Fit Thermal Models

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Goal

- Fit series of thermal models found in `rTPC` to data collected in the Derryberry lab.
- Intial analysis should be with GLM and mixture models.

Set up

Install libraries

```
## install packages user might not have by replacing FALSE with TRUE
if(FALSE) {
    BiocManager::install("mixOmics") ## needed by RVAideMemoire
    install.packages(c("RSQLite", "nls.multstart", "lme4", "RVAideMemoire"))
    ##  Install the thermal curve package from git_hub, not cran
    remotes::install_github("padpadpadpad/rTPC")

}

## load libraries
library(stats)
require(MASS) # provides negative binomial fitting:  glm.nb
```

```
## Loading required package: MASS
```

```
library(RSQLite)  # Don't think we need this.
library(rTPC)  ##
library(nls.multstart)
library(broom)
library(tidyverse)
```

```
## -- Attaching packages
## ------------------------------------------------------------------ tidyverse
## 1.3.2 --
```

```
## v ggplot2 3.3.6           v purrr   0.3.4
## v tibble  3.1.8           v dplyr   1.0.99.9000
## v tidyr   1.2.0.9000      v stringr 1.4.1
## v readr   2.1.2           v forcats 0.5.2
## -- Conflicts --------------------------------------------------------------------- tidyverse_conflic
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
## x dplyr::select() masks MASS::select()
```

```
require(ggplot2)
require(ggpubr)
```

```
## Loading required package: ggpubr
```

```
require(viridisLite)
```

```
## Loading required package: viridisLite
```

```
#options(ggplot2.continuous.colour="viridis",
#         ggplot2.discrete.colour="viridis",
#         ggplot2.scale_fill_discrete = scale_fill_viridis_d,
#         ggplot2.scale_fill_continuous = scale_fill_viridis_c)

require(GGally)
```

```
## Loading required package: GGally
## Registered S3 method overwritten by 'GGally':
##   method from
##   +.gg   ggplot2
```

```
require(reshape2)
```

```
## Loading required package: reshape2
##
## Attaching package: 'reshape2'
##
## The following object is masked from 'package:tidyr':
##
##     smiths
```

```
require(lme4)
```

```
## Loading required package: lme4
## Loading required package: Matrix
##
## Attaching package: 'Matrix'
##
## The following objects are masked from 'package:tidyr':
##
##     expand, pack, unpack
```

```
require(RVAideMemoire) # provides overdisp.glmer()
```

```
## Loading required package: RVAideMemoire
## *** Package RVAideMemoire v 0.9-81-2 ***
##
## Attaching package: 'RVAideMemoire'
##
## The following object is masked from 'package:lme4':
##
##     dummy
##
## The following object is masked from 'package:broom':
##
##     bootstrap
```

Load Data

```
## Read in ZEFI Data sets
## Treat 'repeatability' as round = 0
## Add round info

## Repeatability was done between round 1 and 2, female was present, but only one temp. so treating as

git_root <- system("git rev-parse --show-toplevel", intern = TRUE)

data_raw = list()

data_raw[[1]] <- read.csv(file.path(git_root, "data", "raw_data", "HSPi-Round-1-Heat-Trials.csv")) %>%
    ## Note T237 and T230 are missing numbers in the song_count column
    ## so we are filtering these observations out until they are found
    filter(!is.na(song_count))

data_raw[[2]] <- read.csv(file.path(git_root, "data", "raw_data", "HSPi-Repeatability-Song-Count.csv"))
    mutate(round = 2) %>%
    group_by(male) %>%
    mutate(test_order = rank(date)) %>%
    ungroup()

data_raw[[3]] <-read.csv(file.path(git_root, "data", "raw_data", "HSPi-Round-2-Heat-Trials.csv")) %>%
    mutate(round = 3) #%>%
#    group_by(male) %>% mutate(total_count_round_3 = sum(song_count) )

## Join data and discard empty columns
data_full <- full_join(data_raw[[1]], data_raw[[2]]) %>%
    full_join(data_raw[[3]]) %>%
    discard(~all(is.na(.) | . =="")) %>% ## get rid of columns of only NA
    mutate(trial_completed = !(is.na(song_count)) ) %>%
    mutate(song_count = ifelse(is.na(song_count), 0, song_count)) %>%
    mutate(song_count = song_count*1.0) %>% ## convert to a double so it's not treated as an integer
    mutate(chamber = as.factor(chamber), male = as.factor(male)) %>%
    ## create a global variable trial_order based on individual rounds
    mutate(trial_index = as.integer(round*10+test_order)) %>%
    mutate(song_count_plus_1 = (song_count + 1)) %>%
    mutate(log_song_count_plus_1 = log(song_count + 1)) %>%
    mutate(temp_target = as.numeric(temp_target)) %>%
    ## Add column with total song_count for a given round
    group_by(male, round ) %>% mutate(count_total_round = sum(song_count) ) %>%
    ungroup() %>%
    mutate() ## Dummy function so we can comment out lines above it w/o any issues
```

```
## Joining, by = c("male", "chamber", "date", "song_count", "counter", "test_order", "temp_target", "rou
## Joining, by = c("male", "chamber", "date", "song_count", "counter", "test_order", "temp_target", "rou
```

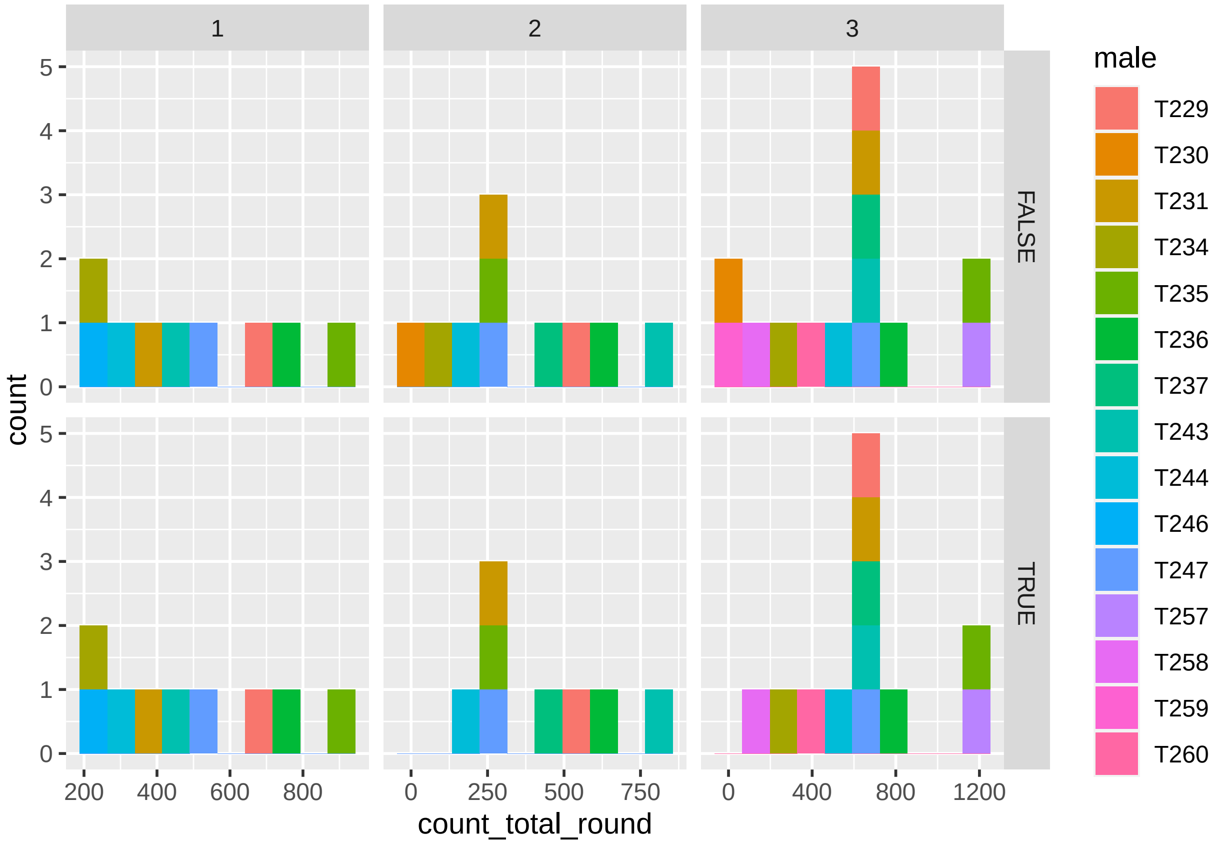
Second Analysis for Liz

Examine Data

```
data_count_total <- data_full %>% group_by(round) %>%
    select(male, round, count_total_round)  %>%
    distinct() %>% mutate(filtered = FALSE)

data_count_total_filter <- data_count_total %>%
    filter(count_total_round > 150) %>%
    mutate(filtered = TRUE)


data_tmp <- full_join(data_count_total, data_count_total_filter)
```

```
## Joining, by = c("male", "round", "count_total_round", "filtered")
```

```
t <- ggplot(data_tmp, aes(count_total_round, fill = male)) +
    geom_histogram(bins = 10) #+
#    scale_x_log10()
hist_count_total <- t +
    facet_grid(cols =vars(round), rows = vars(filtered), scales = "free_x")
hist_count_total
```



```
data <- data_full #%>% filter(round ==3)

data %>% group_by(temp_target) %>%
    summarize(ave = mean(song_count), sd = sd(song_count), n = length(song_count), n_completed = sum(tr
```

```
## # A tibble: 5 x 5
##   temp_target   ave    sd     n n_completed
##         <dbl> <dbl> <dbl> <int>       <int>
## 1          27 124.  105.     24          24
## 2          35 103.   82.4    23          23
## 3          40 112.   84.6    53          53
## 4          42 112.   96.1    23          23
## 5          44  78.2  78.5    23          22
```

```
## Look at occurrance of males across rounds
tmp1 <- data_full %>%
    filter(round==1) %>%
    pull(male) %>%
    unique(); tmp1
```

```
## [1] T236 T243 T246 T247 T234 T231 T244 T235 T229
## 15 Levels: T229 T230 T231 T234 T235 T236 T237 T243 T244 T246 T247 T257 ... T260
```

```r
tmp2 <- data_full %>%
    filter(round %in% c(2,3)) %>%
    pull(male) %>%
    unique() ; tmp2
```

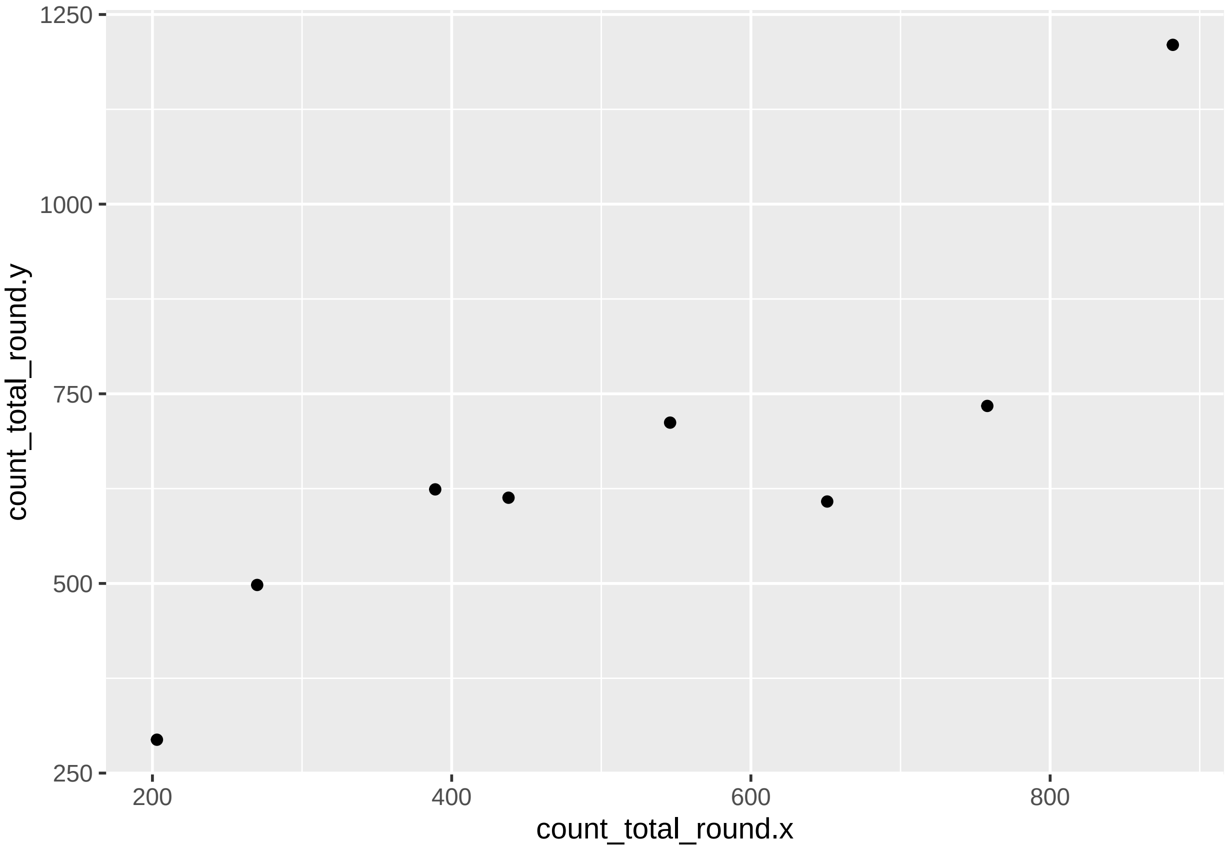
```
##  [1] T247 T236 T243 T234 T244 T231 T235 T229 T237 T230 T259 T258 T257 T260
## 15 Levels: T229 T230 T231 T234 T235 T236 T237 T243 T244 T246 T247 T257 ... T260
```

```r
lapply(list(tmp1, tmp2, intersect(tmp1, tmp2)), length)
```

```
## [[1]]
## [1] 9
##
## [[2]]
## [1] 14
##
## [[3]]
## [1] 8
```

Compare `count_total_round` between round 1 and 3

```r
x <- data_count_total %>% filter(round ==1) %>% select(male, count_total_round, round)
y <- data_count_total %>% filter(round ==3) %>% select(male, count_total_round, round)

data_xy <- full_join(x = x, y = y, by = "male") %>% na.omit()

ggplot(data_xy) +
    aes(x = count_total_round.x, y = count_total_round.y) +
    geom_point()
```



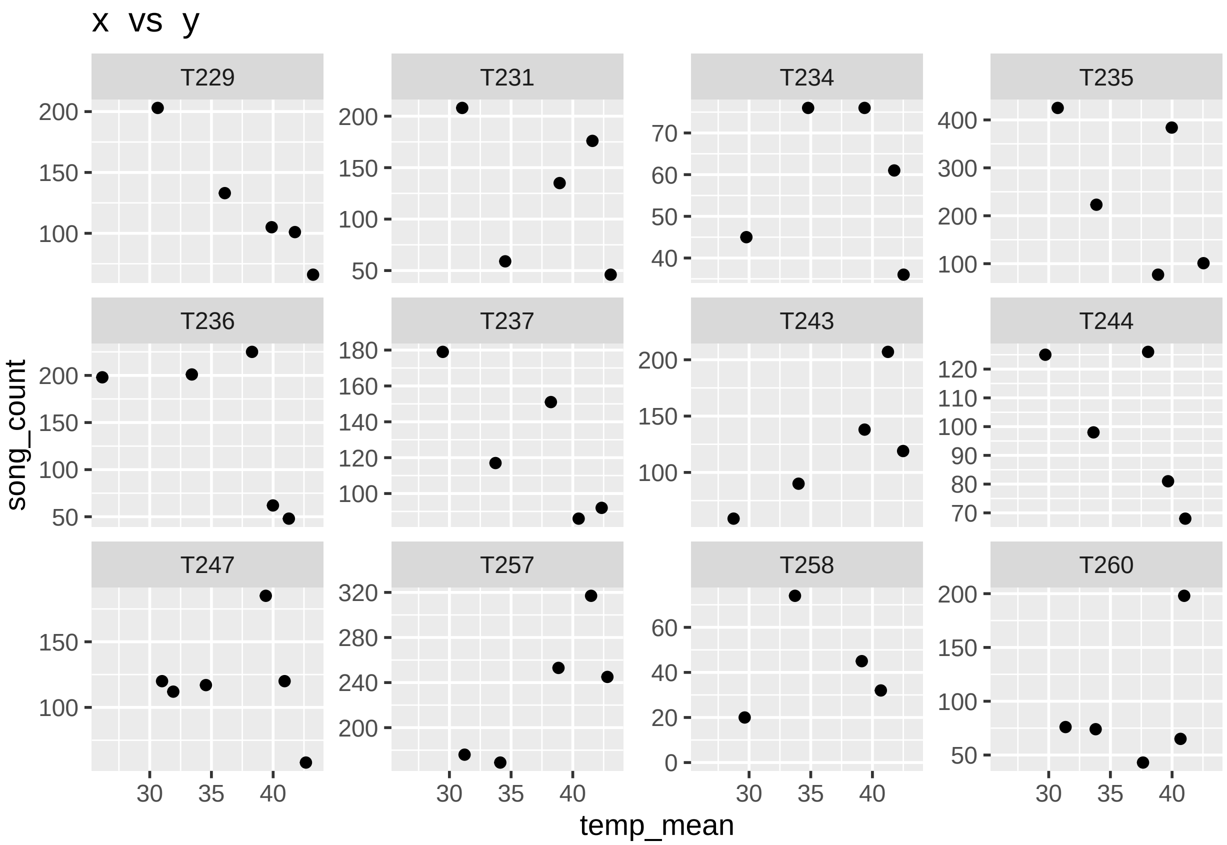
Result

- We see consistancy between `count_total_round` which is good
- Note one male has `trial_completed = FALSE` and, thus, `temp_mean = NA`. In future will create new column `temp_working` and use `temp_target` for this instance and `temp_mean` for remaining ones.

Plot Filtered Data

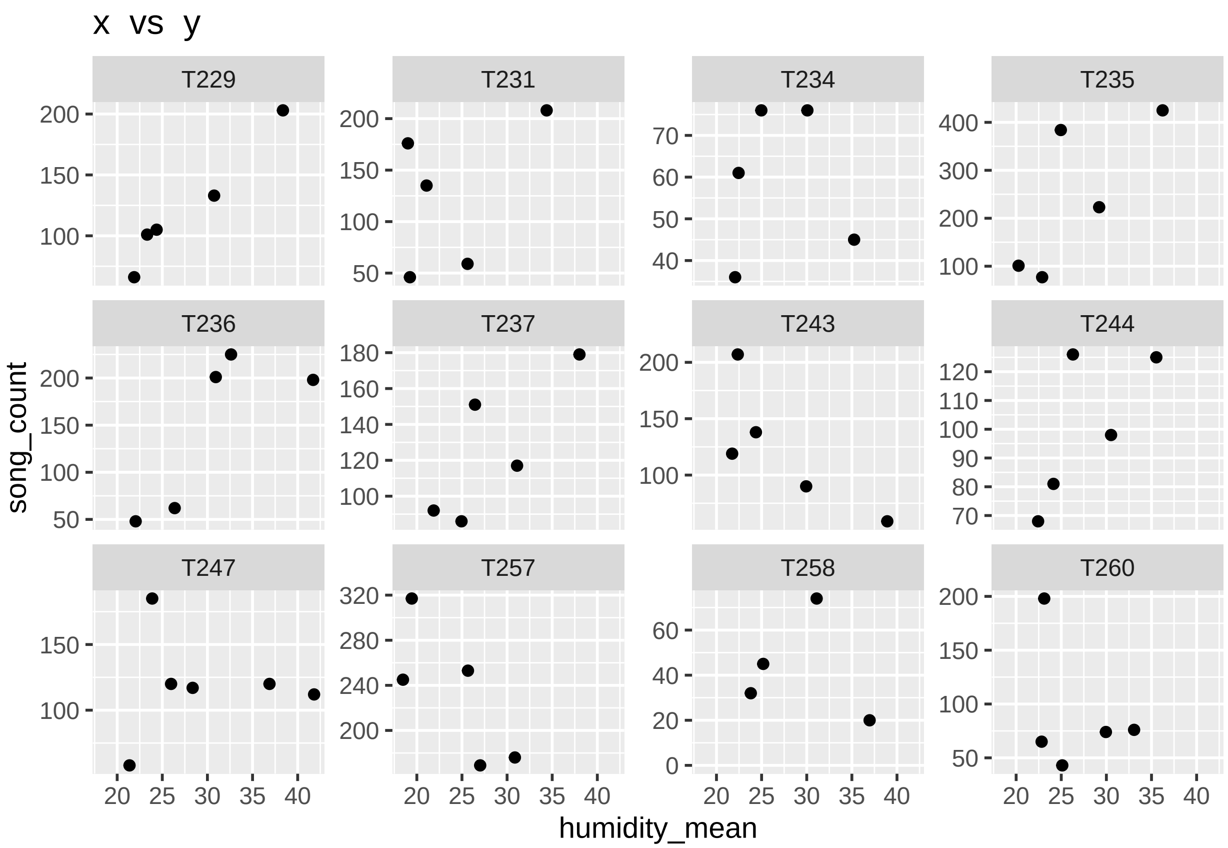
```
data <- data_full %>%
    filter(round==3) %>%
    filter(count_total_round >=100)

xlab <- "Temperature"
ylab <- "song_count"

plot_temp_data <-
    ggplot(data) +
    aes(x = temp_mean,
        y = song_count) +
    facet_wrap("male", scales = "free_y") +
    geom_point() +
    labs( title = paste( substitute(x), " vs ", substitute(y)))
last_plot()
```

```
## Warning: Removed 1 rows containing missing values (geom_point).
```



```
## Create again for humidity

xlab <- "humidity"
ylab <- "song_count"

plot_humidity_data <-
    ggplot(data) +
    aes(x = humidity_mean,
        y = song_count) +
    facet_wrap("male", scales = "free_y") +
    geom_point() +
    labs( title = paste( substitute(x), " vs ", substitute(y)))
last_plot()
```

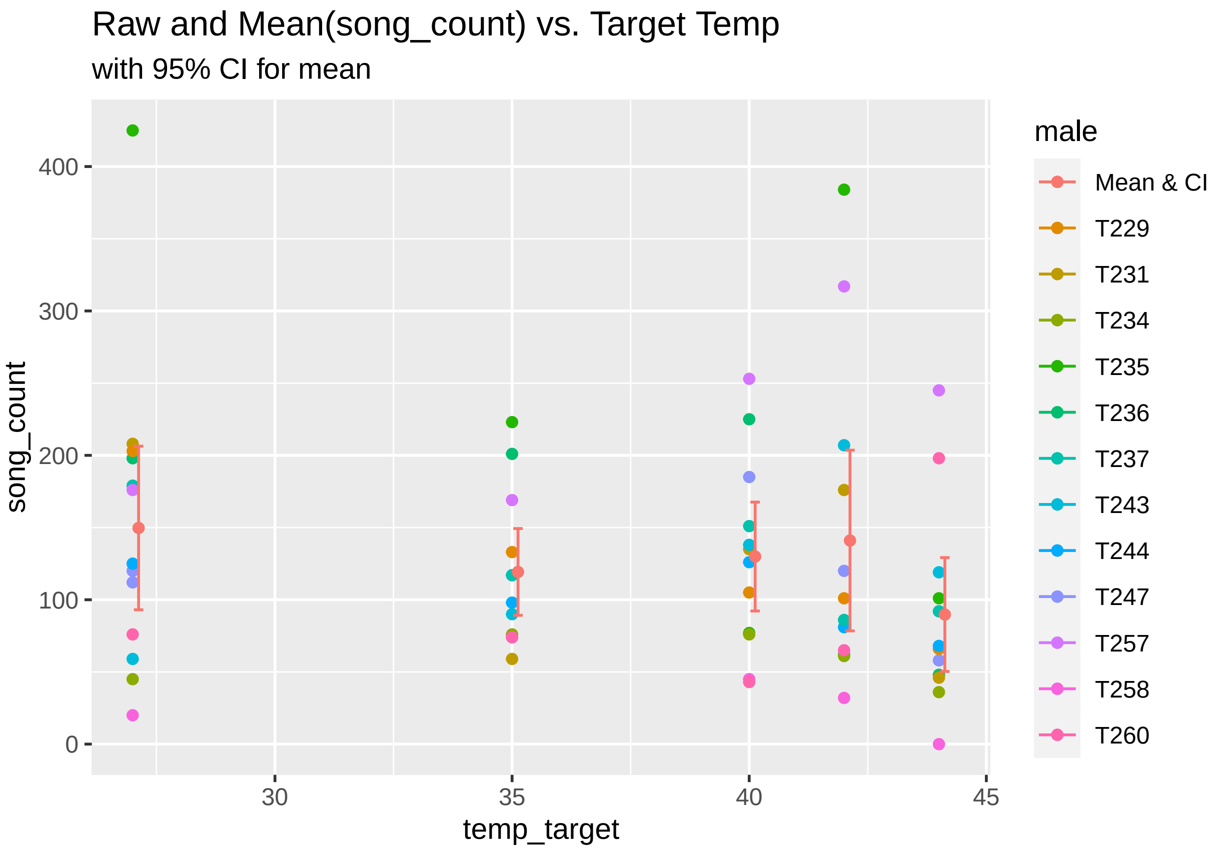
```
## Warning: Removed 1 rows containing missing values (geom_point).
```



Work with mean

- This approach won't work because `temp_target` varies greatly from `temp_mean`.

```
plot_combine <- ggplot(data) +
                  aes(x = temp_target, y = song_count, color = male) +
                  geom_point()
# last_plot()

data_summarize <-
    data %>% group_by(temp_target) %>%
    summarize(song_mean = mean(song_count),
              song_sd = sd(song_count),
              song_n= dplyr::n(),
              song_se = song_sd/sqrt(song_n),
              song_ci = song_se*1.96
              )


plot_summarize <- ggplot(data_summarize) +
    aes(x = temp_target, y = song_mean) +
    geom_point()+
    geom_errorbar(aes(ymin=song_mean - song_ci, ymax=song_mean+song_ci), width=.2)
# last_plot()

plot_combine +
    geom_point(data = data_summarize, aes(x = temp_target+0.125, y = song_mean, colour = "Mean & CI"))+
    geom_errorbar(data = data_summarize, aes(x = temp_target+0.125,
                                             y = song_mean,
                                             ymin=song_mean - song_ci,
                                             ymax=song_mean+song_ci,
                                             colour= "Mean & CI"), width=.2) +
    labs(title = "Raw and Mean(song_count) vs. Target Temp",
         subtitle = "with 95% CI for mean")
```



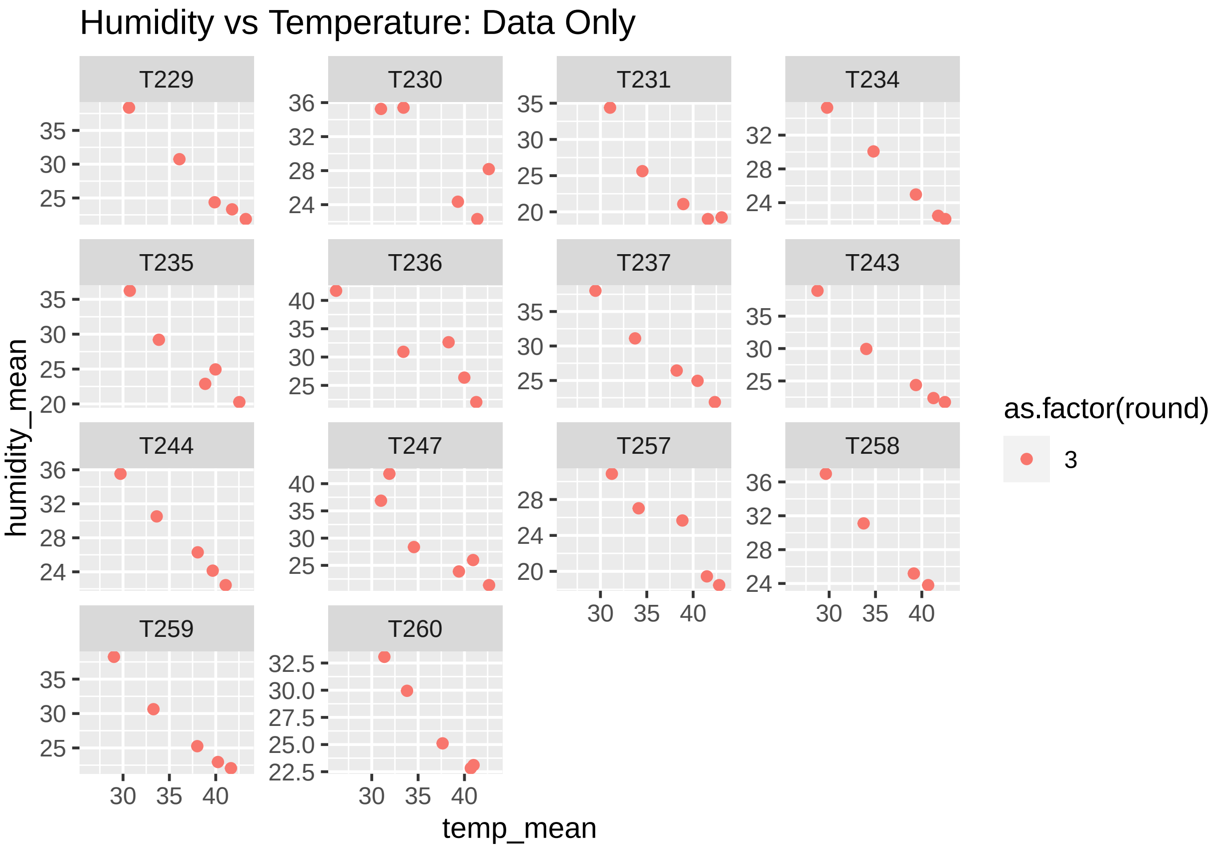
Result

- Data is noisy.
- Note `temp_target` is not necessarily accurate.

Humidity vs. Temp

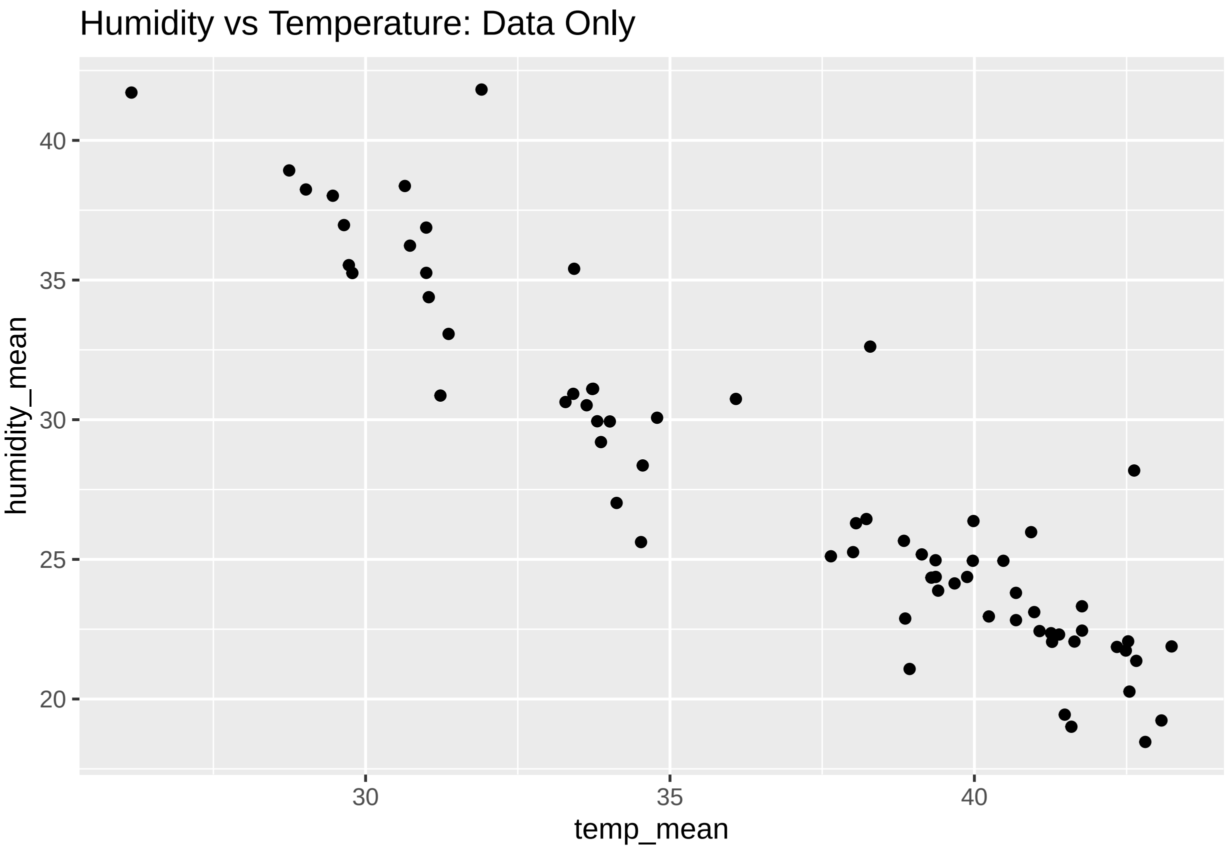
```
data <- data_full %>% filter(round == 3)

## As one might expect, Humidity is negatively correlated with temperature
ylab = "temp_mean"
plot_data_humidity_vs_temp <-
    ggplot(data = data) +
    aes(x = temp_mean,
        y = humidity_mean,
        color = as.factor(round)) +
    facet_wrap("male", scales = "free_y") +
    geom_jitter() +
    labs( title = "Humidity vs Temperature: Data Only")
last_plot()
```

```
## Warning: Removed 1 rows containing missing values (geom_point).
```



```
plot_data_humidity_vs_temp_combined <-
    ggplot(data = data) +
    aes(x = temp_mean,
        y = humidity_mean
        ) +
    geom_point() +
    labs( title = "Humidity vs Temperature: Data Only")
last_plot()
```

```
## Warning: Removed 1 rows containing missing values (geom_point).
```



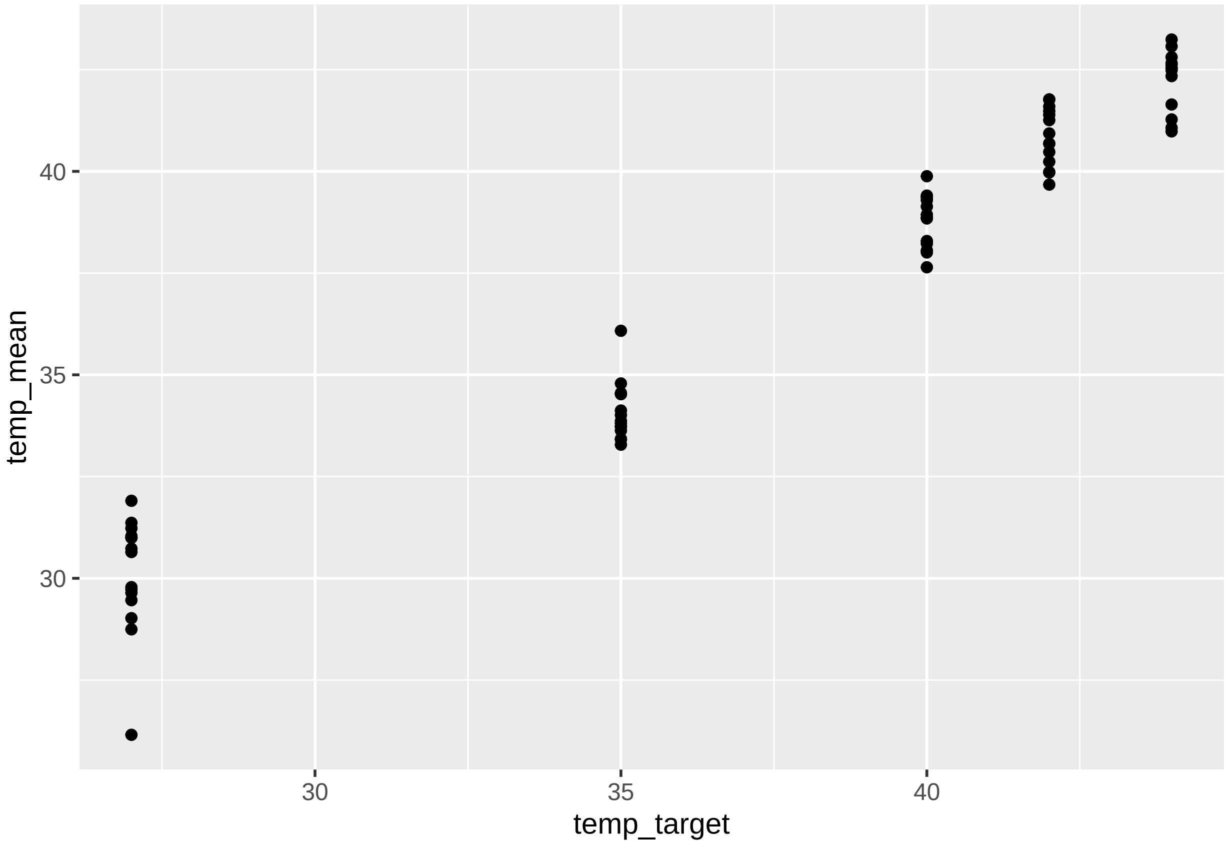
Result

- These values clearly co-vary.
- Should consider using
  - Vapor Pressure Deficit
    - Uses temp to calculate max humidity and then looks at difference with relative humidity.
  - Heat Index
    - Adjusted for birds if available
    - Use just first terms (`c_1 + c_2 T + c_3 R + c_4 T R + ...`)

Compare `temp_target` and `temp_mean`

```
p <- ggplot(data, aes(x = temp_target, y = temp_mean)) +
    geom_point()
p
```

```
## Warning: Removed 1 rows containing missing values (geom_point).
```



Result

- Lots of variation thatn sometimes spans between `temp_target` categories.
- Clearly we want to work with `temp_mean`, rather than `temp_target`. As a result, only round = 3 since we don't have this data for the other rounds.

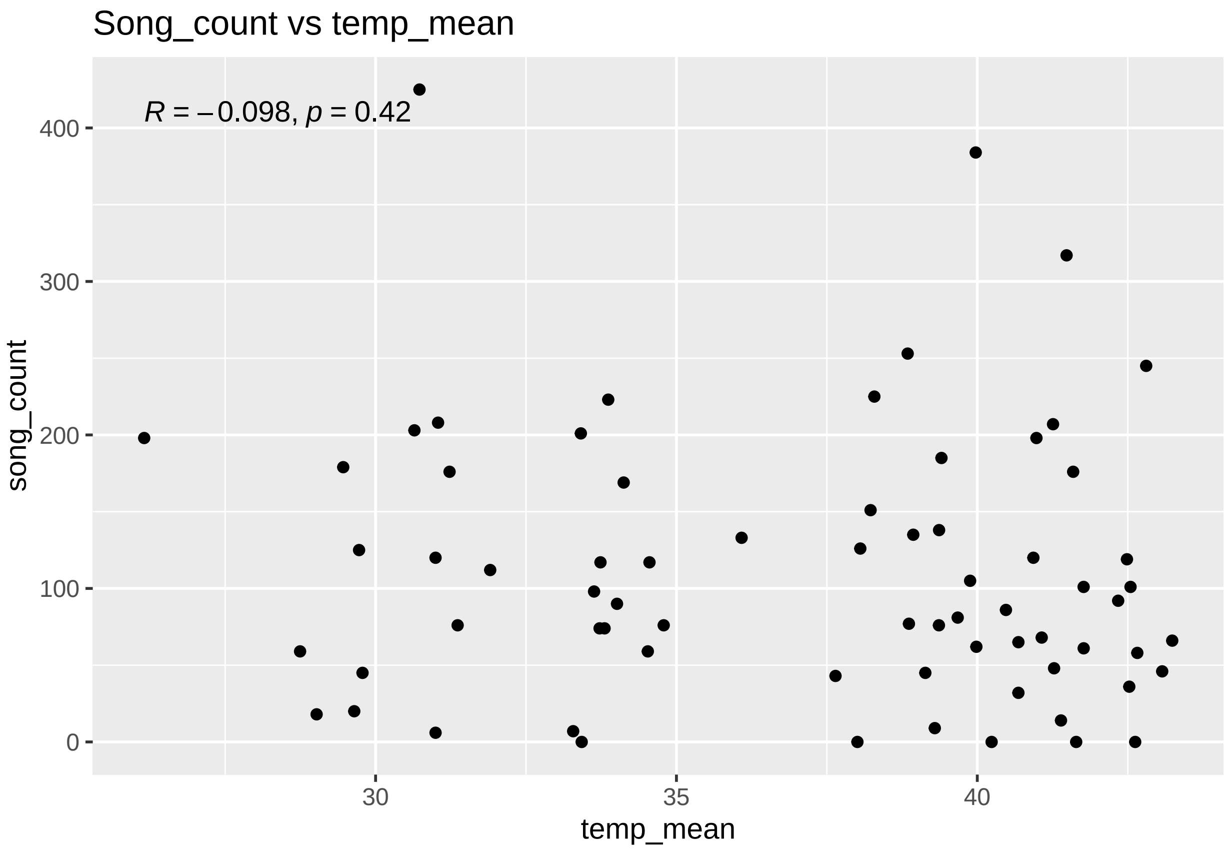
Compare song_count to `temp_mean` and `temp_humidity`

Plot

```
p <- ggplot(data, aes(x = temp_mean, y = song_count), color = male) +
    geom_point() +
    stat_cor() +
labs(title = "Song_count vs temp_mean")
last_plot()
```

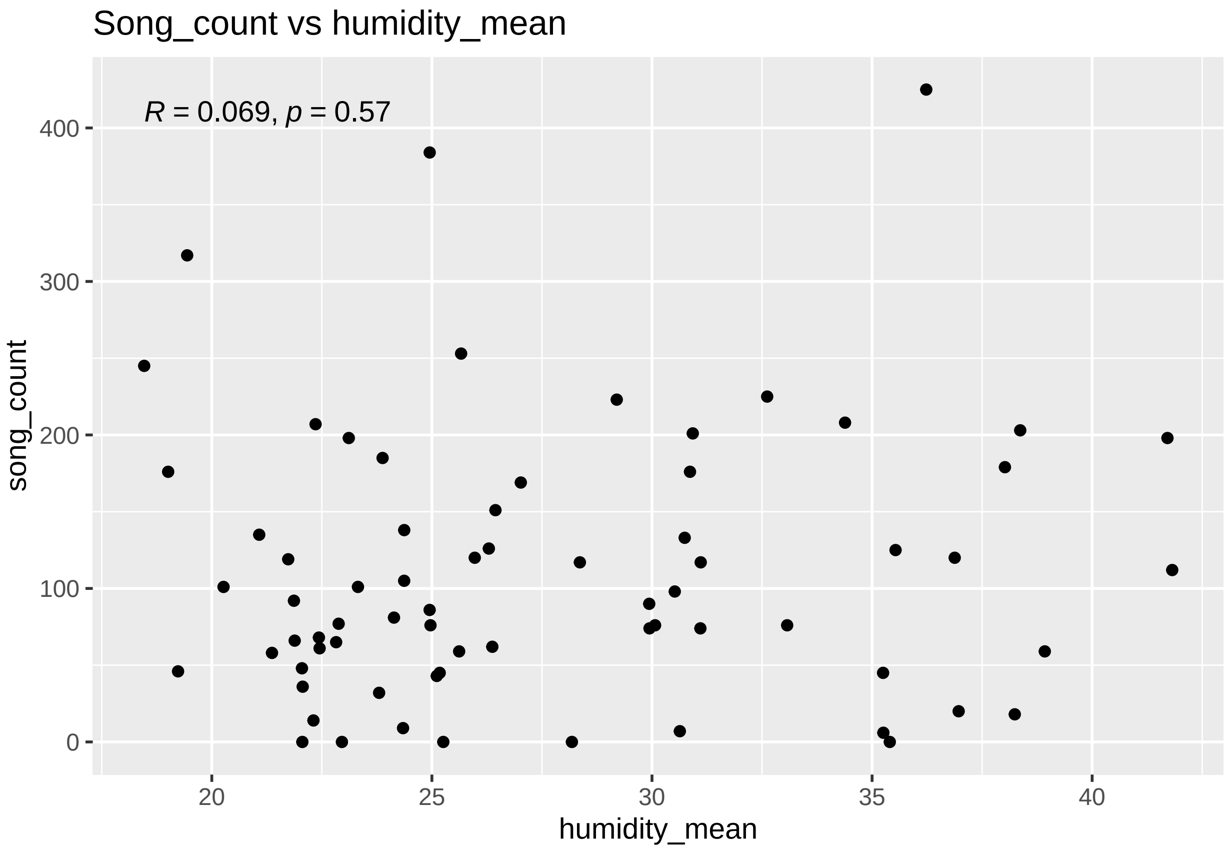
```
## Warning: Removed 1 rows containing non-finite values (stat_cor).
```

```
## Warning: Removed 1 rows containing missing values (geom_point).
```



```
p <- ggplot(data, aes(x = humidity_mean, y = song_count), color = male) +
    geom_point() +
    stat_cor() +
    labs(title = "Song_count vs humidity_mean")
last_plot()
```

```
## Warning: Removed 1 rows containing non-finite values (stat_cor).
## Removed 1 rows containing missing values (geom_point).
```



```
knitr::knit_exit()
```