

# Experimental Data Analysis

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## Packages

define not-in function:

```
`%nin%` = Negate(`%in%`)
```

## 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 Experiment",
                                  "Mid Experiment",
                                  "After Experiment",
                                  "After Experiment",
                                  "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 Experiment:35
##              1st Qu.:66.00  1st Qu.:2021-04-26  Mid Experiment   :35
##              Median :68.00  Median :2021-05-03  After Experiment :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             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
##
##
##
```

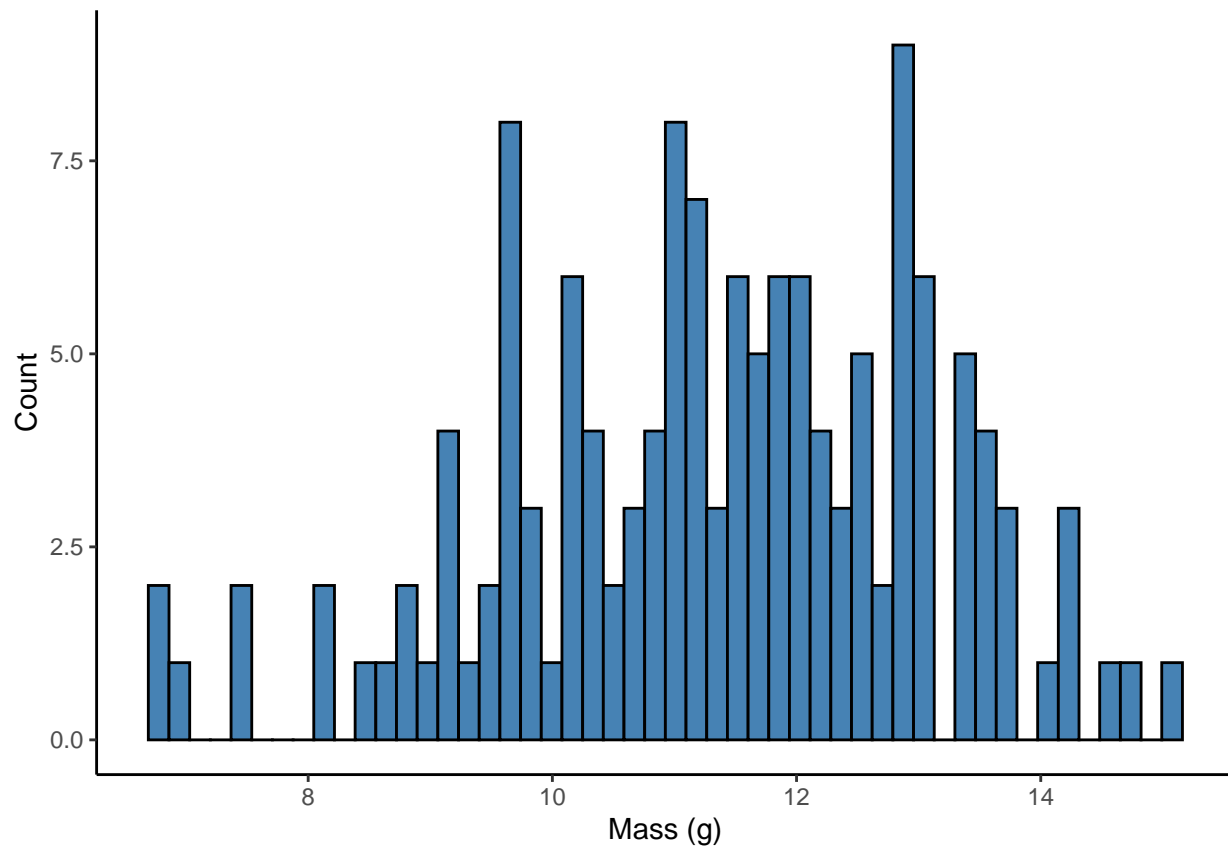
## Export Data Frames for Power Analyses

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

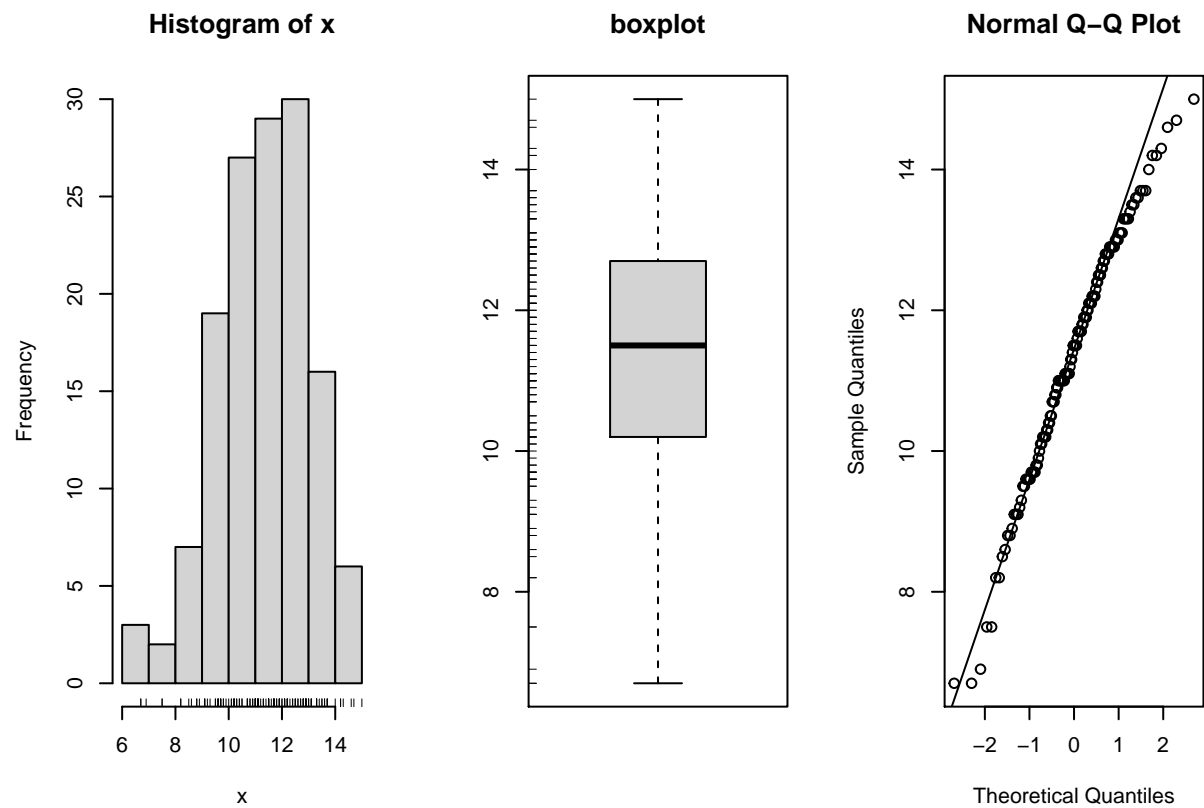
## Data Distributions

### 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)
```



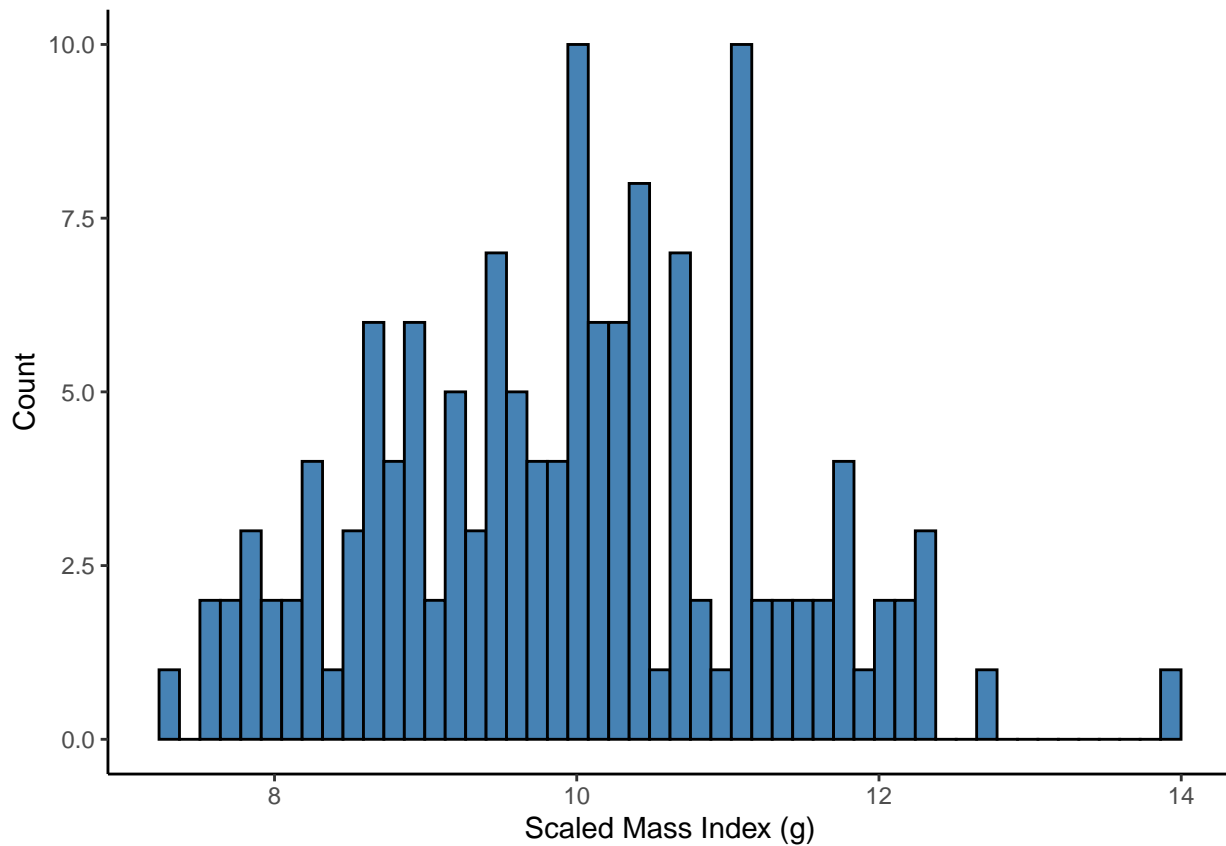
```
shapiro.test(all_dat$mass_g)
```

```
##  
##  Shapiro-Wilk normality test  
##  
## data:  all_dat$mass_g  
## W = 0.98437, p-value = 0.1144
```

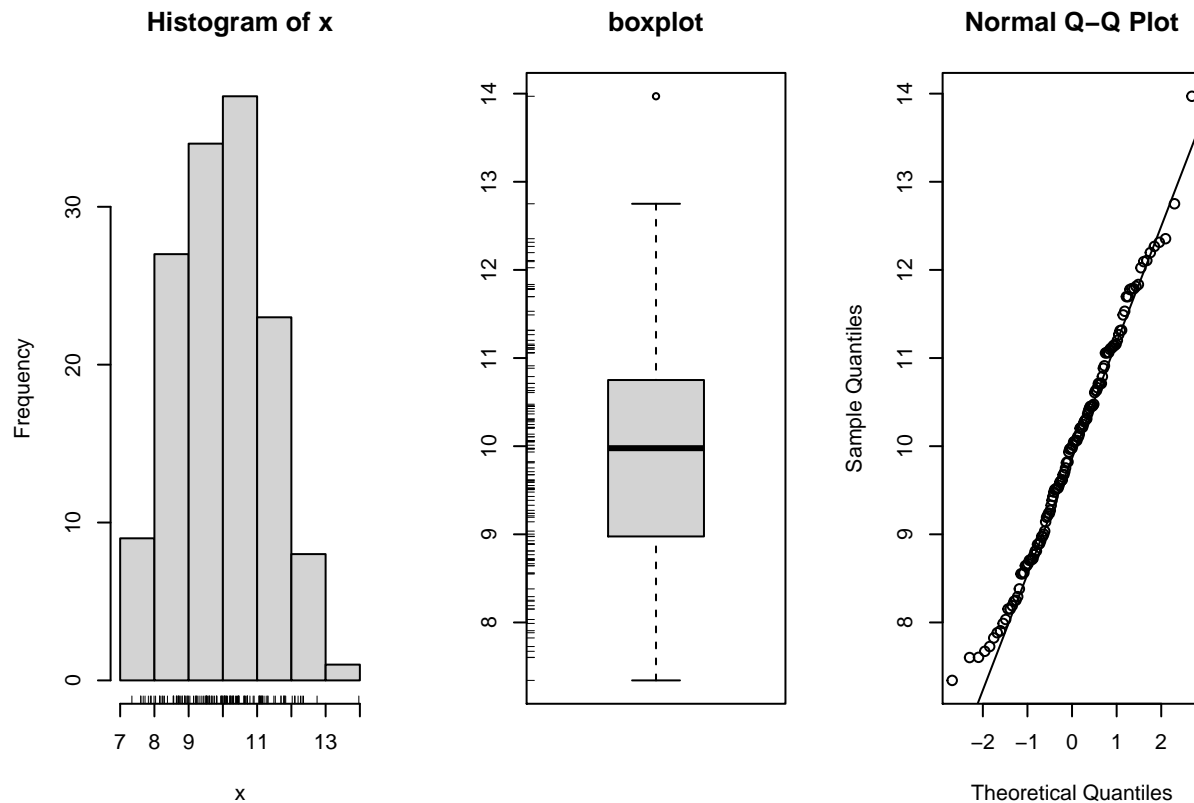
Mass distribution not normal, skewed to the left.

## 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)
```



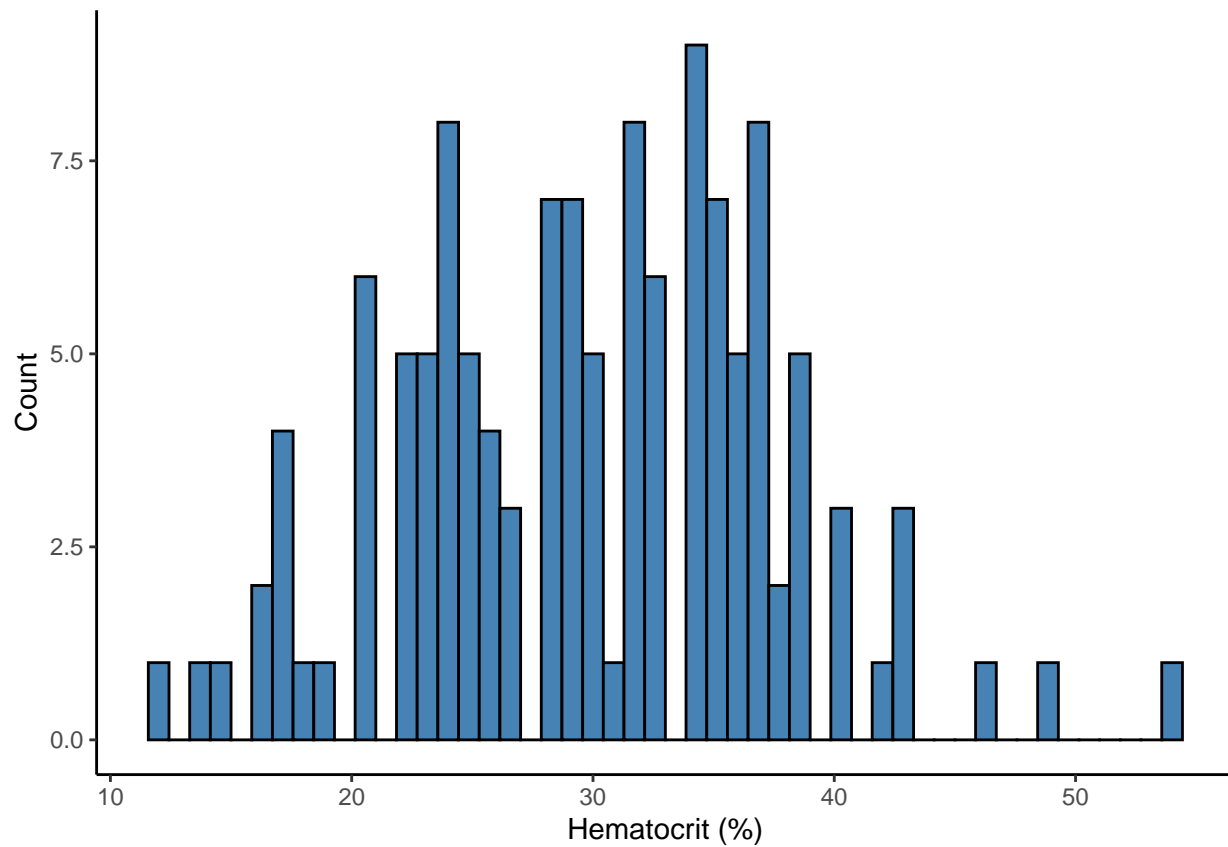
```
shapiro.test(all_dat$SMI)
```

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

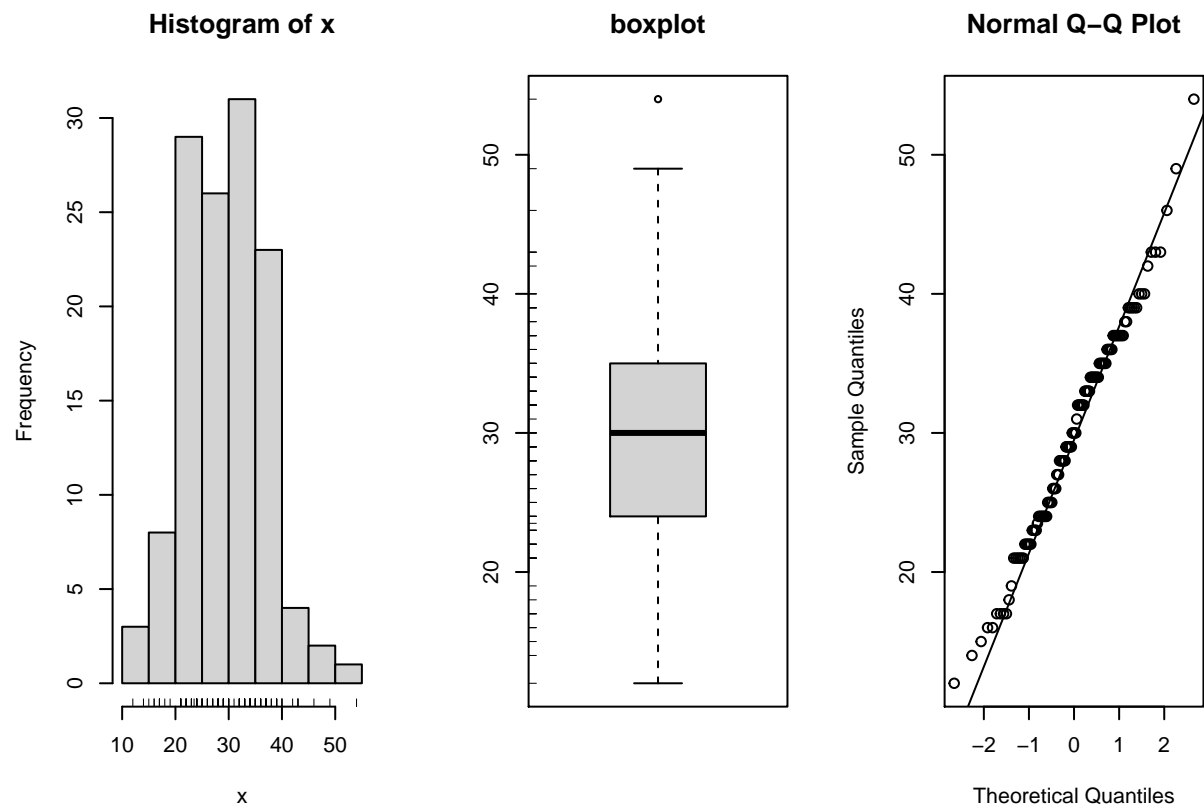
## Hematocrit

```
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)
```

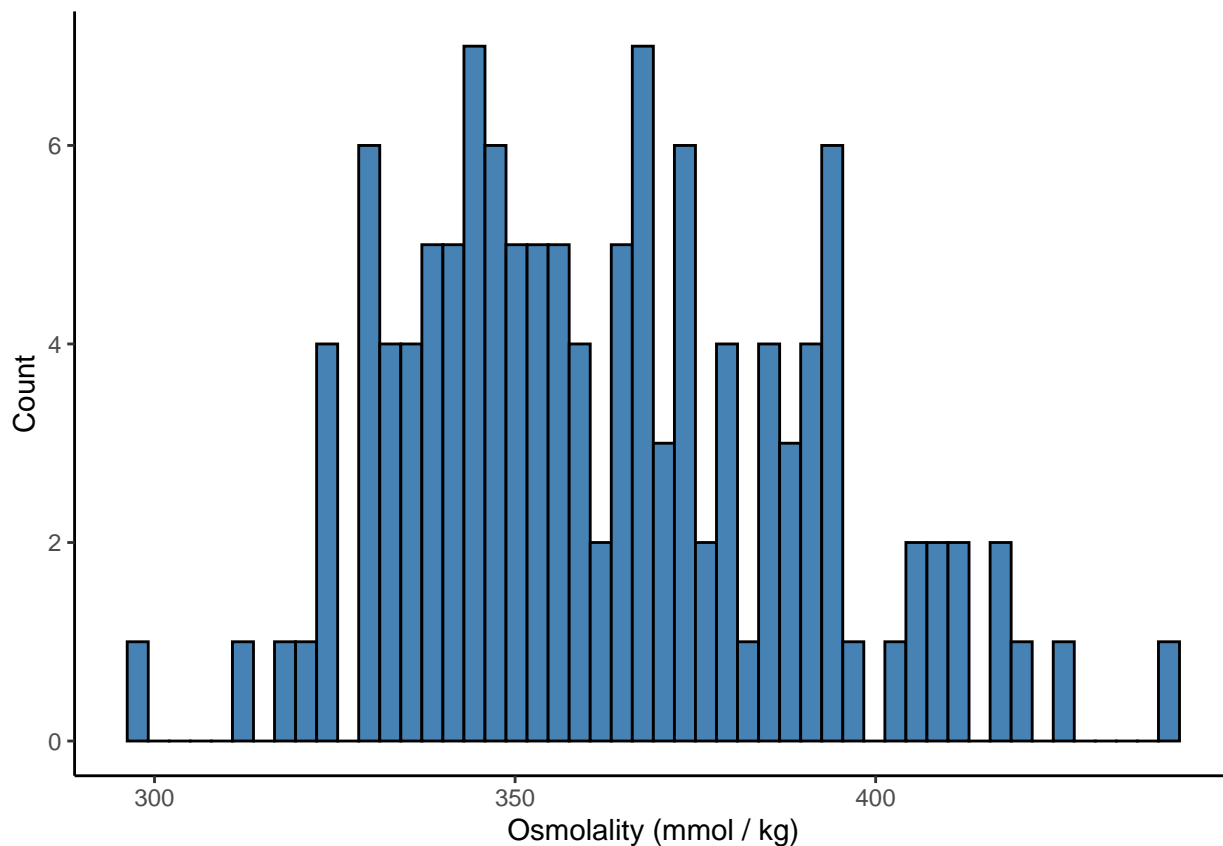
```
##  
##  Shapiro-Wilk normality test  
##  
## data:  all_dat$hematocrit_percent  
## W = 0.98872, p-value = 0.385
```

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

## Osmolality

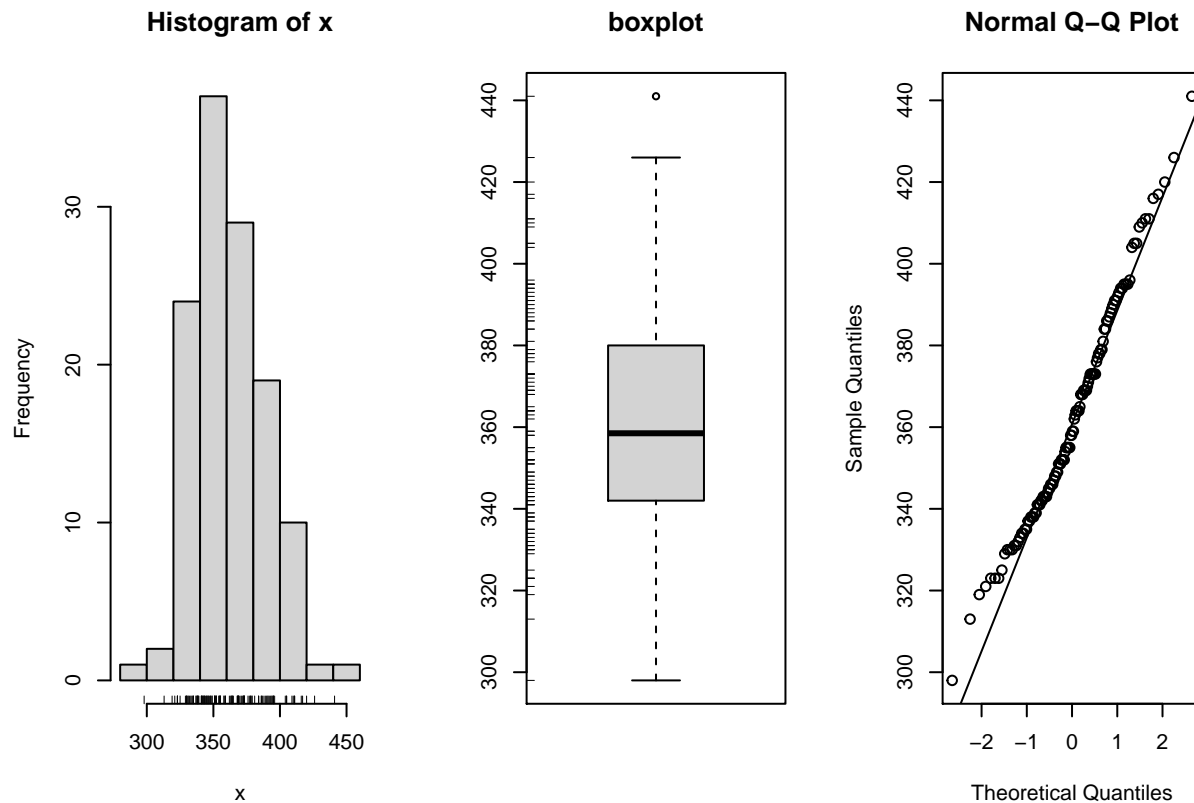
```
all_dat %>%  
  ggplot(., aes(x = osmolality_mmol_kg)) +  
  geom_histogram(color = "black", fill="steelblue", bins=50) +  
  theme_classic() +  
  xlab("Osmolality (mmol / kg)") +  
  ylab("Count")
```

```
## 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_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)
```

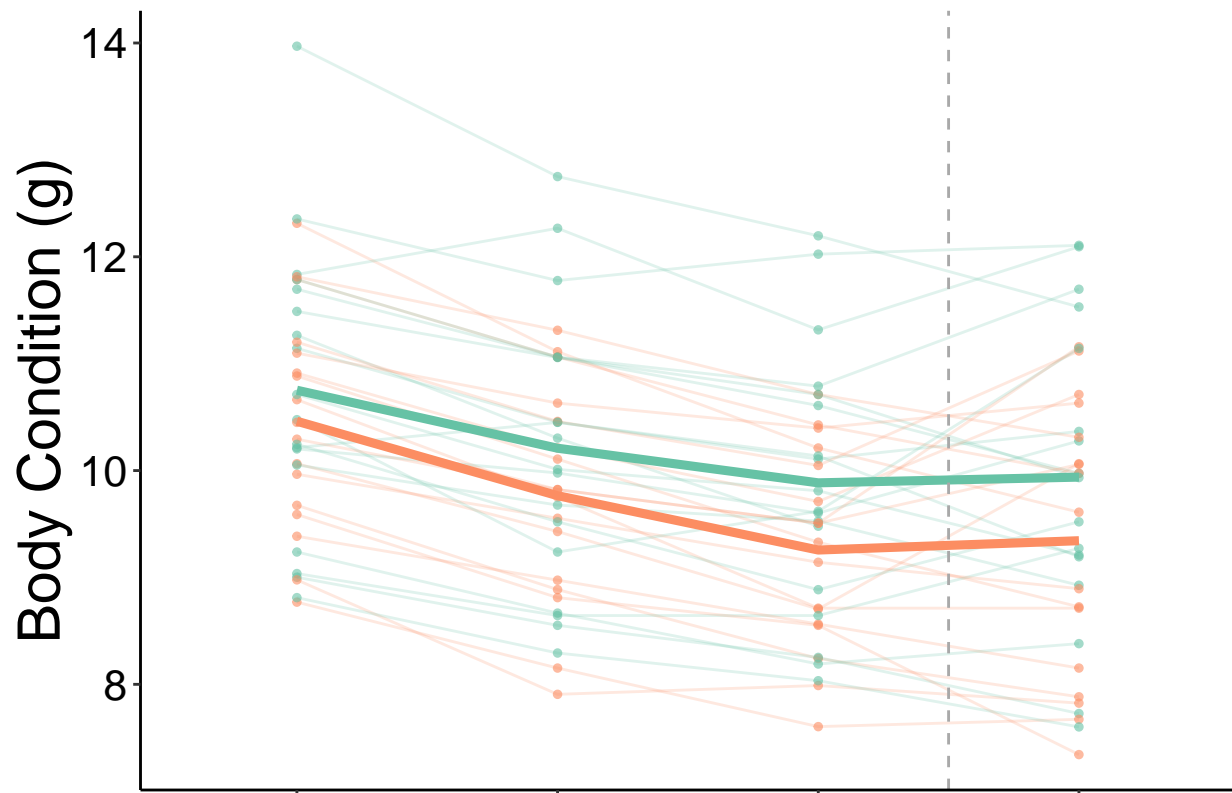
```
all_dat_mean_osml <- all_dat %>%
  dplyr::filter(complete.cases(osmolality_mmol_kg)) %>%
```

```
group_by(humidity_tmt_percent, day) %>%
summarise(osml_mean = mean(osmolality_mmol_kg))
```

## `summarise()` regrouping output by 'humidity\_tmt\_percent' (override with `.groups` argument)

## SMI ~ Time

```
ggplot() +
  geom_point(data = all_dat,
    aes(x = day,
        y = SMI,
        color = 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),
    alpha = 0.2) +
  geom_line(data = all_dat_mean_SMI,
    aes(x = day,
        y = SMI_mean,
        group = humidity_tmt_percent,
        color = humidity_tmt_percent),
    size = 1.6,
    alpha = 1) +
  theme_classic() +
  scale_color_brewer(palette = "Set2",
    name = "") +
  xlab("") +
  ylab("Body Condition (g)") +
  geom_vline(xintercept = 3.5,
    linetype = "dashed",
    color = "darkgrey") +
  theme(text = element_text(color = "black",
    family = "sans",
    size = 22),
    axis.text = element_text(color = "black",
    family = "sans",
    size = 16),
    axis.text.x = element_blank(),
    legend.text = element_text(color = "black",
    family = "sans",
    size = 24),
    legend.text.align = 0,
    legend.position = "none",
    plot.margin = unit(c(0.2,0,0,0.4), "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
            ),
            size = 1,
            alpha = 0.6) +
  geom_line(data = all_dat,
            aes(x = day,
                y = hematocrit_percent,
                group = individual_ID,
                color = humidity_tmt_percent),
            alpha = 0.2) +
  geom_line(data = all_dat_mean_hct,
            aes(x = day,
                y = hct_mean,
                group = humidity_tmt_percent,
```

```

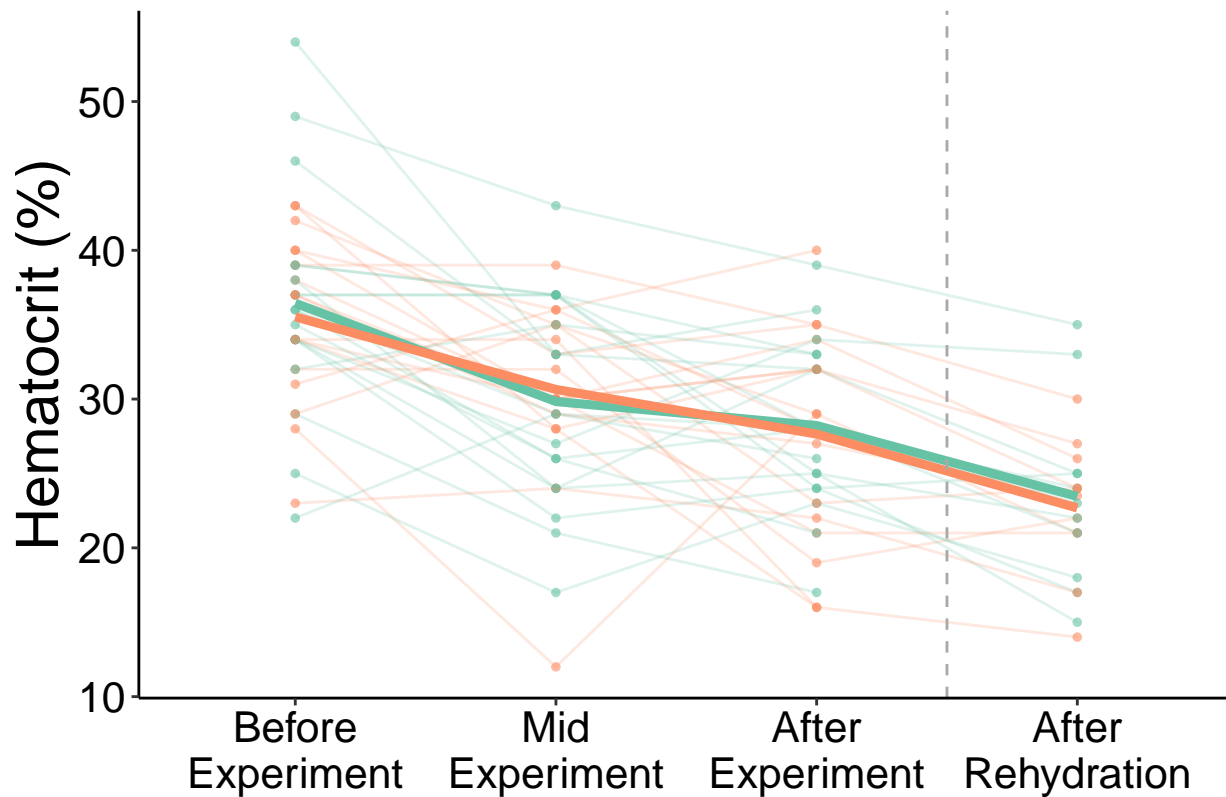
        color = humidity_tmt_percent),
        size = 1.6,
        alpha = 1) +
theme_classic() +
scale_color_brewer(palette = "Set2",
                    name = "") +
scale_x_discrete(labels = c("Before\nExperiment",
                             "Mid\nExperiment",
                             "After\nExperiment",
                             "After\nRehydration")) +

xlab("") +
ylab("Hematocrit (%)") +
geom_vline(xintercept = 3.5,
            linetype = "dashed",
            color = "darkgrey") +
theme(text = element_text(color = "black",
                           family = "sans",
                           size = 22),
      axis.text = element_text(color = "black",
                                family = "sans",
                                size = 16),
      legend.text = element_text(color = "black",
                                  family = "sans",
                                  size = 24),
      legend.text.align = 0,
      legend.position = "none",
      plot.margin = unit(c(0.2,0,0,0.4), "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
            ),
            size = 1,
            alpha = 0.6) +
  geom_line(data = all_dat,
            aes(x = day,
                y = osmolality_mmol_kg,
                group = individual_ID,
                color = humidity_tmt_percent),
            alpha = 0.2) +
  geom_line(data = all_dat_mean_osml,
            aes(x = day,
                y = osml_mean,
                group = humidity_tmt_percent,
```

```

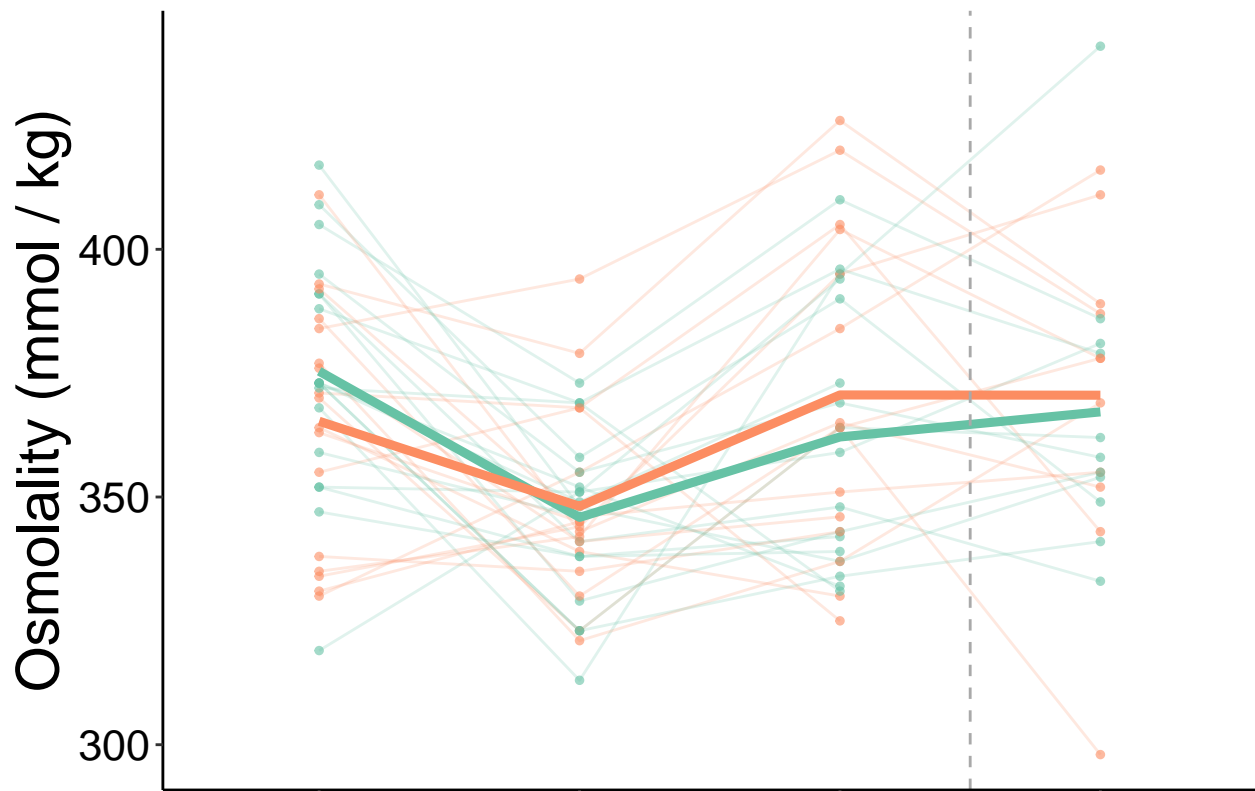
        color = humidity_tmt_percent),
        size = 1.6,
        alpha = 1) +
theme_classic() +
scale_color_brewer(palette = "Set2",
                    name = "") +

xlab("") +
ylab("Osmolality (mmol / kg)") +
geom_vline(xintercept = 3.5,
            linetype = "dashed",
            color = "darkgrey") +
theme(text = element_text(color = "black",
                           family = "sans",
                           size = 22),
      axis.text = element_text(color = "black",
                                family = "sans",
                                size = 16),
      axis.text.x = element_blank(),
      legend.text = element_text(color = "black",
                                  family = "sans",
                                  size = 24),
      legend.text.align = 0,
      legend.position = "none",
      plot.margin = unit(c(0.2,0,0,0.1), "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).
```



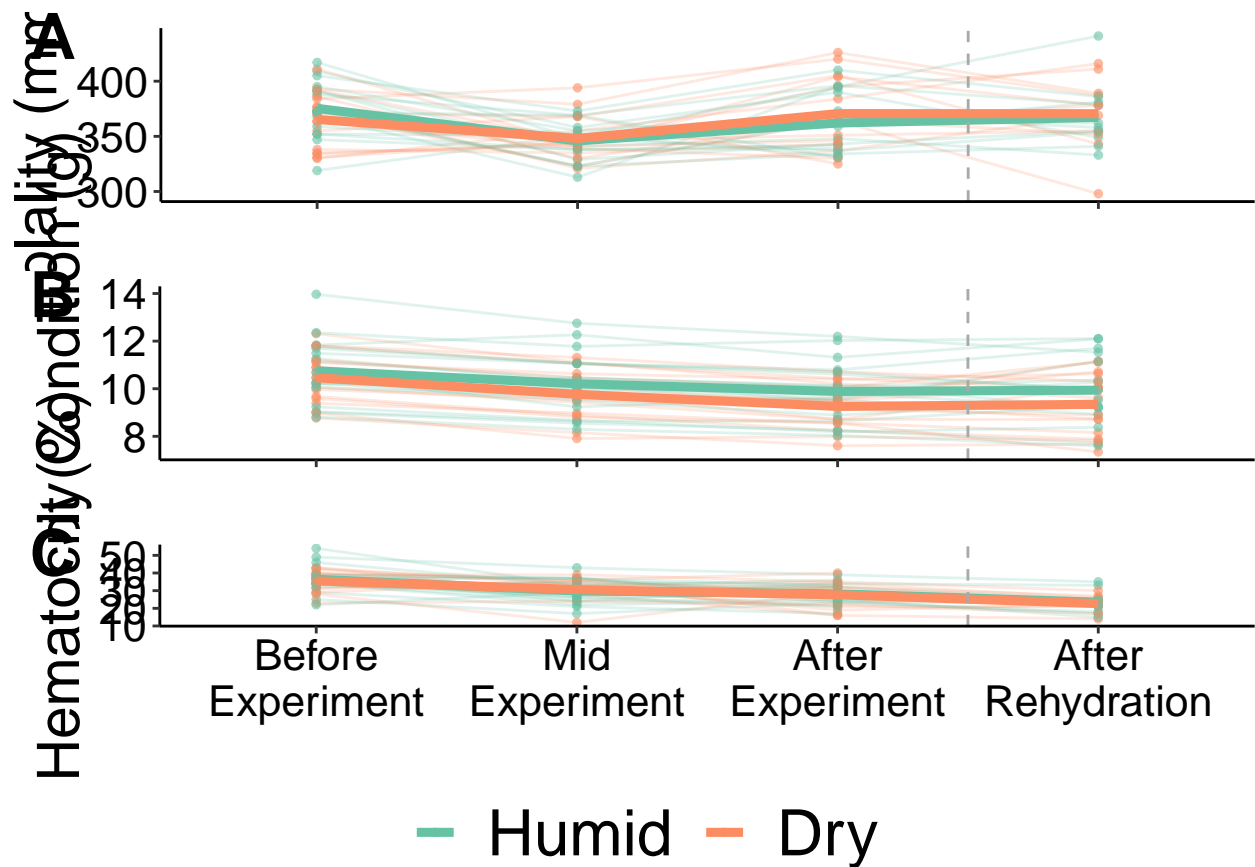
```
# export figure
#ggsave(filename = "tmt_effects_osml.jpeg",
#       plot = tmt_effects_osml,
#       path = "./final_figures",
#       device = "jpeg",
#       dpi = 1200,
#       width = 5, height = 4)
```

## Multi-Figure

```
ggarrange(tmt_effects_osml, tmt_effects_SMI, tmt_effects_hct,
  ncol = 1, nrow = 3,
  labels = c("A", "B", "C"),
  font.label = list(size = 24, face = "bold", color = "black"),
  vjust = c(1, 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 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_fig.jpeg",
        plot = tmt_multi_fig,
        path = "./final_figures",
        device = "jpeg",
        dpi = 1200,
        width = 6, height = 12)
```

## CEWL

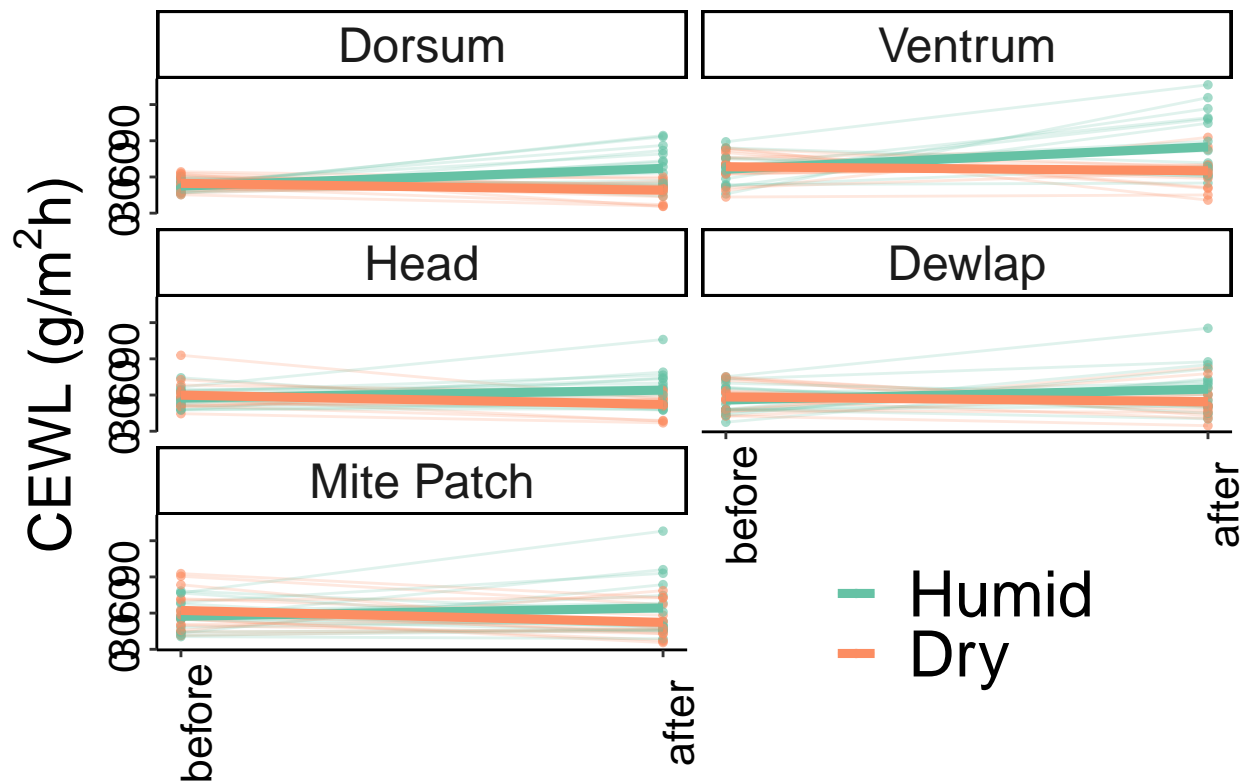
```
CEWL %>%
  ggplot(data = .) +
  geom_point(aes(x = n_day,
                 y = TEWL_g_m2h,
                 color = humidity_tmt_percent),
            size = 1,
            alpha = 0.6) +
  geom_line(aes(x = n_day,
                 y = TEWL_g_m2h,
                 group = individual_ID,
                 color = humidity_tmt_percent),
            alpha = 0.2) +
  stat_smooth(aes(x = n_day,
```



```

        y = TEWL_g_m2h,
        color = humidity_tmt_percent
    ),
    formula = y ~ x,
    method = "lm",
    se = F,
    size = 1.6,
    alpha = 1) +
theme_classic() +
scale_color_brewer(palette = "Set2",
                    name = ""
                    #name = "Humidity\nTreatment"
                    ) +
facet_wrap(~region, ncol = 2) +
scale_x_continuous(breaks = c(0, 1),
                    labels = c("0" = "before", "1" = "after"))
) +
xlab("") +
ylab(bquote('CEWL (g/*m^2*h)')) +
theme(text = element_text(color = "black",
                           family = "sans",
                           size = 22),
      axis.text = element_text(color = "black",
                                family = "sans",
                                size = 16,
                                angle = 90),
      legend.text = element_text(color = "black",
                                  family = "sans",
                                  size = 24),
      legend.text.align = 0,
      legend.position = c(0.75,0.12),
      #legend.justification = c(1, 1)
) -> CEWL_tmt_fig
CEWL_tmt_fig

```



```
# export figure
ggsave(filename = "tmt_effects_CEWL.jpeg",
  plot = CEWL_tmt_fig,
  path = "./final_figures",
  device = "jpeg",
  dpi = 1200,
  width = 6, height = 9)
```

## Models

### SMI

Check whether means started out different:

```
SMI_diff_lm <- all_dat_no_rehab %>%
  dplyr::filter(day == "Before Experiment") %>%
  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 Experiment") %>%
  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))
```

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

```
drop1(SMI_mod1)
```

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

```
## Single term deletions
```

```
##
```

```
## Model:
```

```
## SMI ~ day * humidity_tmt_percent + (1 | trial_number)
```

```
##              npar      AIC
```

```
## <none>              337.25
```

```
## day:humidity_tmt_percent    2 333.66
```

```

# drop interaction term
SMI_mod2 <- lme4::lmer(data = all_dat_no_rehab,
  SMI ~ day + humidity_tmt_percent +
  (1|trial_number))

## 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)
##          npar      AIC
## <none>          333.66
## day             2 343.71
## humidity_tmt_percent 1 335.89

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

```

```

## boundary (singular) fit: see ?isSingular
drop1(SMI_mod3)

```

```

## boundary (singular) fit: see ?isSingular

## Single term deletions
##
## Model:
## SMI ~ day + (1 | trial_number)
##          npar      AIC
## <none>          335.89
## day             2 345.42

```

```

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

```

```

## 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))
```

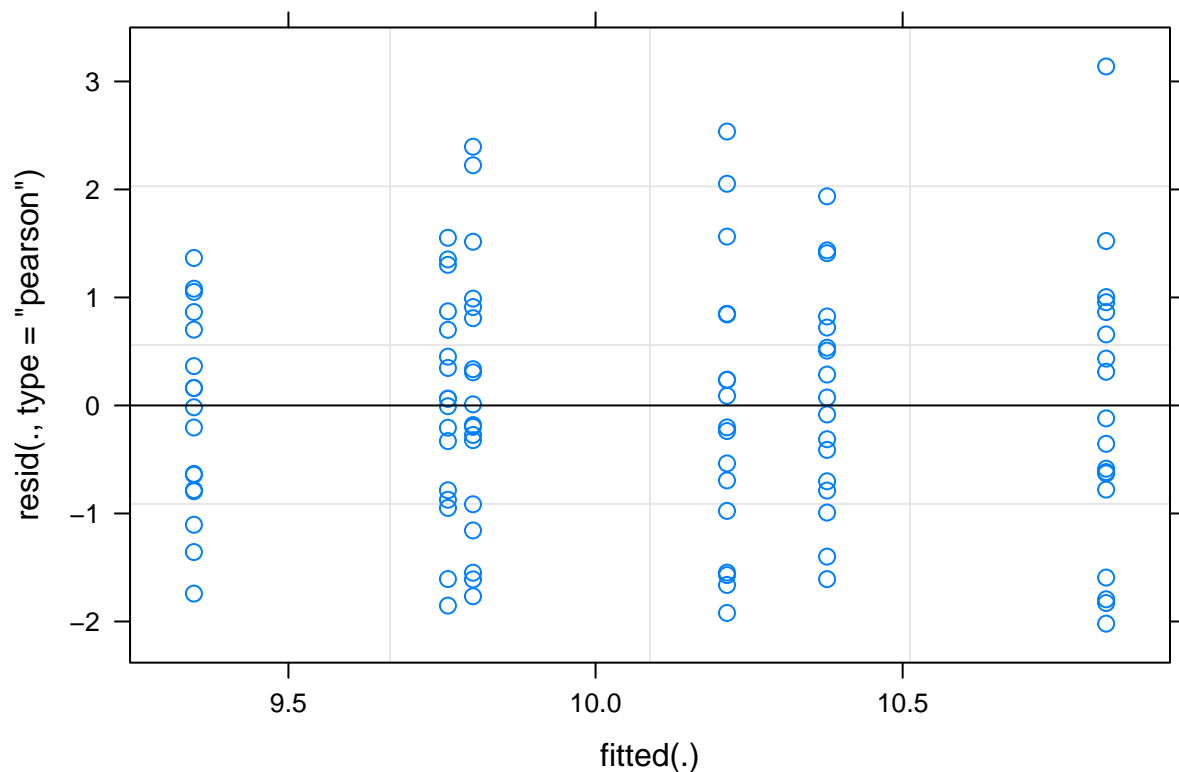
```
## Warning in aictab.AIClmerMod(cand.set = SMI_models, modnames = SMI_mod_names):
## Model selection for fixed effects is only appropriate with ML estimation:
## REML (default) should only be used to select random effects for a constant set of fixed effects
```

```
SMI_AICc
```

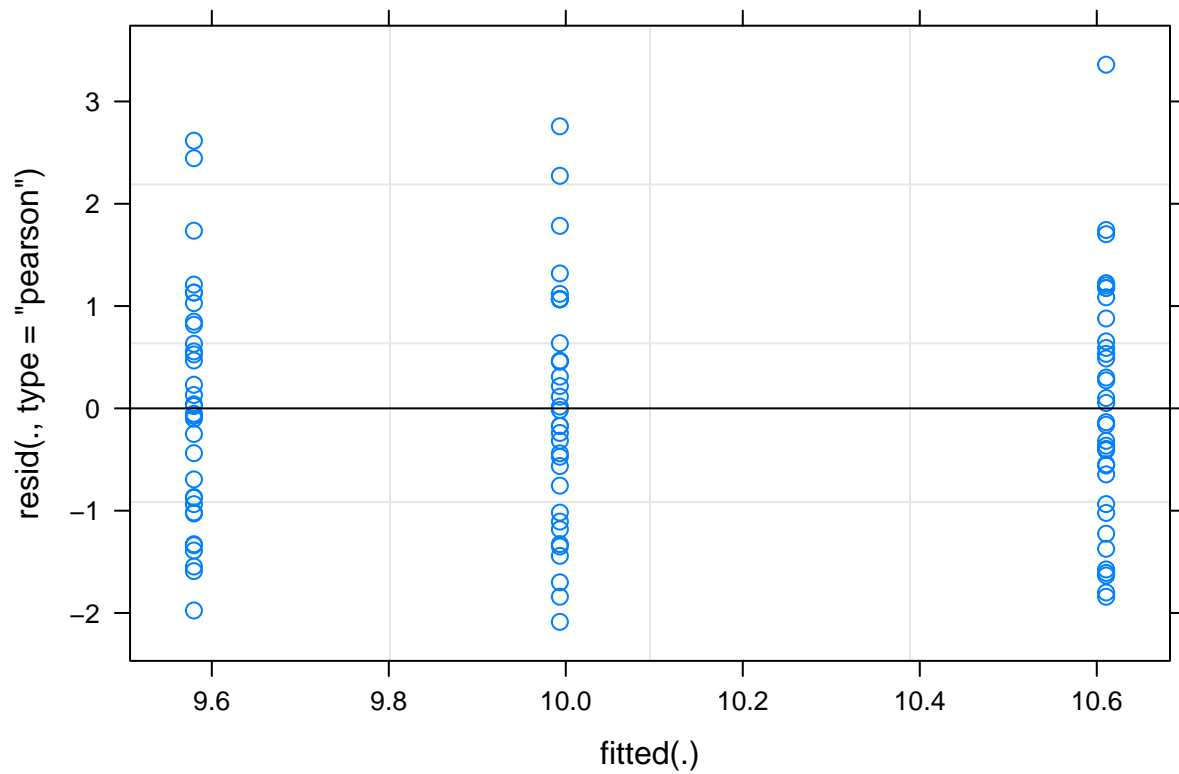
```
##           Modnames K      AICc Delta_AICc  Modellik      AICcWt
## 2 (model 2) ~ day + humidity 6 340.1152  0.0000000  1.0000000  0.520810202
## 3           (model 3) ~ day 5 340.8080  0.6928134  0.70722480  0.368329889
## 1 (model 1) ~ day * humidity 8 343.3932  3.2780742  0.19416692  0.101124113
## 4           null model 3 348.0743  7.9591527  0.01869356  0.009735796
##      Res.LL      Cum.Wt
## 2 -163.6290  0.5208102
## 3 -165.1010  0.8891401
## 1 -162.9466  0.9902642
## 4 -170.9183  1.0000000
```

### Check Conditions of Top Models

```
plot(SMI_mod2)
```



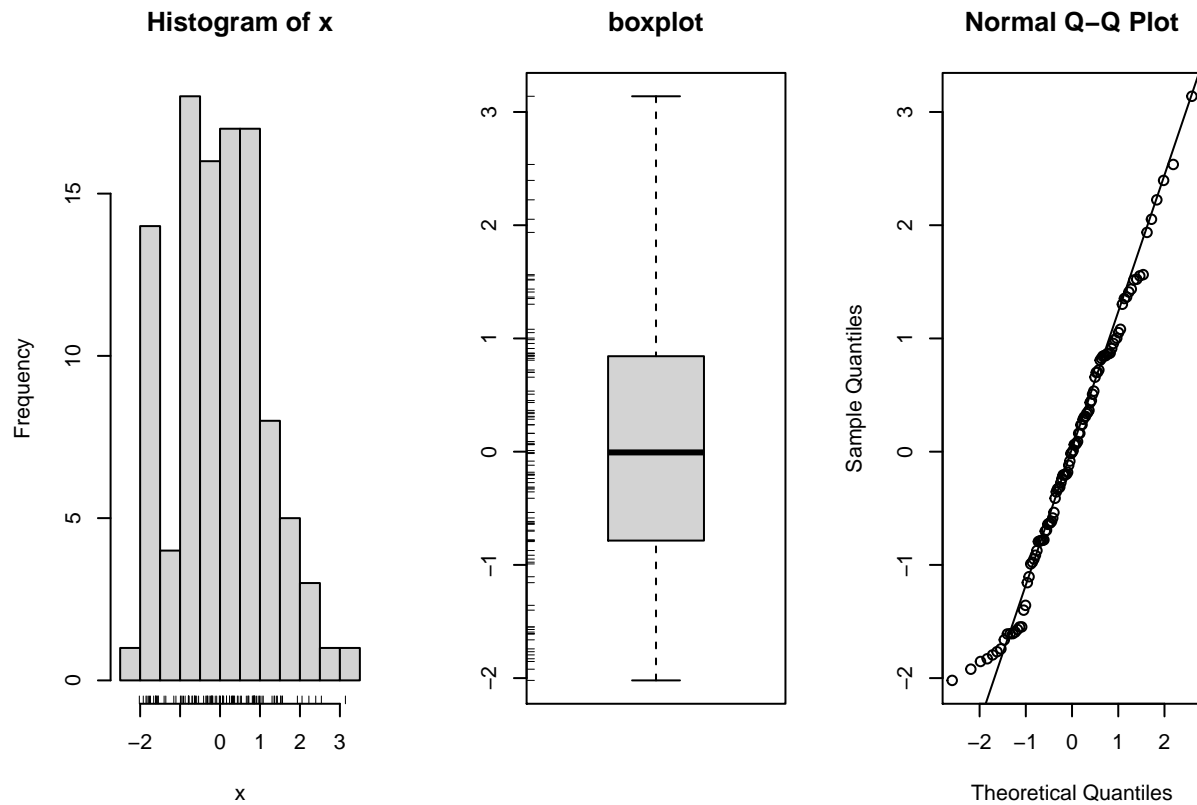
```
plot(SMI_mod3)
```



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

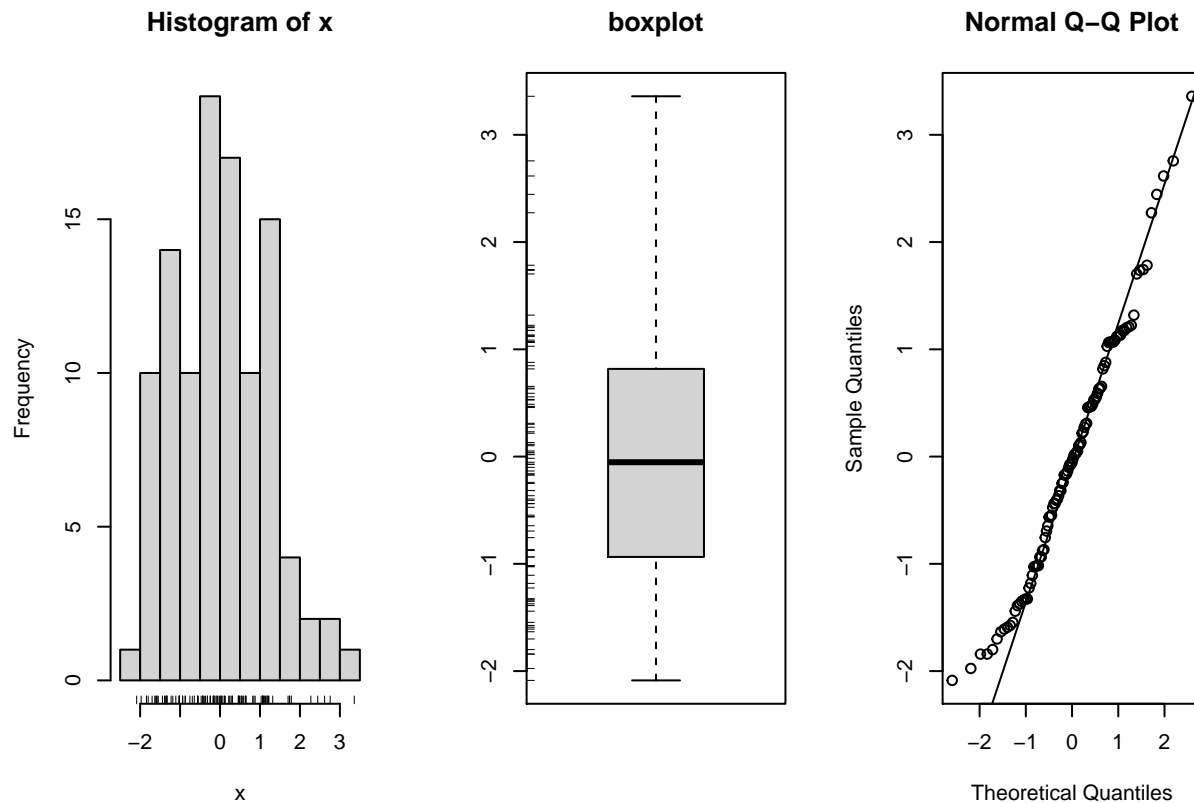
```
simple.eda(residuals(SMI_mod2))
```



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

```
##
##  Shapiro-Wilk normality test
##
## data:  residuals(SMI_mod2)
## W = 0.98165, p-value = 0.1551
```

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



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

```
##
##  Shapiro-Wilk normality test
##
## data:  residuals(SMI_mod3)
## W = 0.97886, p-value = 0.09175
```

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))
```

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

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

```
## 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))
summary(hct_mod1)

## Linear mixed model fit by REML ['lmerMod']
## Formula: hematocrit_percent ~ day * humidity_tmt_percent + (1 | trial_number)
## Data: .
##
## REML criterion at convergence: 665.8
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.1677 -0.5501  0.0365  0.5956  2.6381
##
## Random effects:
##  Groups      Name      Variance Std.Dev.
##  trial_number (Intercept)  7.185   2.681
##  Residual                38.959   6.242
## Number of obs: 105, groups: trial_number, 4
##
## Fixed effects:
##
##              Estimate Std. Error t value
## (Intercept)      36.0220    1.9995  18.016
## dayMid Experiment    -6.6111    2.0806  -3.178
## dayAfter Experiment  -8.2222    2.0806  -3.952
## humidity_tmt_percentDry -0.8797    2.1115  -0.417
## dayMid Experiment:humidity_tmt_percentDry  1.7288    2.9853   0.579
## dayAfter Experiment:humidity_tmt_percentDry  0.3399    2.9853   0.114
##
## Correlation of Fixed Effects:
##              (Intr) dyMdEx dyAftE hmd__D dME:__
## dyMdExprmnt -0.520
## dyAftExprm -0.520  0.500
## hmdty_tmt_D -0.514  0.493  0.493
## dyMExpr:__D  0.363 -0.697 -0.348 -0.707
## dyAExpr:__D  0.363 -0.348 -0.697 -0.707  0.500
drop1(hct_mod1)

## Single term deletions
##
## Model:
## hematocrit_percent ~ day * humidity_tmt_percent + (1 | trial_number)
##              npar      AIC
```

```

## <none> 699.17
## day:humidity_tmt_percent 2 695.56
# 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))
summary(hct_mod2)

## Linear mixed model fit by REML ['lmerMod']
## Formula: hematocrit_percent ~ day + humidity_tmt_percent + (1 | trial_number)
## Data: .
##
## REML criterion at convergence: 674
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.10869 -0.60033  0.02219  0.62265  2.71370
##
## Random effects:
##   Groups       Name             Variance Std.Dev.
##   trial_number (Intercept)  7.224    2.688
##   Residual                38.312    6.190
## Number of obs: 105, groups: trial_number, 4
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)      35.685      1.812  19.698
## dayMid Experiment    -5.771      1.480  -3.901
## dayAfter Experiment   -8.057      1.480  -5.445
## humidity_tmt_percentDry -0.190      1.210  -0.157
##
## Correlation of Fixed Effects:
##              (Intr) dyMdEx dyAftE
## dyMdExprmnt -0.408
## dyAftrExprm -0.408  0.500
## hmdty_tmt_D -0.326  0.000  0.000
drop1(hct_mod2)

## Single term deletions
##
## Model:
## hematocrit_percent ~ day + humidity_tmt_percent + (1 | trial_number)
##              npar      AIC
## <none>              695.56
## day              2 719.67
## humidity_tmt_percent 1 693.59
# drop humidity tmt
hct_mod3 <- all_dat_no_rehab %>%
  dplyr::filter(complete.cases(hematocrit_percent)) %>%
  lme4::lmer(data = .,
             hematocrit_percent ~ day +

```

```

      (1|trial_number))
summary(hct_mod3)

## Linear mixed model fit by REML ['lmerMod']
## Formula: hematocrit_percent ~ day + (1 | trial_number)
## Data: .
##
## REML criterion at convergence: 676.2
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.14009 -0.58850  0.00871  0.64072  2.74219
##
## Random effects:
##  Groups      Name      Variance Std.Dev.
## trial_number (Intercept)  7.253   2.693
## Residual              37.932   6.159
## Number of obs: 105, groups: trial_number, 4
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)    35.592     1.712  20.794
## dayMid Experiment  -5.771     1.472  -3.920
## dayAfter Experiment -8.057     1.472  -5.473
##
## Correlation of Fixed Effects:
##              (Intr) dyMdEx
## dyMdExprmnt -0.430
## dyAftrExprm -0.430  0.500

```

```

drop1(hct_mod3)

## Single term deletions
##
## Model:
## hematocrit_percent ~ day + (1 | trial_number)
##      npar    AIC
## <none>    693.59
## day      2 717.69

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

```

```

## Linear mixed model fit by REML ['lmerMod']
## Formula: hematocrit_percent ~ 1 + (1 | trial_number)
## Data: .
##
## REML criterion at convergence: 709.3
##
## Scaled residuals:

```

```
##      Min      1Q   Median      3Q      Max
## -2.91350 -0.66552  0.08156  0.65205  3.07663
##
## Random effects:
##   Groups      Name      Variance Std.Dev.
## trial_number (Intercept)  6.579   2.565
## Residual                49.162   7.012
## Number of obs: 105, groups: trial_number, 4
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)   31.011      1.467    21.14
```

## 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:
```

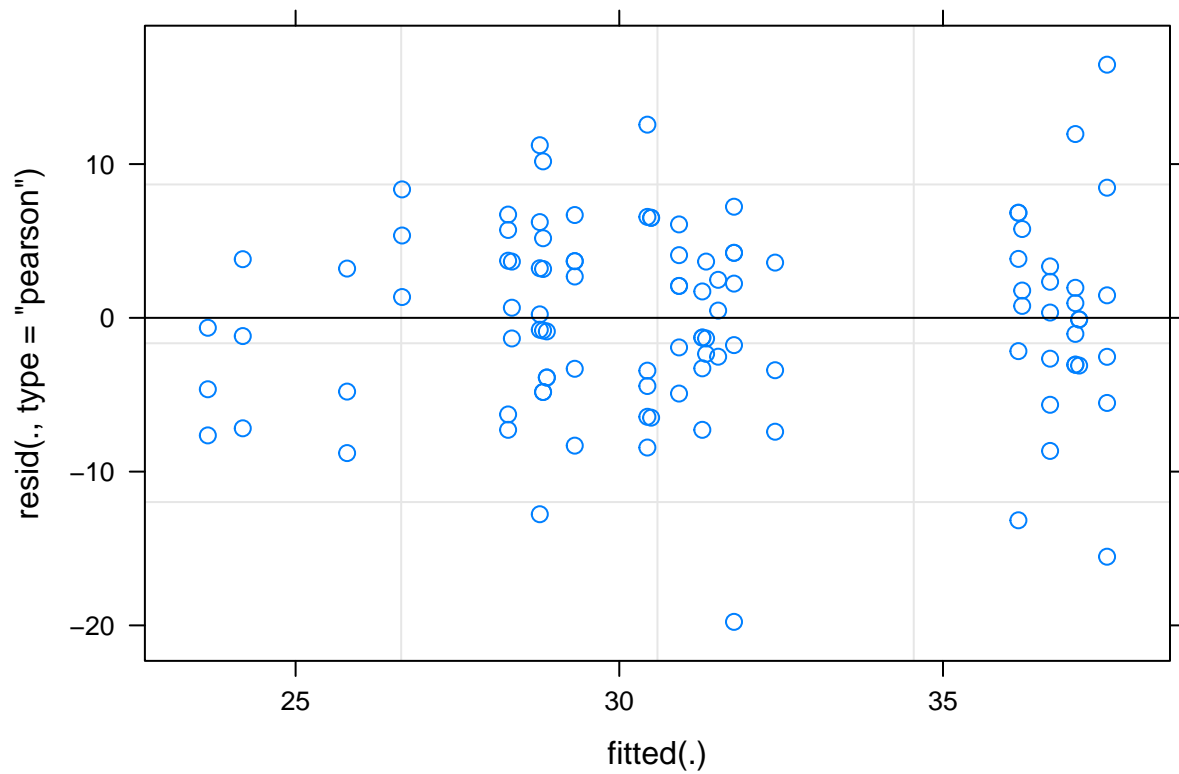
```
## REML (default) should only be used to select random effects for a constant set of fixed effects
```

```
hct_AICc
```

```
##           Modnames K      AICc Delta_AICc      Modellik      AICcWt
## 1 (model 1) ~ day * humidity 8 683.3443   0.000000 1.000000e+00 7.398247e-01
## 3      (model 3) ~ day 5 686.8142   3.469934 1.764060e-01 1.305095e-01
## 2 (model 2) ~ day + humidity 6 686.8272   3.482907 1.752655e-01 1.296657e-01
## 4      null model 3 715.5004  32.156093 1.040862e-07 7.700553e-08
##      Res.LL      Cum.Wt
## 1 -332.9222 0.7398247
## 3 -338.1041 0.8703342
## 2 -336.9850 0.9999999
## 4 -354.6314 1.0000000
```

## Check Conditions of Top Model

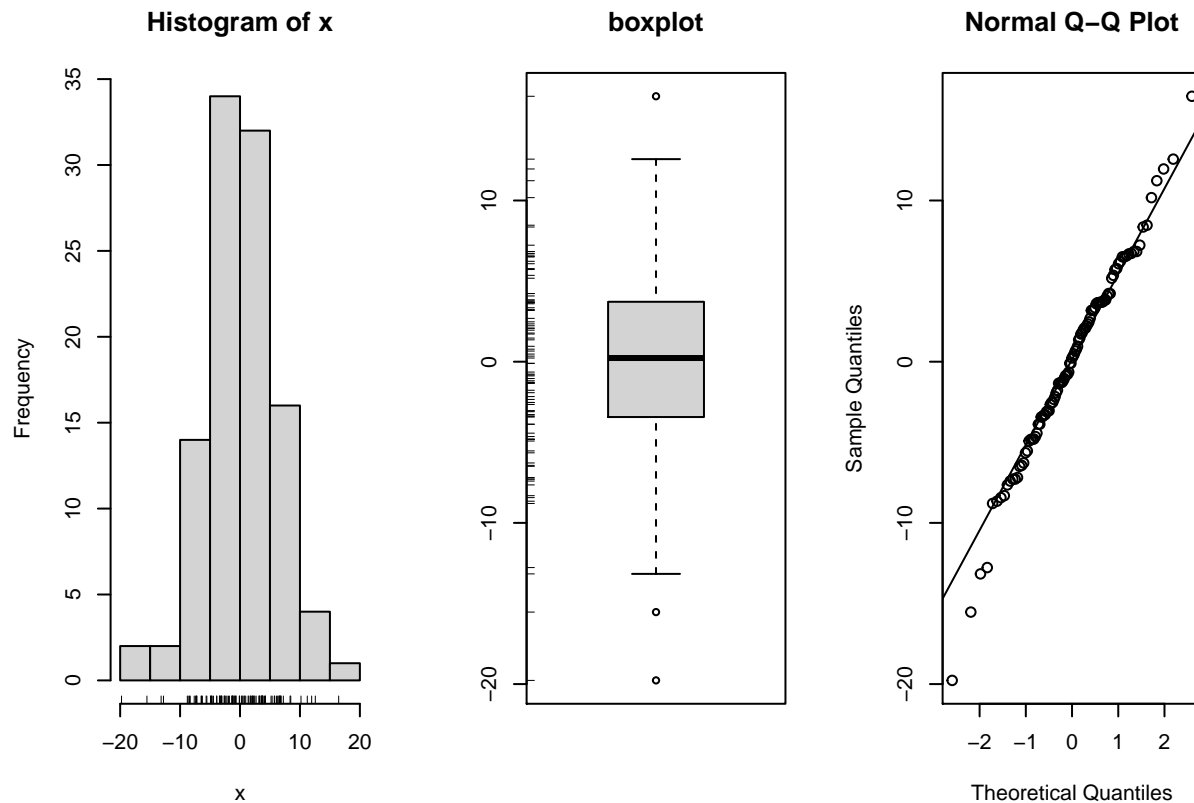
```
plot(hct_mod1)
```



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 = 0.98802, p-value = 0.4735
```

residuals are normally distributed!

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

```
hct_mod1p <- lmerTest::lmer(data = all_dat_no_rehab,
  SMI ~ day * humidity_tmt_percent +
  (1|trial_number))
```

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

## Export

```
write.csv(hct_AICc, "./best_models/exp_effects_hct_mod_rankings.csv")
write.csv(broom.mixed::tidy(hct_mod1),
  "./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))
summary(osml_mod1)

## Linear mixed model fit by REML ['lmerMod']
## Formula: osmolality_mmol_kg ~ day * humidity_tmt_percent + (1 | trial_number)
## 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.
## trial_number (Intercept) 313.5         17.71
## Residual                393.8         19.84
## Number of obs: 102, groups: trial_number, 4
##
## Fixed effects:
##
##              Estimate Std. Error t value
## (Intercept)      378.509     10.035   37.719
## dayMid Experiment    -29.500      6.615   -4.460
## dayAfter Experiment  -13.885      6.713   -2.068
## humidity_tmt_percentDry -10.215      6.713   -1.522
## dayMid Experiment:humidity_tmt_percentDry 12.324      9.491    1.298
## dayAfter Experiment:humidity_tmt_percentDry 17.783      9.721    1.829
##
## Correlation of Fixed Effects:
##              (Intr) dyMdEx dyAftE hmd__D dME:__
## dyMdExprmnt -0.330
## dyAftExprm  -0.326  0.493
## hmdty_tmt_D -0.326  0.493  0.485
## dyMExpr:__D  0.230 -0.697 -0.343 -0.707
## dyAExpr:__D  0.224 -0.340 -0.690 -0.690  0.488
drop1(osml_mod1)

## Single term deletions
##
## Model:
## osmolality_mmol_kg ~ day * humidity_tmt_percent + (1 | trial_number)
##              npar      AIC
## <none>              920.78
## day:humidity_tmt_percent  2 920.47

# 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))
summary(osml_mod2)

```

```

## Linear mixed model fit by REML ['lmerMod']
## Formula: osmolality_mmol_kg ~ day + humidity_tmt_percent + (1 | trial_number)
## 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.
##   trial_number (Intercept) 314.5        17.74
##   Residual                400.2        20.01
## Number of obs: 102, groups: trial_number, 4
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)    373.7599     9.7086  38.498
## dayMid Experiment   -23.5143     4.7822  -4.917
## dayAfter Experiment   -5.3904     4.9001  -1.100
## humidity_tmt_percentDry -0.4143     3.9679  -0.104
##
## Correlation of Fixed Effects:
##              (Intr) dyMdEx dyAftE
## dyMdExprmnt -0.246
## dyAftExprm -0.245  0.488
## hmdty_tmt_D -0.200  0.000  0.013
drop1(osml_mod2)

## Single term deletions
##
## Model:
## osmolality_mmol_kg ~ day + humidity_tmt_percent + (1 | trial_number)
##              npar      AIC
## <none>              920.47
## day                2 940.51
## humidity_tmt_percent 1 918.48

# 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))
summary(osml_mod3)

## Linear mixed model fit by REML ['lmerMod']
## Formula: osmolality_mmol_kg ~ day + (1 | trial_number)
## 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.
## trial_number (Intercept) 314.6    17.74
## Residual                396.1    19.90
## Number of obs: 102, groups: trial_number, 4
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)      373.559      9.507  39.294
## dayMid Experiment   -23.514      4.757  -4.943
## dayAfter Experiment  -5.384      4.874  -1.105
##
## Correlation of Fixed Effects:
##              (Intr) dyMdEx
## dyMdExprmnt -0.250
## dyAftExprm  -0.246  0.488

```

```

drop1(osml_mod3)

## Single term deletions
##
## Model:
## osmolality_mmol_kg ~ day + (1 | trial_number)
##      npar      AIC
## <none>      918.48
## day        2 938.52

```

```

# 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))
summary(osml_mod_null)

```

```

## Linear mixed model fit by REML ['lmerMod']
## Formula: osmolality_mmol_kg ~ 1 + (1 | trial_number)
##   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.
## trial_number (Intercept) 312.8    17.69
## Residual                495.7    22.26
## Number of obs: 102, groups: trial_number, 4
##
## Fixed effects:

```

```
##           Estimate Std. Error t value
## (Intercept) 363.791      9.138   39.81
```

## 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:
```

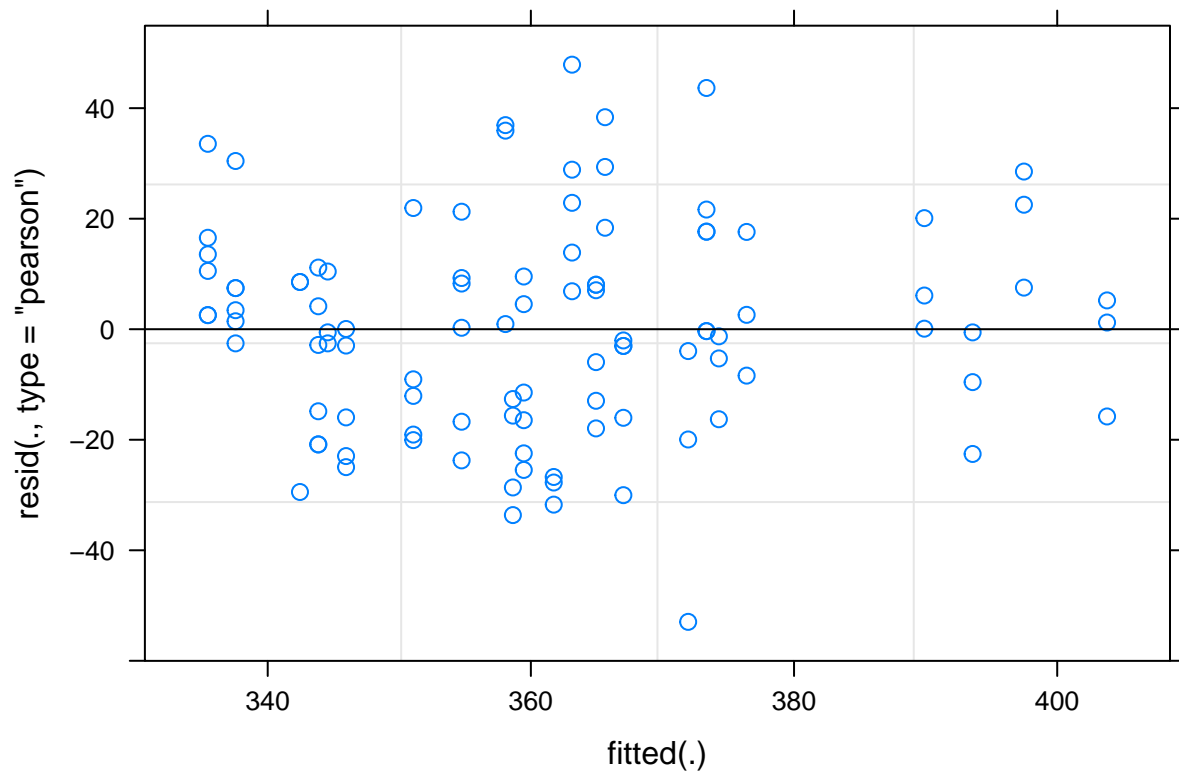
```
## REML (default) should only be used to select random effects for a constant set of fixed effects
```

```
osml_AICc
```

```
##           Modnames K      AICc Delta_AICc      Modellik      AICcWt
## 1 (model 1) ~ day * humidity 8 889.6525    0.00000 1.000000e+00 9.954995e-01
## 2 (model 2) ~ day + humidity 6 900.9910   11.33850 3.450450e-03 3.434921e-03
## 3      (model 3) ~ day 5 903.3319   13.67941 1.070421e-03 1.065604e-03
## 4      null model 3 932.6549   43.00242 4.593485e-10 4.572812e-10
##      Res.LL      Cum.Wt
## 1 -436.0521 0.9954995
## 2 -444.0534 0.9989344
## 3 -446.3535 1.0000000
## 4 -463.2050 1.0000000
```

## Check Conditions of Top Model

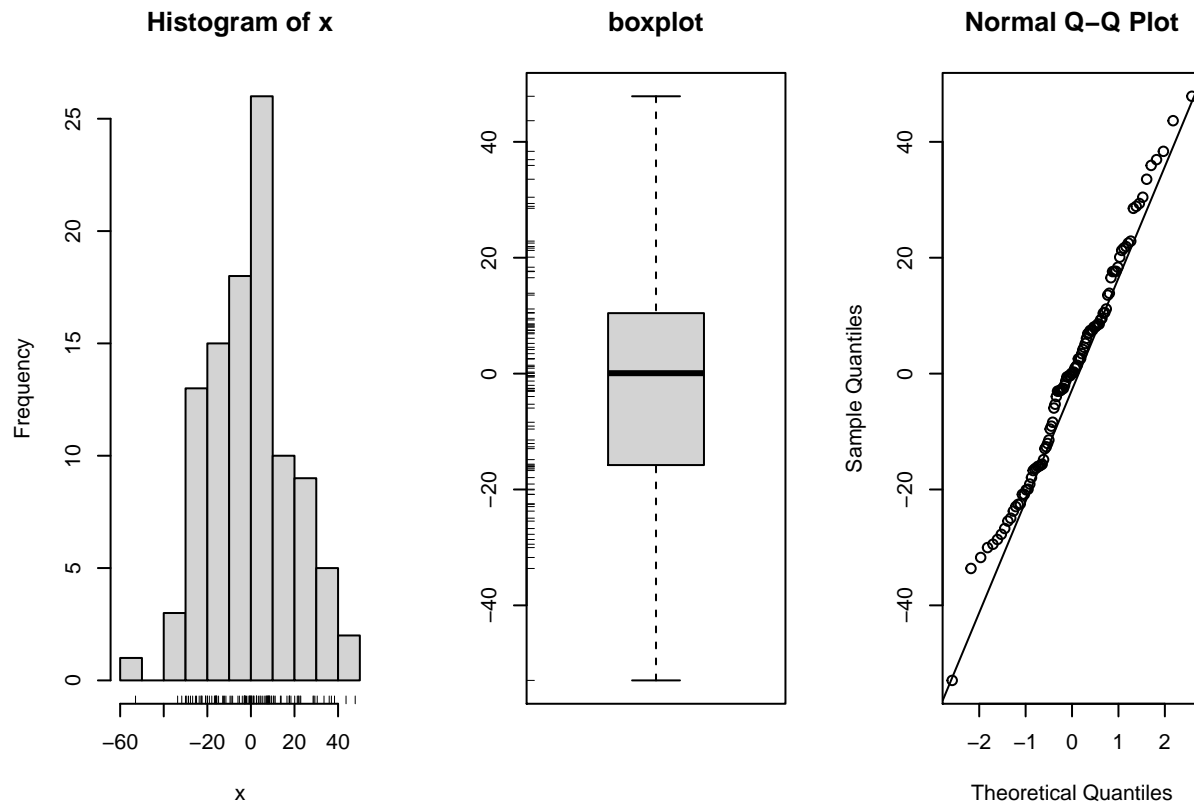
```
plot(osml_mod1)
```



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,
  SMI ~ day * humidity_tmt_percent +
  (1|trial_number))
```

```
## 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
## regionVentrurn    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:regionVentrurn  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:regionVentrurn -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:regionVentrurn -2.37516     7.76641   -0.306
## dayAfter:humidity_tmt_percentDry:regionHead  5.28070     7.76641    0.680
## dayAfter:humidity_tmt_percentDry:regionDewlap  5.66684     7.82338    0.724
## dayAfter:humidity_tmt_percentDry:regionMite Patch 1.47809     7.83657    0.189
##
## Correlation matrix not shown by default, as p = 21 > 12.
## Use print(x, correlation=TRUE) or
##      vcov(x)          if you need it
drop1(CEWL_mod1)

## Single term deletions

```

```

##
## Model:
## TEWL_g_m2h ~ day * humidity_tmt_percent * region + cloacal_temp_C +
##   (1 | trial_number/individual_ID)
##               npar      AIC
## <none>                2570.1
## cloacal_temp_C         1 2628.2
## day:humidity_tmt_percent:region  4 2563.8
# drop triple interaction
CEWL_mod2 <- lme4::lmer(data = CEWL,
  TEWL_g_m2h ~ day * (humidity_tmt_percent + region) +
    humidity_tmt_percent * region +
    cloacal_temp_C +
    (1|trial_number/individual_ID))
summary(CEWL_mod2)

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

```

```

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

drop1(CEWL_mod2)

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

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

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

```

```

## dayAfter: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
## regionVentrurn  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
## regionVentrurn      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
## regionVentrurn            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
## regionVentrurn    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
## regionVentrurn  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
## 1 (model 1) ~ day * humidity * region + cloacal temp
## 2 (model 2) ~ day * humidity + day * region + humidity * region + cloacal temp
## 3 (model 3) ~ day * humidity + day * region + cloacal temp
## 4 (model 4) ~ day * humidity + region + cloacal temp
## 5 (model 5) ~ day * humidity + region
## 6 (model 6) ~ day + humidity + region
```

```
## 7 (model 7) ~ day + region
## 8 (model 8) ~ region
## 9 null model
```

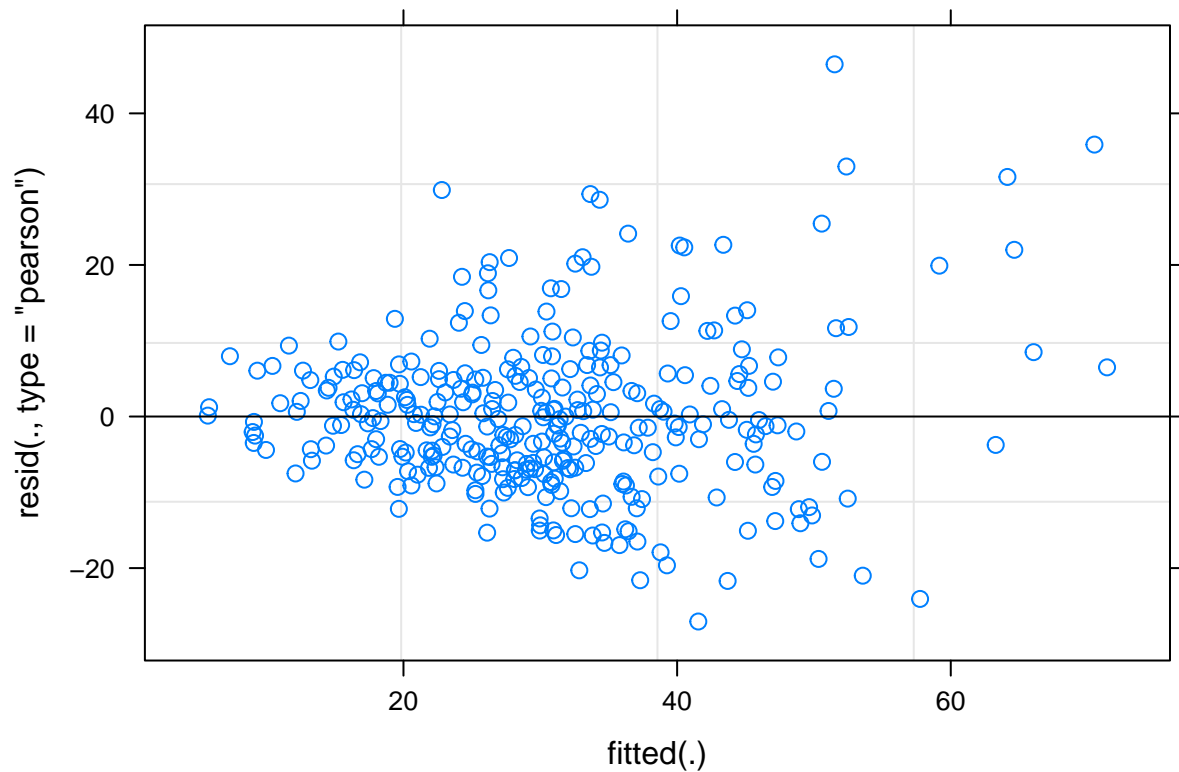
##	K	AICc	Delta_AICc	ModelLik	AICcWt	Res.LL	Cum.Wt
## 1	24	2493.777	0.00000	1.000000e+00	9.994309e-01	-1220.895	0.9994309
## 2	20	2508.727	14.95000	5.670846e-04	5.667619e-04	-1232.986	0.9999977
## 3	16	2519.710	25.93355	2.336689e-06	2.335359e-06	-1242.975	1.0000000
## 4	12	2535.175	41.39888	1.024111e-09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

The FULL model is the best model.

### 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)
```



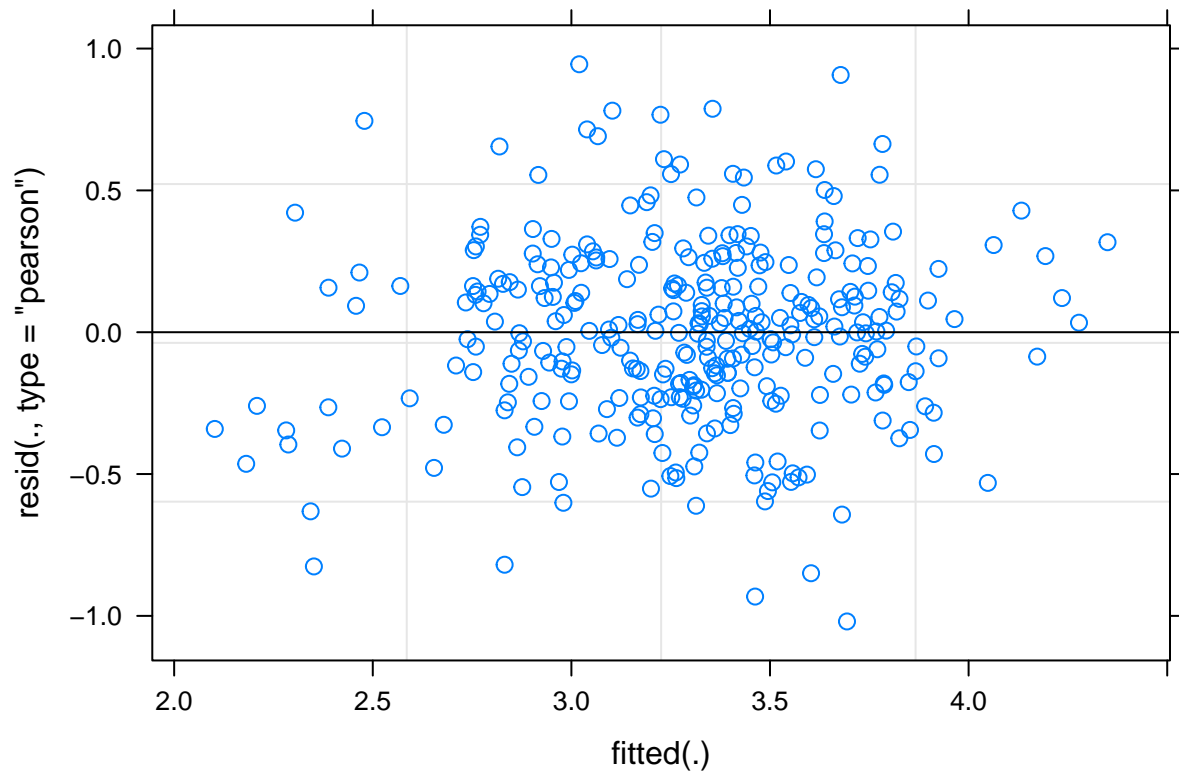
clear fanning shape... L & E are not satisfied.

### Transform CEWL

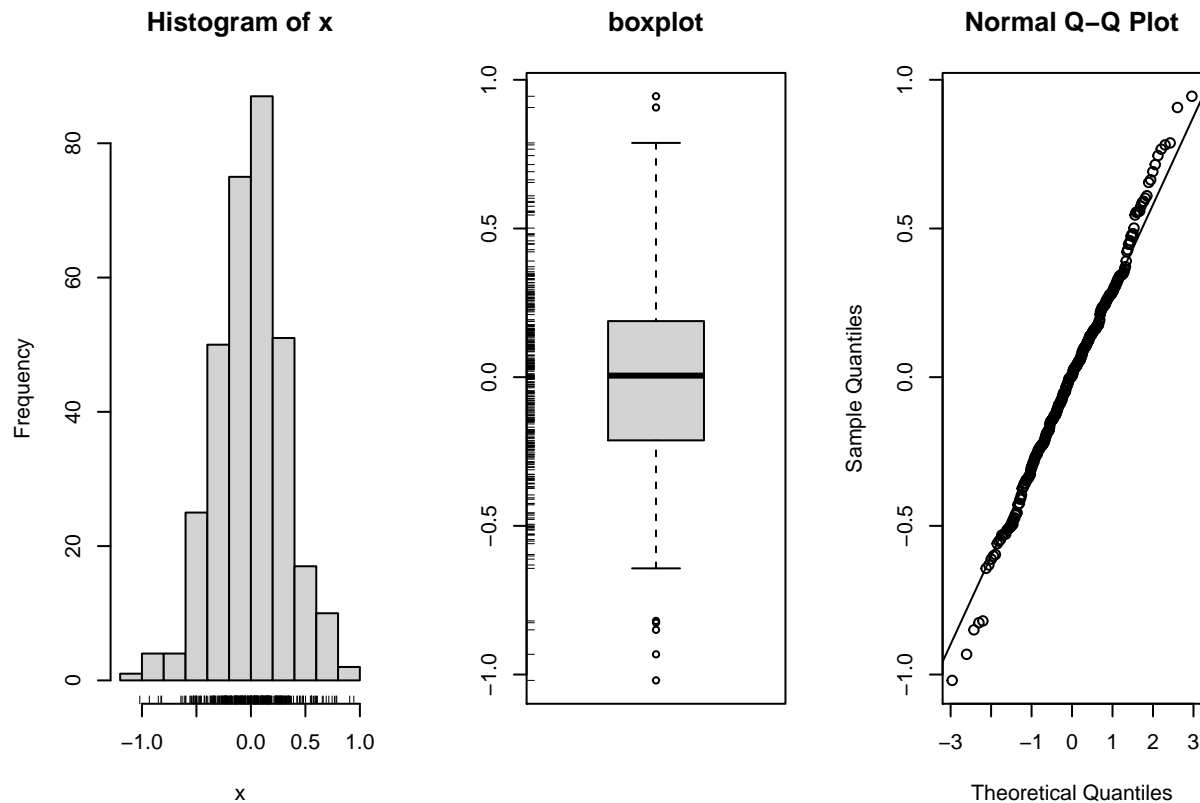
Log-transformation worked well in the capture analysis, so try that here.

```
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
## regionVentrurn                    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:regionVentrurn           -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:regionVentrurn -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:regionVentrurn 0.26103    0.24004
## dayAfter:humidity_tmt_percentDry:regionHead 0.24592    0.24004
## dayAfter:humidity_tmt_percentDry:regionDewlap 0.21627    0.24178
## dayAfter:humidity_tmt_percentDry:regionMite Patch 0.14559    0.24220
##                                     df t value Pr(>|t|)
## (Intercept)                       173.23775  -0.467 0.640762
## dayAfter                          279.57165   5.121 5.66e-07
## humidity_tmt_percentDry           211.50009   0.189 0.850623
## regionVentrurn                    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:regionVentrurn           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:regionVentrurn 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:regionVentrurn 273.55964   1.087 0.277812
## dayAfter:humidity_tmt_percentDry:regionHead 273.55964   1.024 0.306507
## dayAfter:humidity_tmt_percentDry:regionDewlap 274.65325   0.895 0.371833
## dayAfter:humidity_tmt_percentDry:regionMite Patch 273.87346   0.601 0.548266
##

```

```

## (Intercept)
## dayAfter ***
## humidity_tmt_percentDry
## regionVentrurn ***
## regionHead .
## regionDewlap
## regionMite Patch
## cloacal_temp_C ***
## dayAfter:humidity_tmt_percentDry ***
## dayAfter:regionVentrurn
## dayAfter:regionHead
## dayAfter:regionDewlap
## dayAfter:regionMite Patch
## humidity_tmt_percentDry:regionVentrurn
## humidity_tmt_percentDry:regionHead
## humidity_tmt_percentDry:regionDewlap
## humidity_tmt_percentDry:regionMite Patch
## dayAfter:humidity_tmt_percentDry:regionVentrurn
## dayAfter:humidity_tmt_percentDry:regionHead
## dayAfter:humidity_tmt_percentDry:regionDewlap
## dayAfter:humidity_tmt_percentDry:regionMite Patch
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

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

```

## Export

```

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")

```