FINAL PROJECT\_120919 YMaze\_SA Cyt1 flfl

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## Introduction

## Import Data

##install.packages('tidyverse')  
library (tidyverse)  
##install.packages('ggplot2')  
library (ggplot2)  
#install.packages('dplyr')  
library(dplyr)  
##install.packages('readxl')  
library (rio)  
  
## load csv files - the input file name has to be updates each time and the file needs to be in the same project folder than the code  
data <- read\_csv("102819 YMaze\_SA Cyt1 flfl Data\_Seq.csv",)  
head(data)

## # A tibble: 6 x 129  
## Test Animal Treatment Time Date Distance `Visited zones` X8 X9 X10   
## <dbl> <dbl> <chr> <tim> <chr> <dbl> <chr> <chr> <chr> <chr>  
## 1 1 4667 Cre 12:14 10/2~ 11.4 Arm 1 Cent~ Arm 1 Cent~  
## 2 2 4668 ctrl 12:21 10/2~ 14.4 Arm 1 Cent~ Arm 3 Cent~  
## 3 3 4669 ctrl 12:28 10/2~ 14.3 Arm 1 Cent~ Arm 3 Cent~  
## 4 4 5054 cre 12:36 10/2~ 14.4 Arm 1 Cent~ Arm 3 Cent~  
## 5 5 5055 ctrl 12:43 10/2~ 12.8 Arm 1 Cent~ Arm 2 Cent~  
## 6 6 4673 cre 12:50 10/2~ 9.71 Arm 1 Cent~ Arm 3 Cent~  
## # ... with 119 more variables: X11 <chr>, X12 <chr>, X13 <chr>, X14 <chr>,  
## # X15 <chr>, X16 <chr>, X17 <chr>, X18 <chr>, X19 <chr>, X20 <chr>,  
## # X21 <chr>, X22 <chr>, X23 <chr>, X24 <chr>, X25 <chr>, X26 <chr>,  
## # X27 <chr>, X28 <chr>, X29 <chr>, X30 <chr>, X31 <chr>, X32 <chr>,  
## # X33 <chr>, X34 <chr>, X35 <chr>, X36 <chr>, X37 <chr>, X38 <chr>,  
## # X39 <chr>, X40 <chr>, X41 <chr>, X42 <chr>, X43 <chr>, X44 <chr>,  
## # X45 <chr>, X46 <chr>, X47 <chr>, X48 <chr>, X49 <chr>, X50 <chr>,  
## # X51 <chr>, X52 <chr>, X53 <chr>, X54 <chr>, X55 <chr>, X56 <chr>,  
## # X57 <chr>, X58 <chr>, X59 <chr>, X60 <chr>, X61 <chr>, X62 <chr>,  
## # X63 <chr>, X64 <chr>, X65 <chr>, X66 <chr>, X67 <chr>, X68 <chr>,  
## # X69 <chr>, X70 <chr>, X71 <chr>, X72 <chr>, X73 <chr>, X74 <chr>,  
## # X75 <chr>, X76 <chr>, X77 <chr>, X78 <chr>, X79 <chr>, X80 <chr>,  
## # X81 <chr>, X82 <chr>, X83 <chr>, X84 <chr>, X85 <chr>, X86 <chr>,  
## # X87 <chr>, X88 <chr>, X89 <chr>, X90 <chr>, X91 <chr>, X92 <chr>,  
## # X93 <chr>, X94 <chr>, X95 <chr>, X96 <chr>, X97 <chr>, X98 <chr>,  
## # X99 <chr>, X100 <chr>, X101 <chr>, X102 <chr>, X103 <chr>, X104 <chr>,  
## # X105 <chr>, X106 <chr>, X107 <chr>, X108 <chr>, X109 <chr>, X110 <chr>, ...

## Tidying

n<-nrow(data)  
  
for (i in 1:n){  
 animali<- data[i,]  
 animali<- animali %>% select ('Visited zones', contains("X")) %>% gather(variable, sequence) %>% select(sequence) %>% filter(sequence !=('Center'))  
 animali<-animali %>% mutate (onebefore= lag(sequence)) %>% mutate (twobefore=lag(onebefore)) %>% mutate(threebefore=lag(twobefore)) %>%   
 mutate (alternation1= ifelse(sequence=='Arm 1'& onebefore=='Arm 2' & twobefore=='Arm 3',1,0)) %>%   
 mutate (alternation2= ifelse(sequence=='Arm 1'& onebefore=='Arm 3' & twobefore=='Arm 2',1,0)) %>%   
 mutate (alternation3= ifelse(sequence=='Arm 2'& onebefore=='Arm 3' & twobefore=='Arm 1',1,0)) %>%   
 mutate (alternation4= ifelse(sequence=='Arm 2'& onebefore=='Arm 1' & twobefore=='Arm 3',1,0)) %>%   
 mutate (alternation5= ifelse(sequence=='Arm 3'& onebefore=='Arm 1' & twobefore=='Arm 2',1,0)) %>%   
 mutate (alternation6= ifelse(sequence=='Arm 3'& onebefore=='Arm 2' & twobefore=='Arm 1',1,0)) %>%   
 mutate (alternation7= ifelse(sequence=='Arm 1'& onebefore=='Arm 2' & twobefore=='Arm 2' & threebefore=='Arm 3',1,0)) %>%   
 mutate (alternation8= ifelse(sequence=='Arm 1'& onebefore=='Arm 3' & twobefore=='Arm 3' & threebefore=='Arm 2',1,0)) %>%   
 mutate (alternation9= ifelse(sequence=='Arm 2'& onebefore=='Arm 1' & twobefore=='Arm 1' & threebefore=='Arm 3',1,0)) %>%   
 mutate (alternation10= ifelse(sequence=='Arm 2'& onebefore=='Arm 3' & twobefore=='Arm 3' & threebefore=='Arm 1',1,0)) %>%   
 mutate (alternation11= ifelse(sequence=='Arm 3'& onebefore=='Arm 2' & twobefore=='Arm 2' & threebefore=='Arm 1',1,0)) %>%   
 mutate (alternation12= ifelse(sequence=='Arm 3'& onebefore=='Arm 1' & twobefore=='Arm 1' & threebefore=='Arm 2',1,0)) %>%   
   
 mutate(A1=as.numeric(alternation1)) %>%   
 mutate(A2=as.numeric(alternation2)) %>%   
 mutate(A3=as.numeric(alternation3)) %>%   
 mutate(A4=as.numeric(alternation4)) %>%   
 mutate(A5=as.numeric(alternation5)) %>%   
 mutate(A6=as.numeric(alternation6)) %>%   
 mutate(A7=as.numeric(alternation7)) %>%   
 mutate(A8=as.numeric(alternation8)) %>%   
 mutate(A9=as.numeric(alternation9)) %>%   
 mutate(A10=as.numeric(alternation10)) %>%   
 mutate(A11=as.numeric(alternation11)) %>%   
 mutate(A12=as.numeric(alternation12)) %>%   
   
 mutate(alternation=A1+A2+A3+A4+A5+A6+A7+A8+A9+A10+A11+A12) %>%   
   
 select(sequence, onebefore, twobefore, threebefore, alternation)  
 animali<-animali[-c(1,2),]  
  
 a<-sum(animali$alternation, na.rm=T)  
 #a  
 entries<-nrow(animali)  
 #entries  
 percentage<-a/entries \*100  
 #as.numeric(percentage)  
 ci<-c(data$Animal[i], data$Treatment[i], data$Distance[i], entries, percentage)  
 if (i==1) {final<-rbind(ci)} else {final<-rbind(final,ci)}  
}  
  
colnames(final)<-c('Animal','Treatment','Distance','Entries','Alternation')  
final<-as.data.frame(final)  
final<-final %>% arrange(Animal)  
final

## Animal Treatment Distance Entries Alternation  
## 1 4667 Cre 11.376 26 57.6923076923077  
## 2 4668 ctrl 14.446 44 47.7272727272727  
## 3 4669 ctrl 14.271 30 60  
## 4 4670 ctrl 15.424 42 54.7619047619048  
## 5 4671 cre 14.41 45 42.2222222222222  
## 6 4673 cre 9.707 26 46.1538461538462  
## 7 4674 ctrl 16.393 44 45.4545454545455  
## 8 4675 cre 13.43 39 46.1538461538462  
## 9 4676 ctrl 12.558 30 36.6666666666667  
## 10 4677 cre 18.316 47 53.1914893617021  
## 11 4678 ctrl 18.774 42 45.2380952380952  
## 12 4679 ctrl 16.943 43 46.5116279069767  
## 13 4696 cre 8.588 23 30.4347826086957  
## 14 4700 cre 17.731 47 53.1914893617021  
## 15 4701 cre 25.909 60 55  
## 16 4702 ctrl 19.978 52 50  
## 17 5054 cre 14.377 32 59.375  
## 18 5055 ctrl 12.845 41 43.9024390243902

write.csv(final, file="BIOF339 FINAL PROJECT\_Ymaze Cyt1 flfl\_tidy.csv")

## Statistical Analysis

final2 <- final %>% mutate(Treatment=toupper(Treatment)) %>% mutate(Treatment=as.factor(Treatment)) %>% mutate(Alternation=as.numeric(as.character(Alternation))) %>% mutate(Distance=as.numeric(as.character(Distance))) %>% mutate(Animal=as.character(Animal)) %>% mutate(Entries=as.numeric(as.character(Entries)))  
  
str(final2)

## 'data.frame': 18 obs. of 5 variables:  
## $ Animal : chr "4667" "4668" "4669" "4670" ...  
## $ Treatment : Factor w/ 2 levels "CRE","CTRL": 1 2 2 2 1 1 2 1 2 1 ...  
## $ Distance : num 11.4 14.4 14.3 15.4 14.4 ...  
## $ Entries : num 26 44 30 42 45 26 44 39 30 47 ...  
## $ Alternation: num 57.7 47.7 60 54.8 42.2 ...

YMAze\_ttest <- t.test(Alternation~Treatment, data=final2) %>%   
 broom::tidy()  
print(YMAze\_ttest)

## # A tibble: 1 x 10  
## estimate estimate1 estimate2 statistic p.value parameter conf.low conf.high  
## <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>  
## 1 1.46 49.3 47.8 0.389 0.703 14.7 -6.56 9.48  
## # ... with 2 more variables: method <chr>, alternative <chr>

Distance\_ttest <- t.test(Distance~Treatment, data=final2) %>%   
 broom::tidy()  
print(Distance\_ttest)

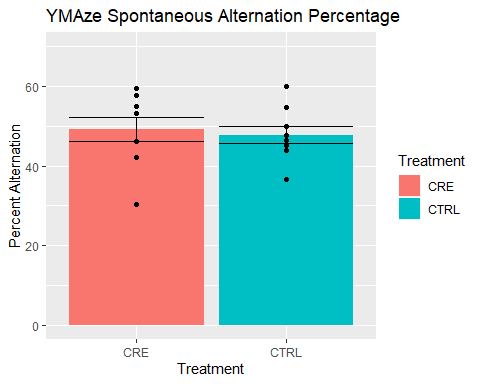
## # A tibble: 1 x 10  
## estimate estimate1 estimate2 statistic p.value parameter conf.low conf.high  
## <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>  
## 1 -0.865 14.9 15.7 -0.443 0.666 11.5 -5.14 3.41  
## # ... with 2 more variables: method <chr>, alternative <chr>

## Graphs

sem <- function(x) sqrt(var(x, na.rm=T)/sum(!is.na(x)))  
plot\_data <- final2 %>%   
 group\_by(Treatment) %>%   
 summarise(meanAlt = mean(Alternation), semAlt=sem(Alternation))  
plot\_data

## # A tibble: 2 x 3  
## Treatment meanAlt semAlt  
## <fct> <dbl> <dbl>  
## 1 CRE 49.3 3.03  
## 2 CTRL 47.8 2.22

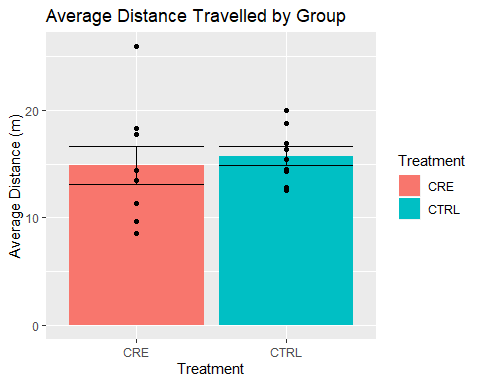
ttest\_plot <- ggplot(data = plot\_data,  
 mapping = aes(x = Treatment, y=meanAlt, fill=Treatment)) +  
 geom\_col()+  
 labs(x= "Treatment", y= "Percent Alternation", title= "YMAze Spontaneous Alternation Percentage") +  
 geom\_errorbar(aes(ymin=meanAlt - semAlt, ymax= meanAlt+semAlt)) +  
 ylim(0,70)  
  
ttest\_plot <- ttest\_plot + geom\_point(data=final2, mapping = aes(x=Treatment, y=Alternation, group=Treatment), show.legend = FALSE)  
print(ttest\_plot)



plot\_data\_dist <- final2 %>%   
 group\_by(Treatment) %>%   
 summarise(meanDist = mean(Distance), semDist=sem(Distance))  
plot\_data\_dist

## # A tibble: 2 x 3  
## Treatment meanDist semDist  
## <fct> <dbl> <dbl>  
## 1 CRE 14.9 1.76   
## 2 CTRL 15.7 0.846

distance\_plot <-plot\_data\_dist %>%   
 ggplot(mapping=aes(x=Treatment, y=meanDist, fill=Treatment))+  
 geom\_col()+  
 labs(x="Treatment", y="Average Distance (m)", title="Average Distance Travelled by Group")+  
 geom\_errorbar(aes(ymin=meanDist - semDist, ymax= meanDist+semDist))  
  
distance\_plot <- distance\_plot + geom\_point(data=final2, mapping = aes(x=Treatment, y=Distance, group=Treatment), show.legend = FALSE)  
print(distance\_plot)



## Conclusion