Experimental Data Analysis

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July 2021

Contents

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:

```r
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)

```r
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.

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

summary(all_dat)
```

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

```
##      conclusion        SVL_mm         capture_date               day
##   complete:139   Min.   :59.00   Min.   :2021-04-19   Min.   : 0.000
##                  1st Qu.:66.00   1st Qu.:2021-04-26   1st Qu.: 2.000
##                  Median :68.00   Median :2021-05-03   Median : 4.000
##                  Mean   :67.66   Mean   :2021-05-01   Mean   : 5.547
##                  3rd Qu.:70.00   3rd Qu.:2021-05-10   3rd Qu.: 9.000
##                  Max.   :73.00   Max.   :2021-05-10   Max.   :11.000
##
##        SMI
##   Min.   : 7.343
##   1st Qu.: 8.976
##   Median : 9.977
##   Mean   : 9.958
##   3rd Qu.:10.751
##   Max.   :13.970
##
```

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

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

re-order some factors:

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

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

```r
                    # 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                         3:110
##  Mean   :0.5    Mean   :23.11    Mean   :25                         4:118
##  3rd Qu.:1.0    3rd Qu.:24.75    3rd Qu.:25
##  Max.   :1.0    Max.   :28.00    Max.   :25
##
##     conclusion      notes
##  complete:326    Length:326
##                  Class :character
##                  Mode  :character
##
##
##
##
```

Check that data looks correct:

```
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
##
##
##
```
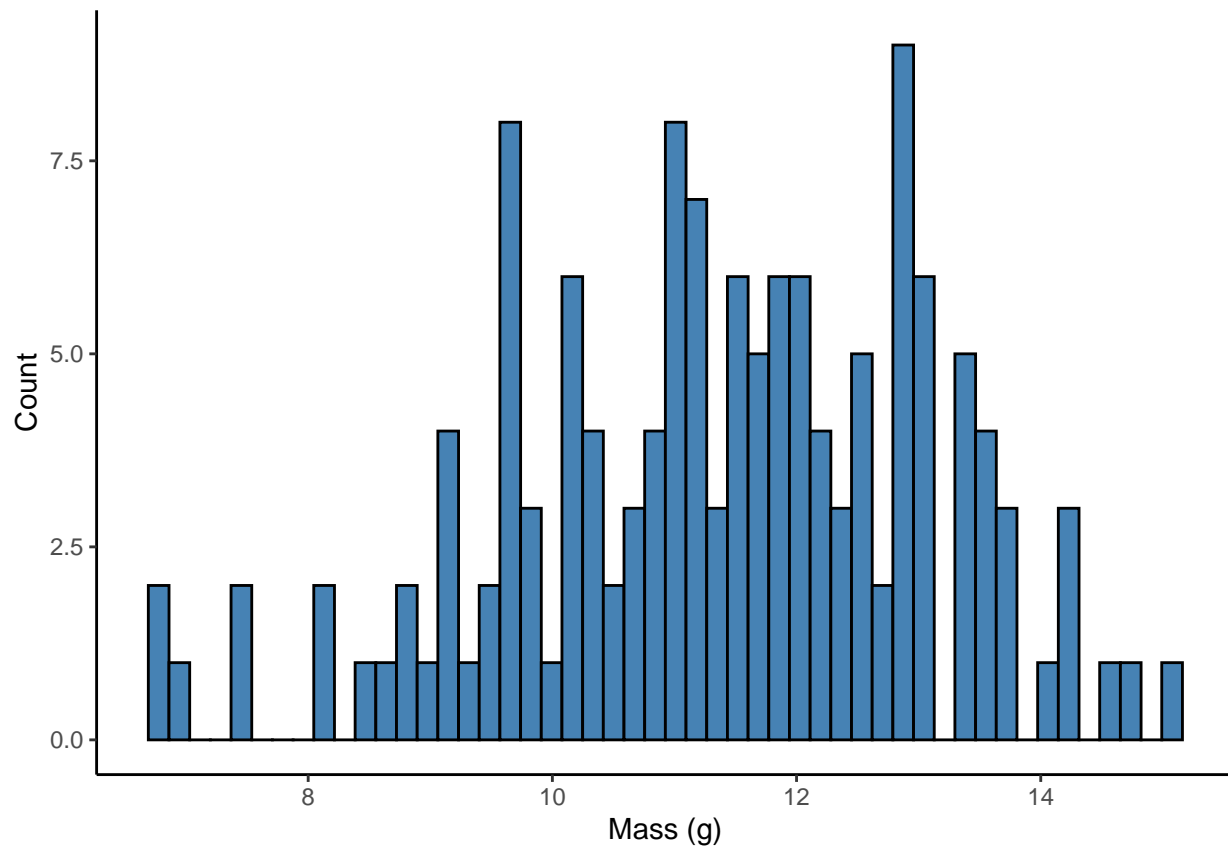
Export Data Frames for Power Analyses

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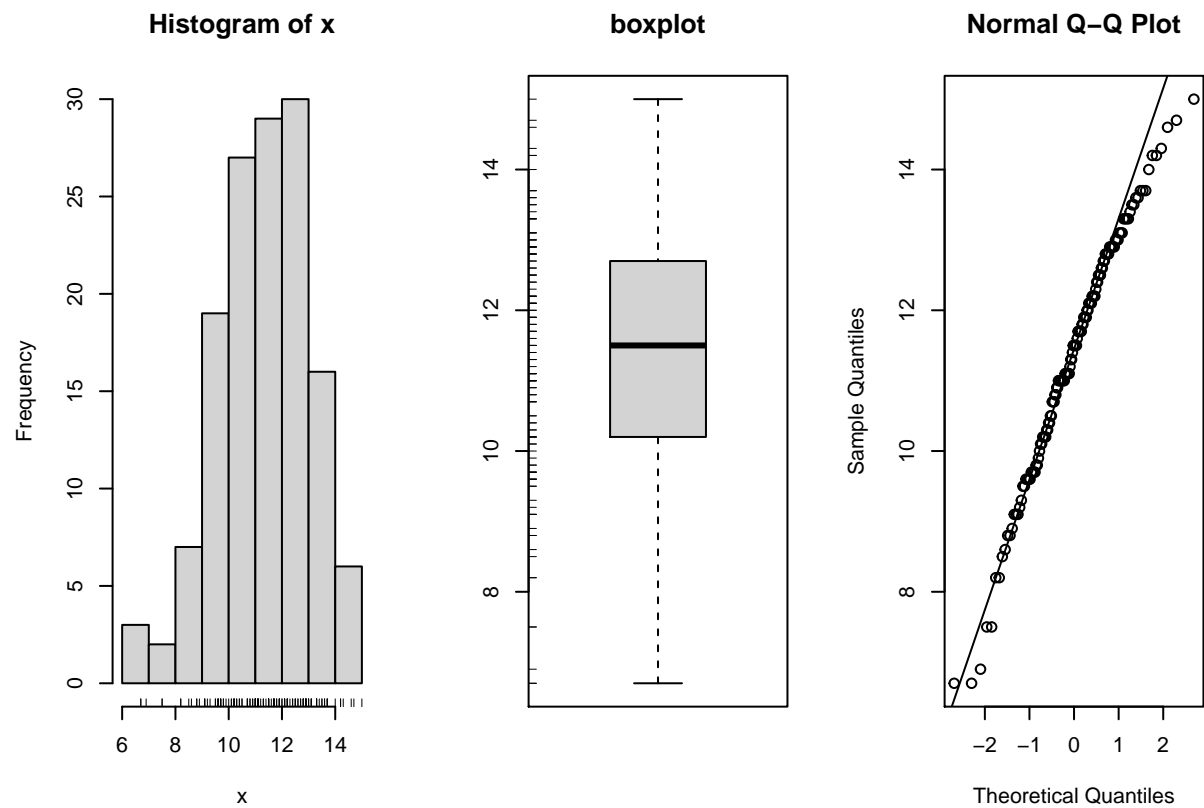
Data Distributions

Mass

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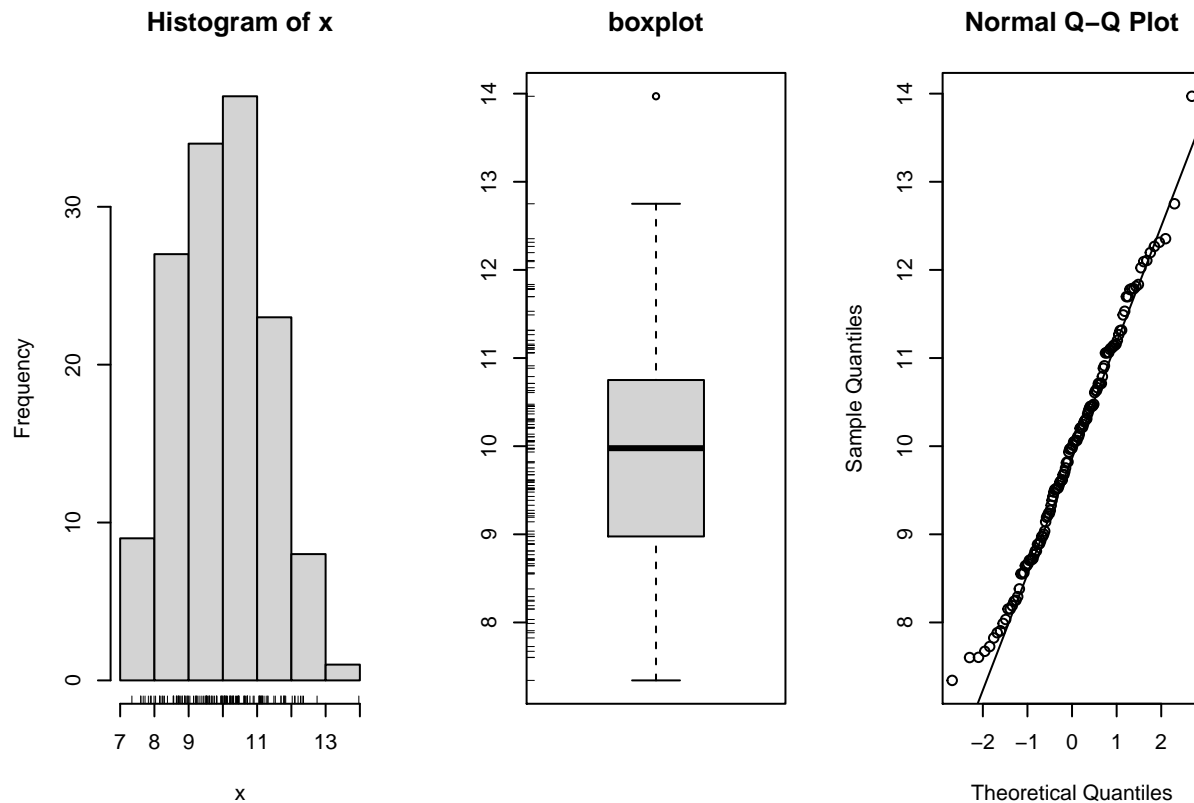
```
shapiro.test(all_dat$mass_g)
```

```
##
##  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")
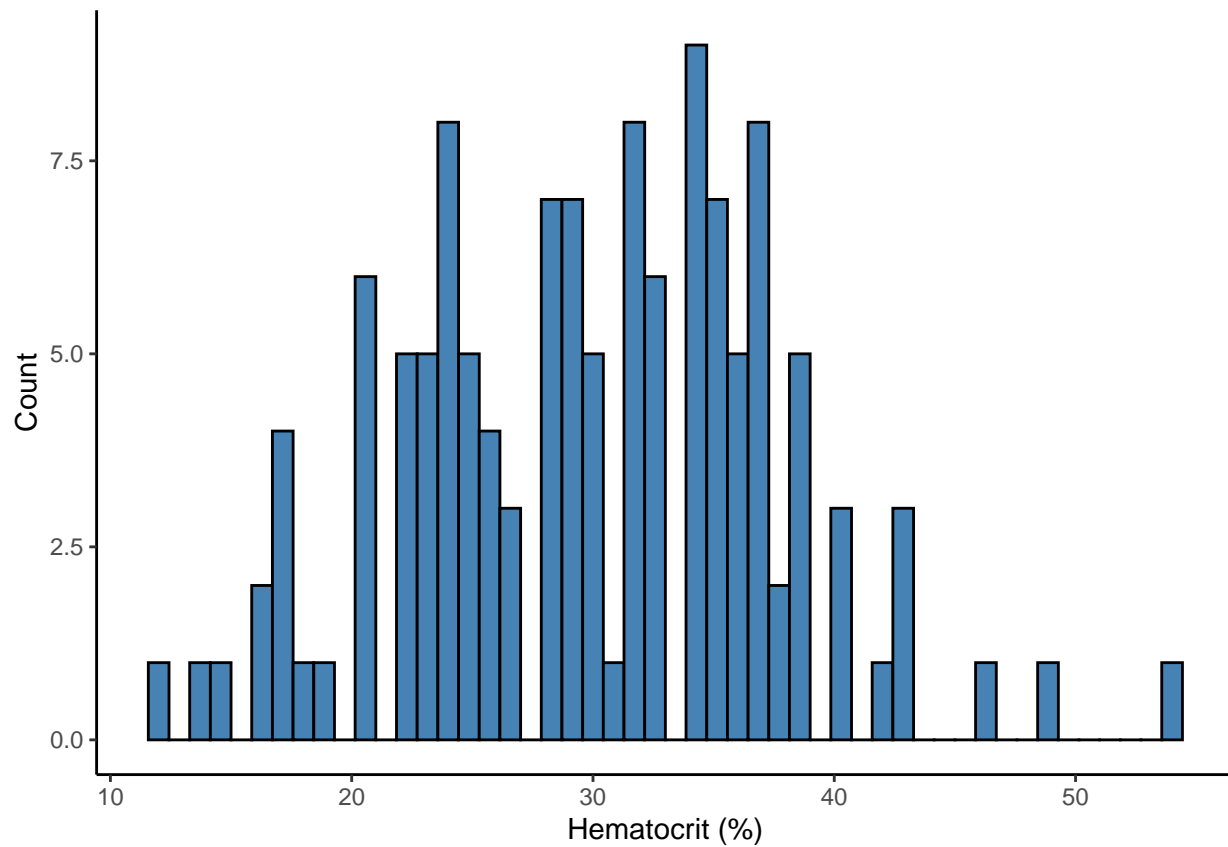```



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

Histogram of x   **boxplot**   **Normal Q–Q Plot**
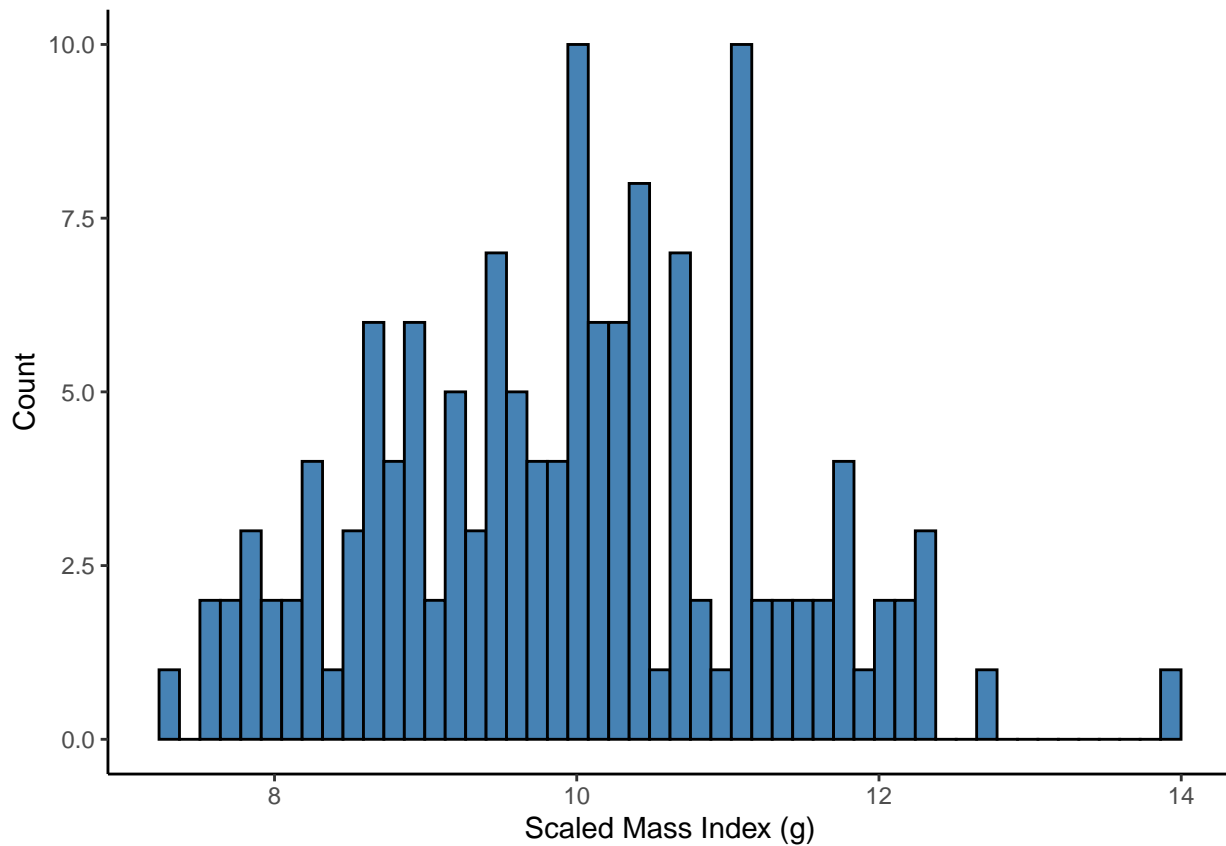
```r
shapiro.test(all_dat$SMI)
```

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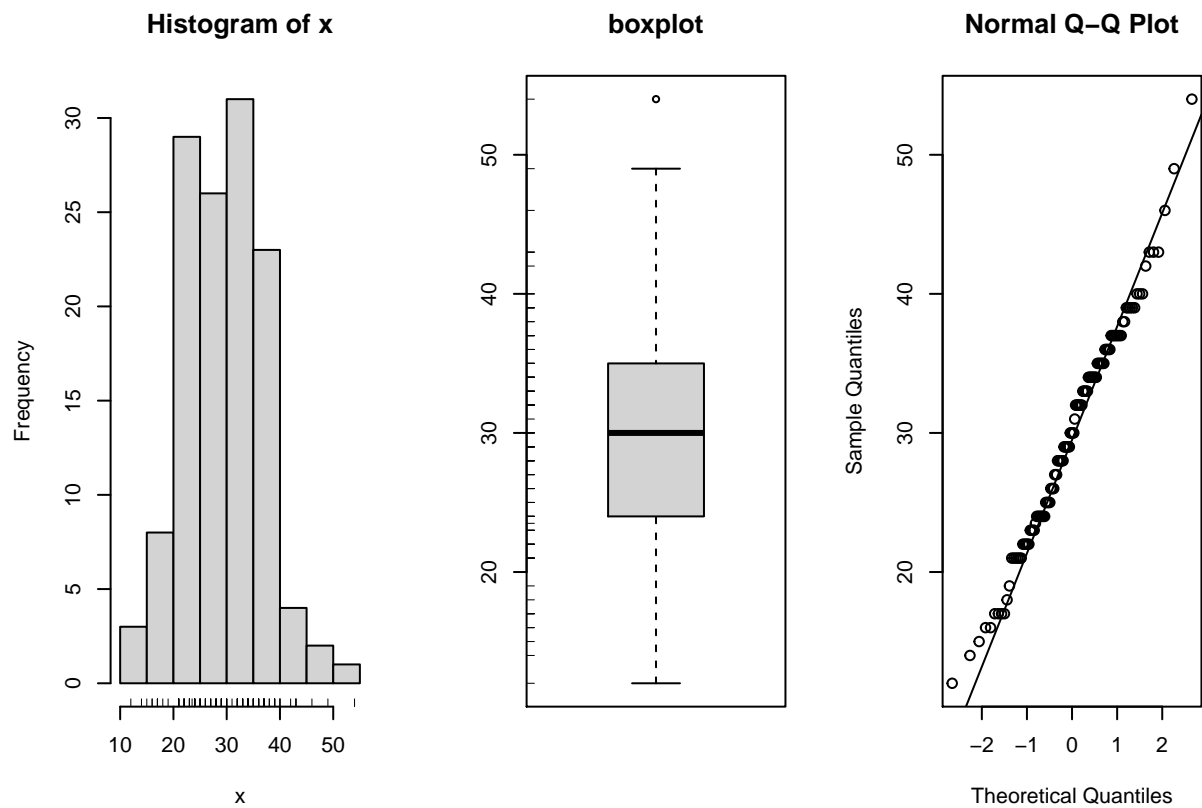
Hematocrit

```r
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)
```


15

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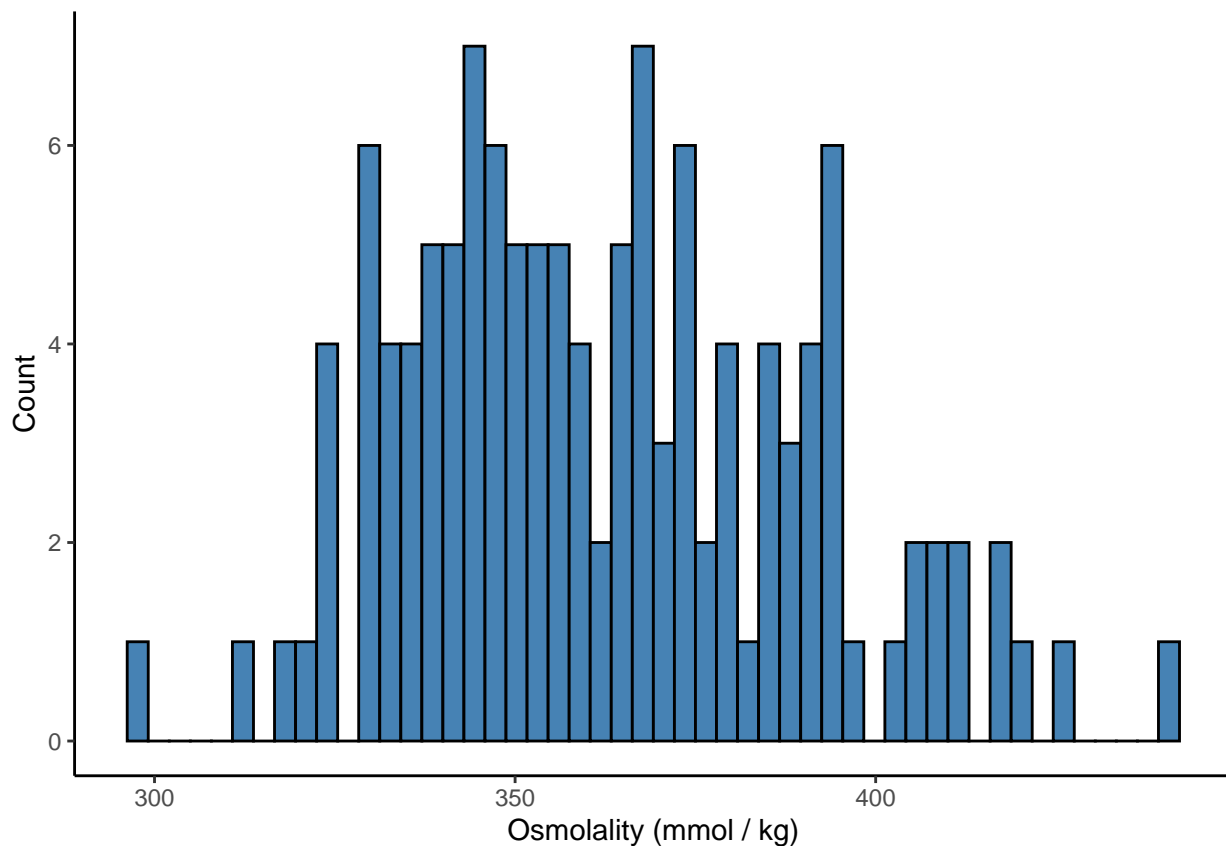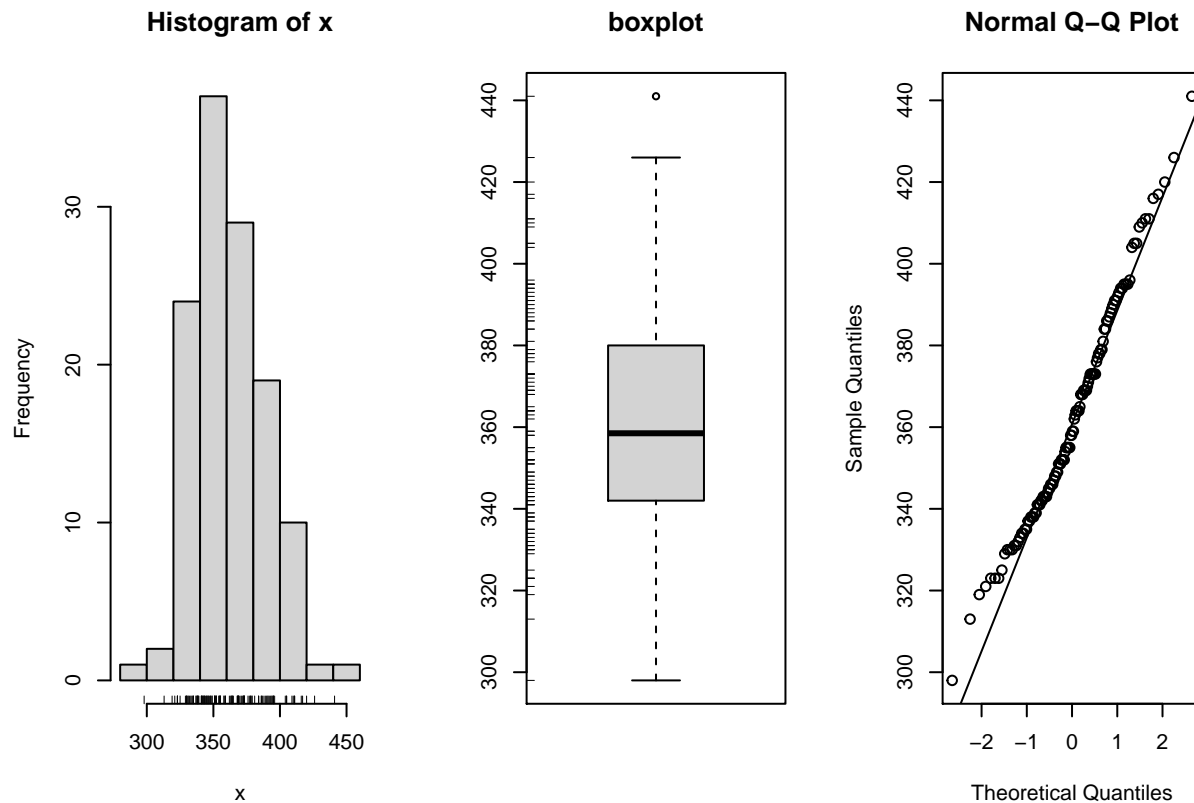
```
##
##  Shapiro-Wilk normality test
##
## data:  all_dat$osmolality_mmol_kg
## W = 0.9801, p-value = 0.06427
```

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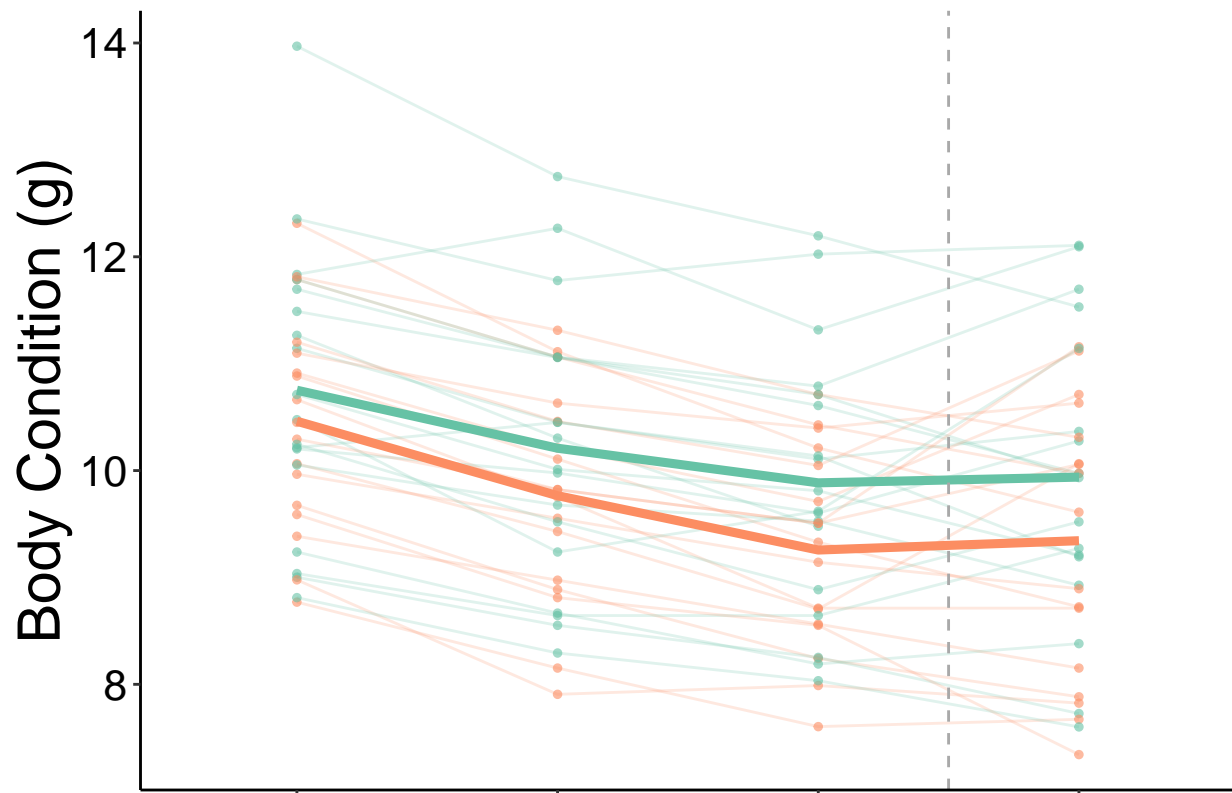
```
# export figure
#ggsave(filename = "tmt_effects_SMI.jpeg",
 #      plot = tmt_effects_SMI,
  #     path = "./final_figures",
   #    device = "jpeg",
    #   dpi = 1200,
     #  width = 5, height = 4)
```

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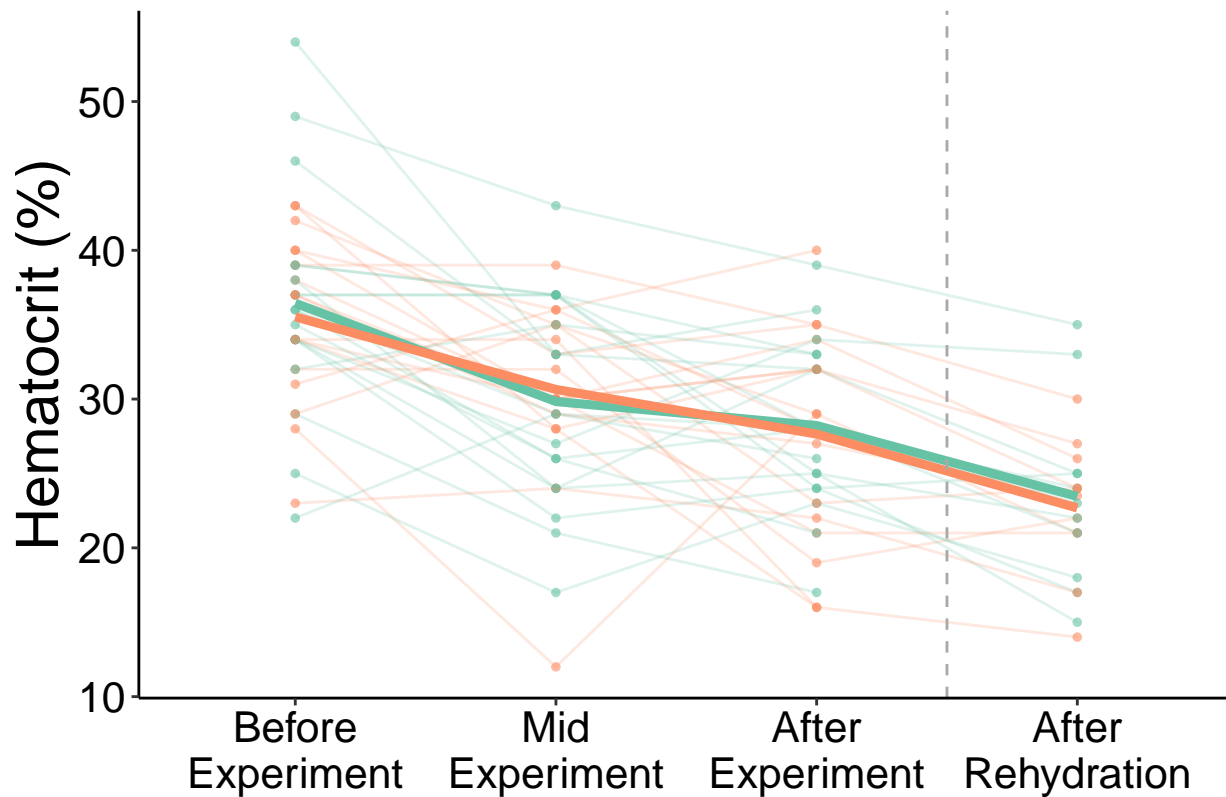
Warning: Removed 12 rows containing missing values (geom_point).

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
```
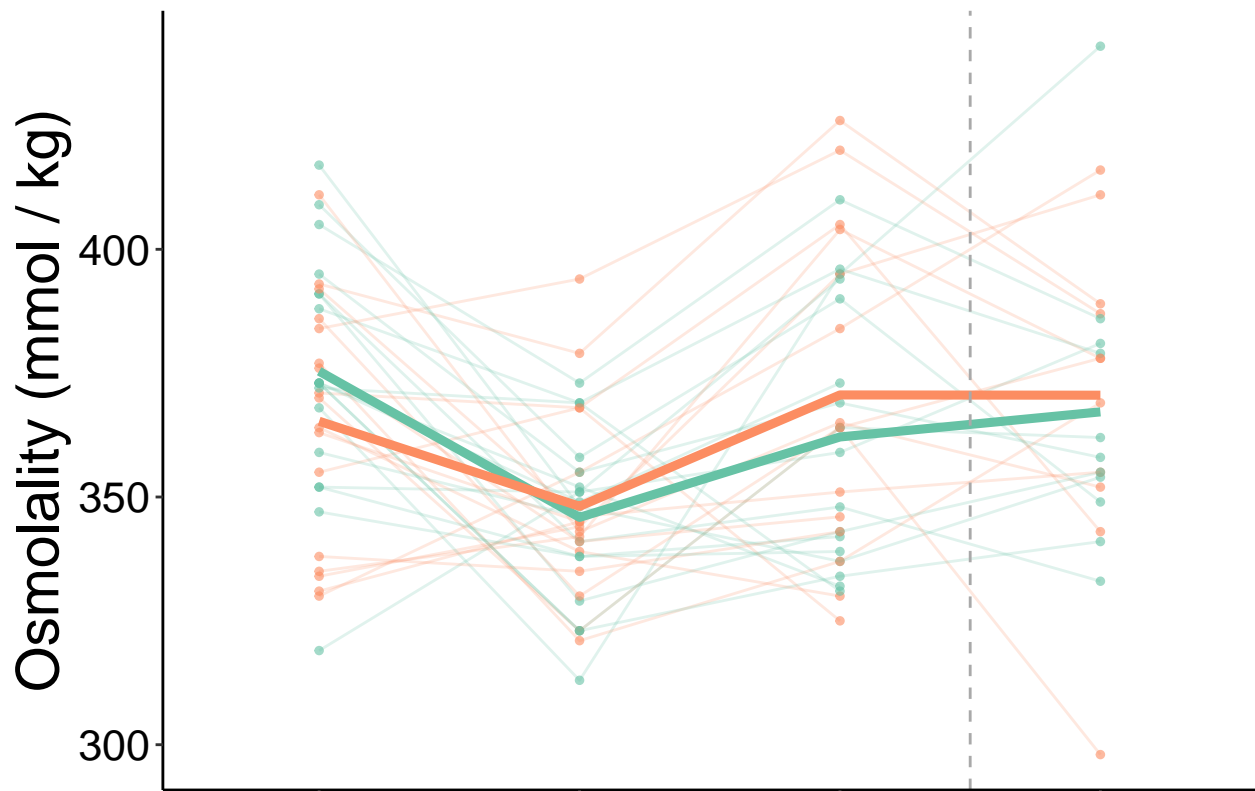
Warning: Removed 15 rows containing missing values (geom_point).

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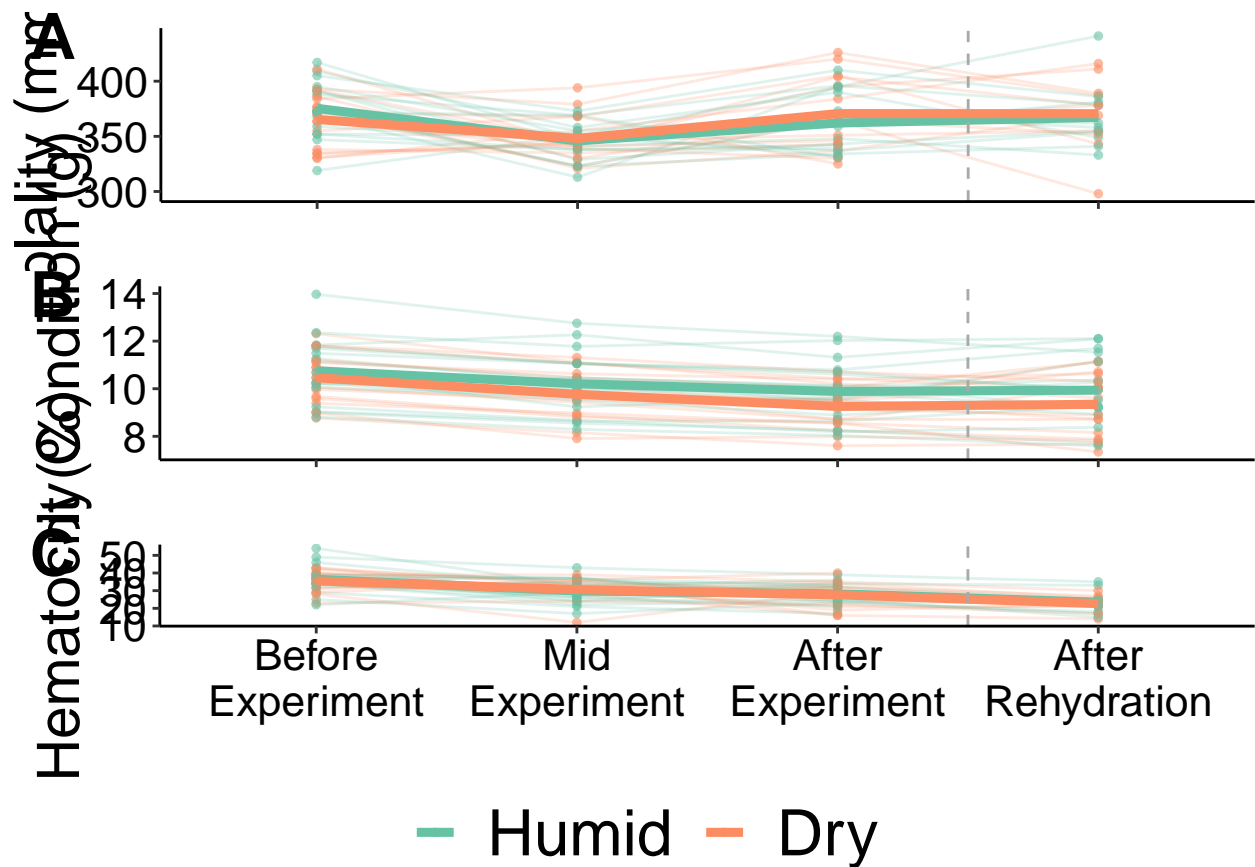
```
# export figure
ggsave(filename = "tmt_multi_fig.jpeg",
       plot = tmt_multi_fig,
       path = "./final_figures",
       device = "jpeg",
       dpi = 1200,
       width = 6, height = 12)
```

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,
```

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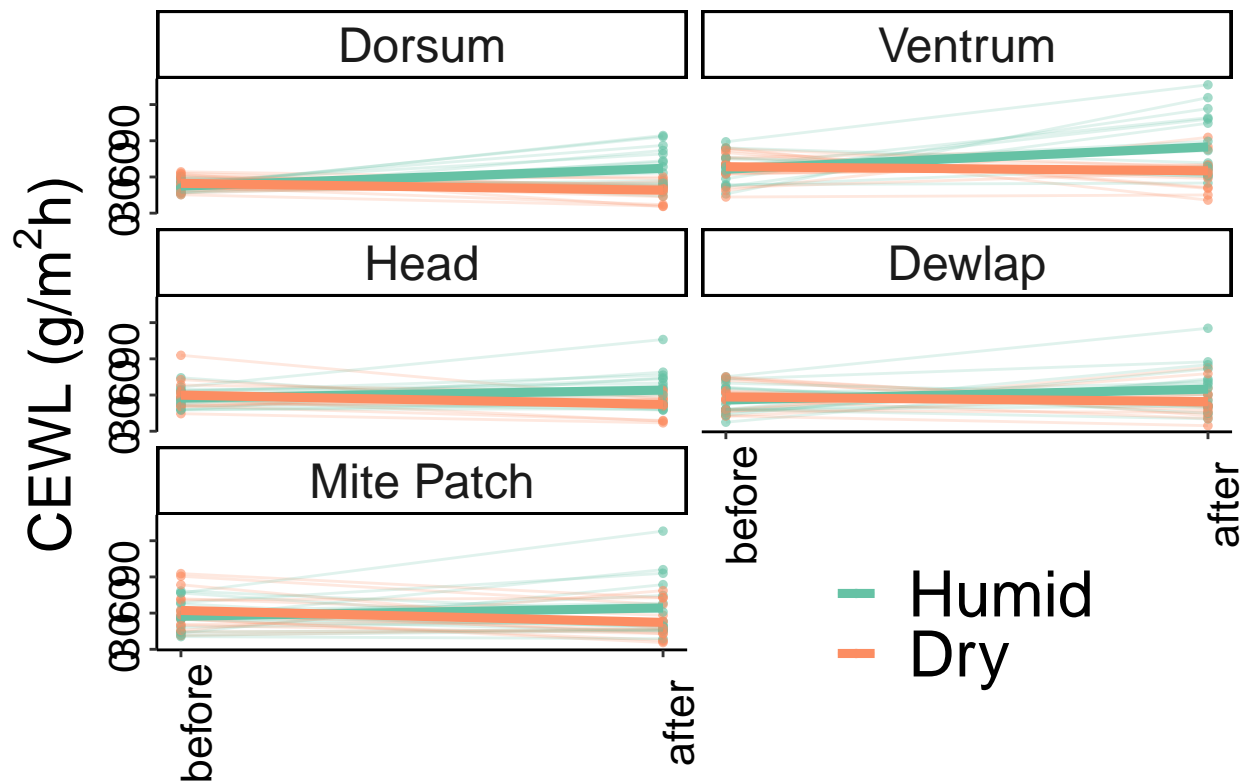
```
# export figure
ggsave(filename = "tmt_effects_CEWL.jpeg",
       plot = CEWL_tmt_fig,
       path = "./final_figures",
       device = "jpeg",
       dpi = 1200,
       width = 6, height = 9)
```

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
```

```r
# 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

```r
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

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

boundary (singular) fit: see ?isSingular

```r
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

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

boundary (singular) fit: see ?isSingular

Selection

```r
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 1.00000000 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)
```
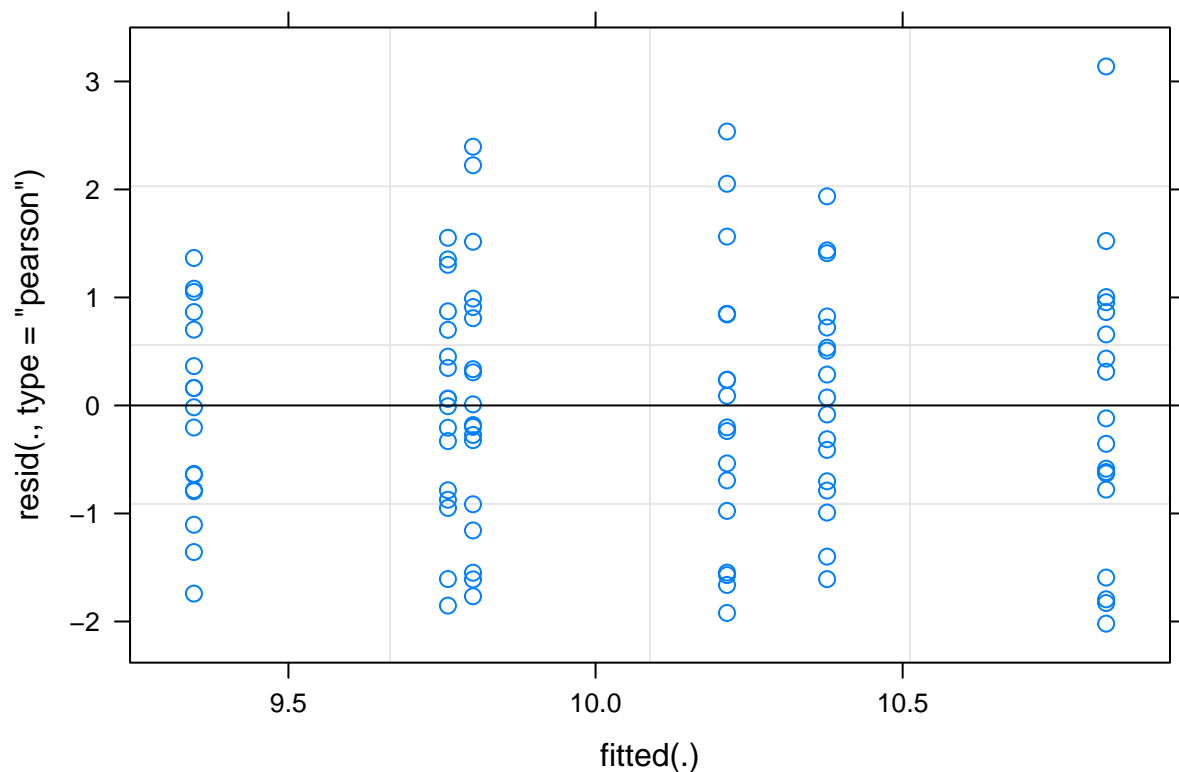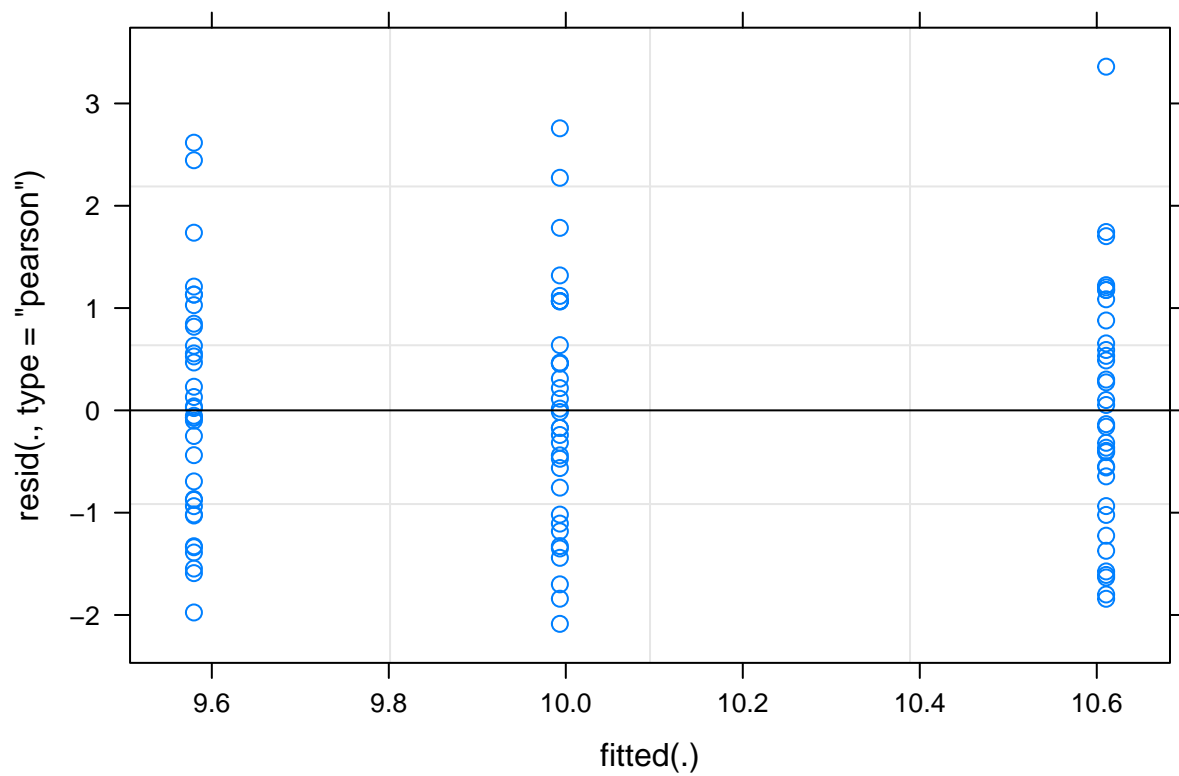


```
plot(SMI_mod3)
```
```

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))
```

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

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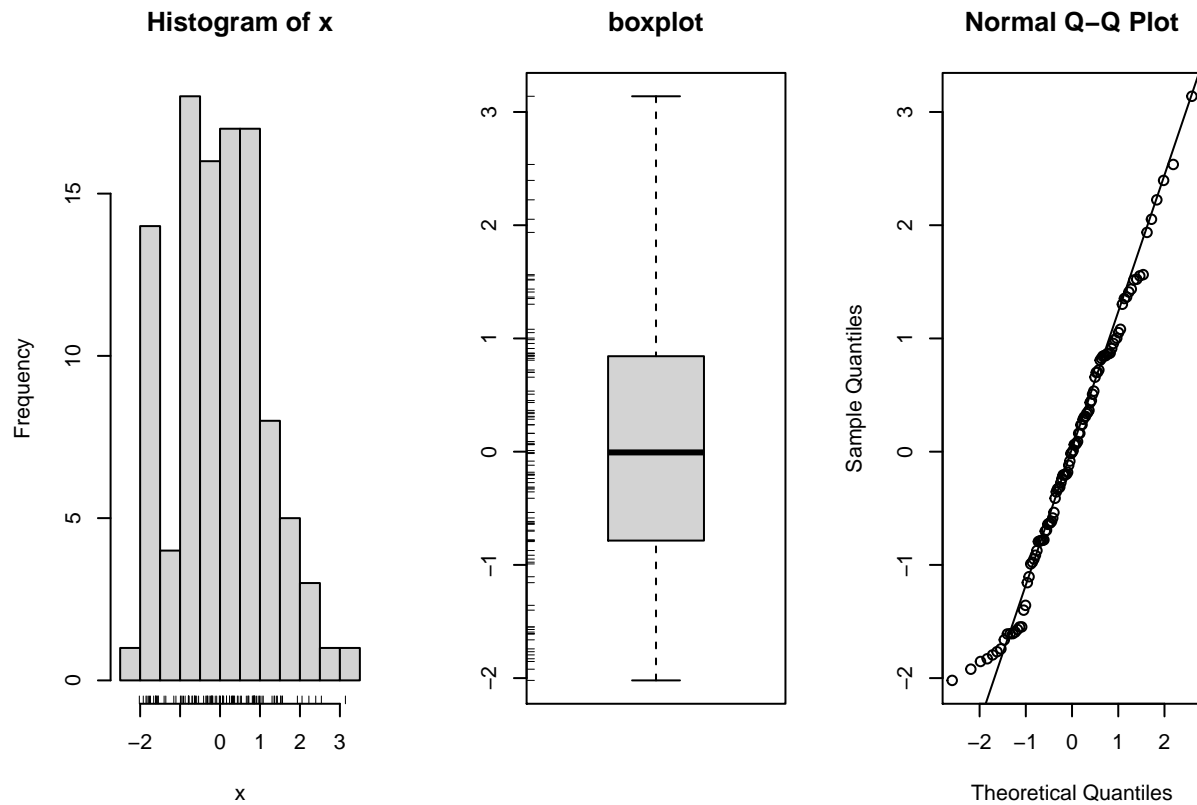
```
##
##  Shapiro-Wilk normality test
##
## data:  residuals(SMI_mod2)
## W = 0.98165, p-value = 0.1551
```

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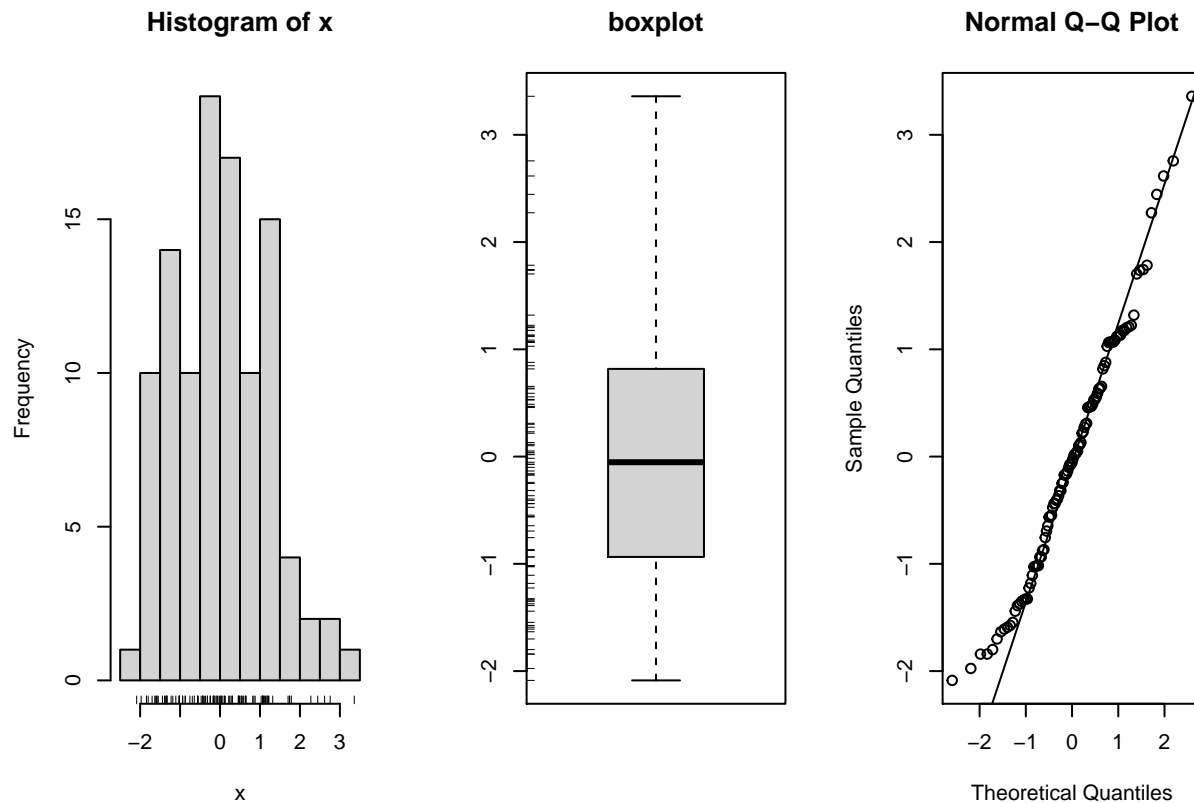
```
shapiro.test(residuals(SMI_mod3))
```

```
##
##  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
## dyAftrExprm -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
```

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

```r
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
```

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

```
                (1|trial_number))
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

```r
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
```

```r
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

```r
plot(hct_mod1)
```
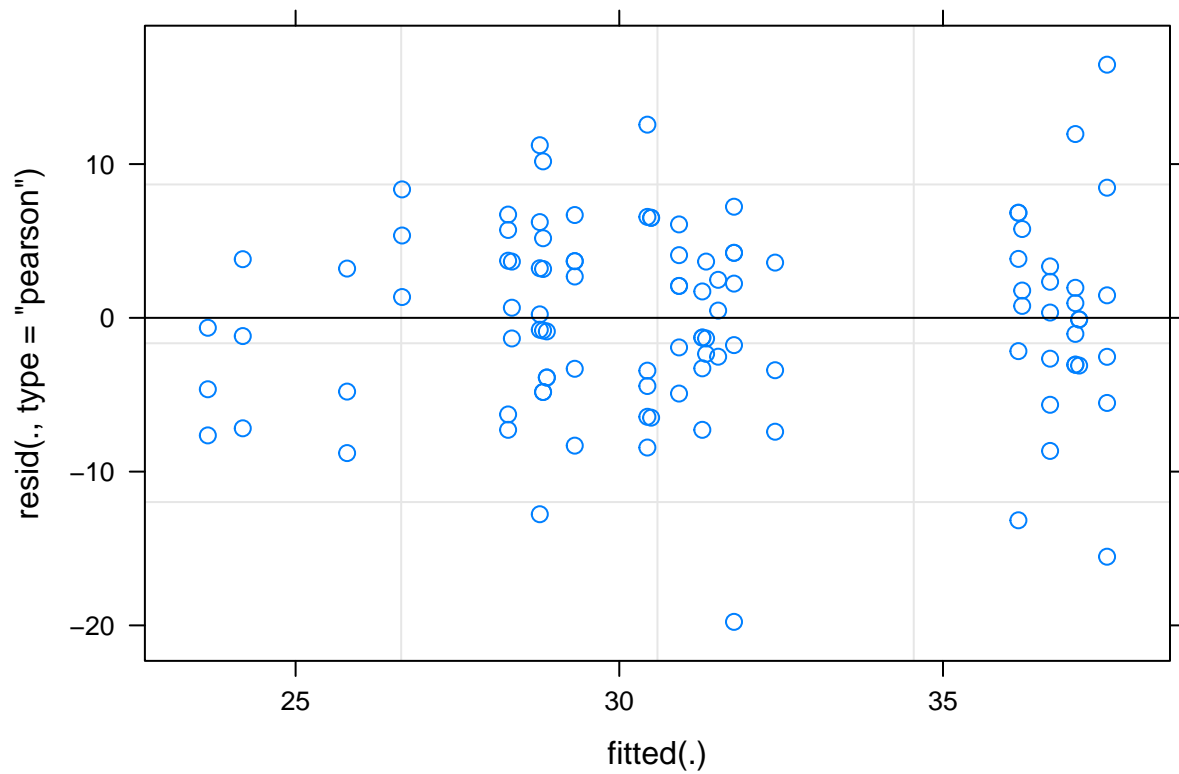
looks okay

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))
```
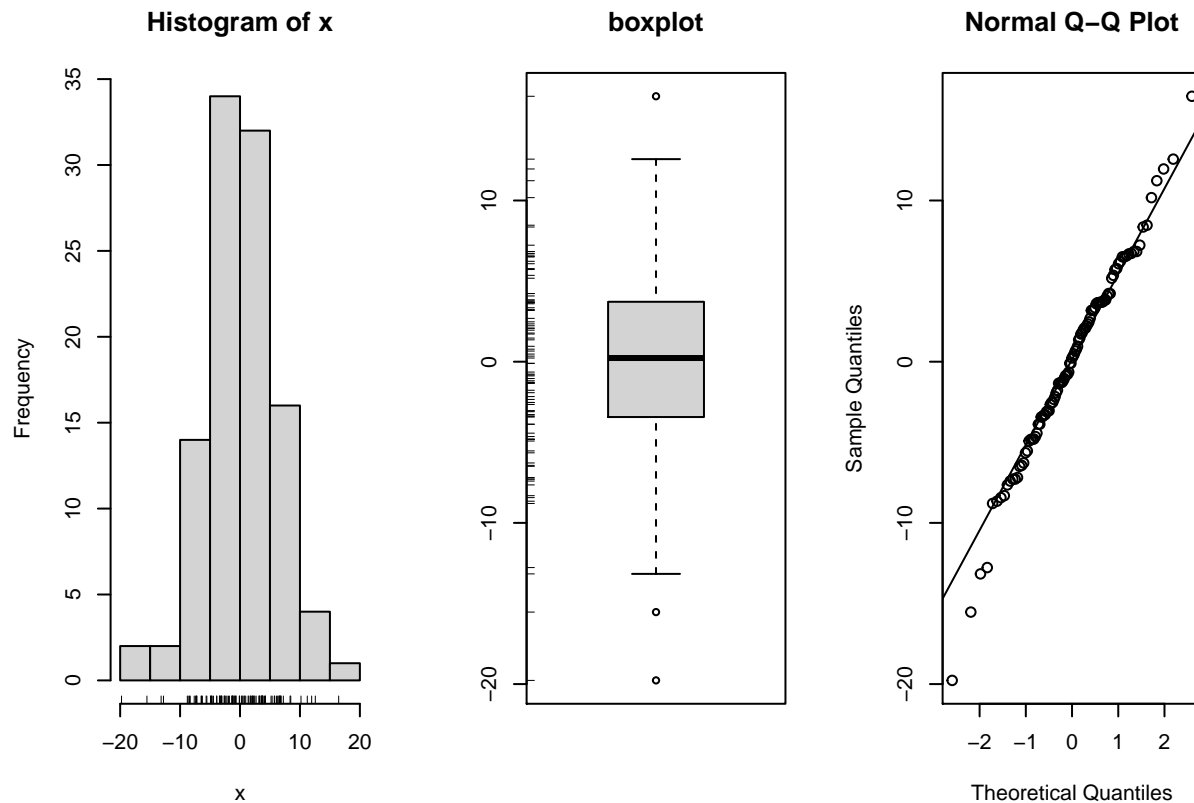
```r
shapiro.test(residuals(hct_mod1))
```

```
##
##  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:

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

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

Export

```r
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

```r
osml_mod1 <- all_dat_no_rehab %>%
  dplyr::filter(complete.cases(osmolality_mmol_kg)) %>%
```

```r
  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
## dyAftrExprm -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
```

```r
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
```

```r
# 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
## dyAftrExprm -0.245  0.488
## hmdty_tmt_D -0.200  0.000  0.013
```

```r
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
```

```r
# drop humidity tmt
osml_mod3 <- all_dat_no_rehab %>%
  dplyr::filter(complete.cases(osmolality_mmol_kg)) %>%
  lme4::lmer(data = .,
             osmolality_mmol_kg ~ day +
             (1|trial_number))
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
## dyAftrExprm -0.246  0.488
```

```r
drop1(osml_mod3)
```

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

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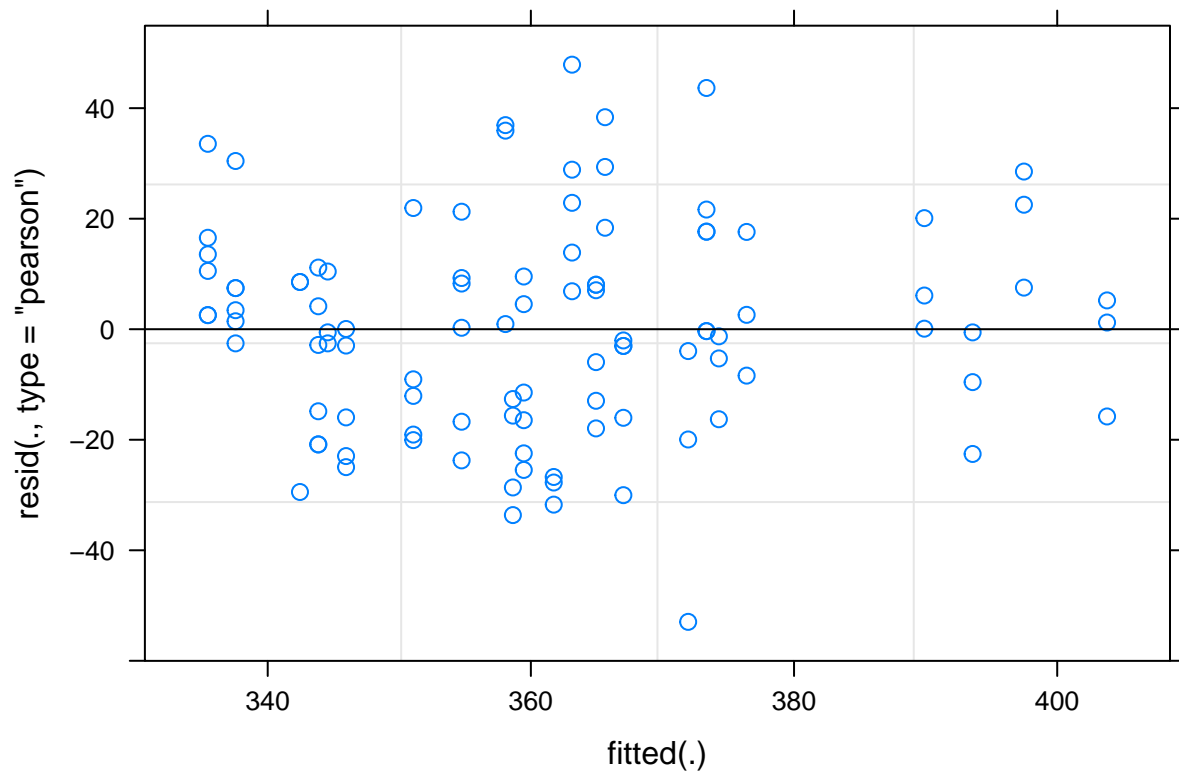
looks pretty good

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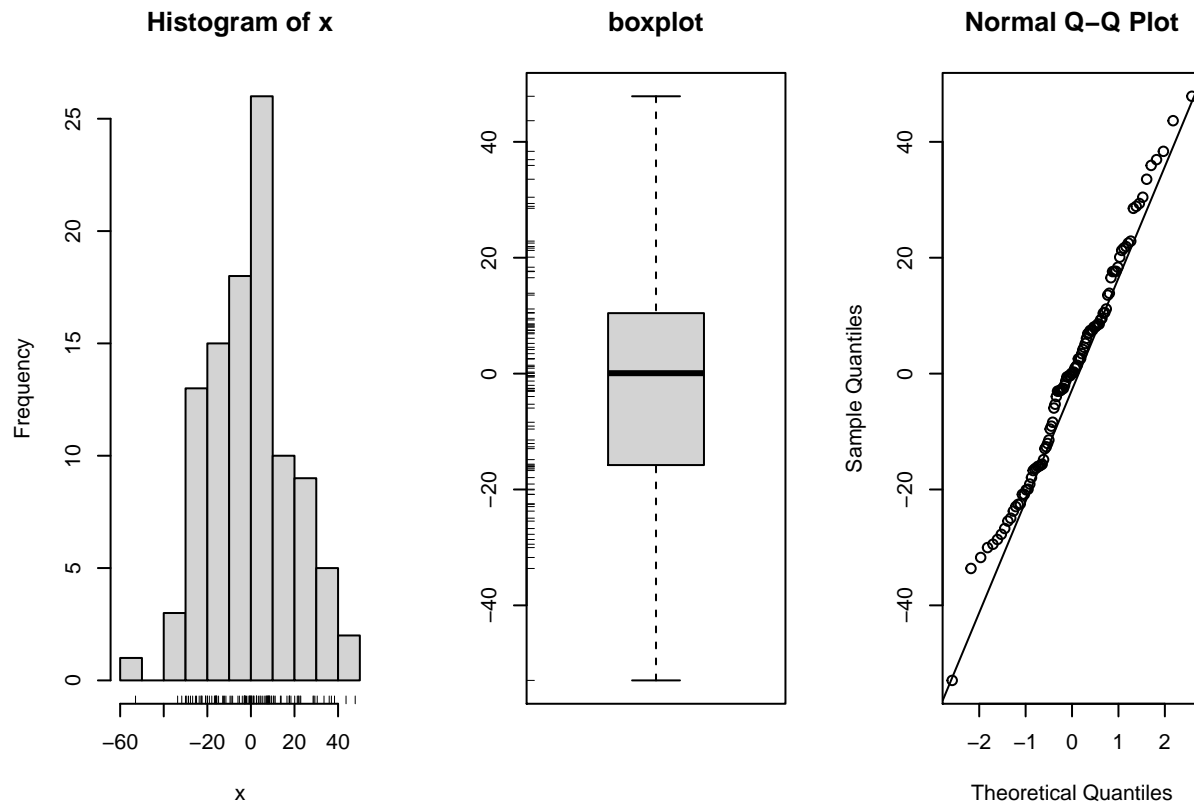
```r
shapiro.test(residuals(osml_mod1))
```

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

residuals are normally distributed!

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

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

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

Export

```r
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

```r
# FULL model
CEWL_mod1 <- lme4::lmer(data = CEWL,
```

```
               TEWL_g_m2h ~ day * humidity_tmt_percent * region +
               cloacal_temp_C +
               (1|trial_number/individual_ID))
summary(CEWL_mod1)
```

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

```
drop1(CEWL_mod1)
```

```
## Single term deletions
```

```
## 
## Model:
## TEWL_g_m2h ~ day * humidity_tmt_percent * region + cloacal_temp_C +
##     (1 | trial_number/individual_ID)
##                                      npar   AIC
## <none>                                     2570.1
## cloacal_temp_C                        1 2628.2
## day:humidity_tmt_percent:region       4 2563.8
```

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

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

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

```r
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
```

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

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

```
## dayAfter:regionVentrum            3.7183    3.8575   0.964
## dayAfter:regionHead              -4.5610    3.8575  -1.182
## dayAfter:regionDewlap            -0.2458    3.8845  -0.063
## dayAfter:regionMite Patch        -5.2131    3.8900  -1.340
##
## Correlation matrix not shown by default, as p = 13 > 12.
## Use print(x, correlation=TRUE)  or
##     vcov(x)        if you need it
```
```r
drop1(CEWL_mod3)
```
```
## Single term deletions
##
## Model:
## TEWL_g_m2h ~ day * (humidity_tmt_percent + region) + cloacal_temp_C +
##     (1 | trial_number/individual_ID)
##                          npar    AIC
## <none>                        2559.0
## cloacal_temp_C            1 2616.1
## day:humidity_tmt_percent  1 2618.8
## day:region                4 2558.4
```
```r
# drop day*region interaction
CEWL_mod4 <- lme4::lmer(data = CEWL,
             TEWL_g_m2h ~ day * humidity_tmt_percent + region +
             cloacal_temp_C +
             (1|trial_number/individual_ID))
summary(CEWL_mod4)
```
```
## Linear mixed model fit by REML ['lmerMod']
## Formula: TEWL_g_m2h ~ day * humidity_tmt_percent + region + cloacal_temp_C +
##     (1 | trial_number/individual_ID)
##    Data: CEWL
##
## REML criterion at convergence: 2510.2
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.3478 -0.6058 -0.1117  0.4446  3.9319
##
## Random effects:
##  Groups                     Name         Variance Std.Dev.
##  individual_ID:trial_number (Intercept)  38.023   6.166
##  trial_number               (Intercept)   8.872   2.979
##  Residual                                123.111  11.096
## Number of obs: 326, groups:  individual_ID:trial_number, 33; trial_number, 4
##
## Fixed effects:
##                            Estimate Std. Error t value
## (Intercept)                -69.3758    11.8197  -5.869
## dayAfter                    18.2632     1.9251   9.487
## humidity_tmt_percentDry      0.7605     2.7927   0.272
## regionVentrum               15.7651     1.9396   8.128
## regionHead                   2.9138     1.9396   1.502
## regionDewlap                 3.0977     1.9483   1.590
```
```
                                    48
```

```
## 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
```

```r
drop1(CEWL_mod7)
```

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

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

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

```
## 
## Correlation of Fixed Effects:
##            (Intr) rgnVnt regnHd rgnDwl
## regionVntrm -0.278
## regionHead  -0.278  0.504
## regionDewlp -0.277  0.502  0.502
## reginMtPtch -0.276  0.500  0.500  0.498
```

```
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
```

```
##                                                                    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 homoskedactic relative to y_hat (or x). Plotting residuals shows us whether the data meets linearity and equal variance assumptions:

```
plot(CEWL_mod1)
```
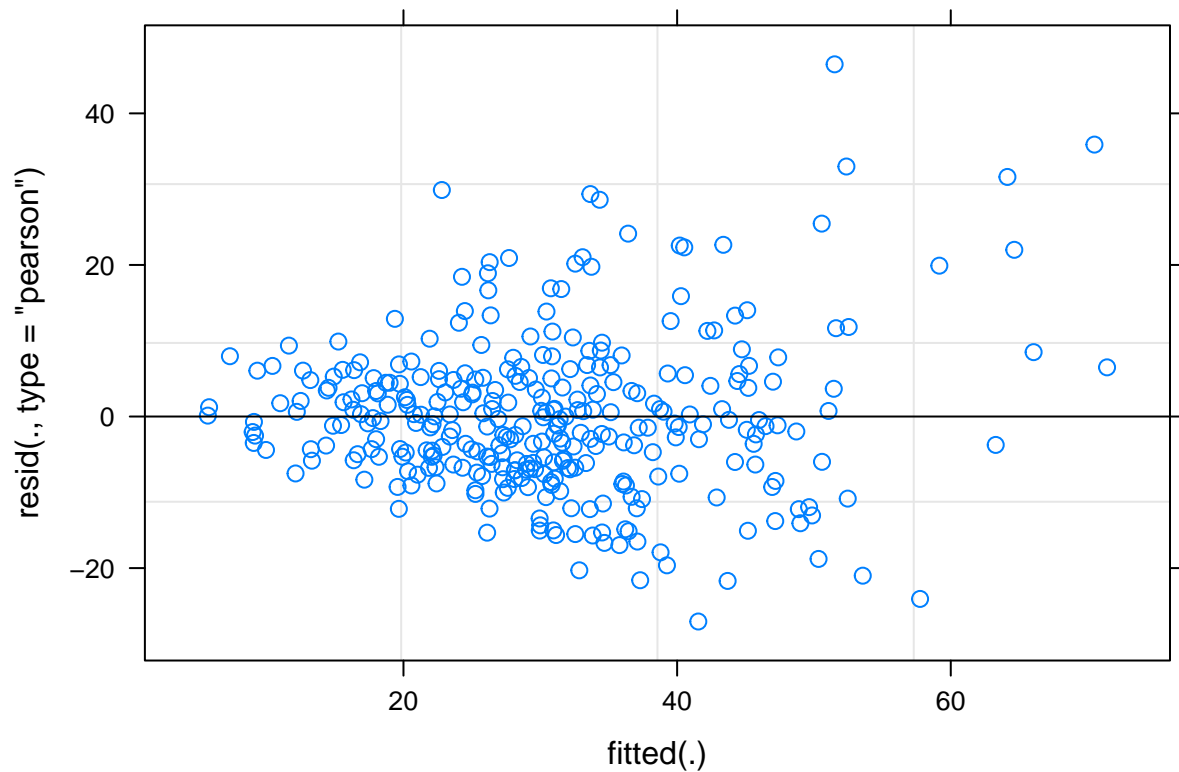

clear fanning shape... L & E are not satisfied.

Transform CEWL

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

```
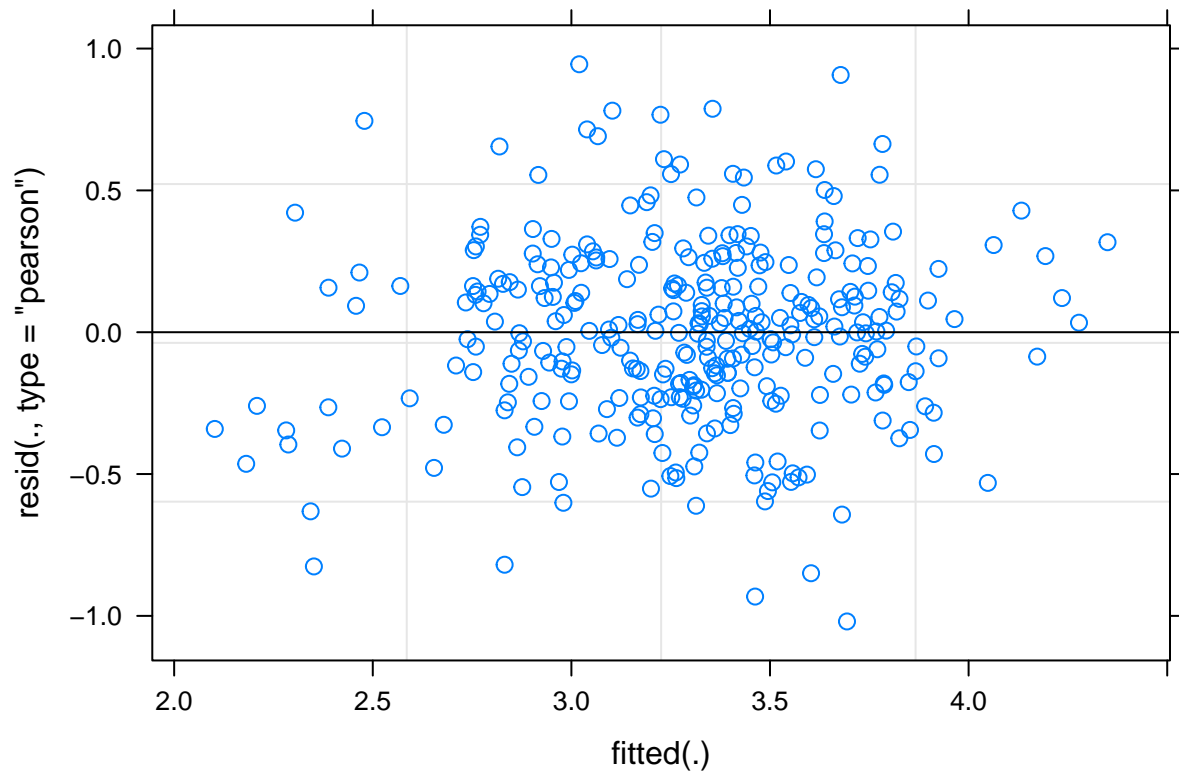CEWL_mod1t <- lme4::lmer(data = CEWL,
              log(TEWL_g_m2h) ~ day * humidity_tmt_percent * region +
```

```
            cloacal_temp_C +
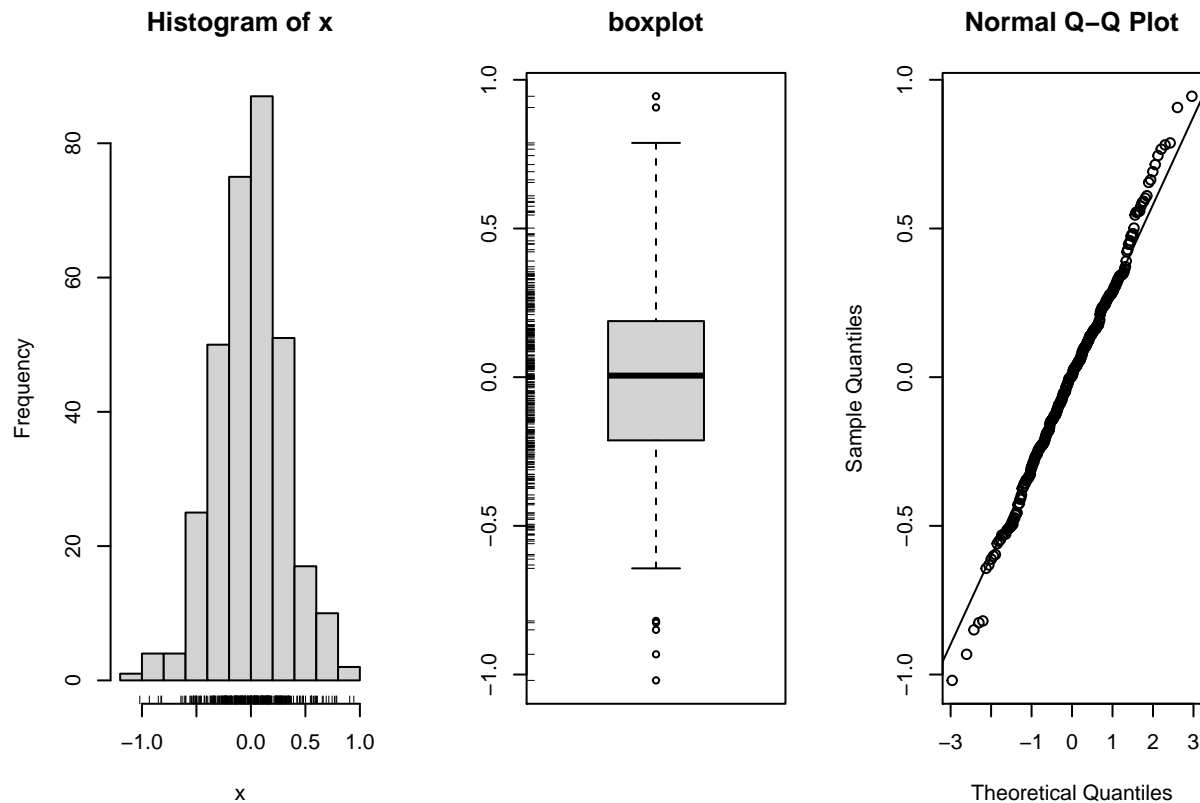            (1|trial_number/individual_ID))
plot(CEWL_mod1t)
```



```
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
## regionVentrum                                       0.45536    0.11771
## regionHead                                          0.19454    0.11771
## regionDewlap                                        0.02448    0.11968
## regionMite Patch                                    0.10936    0.11771
## cloacal_temp_C                                      0.13669    0.01501
## dayAfter:humidity_tmt_percentDry                   -0.82882    0.17069
## dayAfter:regionVentrum                             -0.02994    0.16787
## dayAfter:regionHead                                -0.22825    0.16787
## dayAfter:regionDewlap                              -0.05098    0.16879
## dayAfter:regionMite Patch                          -0.24118    0.16930
## humidity_tmt_percentDry:regionVentrum              -0.05006    0.16904
## humidity_tmt_percentDry:regionHead                 -0.03247    0.16904
## humidity_tmt_percentDry:regionDewlap                0.05969    0.17042
## humidity_tmt_percentDry:regionMite Patch            0.06529    0.17063
## dayAfter:humidity_tmt_percentDry:regionVentrum      0.26103    0.24004
## dayAfter:humidity_tmt_percentDry:regionHead         0.24592    0.24004
## dayAfter:humidity_tmt_percentDry:regionDewlap       0.21627    0.24178
## dayAfter:humidity_tmt_percentDry:regionMite Patch   0.14559    0.24220
##                                                           df t value Pr(>|t|)
## (Intercept)                                        173.23775  -0.467 0.640762
## dayAfter                                           279.57165   5.121 5.66e-07
## humidity_tmt_percentDry                            211.50009   0.189 0.850623
## regionVentrum                                      273.43987   3.869 0.000137
## regionHead                                         273.43987   1.653 0.099524
## regionDewlap                                       273.94809   0.205 0.838091
## regionMite Patch                                   273.43987   0.929 0.353650
## cloacal_temp_C                                     265.46375   9.107  < 2e-16
## dayAfter:humidity_tmt_percentDry                   274.19820  -4.856 2.02e-06
## dayAfter:regionVentrum                             273.68460  -0.178 0.858566
## dayAfter:regionHead                                273.68460  -1.360 0.175037
## dayAfter:regionDewlap                              275.46822  -0.302 0.762859
## dayAfter:regionMite Patch                          273.95495  -1.425 0.155428
## humidity_tmt_percentDry:regionVentrum              273.43987  -0.296 0.767347
## humidity_tmt_percentDry:regionHead                 273.43987  -0.192 0.847838
## humidity_tmt_percentDry:regionDewlap               273.69087   0.350 0.726414
## humidity_tmt_percentDry:regionMite Patch           273.72770   0.383 0.702305
## dayAfter:humidity_tmt_percentDry:regionVentrum     273.55964   1.087 0.277812
## dayAfter:humidity_tmt_percentDry:regionHead        273.55964   1.024 0.306507
## dayAfter:humidity_tmt_percentDry:regionDewlap      274.65325   0.895 0.371833
## dayAfter:humidity_tmt_percentDry:regionMite Patch  273.87346   0.601 0.548266
## 
```

```
## (Intercept)
## dayAfter                                              ***
## humidity_tmt_percentDry
## regionVentrum                                         ***
## regionHead                                            .
## regionDewlap
## regionMite Patch
## cloacal_temp_C                                        ***
## dayAfter:humidity_tmt_percentDry                      ***
## dayAfter:regionVentrum
## dayAfter:regionHead
## dayAfter:regionDewlap
## dayAfter:regionMite Patch
## humidity_tmt_percentDry:regionVentrum
## humidity_tmt_percentDry:regionHead
## humidity_tmt_percentDry:regionDewlap
## humidity_tmt_percentDry:regionMite Patch
## dayAfter:humidity_tmt_percentDry:regionVentrum
## dayAfter:humidity_tmt_percentDry:regionHead
## dayAfter:humidity_tmt_percentDry:regionDewlap
## dayAfter:humidity_tmt_percentDry:regionMite Patch
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation matrix not shown by default, as p = 21 > 12.
## Use print(x, correlation=TRUE)  or
##     vcov(x)        if you need it
```

Export

```
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")
```