Process song_count data

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Goal

- Developing code for processing song_count
- Idea is to index processing by date and then have other code load data in output/ found in this
 directory.

Set up

Load libraries

```
## load libraries
library(stats)
require(MASS) # provides negative binomial fitting: qlm.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
                                0.3.5
## v tibble 3.1.8
                      v dplyr 1.0.10
## v tidyr 1.2.1
                      v stringr 1.4.1
          2.1.3
## v readr
                      v forcats 0.5.2
## -- Conflicts -----
## x dplyr::filter() masks stats::filter()
## x dplyr::lag() masks stats::lag()
## x dplyr::select() masks MASS::select()
```

```
library(ggplot2)
library(ggpubr)
library(grid) ## provides textGrob
library(gridExtra)
##
## Attaching package: 'gridExtra'
## The following object is masked from 'package:dplyr':
##
##
       combine
library(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)
library(GGally)
## Registered S3 method overwritten by 'GGally':
##
    method from
##
    +.gg
           ggplot2
library(reshape2)
##
## Attaching package: 'reshape2'
## The following object is masked from 'package:tidyr':
##
##
       smiths
library(lme4)
## Loading required package: Matrix
##
## Attaching package: 'Matrix'
##
## The following objects are masked from 'package:tidyr':
##
##
       expand, pack, unpack
library(nlme)
##
## Attaching package: 'nlme'
## The following object is masked from 'package:lme4':
```

```
##
       lmList
##
##
## The following object is masked from 'package:dplyr':
##
##
       collapse
library(gnm)
library(rsample) ## provides bootstraps()
library(RVAideMemoire) # provides overdisp.glmer()
## *** Package RVAideMemoire v 0.9-81-2 ***
## Attaching package: 'RVAideMemoire'
##
## The following object is masked from 'package:gnm':
##
##
       se
##
## The following object is masked from 'package:lme4':
##
##
       dummy
##
## The following object is masked from 'package:broom':
##
##
       bootstrap
library(humidity) ## provides VPD
library(weathermetrics)
library(latex2exp)
```

Local Functions

```
kprint <- function(input, ...) {
    print(knitr::kable(input, ...))
cat('\n\n<!-- -->\n\n')
}

if(interactive()) {
    file_name <- "testing.Rda"
} else {
    file_name <- knitr::current_input() %>% sub("\\.Rmd", ".Rda", .)
}
```

Plotting settings

```
## From: https://data-se.netlify.app/2018/12/12/changing-the-default-color-scheme-in-ggplot2/
theme_set(theme_minimal(base_size = 9))
theme_update(
    plot.title = element_text(size = rel(1.1)),
    plot.subtitle = element_text(size = rel(1)))

if(!exists("old_opts")) old_opts <- options()  # save old options

options(ggplot2.continuous.colour="viridis")
options(ggplot2.discrete.colour="viridis")
options(ggplot2.discrete.colour="viridis")
options(ggplot2.discrete.fill = "viridis")</pre>
```

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
output_dir <- "output"</pre>
if(!dir.exists(output_dir)) dir.create(output_dir)
git_root <- system("git rev-parse --show-toplevel", intern = TRUE)</pre>
song_data_raw = list()
song_data_raw[[1]] <- read.csv(file.path(git_root, "data", "raw_data", "HSPi-Round-1-Heat-Trials.csv"))</pre>
    ## 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))
song_data_raw[[2]] <- read.csv(file.path(git_root, "data", "raw_data", "HSPi-Repeatability-Song-Count.c</pre>
   mutate(round = 2) %>%
   ungroup()
song_data_raw[[3]] <-read.csv(file.path(git_root, "data", "raw_data", "HSPi-Round-2-Heat-Trials.csv"))
   mutate(round = 3) %>%
    ## Deal with missing temp_mean and humidity_mean values
    ## in round == 3
    ## 2022/10/19 - code no longer needed
    ## group_by(temp_target) %>%
    ##mutate(temp = if_else((round == 3 & is.na(temp_mean)),
    ##
                            mean(temp_mean, na.rm = TRUE),
    ##
                            temp_mean)) %>%
    ##mutate(humidity = if_else((round == 3 & is.na(humidity_mean)),
                                mean(humidity_mean, na.rm = TRUE),
    ##
                                humidity mean)) %>%
   ungroup()
```

```
## Join data and discard empty columns
song_data_full <- full_join(song_data_raw[[1]], song_data_raw[[2]]) %>%
    full join(song data raw[[3]]) %>%
   discard(~all(is.na(.) | . =="")) %% ## get rid of columns of only NA
   mutate(n_obs_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 male specific round and global trial index `trial`
   group_by(male, round) %>%
   mutate(trial_round = rank(date)) %>%
   ungroup() %>%
   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)) %>%
    ## Create generic 'temp' column which is either
    ## temp_mean, if it exists, or temp_target, if it doesn't
   mutate(temp = if_else(is.na(temp_mean),
                         temp_target,
                          temp mean)) %>%
    ## Add column with total song_count for a given round
   group by (male, round) %>%
   mutate(count_total_round = sum(song_count),
          n_obs_round = length(song_count),
           count_mean_round = count_total_round/n_obs_round,
           count_sd_round = sd(song_count),
          count_cv_round = count_sd_round/count_mean_round) %>%
   ungroup(round) %>%
   mutate(count_total = sum(song_count),
          n_obs = length(song_count),
           count_mean = count_total/n_obs) %>%
   mutate(trial = rank(date)) %>%
   mutate(song_prop_round = song_count/count_total_round) %>%
   mutate(song_prop = song_count/count_total) %>%
    ## assuming poisson error
    ## From glm man page
    ## > Non-'NULL' 'weights' can be used to indicate that different
    ## > observations have different dispersions (with the values in
    ## > 'weights' being inversely proportional to the dispersions);
    ## add +1 to deal with single 0
    ## Interpret dispersion as ~ sd(), wt ~ 1/disp = 1/sd var()
   mutate(weight_count = sqrt(1/(song_count + 1))) %>%
    ## need to rescale wts for song_prop data
   mutate(weight_prop = weight_count * count_total_round) %>%
   mutate(svp = SVP(t = temp_mean + 273.15, isK = TRUE), vpd = svp*(1-humidity_mean/100) ) %>%
   rename(bill_date = date_morph_data_collected) %>%
   group_by(round) %>%
   mutate(vpd_offset = vpd - mean(vpd)) %>%
   ungroup() %>%
   relocate(round, trial_round, song_count, song_prop, temp_mean, humidity_mean, .after = male) %%
   mutate() ## Dummy function so we can comment out lines above it w/o any issues
```

```
## Joining, by = c("male", "chamber", "date", "song_count", "counter", "temp_target", "round")
## Joining, by = c("male", "chamber", "date", "song_count", "counter", "test_order", "temp_target", "ro
## Extract information on each male's bill
bird_bill_data <- song_data_full %>%
    select(male, bill_depth, bill_length, bill_width, bill_date)
song_stats <- song_data_full %>%
    select(male, round, n_obs, starts_with("count_")) %>%
   unique()
names(song_stats) <- names(song_stats) %>% sub("^count_", "", .)
## Remove columns on male bills
song_data <- song_data_full %>%
   select( -starts_with("bill_")) %>%
   select( -starts_with(c("count_")))
## Create small subset of data.
song_data_40C \leftarrow song_data \%
    filter(temp_target == 40) %>%
   unique()
dim(song_data_40C)
## [1] 53 28
## Get stats for subset
## Original approach
song_stats_40C <- song_data_40C %>%
    group_by(male) %>%
    summarize(n_obs = length(song_count),
             mean = mean(song_count),
              var = var(song_count, na.rm = TRUE),
              cv = sqrt(var)/mean,
              dispersion = var/mean) %>%
   replace(is.na(.), 0)
d[is.na(d)] <- 0
## Error in d[is.na(d)] <- 0: object 'd' not found</pre>
print("We have 15 males, 5 of which we only have 1 observation at 40C")
## [1] "We have 15 males, 5 of which we only have 1 observation at 40C"
song_stats_40C
## # A tibble: 15 x 6
   male n obs mean var cv dispersion
     <fct> <int> <dbl> <dbl> <dbl>
                                           <dbl>
##
```

```
5 159. 8820. 0.592
## 1 T229
                                         55.6
## 2 T230
               4 2.25 20.2 2
                                          9
## 3 T231
              5 106.
                        9770. 0.929
                                         91.8
## 4 T234
              5 53.4
                       688. 0.491
                                         12.9
                       890. 0.381
## 5 T235
               5 78.4
                                         11.4
## 6 T236
              5 184. 3233. 0.310
                                         17.6
## 7 T237
              4 145.
                        693. 0.181
                                         4.77
                        4218. 0.284
## 8 T243
              5 229
                                         18.4
## 9 T244
              5 78.6 1477. 0.489
                                         18.8
## 10 T246
              1 0
                           0 0
                                         0
## 11 T247
              5 118.
                        3223. 0.483
                                         27.4
## 12 T257
               1 253
                          0
                              0
                                          0
## 13 T258
               1 45
                           0
                              0
                                          0
## 14 T259
                           0
                              0
                                          0
               1
                 0
## 15 T260
               1 43
                           0
                              0
                                          0
comment <- paste0("Data created using file ", file_name, " on ", date())</pre>
save obj <- c("song data", "song data 40C", "song stats", "song stats 40C", "bird bill data")
## Add comments
## Note usage of eval and parse!!
for(x in save_obj) {
   my_exp <- paste0("comment(", x, ") <- \"", comment, "\"")</pre>
                                      #eval(parse(text = my_exp))
   parse(text = my_exp)
}
save(list = save_obj, file = paste0(file.path("output", file_name)) )
```

Plot song_prop

```
g1 <- ggplot(data = song_data) +
    aes(x = temp, y = song_count, color = male) +
    geom_point() +
    labs(title = "Males unfiltered") +
    theme(legend.position="bottom")

males_filtered_disp <- song_stats_40C %>% filter(dispersion < 50) %>% pull(male)

data_filtered <- song_data %>% filter(male %in% males_filtered_disp)

g2 <- ggplot(data = data_filtered) +
    aes(x = temp, y = song_count, color = male) +
    geom_point() +
    labs(title = "Males filtered for dispersion < 50 at 40C") +
    theme(legend.position="bottom")

males_filtered_mean <- song_stats %>% filter(mean > 10) %>% pull(male)
males_filtered <- intersect(males_filtered_mean, males_filtered_disp)
data_filtered <- song_data %>% filter(male %in% males_filtered)
```

```
g3 <- ggplot(data = data_filtered) +
    aes(x = temp, y = song_count, color = male) +
    geom_point() +
    labs(title = "Males filtered for dispersion < 50 at 40C & count_mean < 10)") +
    theme(legend.position="bottom")

grid.arrange(g1, g2, g3, ncol = 2)</pre>
```



