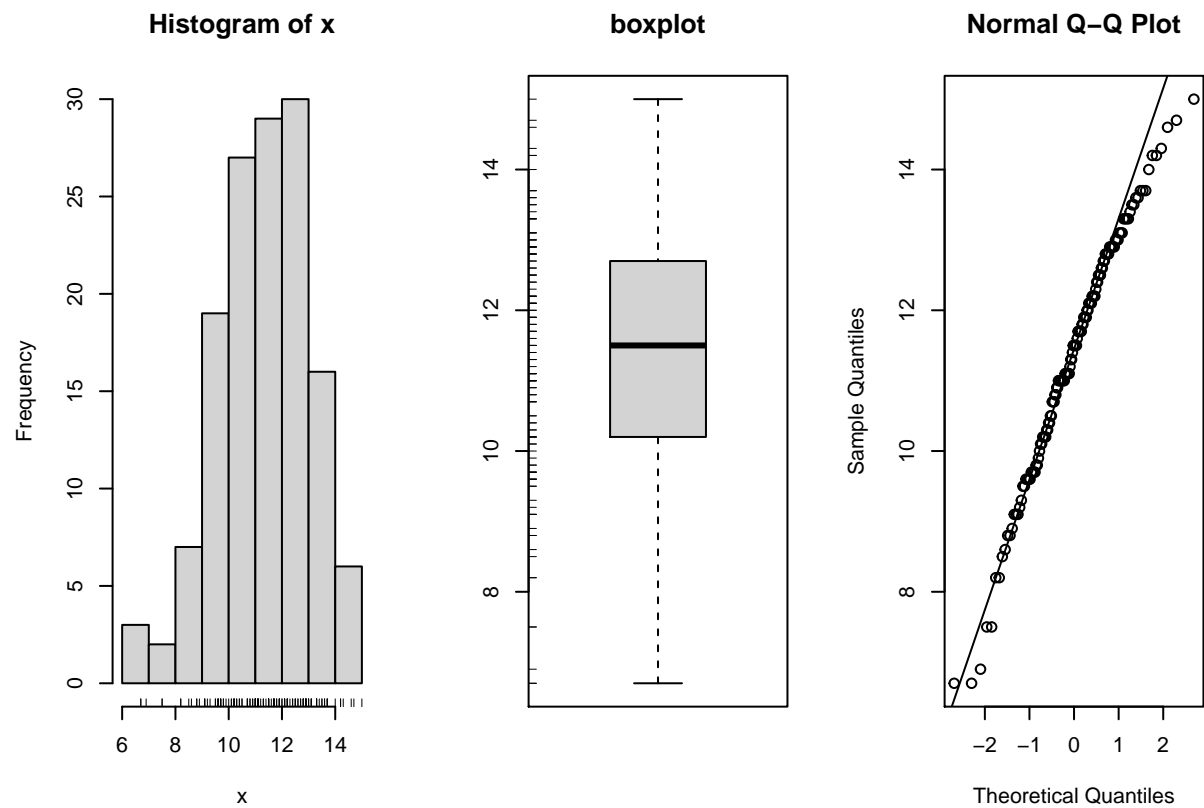
Data Distributions

Mass

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



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

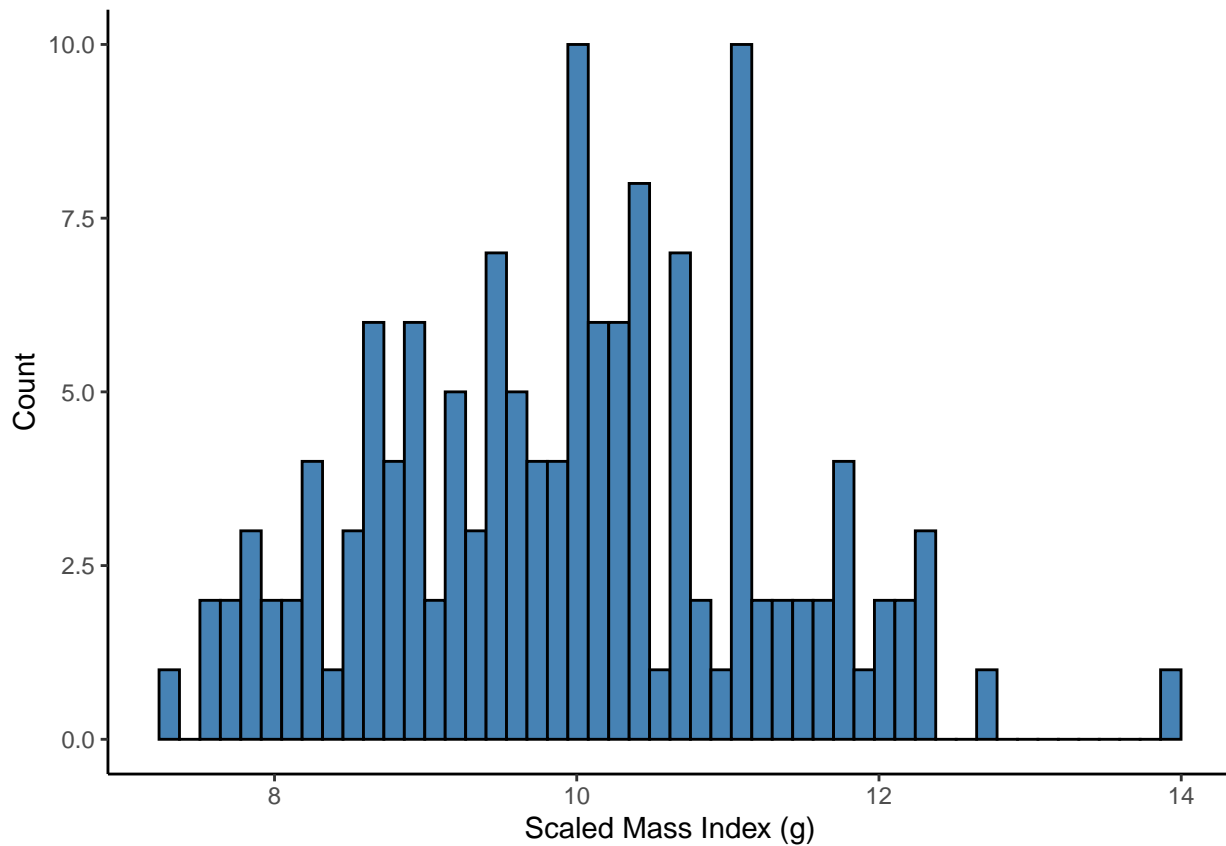


```
shapiro.test(all_dat$mass_g)
```

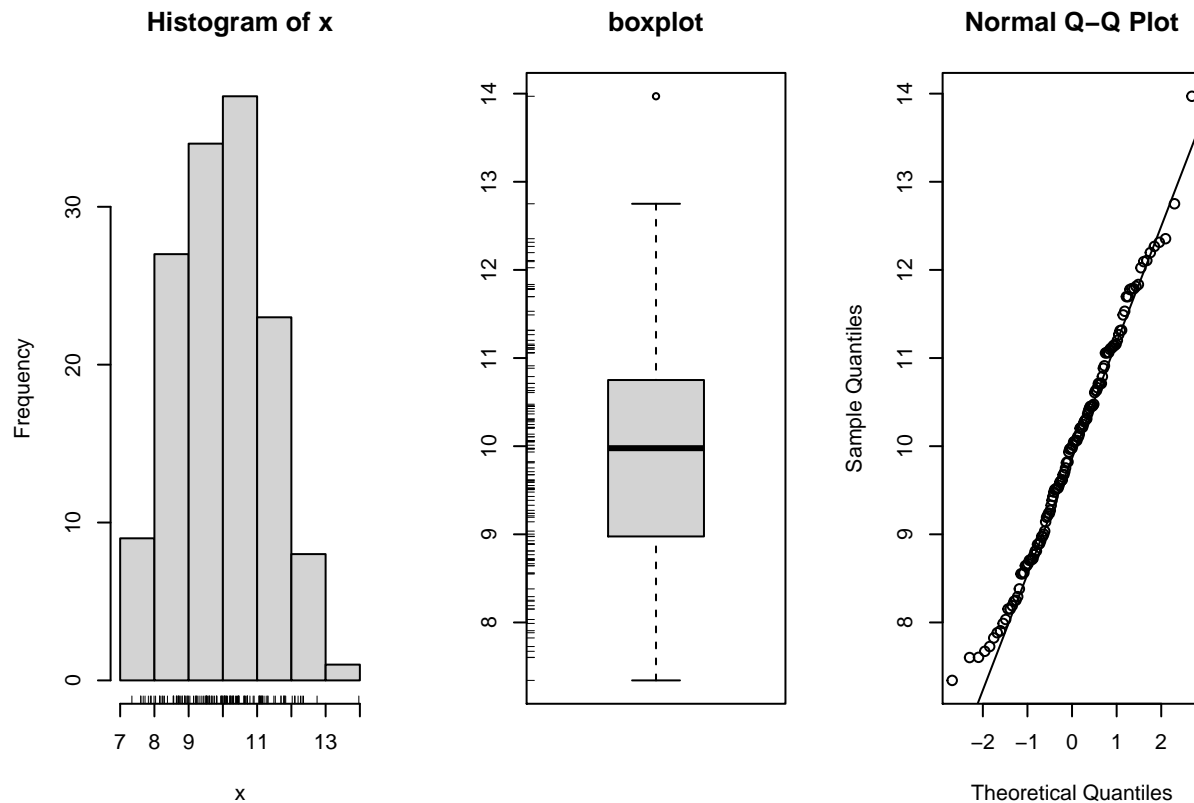
```
##  
##  Shapiro-Wilk normality test  
##  
## data:  all_dat$mass_g  
## W = 0.98437, p-value = 0.1144  
  
Mass distribution not normal, skewed to the left.
```

Scaled Mass Index

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



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



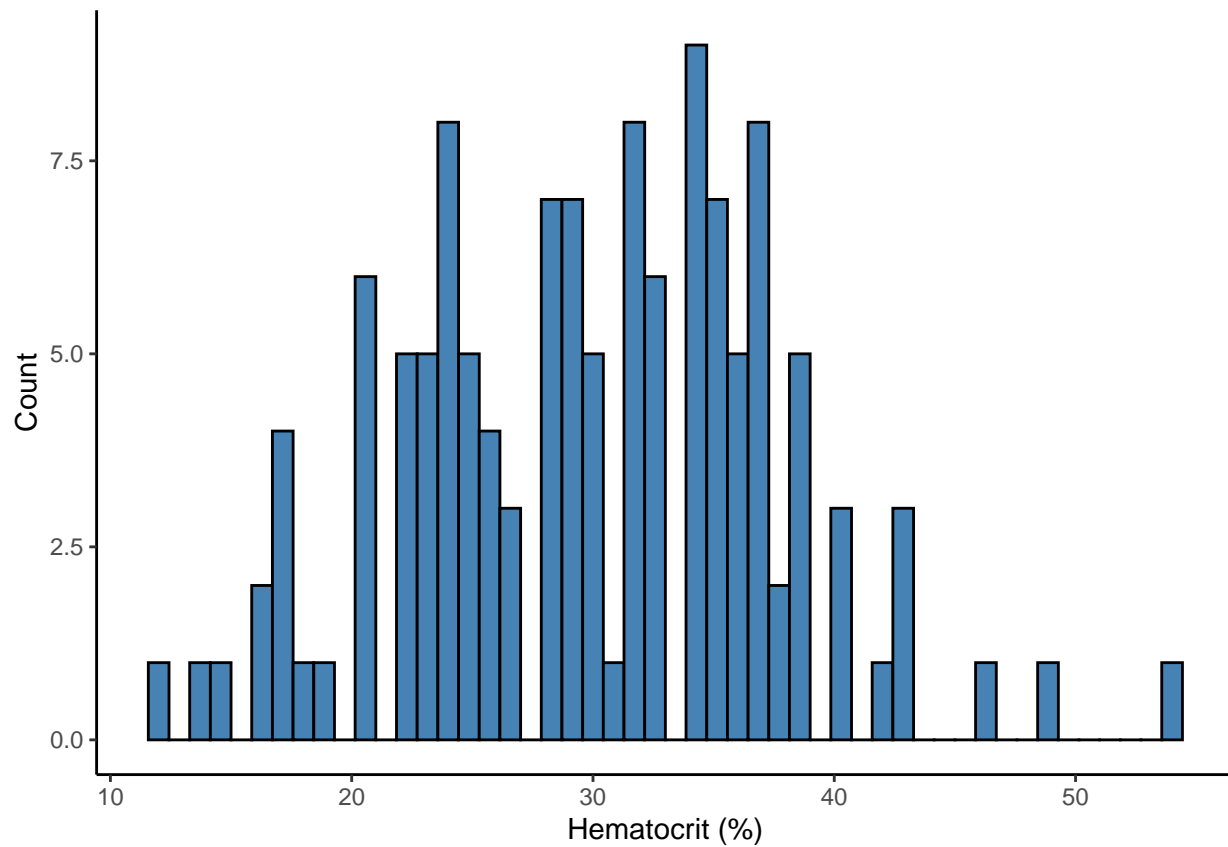
```
shapiro.test(all_dat$SMI)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  all_dat$SMI
## W = 0.98975, p-value = 0.4014
```

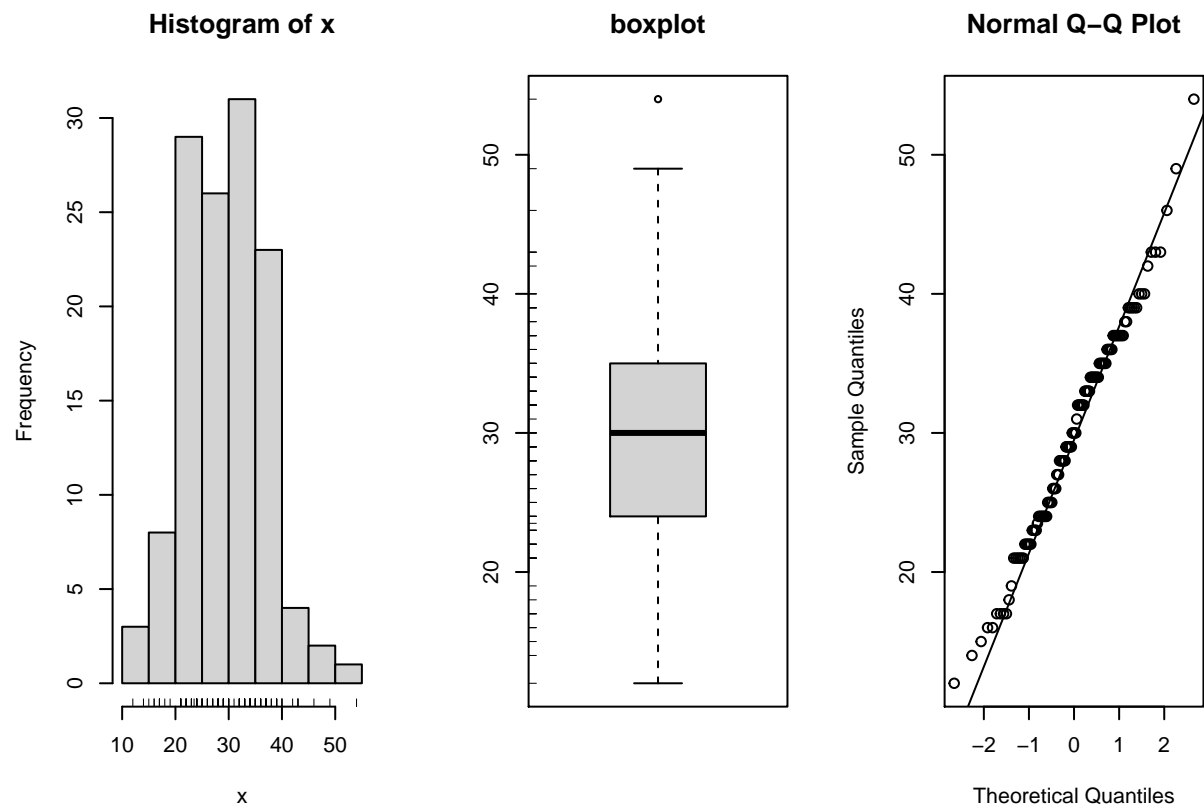
Hematocrit

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

```
## Warning: Removed 12 rows containing non-finite values (stat_bin).
```



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



```
shapiro.test(all_dat$hematocrit_percent)
```

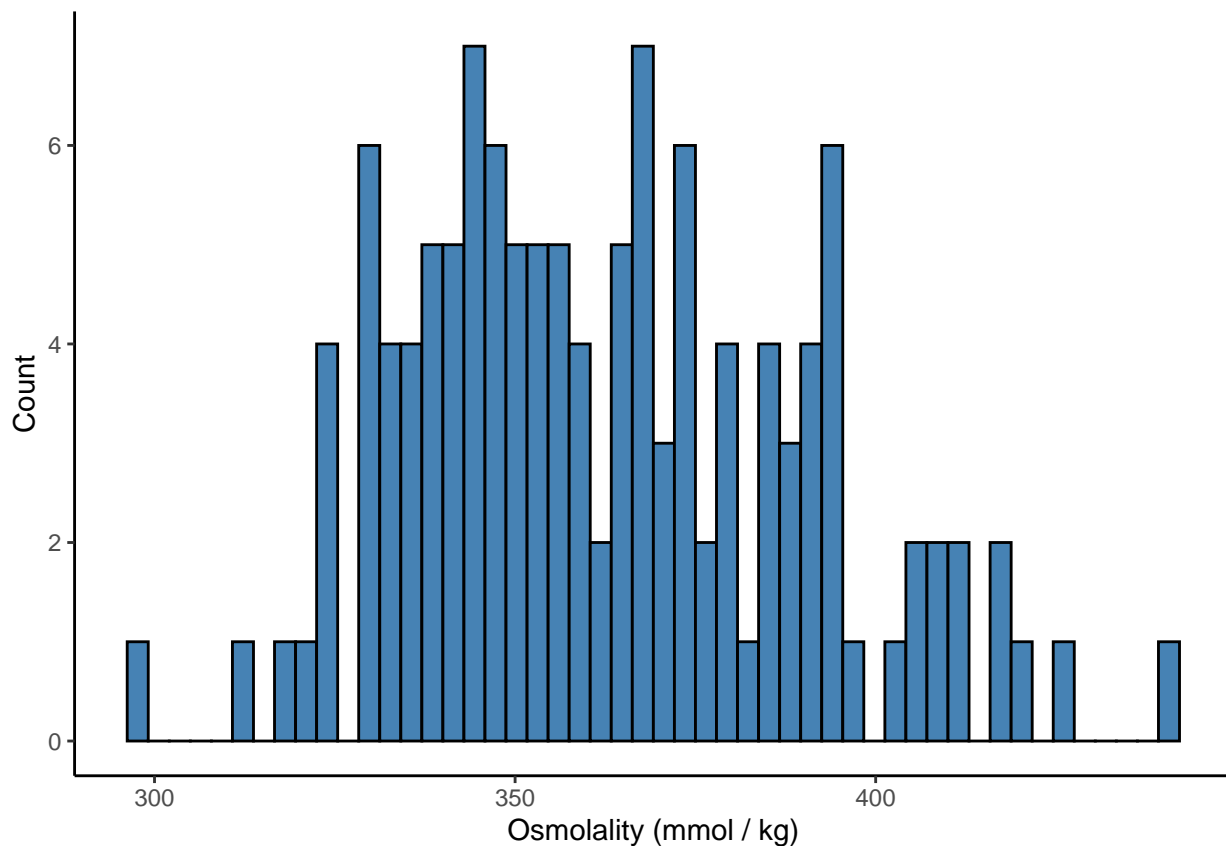
```
##  
## Shapiro-Wilk normality test  
##  
## data:  all_dat$hematocrit_percent  
## W = 0.98872, p-value = 0.385
```

Visually, looks slightly skewed to the right, but statistically, the distribution of hematocrit is normal.

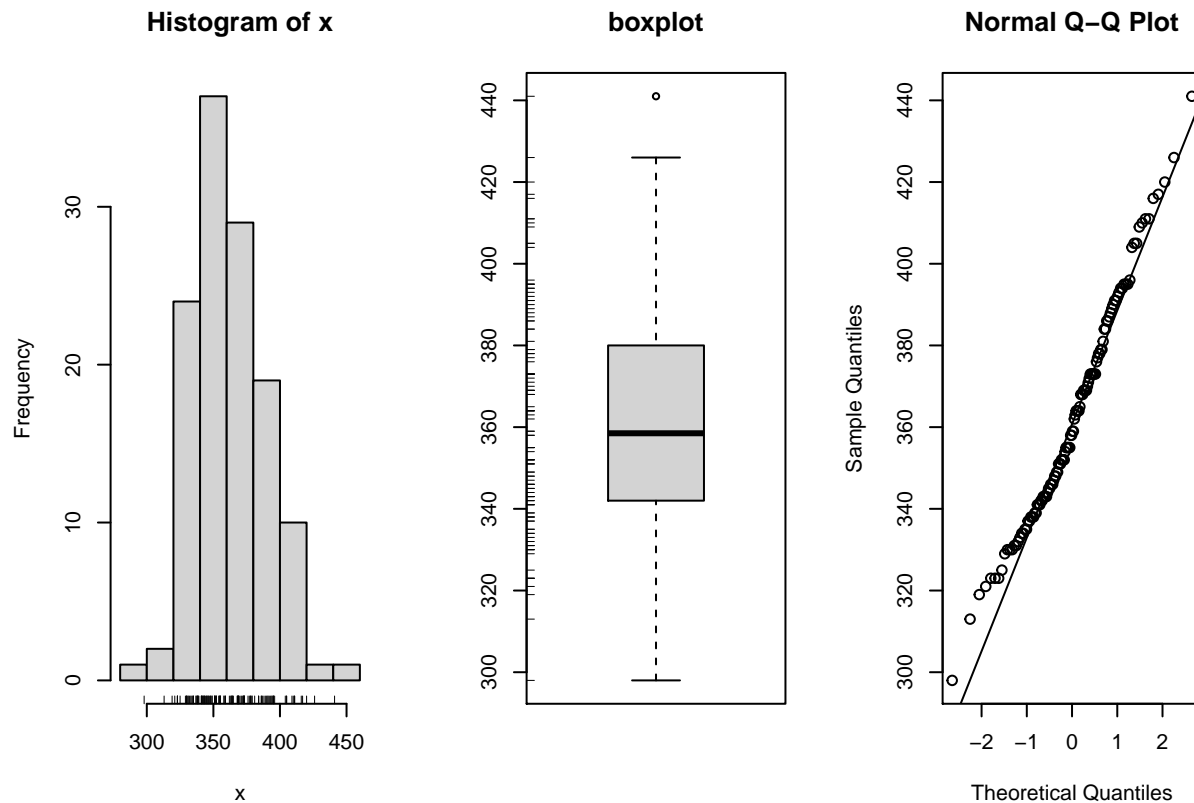
Osmolality

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

```
## Warning: Removed 15 rows containing non-finite values (stat_bin).
```



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

```
shapiro.test(all_dat$osmolality_mmol_kg)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  all_dat$osmolality_mmol_kg
## W = 0.9801, p-value = 0.06427
```

Visually, looks slightly skewed to the right, but statistically, the distribution of osmolality is normal.

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

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)
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.

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

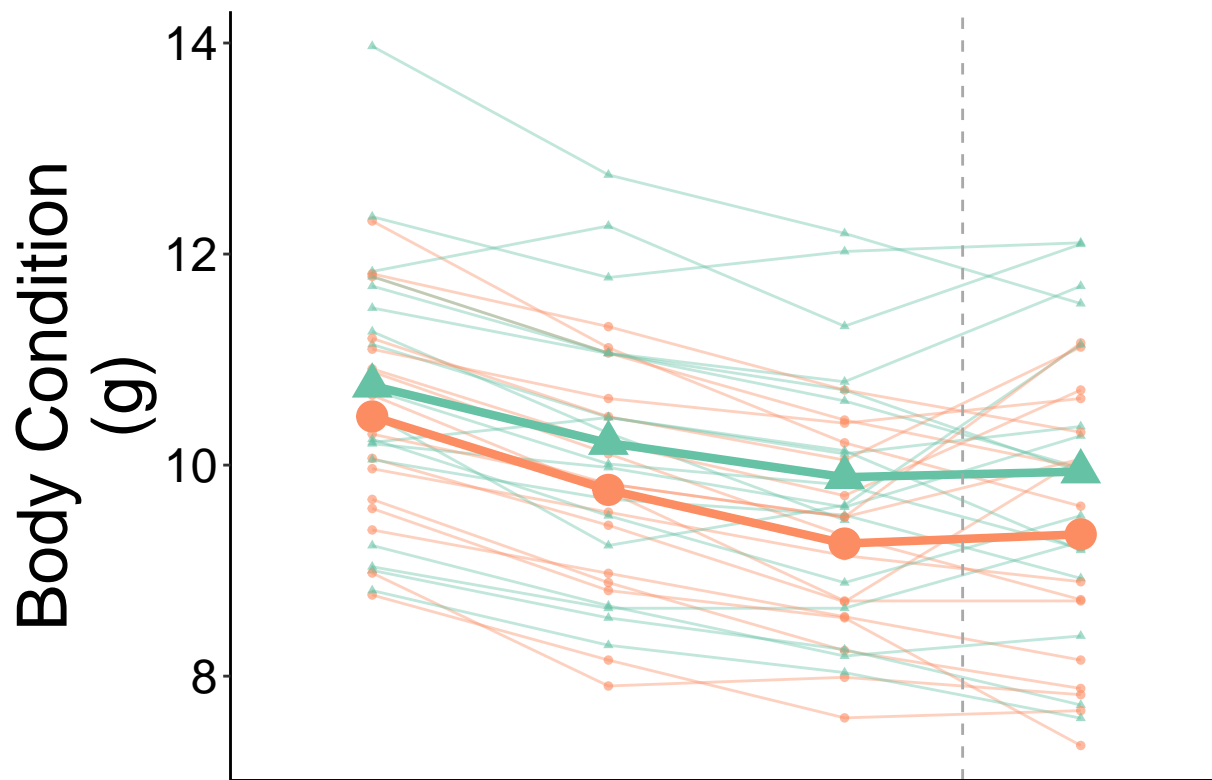
SMI ~ Time

```
ggplot() +
  geom_point(data = all_dat,
    aes(x = day,
        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", "dotted"),
#                       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,
```

```

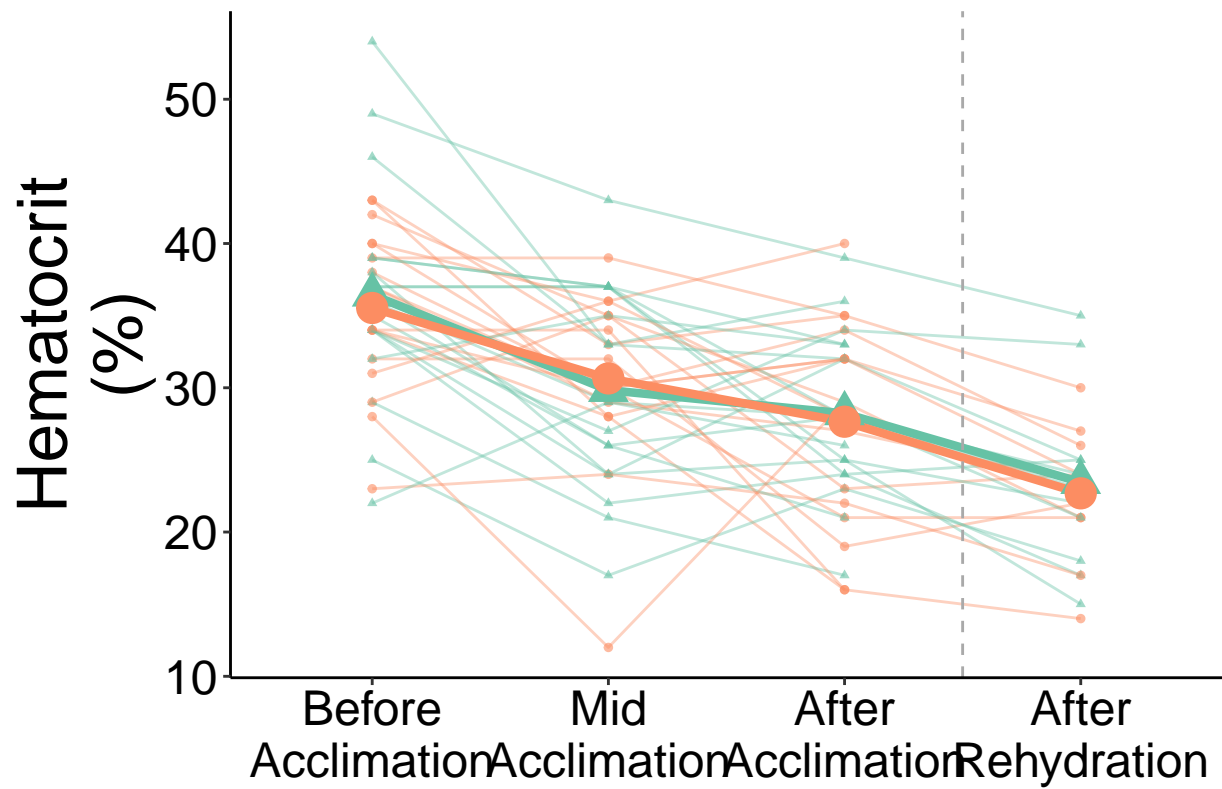
    aes(x = day,
        y = hct_mean,
        group = humidity_tmt_percent,
        color = humidity_tmt_percent,
        #linetype = humidity_tmt_percent
    ),
    size = 1.5,
    alpha = 1) +
geom_point(data = all_dat_mean_hct,
    aes(x = day,
        y = hct_mean,
        color = humidity_tmt_percent,
        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", "dotted"),
#    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,
      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,
```

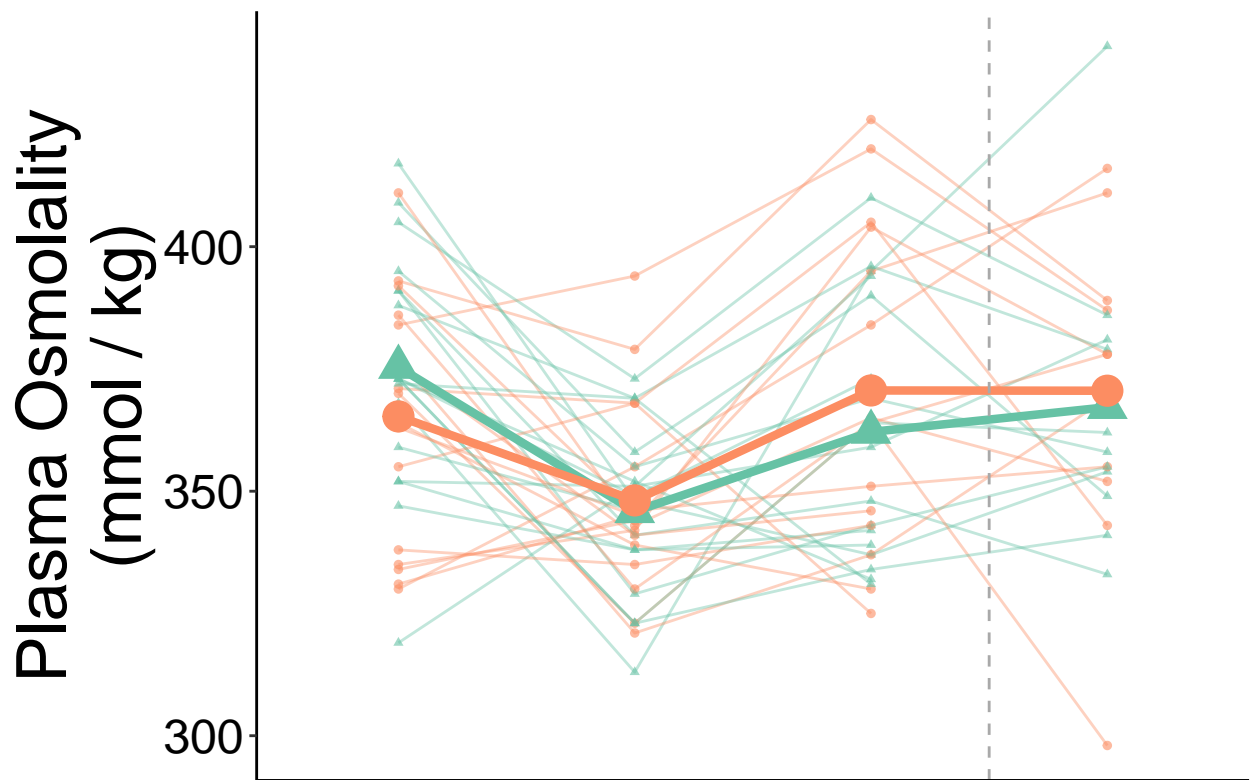
```

    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", "dotted"),
#    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).
```

```
## Warning: Removed 15 row(s) containing missing values (geom_path).
```

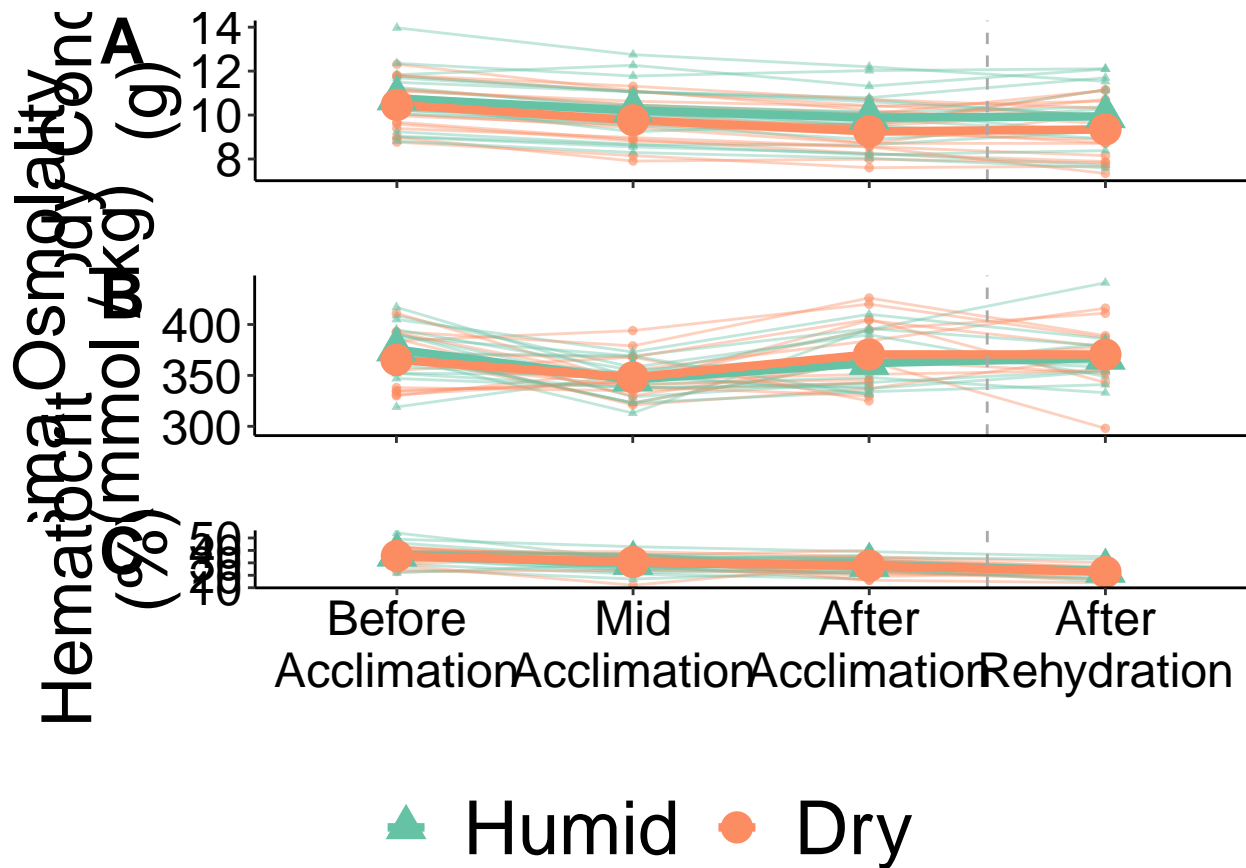



```
# export figure
#ggsave(filename = "tmt_effects_osml.jpeg",
#       plot = tmt_effects_osml,
#       path = "./final_figures",
#       device = "jpeg",
#       dpi = 1200,
#       width = 5, height = 4)
```

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
```

```
## Warning: Removed 15 rows containing missing values (geom_point).
## Warning: Removed 15 row(s) containing missing values (geom_path).
## Warning: Removed 12 rows containing missing values (geom_point).
## Warning: Removed 12 row(s) containing missing values (geom_path).
tmt_multi_fig
```



```
# 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) +
```

```

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", "dotted"),
#                       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

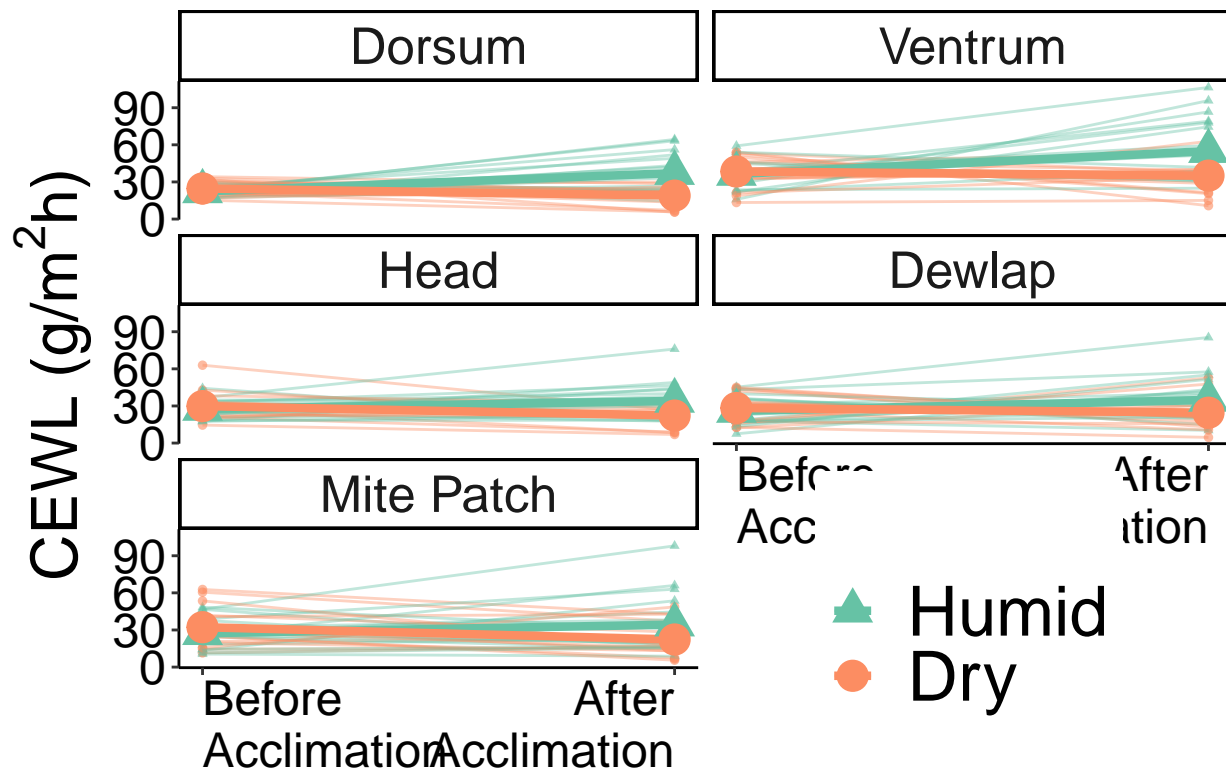
```

```

## Warning: Vectorized input to `element_text()` is not officially supported.
## Results may be unexpected or may change in future versions of ggplot2.

```

CEWL_tmt_fig



```
# 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:

```
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)
```

```
##               Df    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))

```

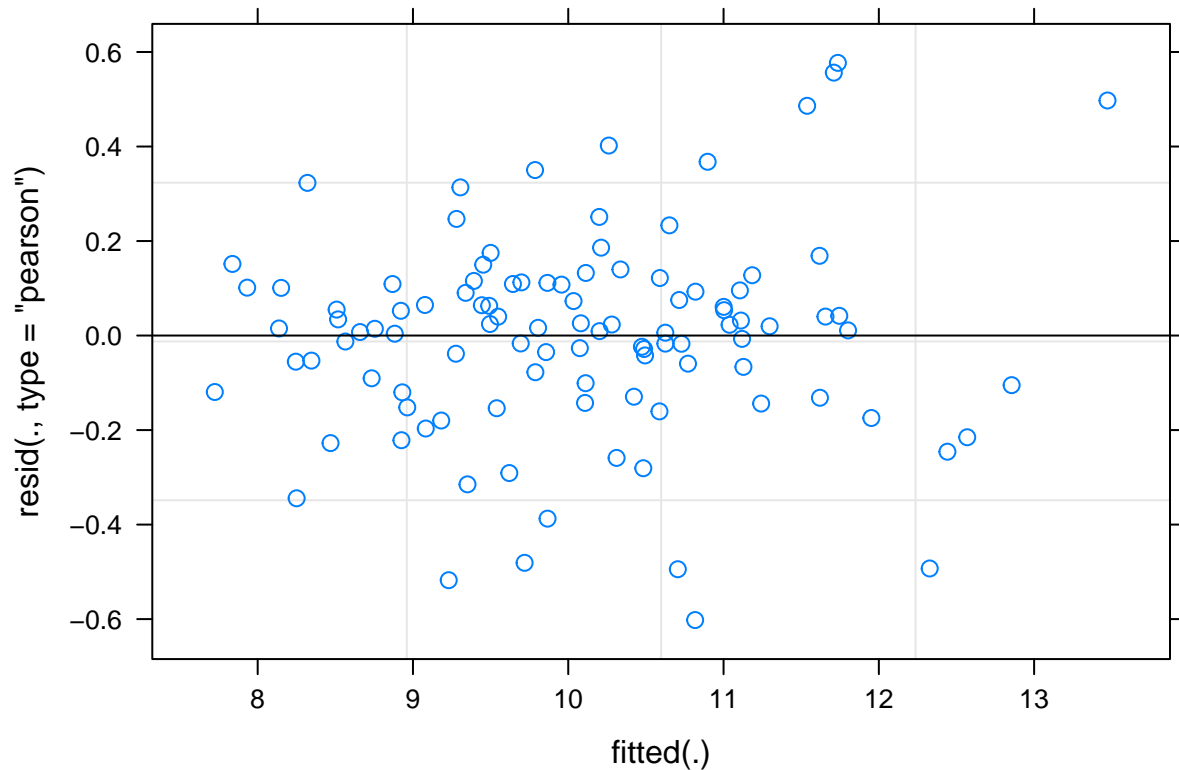
```
## Warning in aictab.AIClmerMod(cand.set = SMI_models, modnames = SMI_mod_names):
## Model selection for fixed effects is only appropriate with ML estimation:
## REML (default) should only be used to select random effects for a constant set of fixed effects
```

```
SMI_AICc
```

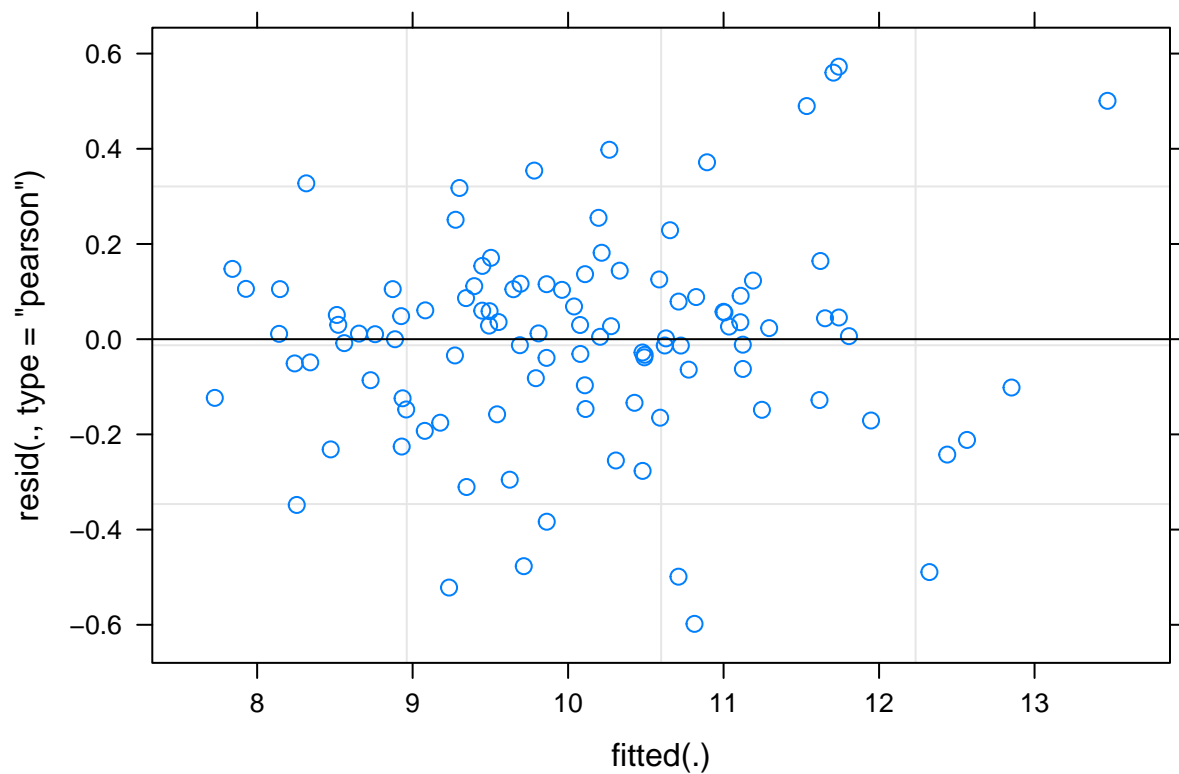
```
##           Modnames K      AICc Delta_AICc      Modellik      AICcWt
## 3      (model 3) ~ day 6 178.1683  0.0000000 1.000000e+00 5.505278e-01
## 2 (model 2) ~ day + humidity 7 179.1421  0.9738317 6.145187e-01 3.383096e-01
## 1 (model 1) ~ day * humidity 9 181.3681  3.1997670 2.019200e-01 1.111626e-01
## 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)
```



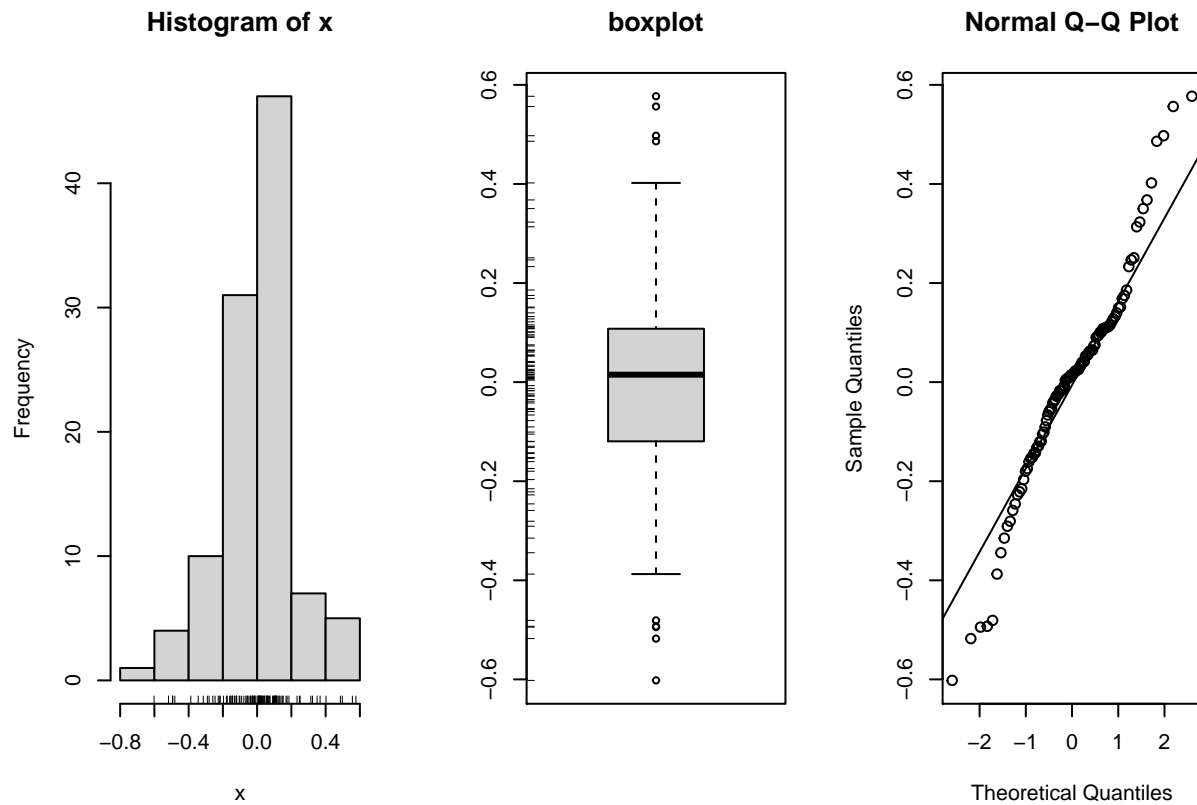
```
car::vif(SMI_mod2)
```

```
##              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

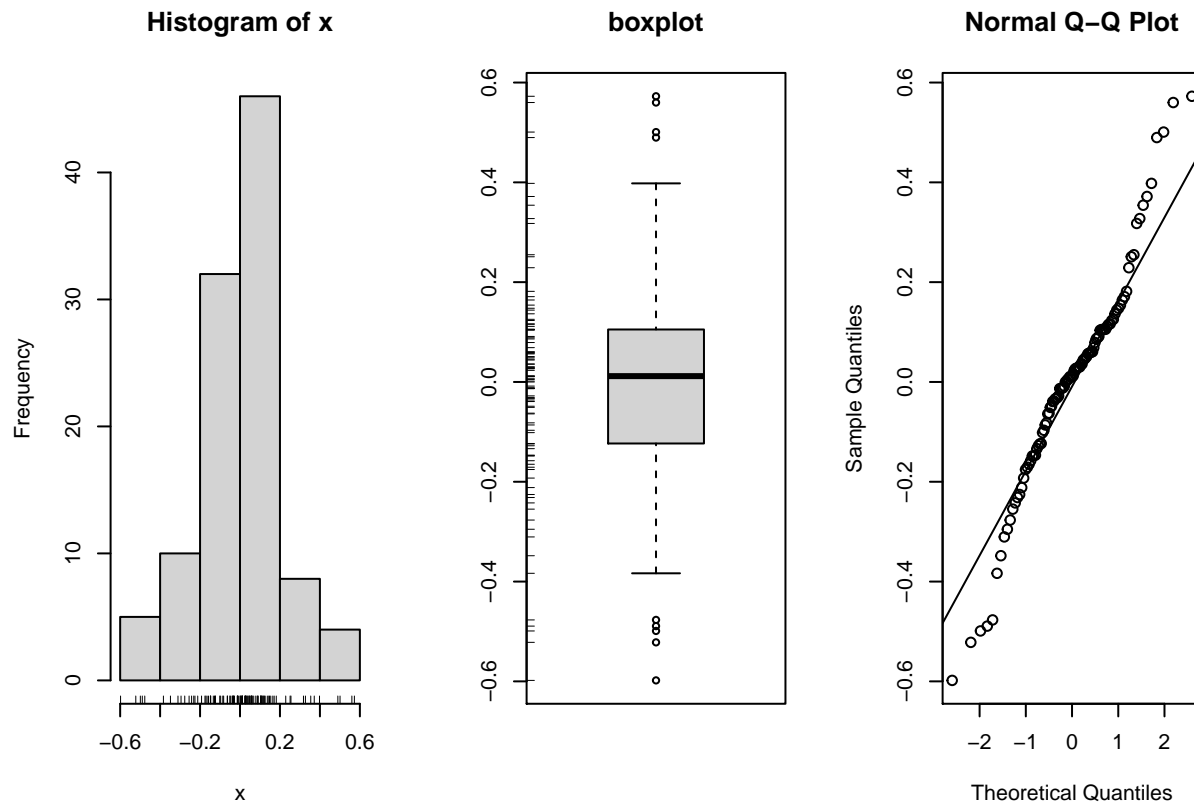
```
simple.eda(residuals(SMI_mod2))
```

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

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

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



```
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:

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

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

```
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
## dyAftAcclm -0.117  0.500
## hmdty_tmt_D -0.691  0.000  0.000
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see ?isSingular
SMI_mod3p <- lmerTest::lmer(data = all_dat_no_rehab,
                           SMI ~ day +
                           (1|trial_number/individual_ID))

## boundary (singular) fit: see ?isSingular
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
## dyAftAcclm  -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
## dyAftAcclm -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
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
# 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
## dyAftAcclm  -0.323  0.500
## hmdty_tmt_D -0.463  0.000  0.000
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

# 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
## dyAftAcclm  -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:
```

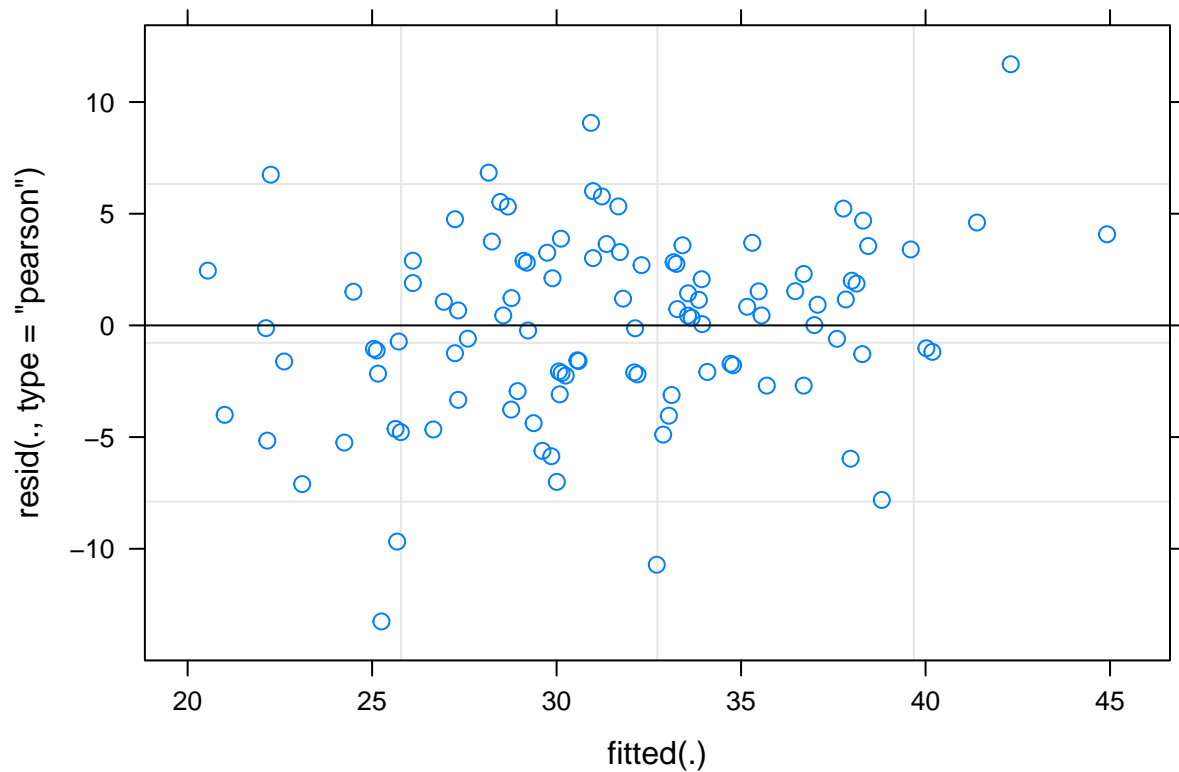
```
## REML (default) should only be used to select random effects for a constant set of fixed effects
```

```
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)
```



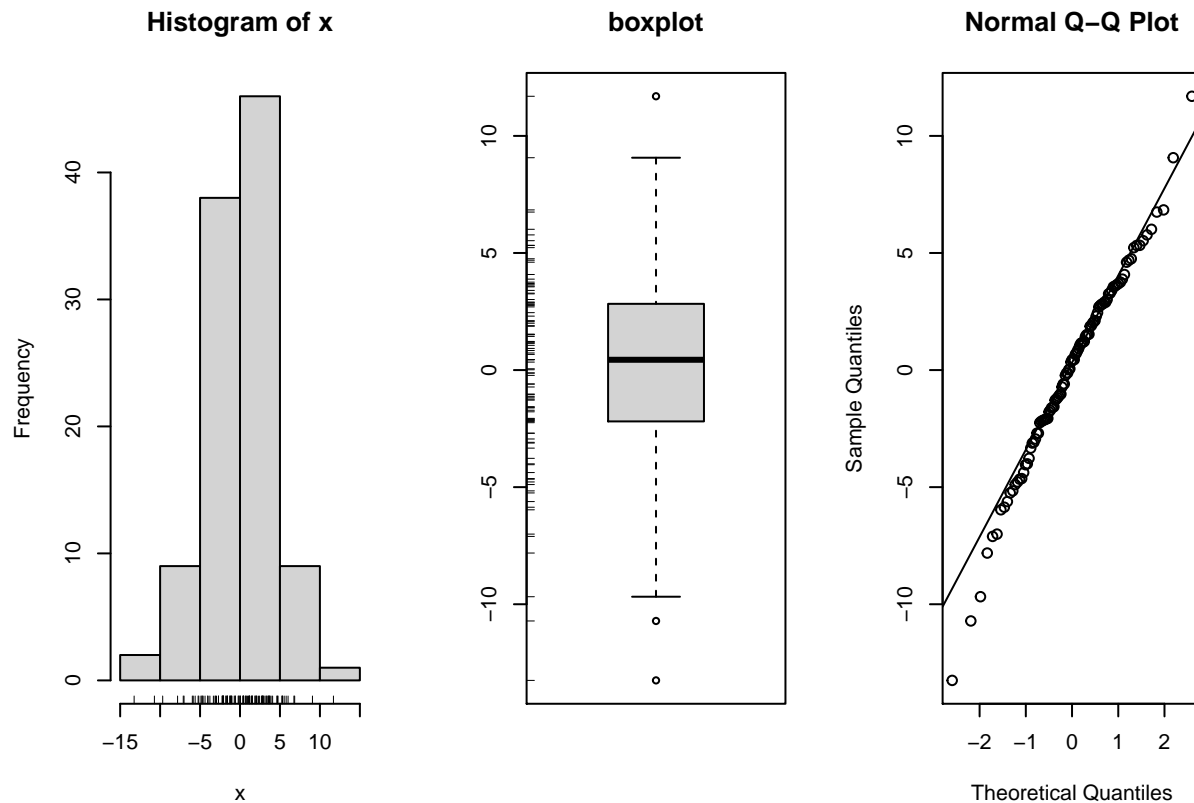
```
car::vif(hct_mod1)
```

```
##           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))
```

```
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:

```
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
## dyAftAcclm -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
## dyAftAcclm  -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

```

```
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
```

```
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

# 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
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
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

# 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
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')

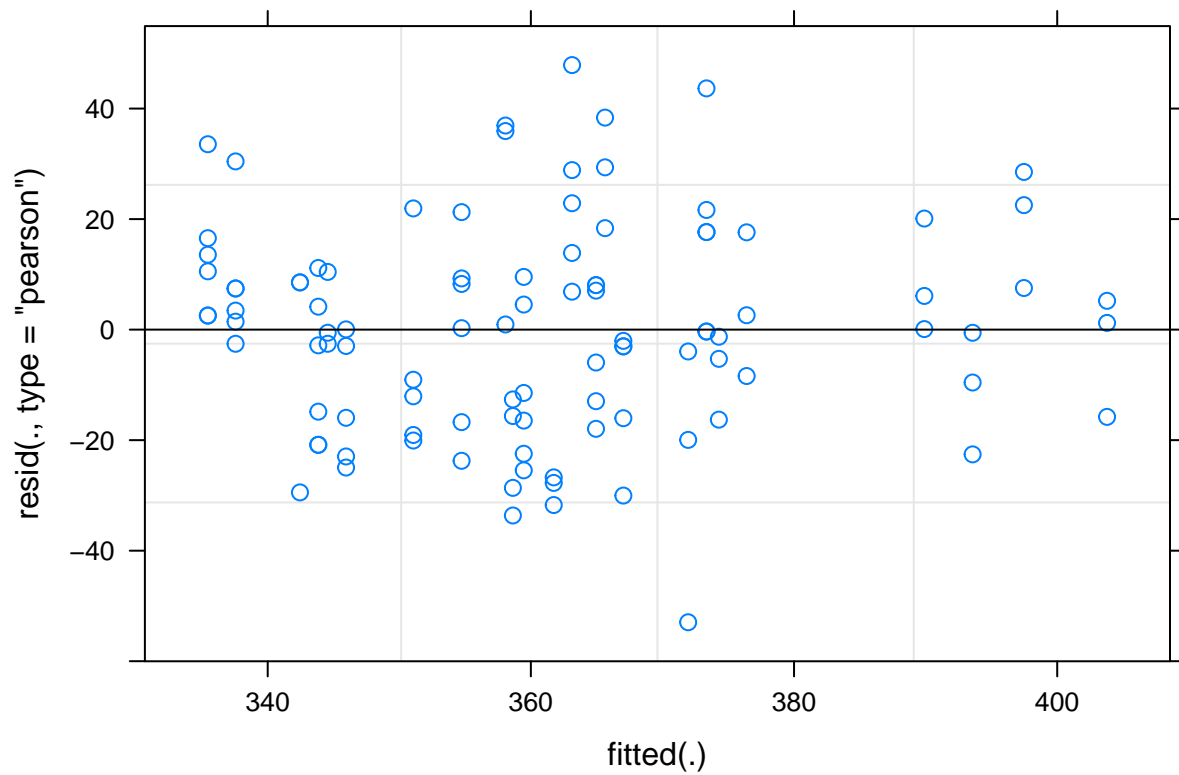
#calculate AIC of each model
osml_AICc <- data.frame(aictab(cand.set = osml_models,
                              modnames = osml_mod_names))
```

```
## 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)
```



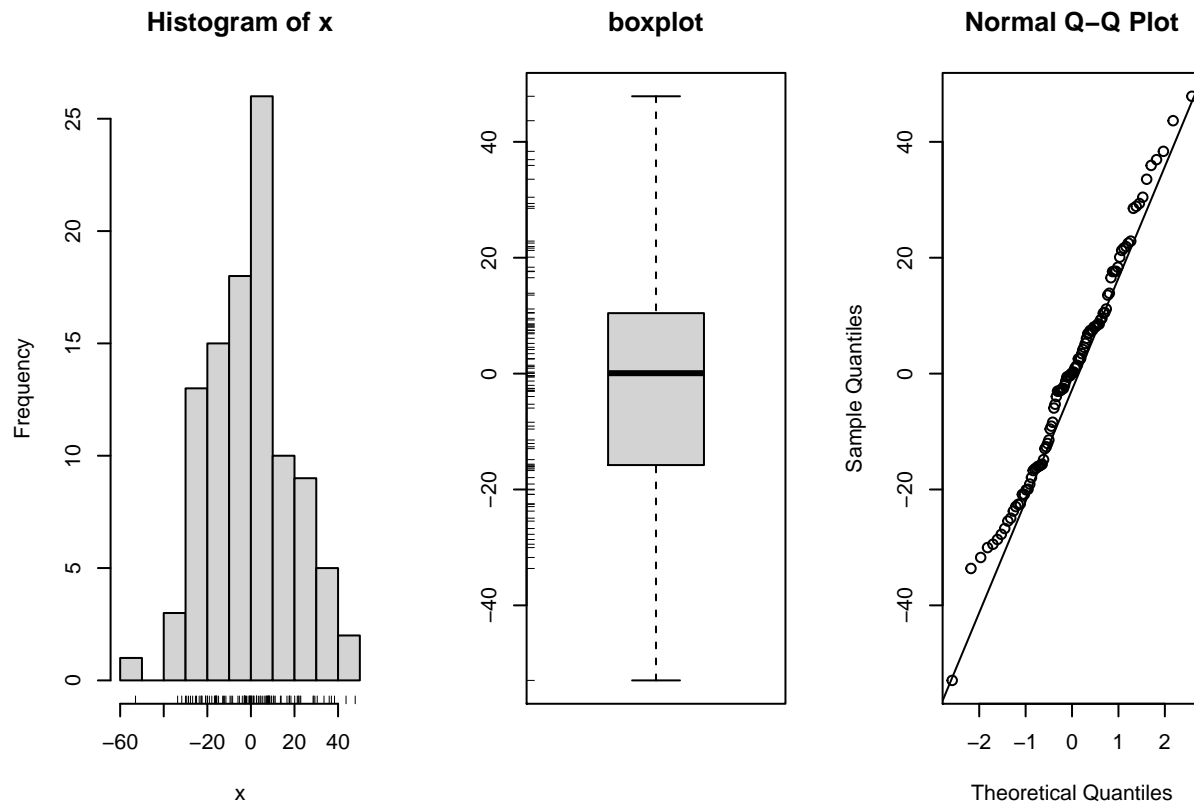
```
car::vif(osml_mod1)
```

```
##              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))
```



```
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:

```
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
```

```
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
## dyAftAcclm -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
## regionVentrurn     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:regionVentrurn  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:regionVentrurn -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)
```

```
##
```

```
## <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
```

```
## regionVentrurn 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:regionVentrurn 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

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

# 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
```

```
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
```

```
# 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

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

# 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

```

```

## 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

```



```

## 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

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

# 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

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

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

Selection

```
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
CEWL_AICc
```

```
##
## 1 Modnames
## 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

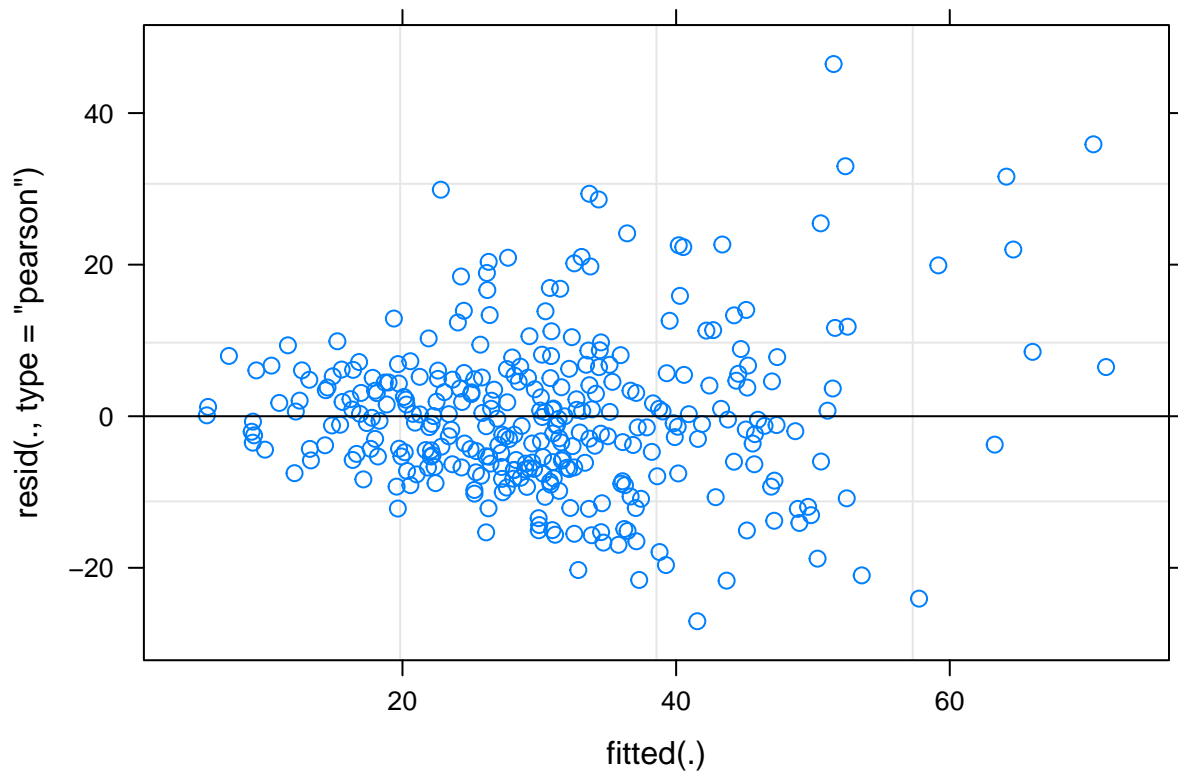
## # A tibble: 20 x 4
## # Groups:   region, humidity_tmt_percent [10]
##   region      humidity_tmt_percent n_day CEWL_mean
##   <fct>         <fct>             <dbl>    <dbl>
## 1 Dorsum      Humid                 0      22.4
## 2 Dorsum      Humid                 1      37.1
## 3 Dorsum      Dry                  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 homoskedastic relative to \hat{y} (or x). Plotting residuals shows us whether the data meets linearity and equal variance assumptions:

```
plot(CEWL_mod1)
```



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

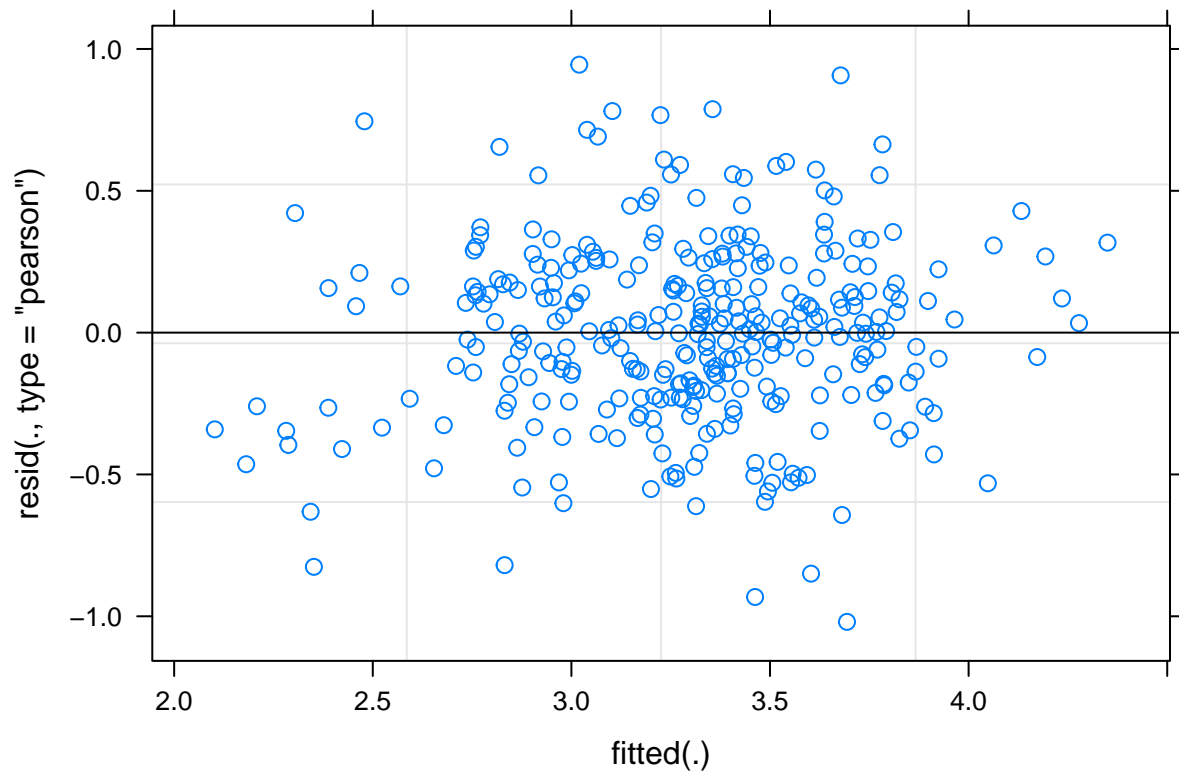
	GVIF	Df	GVIF ^{1/(2*Df)}
## day	10.359562	1	3.218627
## humidity_tmt_percent	3.191166	1	1.786384
## region	227.122403	4	1.970301
## cloacal_temp_C	1.393922	1	1.180645
## day:humidity_tmt_percent	10.993060	1	3.315578
## day:region	697.771225	4	2.267066
## humidity_tmt_percent:region	340.167300	4	2.072343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

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

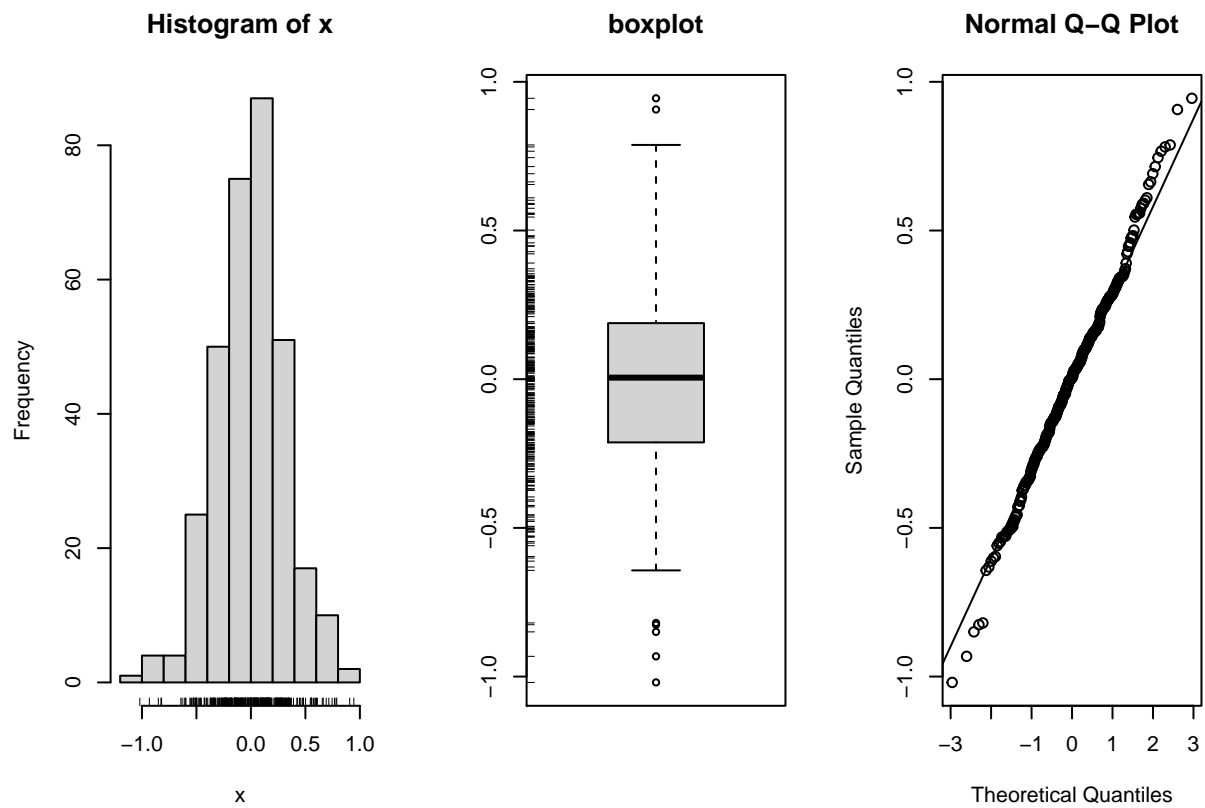
Transform CEWL

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)
```



```
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:regionVentr  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 P 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
## regionVentr 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:regionVentr 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:regionVentr 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:regionVentr 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 P 273.87346 0.601 0.548266
##
## (Intercept)
## dayAfter ***
## humidity_tmt_percentDry
## regionVentr ***
## regionHead .
## regionDewlap
## regionMite Patch
## cloacal_temp_C ***
## dayAfter:humidity_tmt_percentDry ***
## dayAfter:regionVentr
## dayAfter:regionHead
## dayAfter:regionDewlap
## dayAfter:regionMite Patch
## humidity_tmt_percentDry:regionVentr
## humidity_tmt_percentDry:regionHead
## humidity_tmt_percentDry:regionDewlap
## humidity_tmt_percentDry:regionMite Patch
## dayAfter:humidity_tmt_percentDry:regionVentr
## dayAfter:humidity_tmt_percentDry:regionHead
## dayAfter:humidity_tmt_percentDry:regionDewlap
## dayAfter:humidity_tmt_percentDry:regionMite P
## ---
## 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

```
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")
```