models

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2024-12-06

this rmd was mainlyused to create usable code for our models, we created mean values for velocity and nudi angular direction of movement and saved it into a combinedraw file in our clean data folder then edited this into a version without an error we found in the original data called combined_raw_no_spaces.

```
#loading in all my packages

library(here)
```

```
## here() starts at C:/Users/Fiona/OneDrive/Documents/bamfield 2024/DS/Nudireactors Coding and Data/nudi
```

```
library(dplyr)
```

```
##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##     filter, lag

## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
library(tidyverse)
```

```
## -- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
## v forcats   1.0.0     v readr     2.1.5
## v ggplot2   3.5.1     v stringr   1.5.1
## v lubridate 1.9.3     v tibble    3.2.1
## v purrr     1.0.2     v tidyr     1.3.1

## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

```
library(circular)
```

```
## Warning: package 'circular' was built under R version 4.4.2
```

```
##
## Attaching package: 'circular'
##
## The following objects are masked from 'package:stats':
##
##     sd, var
```

```
#loading in all our raw data

rawcons <- read.csv("./raw_data/Meyknecht_Over_Parker_MRNE475_2024_rawcons.csv")

nudisize <- read.csv("./raw_data/Meyknecht_Over_Parker_MRNE475_2024_nudisizeraw.csv")

rawpreds <- read.csv("./raw_data/Meyknecht_Over_Parker_MRNE475_2024_rawpred.csv")%>%
  rename(temp_grp = temp)

#cleaning up the data and getting means and standard deviations

combinedraw <- rbind(rawcons, rawpreds) %>%
  mutate(temp_grp = as.factor(temp_grp)) %>%
  group_by(nudi_num, temp_grp, trial_type) %>%
  summarise(
    mean_angle = mean(fixdeg, na.rm = TRUE),
    sd_angle = sd(fixdeg, na.rm = TRUE),
    mean_vel = mean(v_ms, na.rm = TRUE),
    sd_vel = sd(v_ms, na.rm = TRUE)
  ) %>%
  left_join(y = nudisize, by = "nudi_num") %>% #adding in nudisize to help create a usuable tablefor ou
  mutate(direction_binom = case_when(
    mean_angle >= 0 & mean_angle <= 180 ~ 0,
    mean_angle <= 360 & mean_angle > 180 ~ 1
  ))
```

```
## `summarise()` has grouped output by 'nudi_num', 'temp_grp'. You can override
## using the `.groups` argument.
```

```
# our data had a row with a space so we used this code to fix it
nudi_data_nospaces <- read.csv("clean_data/Meyknecht_Over_Parker_MRNE475_2024_combinedraw.csv")%>%
  mutate(temp_grp = as.factor(temp_grp))
nudi_data_nospaces$trial_type[nudi_data_nospaces$trial_type=="conspecific "] <- "conspecific"

nudi_data_nospaces_xl <- nudi_data_nospaces %>%
  dplyr::select(nudi_num, trial_type, mean_vel, sd_vel)%>%
  filter(trial_type == "conspecific")

write.csv(nudi_data_nospaces_xl, "./clean_data/Meyknecht_Over_Parker_MRNE475_2024_combinedraw_no_spaces
```