

SUPPLEMENTARY FILE 1

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LOAD LIBRARY

▼ Code

```
library(tidyverse)
library(PMCMRplus)
library(skimr)
library(report)
library(readxl)
library(moments)
library(ggtern)
library(PerformanceAnalytics)
library(gtsummary)
library(rcompanion)
library(FSA)
library(gt)
library(pROC)
```

LOAD AND PREP DATA

▼ Code

```
# load data from file
data1 = read_excel("D:/GDrive/My Drive/Writing/Ryuta_Okinawa_LandUse/Squid color/RGB F
behav = read_excel("D:/GDrive/My Drive/Writing/Ryuta_Okinawa_LandUse/Squid color/Squid

# Prep based as factor
data1[,c(2,7)]=lapply(data1[,c(2,7)], factor)

## Li S, Lee D. RGB-D SLAM in dynamic environments using static point weighting. IEEE

# RGB Ratio percentage
data1$R.per=(data1$R/rowSums(data1[,3:5]))*100
data1$G.per=(data1$G/rowSums(data1[,3:5]))*100
data1$B.per=(data1$B/rowSums(data1[,3:5]))*100

data1=relocate(data1,Disruptive,.after = B.per)
```

SKIM DATA

▼ Code

```
skim(data1)%>%
  yank("numeric") %>%
  gt()%>%
  cols_hide(columns = c("n_missing","complete_rate"))%>%
  tab_header(
    title = "Numeric Data Descriptive Statistics"
  ) %>%
  fmt_number(decimals = 3)
```

NUMERIC DATA DESCRIPTIVE STATISTICS								
skim_variable	mean	sd	p0	p25	p50	p75	p100	hist
animal	38.267	22.105	1.000	19.000	38.000	57.000	77.000	■■■■■■■
R	71.453	35.353	3.000	47.000	64.000	90.000	176.000	■■■_■■_
G	80.751	43.311	4.000	43.000	77.000	112.000	214.000	■■■■_■■_
B	94.640	63.436	5.000	36.000	92.000	139.000	243.000	■■■■_■■_
Brightness	81.625	40.559	4.796	46.554	76.003	107.512	207.064	■■■■_■■_
R.per	32.493	13.055	5.357	23.053	32.051	39.273	65.979	■■■_■■_

NUMERIC DATA DESCRIPTIVE STATISTICS								
skim_variable	mean	sd	p0	p25	p50	p75	p100	hist
G.per	32.371	3.327	23.913	30.435	32.218	34.228	48.214	
B.per	35.135	12.803	7.216	27.723	34.483	44.130	60.335	

▼ Code

```
skim(data1)%>%
  yank("factor") %>%
  gt()%>%
    cols_hide(columns = c("n_missing","complete_rate"))%>%
  tab_header(
    title = "Factor Data Descriptive Statistics"
  )
```

FACTOR DATA DESCRIPTIVE STATISTICS			
skim_variable	ordered	n_unique	top_counts
zone	FALSE	3	a: 75, b: 75, c: 75
Disruptive	FALSE	2	No: 180, Yes: 45

DATA VALIDATION

▼ Code

```
# Normality and skweness tests
# Create a data frame with all statistics
result_df <- data.frame(
  Variable = names(data1[,3:9]),
  Shapiro_p = sapply(data1[,3:9], function(x) shapiro.test(x)$p.value),
  Skewness = sapply(data1[,3:9], function(x) skewness(x)),
  Kurtosis = sapply(data1[,3:9], function(x) kurtosis(x))
)

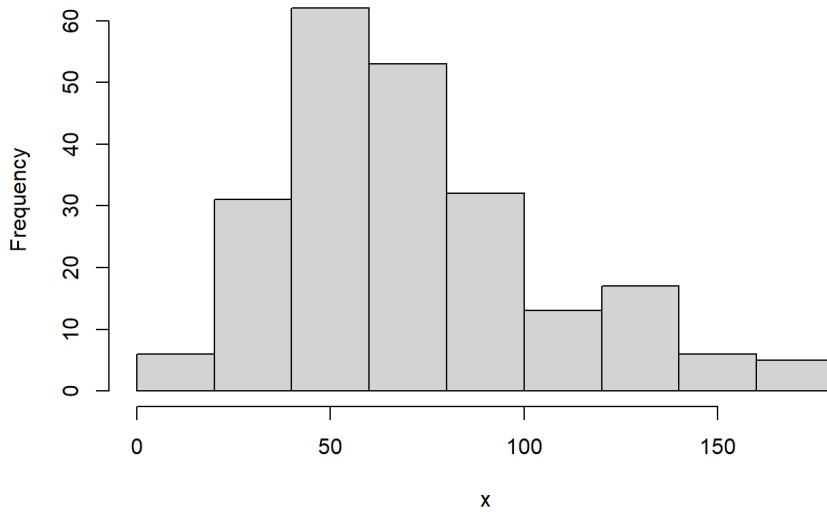
# Create a gt table with title
result_df %>%
  gt() %>%
  tab_header(
    title = "Distribution Statistics"
  ) %>%
  fmt_number(columns = c(Shapiro_p, Skewness, Kurtosis), decimals = 3)
```

DISTRIBUTION STATISTICS			
Variable	Shapiro_p	Skewness	Kurtosis
R	0.000	0.816	0.311
G	0.000	0.520	-0.062
B	0.000	0.374	-0.820
Brightness	0.000	0.561	0.033
R.per	0.000	0.571	-0.005
G.per	0.003	0.363	1.473
B.per	0.005	-0.173	-0.486

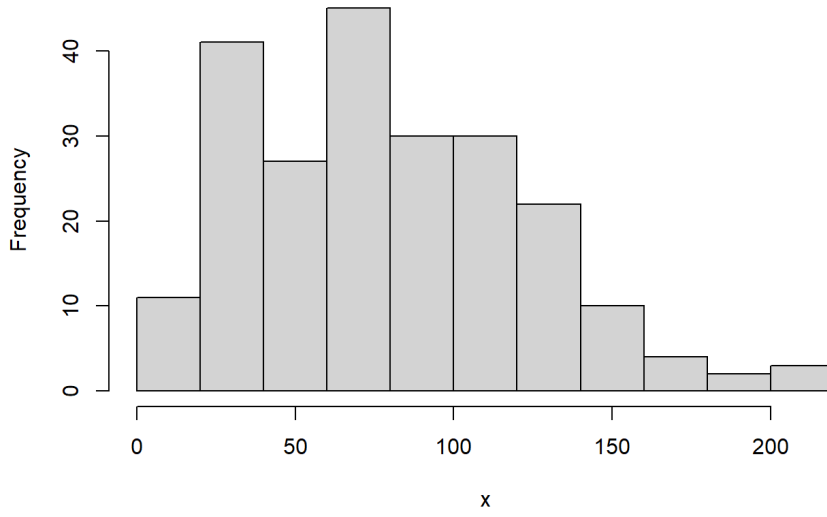
▼ Code

```
lapply(data1[,3:9], function(x) plot(hist(x)))
```

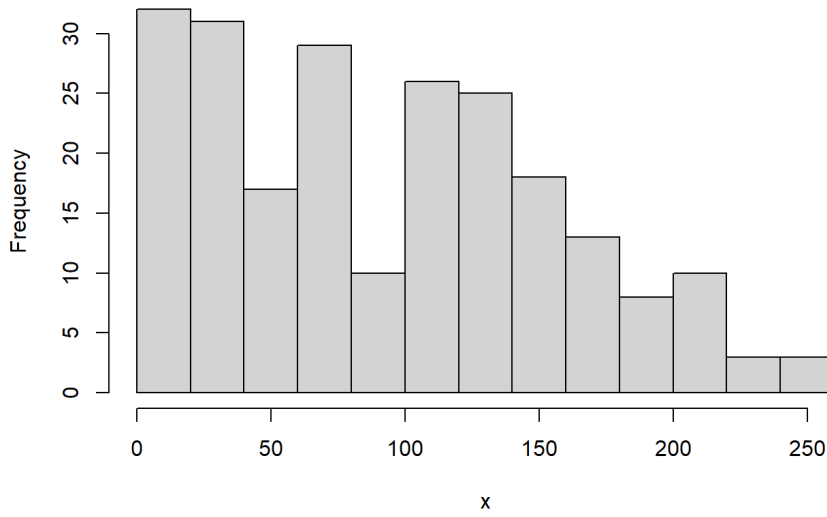
Histogram of x



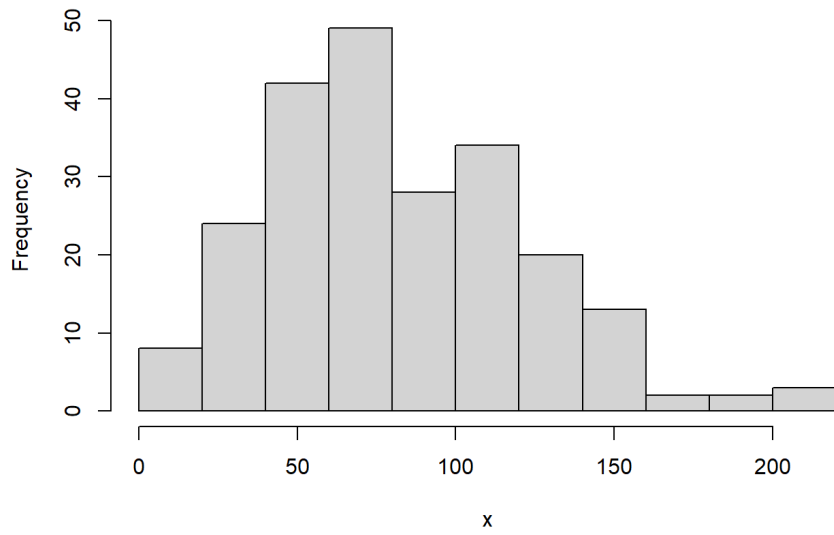
Histogram of x



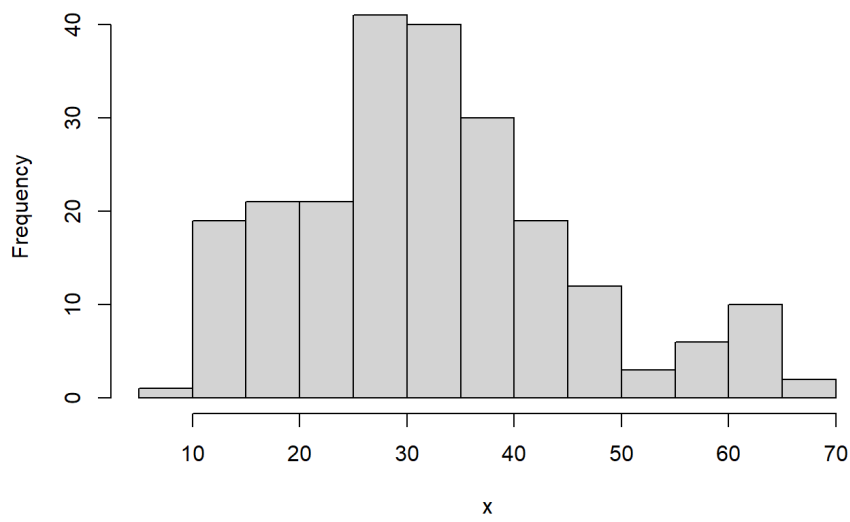
Histogram of x



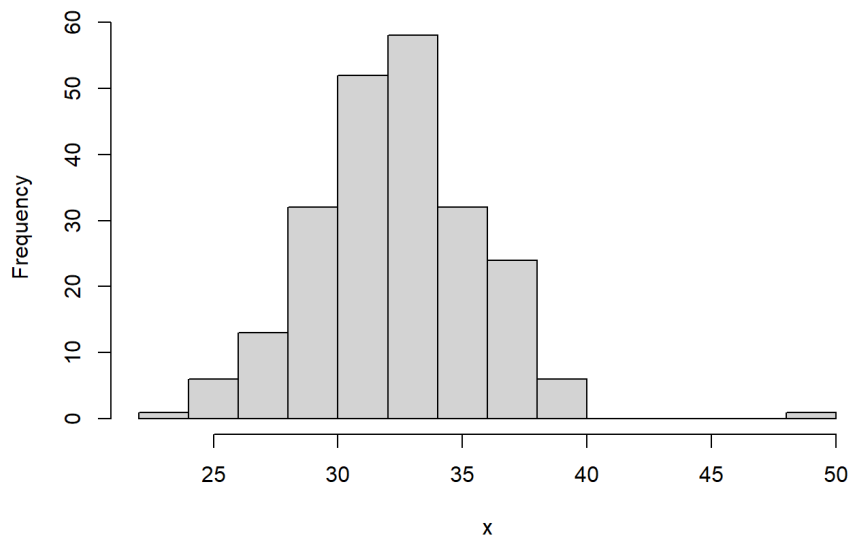
Histogram of x

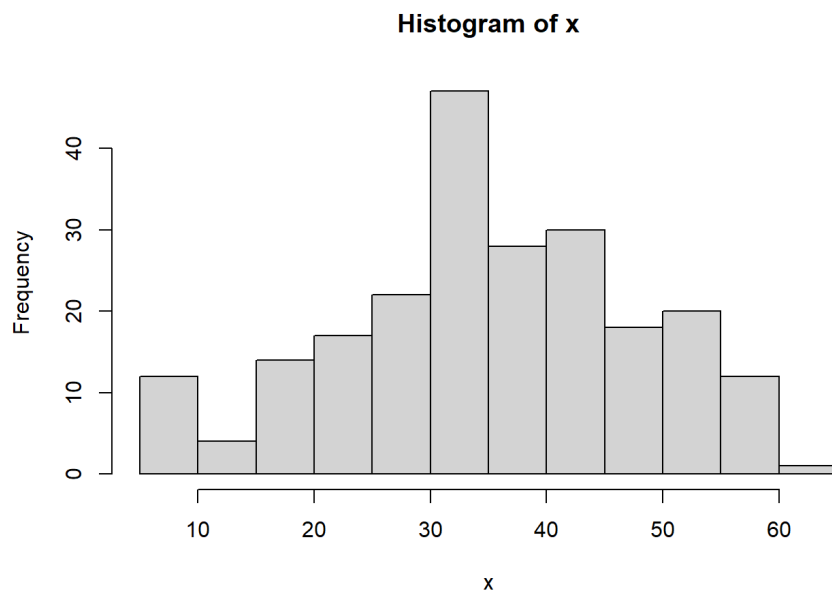


Histogram of x



Histogram of x





\$R
NULL

\$G
NULL

\$B
NULL

\$Brightness
NULL

\$R.per
NULL

\$G.per
NULL

\$B.per
NULL

RGB VALUES BASED ON ZONES

▼ Code

```
zone_difference = function(var1){
  data1%>%
    select(animal,zone, var1)%>%
    pivot_wider(names_from = zone, values_from = var1)%>%
    mutate(ba=b-a)%>%
    mutate(bc=b-c)%>%
    skim()%>%
    yank("numeric") %>%
    gt()%>%
    cols_hide(columns = c("n_missing","complete_rate","hist","p0","p25","p75","p100"))
  tab_header(
    title = paste0(var1," Descriptive Statistics")
  )
}

zone_difference("R")
```

R DESCRIPTIVE STATISTICS			
skim_variable	mean	sd	p50
animal	38.266667	22.20441	38
a	71.946667	35.05166	64
b	79.213333	36.59652	72
c	63.200000	32.93934	59

R DESCRIPTIVE STATISTICS			
skim_variable	mean	sd	p50
ba	7.266667	18.38943	4
bc	16.013333	20.94103	11

▼ Code

```
zone_difference("G")
```

G DESCRIPTIVE STATISTICS			
skim_variable	mean	sd	p50
animal	38.26667	22.20441	38
a	79.54667	41.16588	76
b	95.70667	43.56318	101
c	67.00000	40.81865	63
ba	16.16000	24.89928	11
bc	28.70667	28.81477	22

▼ Code

```
zone_difference("B")
```

B DESCRIPTIVE STATISTICS			
skim_variable	mean	sd	p50
animal	38.26667	22.20441	38
a	90.70667	61.09115	77
b	114.42667	64.40605	119
c	78.78667	60.28094	63
ba	23.72000	35.69865	17
bc	35.64000	40.27931	25

▼ Code

```
zone_difference("Brightness")
```

BRIGHTNESS DESCRIPTIVE STATISTICS			
skim_variable	mean	sd	p50
animal	38.26667	22.20441	38.00000
a	80.43923	38.90327	73.60243
b	95.33636	40.48760	99.30199
c	69.09836	38.41702	61.38813
ba	14.89713	22.82116	12.40201
bc	26.23800	26.56214	21.83999

DISRUPTIVE

▼ Code

```
zone_difference = function(var1){
  data1%>%
    filter(Disruptive=="Yes")%>%
    select(animal,zone, var1)%>%
    pivot_wider(names_from = zone, values_from = var1)%>%
    mutate(ba=b-a)%>%
```

```
mutate(bc=b-c)%>%
  skim()%>%
  yank("numeric") %>%
  gt()%>%
  cols_hide(columns = c("n_missing","complete_rate","hist","p0","p25","p75","p100"))
tab_header(
  title = paste0(var1," Descriptive Statistics")
)
}

zone_difference("R")
```

R DESCRIPTIVE STATISTICS			
skim_variable	mean	sd	p50
animal	43.60000	21.54000	50
a	65.46667	28.02516	56
b	87.53333	36.74792	80
c	54.26667	21.63815	47
ba	22.06667	19.48064	26
bc	33.26667	20.61368	35

▼ Code

```
zone_difference("G")
```

G DESCRIPTIVE STATISTICS			
skim_variable	mean	sd	p50
animal	43.60000	21.54000	50
a	62.00000	26.94704	60
b	112.06667	32.71624	113
c	46.86667	21.13855	38
ba	50.06667	13.72936	54
bc	65.20000	18.90276	62

▼ Code

```
zone_difference("B")
```

B DESCRIPTIVE STATISTICS			
skim_variable	mean	sd	p50
animal	43.60000	21.54000	50
a	55.46667	36.54716	45
b	129.26667	49.74430	119
c	42.33333	31.54060	31
ba	73.80000	32.95495	61
bc	86.93333	39.61325	72

▼ Code

```
zone_difference("Brightness")
```

BRIGHTNESS DESCRIPTIVE STATISTICS			
skim_variable	mean	sd	p50
animal	43.60000	21.54000	50.00000

BRIGHTNESS DESCRIPTIVE STATISTICS			
skim_variable	mean	sd	p50
a	63.08170	26.76210	61.45873
b	108.77283	32.12153	103.74699
c	49.21074	21.55823	40.46701
ba	45.69114	12.29808	47.78869
bc	59.56209	17.14639	55.25066

NON-DISRUPTIVE

▼ Code

```
zone_difference = function(var1){
  data1%>%
    filter(Disruptive=="No")%>%
    select(animal,zone, var1)%>%
    pivot_wider(names_from = zone, values_from = var1)%>%
    mutate(ba=b-a)%>%
    mutate(bc=b-c)%>%
    skim()%>%
    yank("numeric") %>%
    gt()%>%
    cols_hide(columns = c("n_missing","complete_rate","hist","p0","p25","p75","p100"))
  tab_header(
    title = paste0(var1," Descriptive Statistics")
  )
}

zone_difference("R")
```

R DESCRIPTIVE STATISTICS			
skim_variable	mean	sd	p50
animal	36.933333	22.34390	34.5
a	73.566667	36.62331	66.0
b	77.133333	36.57009	69.5
c	65.433333	34.99122	61.0
ba	3.566667	16.26306	3.0
bc	11.700000	18.83047	7.0

▼ Code

```
zone_difference("G")
```

G DESCRIPTIVE STATISTICS			
skim_variable	mean	sd	p50
animal	36.933333	22.34390	34.5
a	83.933333	43.07340	80.0
b	91.616667	45.17953	97.5
c	72.033333	43.06871	69.5
ba	7.683333	19.17050	4.0
bc	19.583333	23.09471	13.5

▼ Code

```
zone_difference("B")
```

B DESCRIPTIVE STATISTICS			
skim_variable	mean	sd	p50
animal	36.933333	22.34390	34.5
a	99.51667	63.00296	108.0
b	110.71667	67.42104	118.5
c	87.90000	62.44420	77.0
ba	11.20000	23.31639	3.0
bc	22.81667	28.74758	12.0

▼ Code

```
zone_difference("Brightness")
```

BRIGHTNESS DESCRIPTIVE STATISTICS			
skim_variable	mean	sd	p50
animal	36.933333	22.34390	34.500000
a	84.778616	40.40480	80.171878
b	91.977242	41.87835	96.937831
c	74.070263	40.18846	67.868953
ba	7.198626	17.77550	5.211342
bc	17.906979	21.49999	12.538154

STATS TEST ON DIFFERENT GROUPS (REPEATED TEST)

FRIEDMAN TEST

▼ Code

```
# Friedman repeated measure test
# Create a function that extracts only the desired components
friedman_test_extract <- function(var1) {
  test_result <- friedman.test(var1 ~ zone | animal, data = data1)
  c(statistic = test_result$statistic,
    parameter = test_result$parameter,
    p.value = test_result$p.value)
}

# Apply the function to each variable
results <- sapply(data1[,3:6], friedman_test_extract)

# Convert to a data frame for better formatting
results_df <- as.data.frame(results)

# Add row names as a new column
results_df <- tibble::rownames_to_column(results_df, var = "Measure")

# Create a nicer table with the gt package
library(gt)
results_df %>%
  gt() %>%
  tab_header(
    title = "Friedman Test Results"
  ) %>%
  fmt_number(columns = -1, decimals = 3) %>% # Format all columns except the first or
  tab_style(
    style = cell_text(weight = "bold"),
    locations = cells_column_labels(columns = everything())
  )
```

FRIEDMAN TEST RESULTS				
Measure	R	G	B	Brightness
statistic.Friedman chi-squared	42.067	52.827	54.460	55.387
parameter.df	2.000	2.000	2.000	2.000
p.value	0.000	0.000	0.000	0.000

FRIEDMAN POST-HOC TEST

▼ Code

```
friedman_posth_func=function(var1){
  frdAllPairsNemenyiTest(var1 ~ zone | animal, data = data1)
}

lapply(data1[,3:6],friedman_posth_func)
```

\$R

```
      a      b
b 0.01188 -
c 0.00095 3.3e-10
```

\$G

```
      a      b
b 0.00545 -
c 0.00013 2e-12
```

\$B

```
      a      b
b 0.00051 -
c 0.00130 1.1e-12
```

\$Brightness

```
      a      b
b 0.00235 -
c 0.00013 3.5e-13
```

DISRUPTIVE VS NON DISRUPTIVE COLOR BRIGHTNESS

▼ Code

```
wilcox.test(R~Disruptive,data1,conf.int=T)
```

Wilcoxon rank sum test with continuity correction

```
data:  R by Disruptive
W = 4250, p-value = 0.6095
alternative hypothesis: true location shift is not equal to 0
95 percent confidence interval:
 -7.000012 12.000030
sample estimates:
difference in location
      2.999932
```

▼ Code

```
wilcox.test(G~Disruptive,data1,conf.int=T)
```

Wilcoxon rank sum test with continuity correction

```
data:  G by Disruptive
W = 4552, p-value = 0.1991
alternative hypothesis: true location shift is not equal to 0
```

95 percent confidence interval:
-4.999981 23.000020
sample estimates:
difference in location
8.000009

▼ Code

```
wilcox.test(B~Disruptive,data1,conf.int=T)
```

Wilcoxon rank sum test with continuity correction

data: B by Disruptive
W = 4863.5, p-value = 0.03737
alternative hypothesis: true location shift is not equal to 0
95 percent confidence interval:
1.00004 46.99999
sample estimates:
difference in location
24.00004

▼ Code

```
wilcox.test(Brightness~Disruptive,data1,conf.int=T)
```

Wilcoxon rank sum test with continuity correction

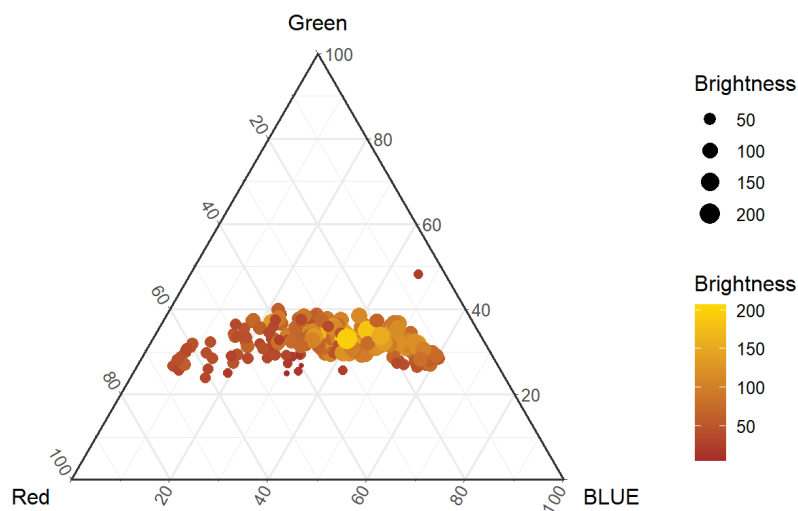
data: Brightness by Disruptive
W = 4697.5, p-value = 0.09762
alternative hypothesis: true location shift is not equal to 0
95 percent confidence interval:
-1.743913 23.532075
sample estimates:
difference in location
9.612739

DATA VISUALIZATION

▼ Code

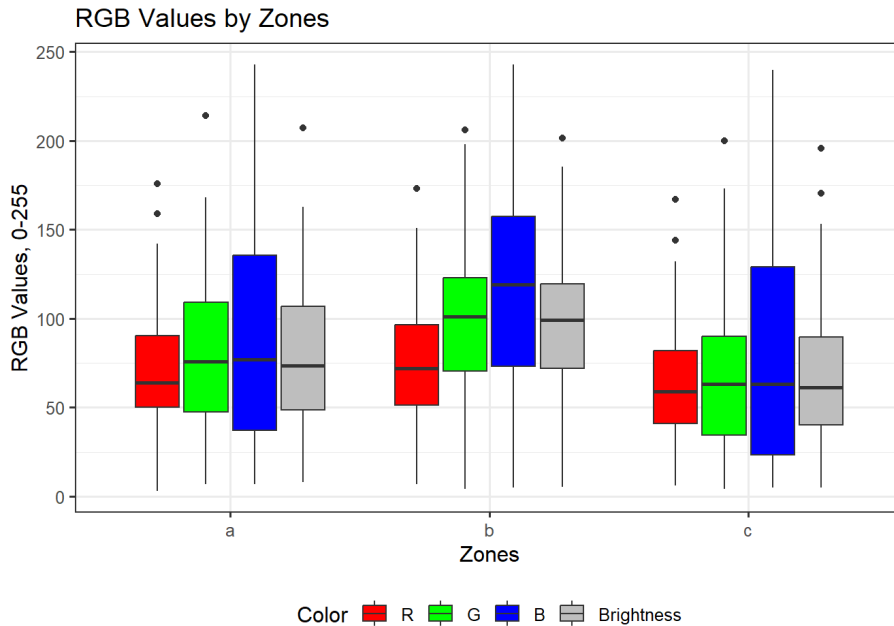
```
# Ternary Graph  
data1 %>% filter(!(zone %in% c("sub.R", "sub.L")))%>% # remove substrate data  
ggtern(aes(x = R, y = G, z = B)) + #ternary graph  
  geom_point(aes(size = Brightness, color = Brightness)) +  
  scale_size_continuous(range = c(1, 5)) +  
  scale_color_continuous(low = "brown", high = "gold") +  
  theme_rgbw() +  
  labs(x = "Red", y = "Green", z = "BLUE",  
       title = "RGB Ternary Plot with Brightness Bubbles") +  
  theme_bw()
```

RGB Ternary Plot with Brightness Bubbles



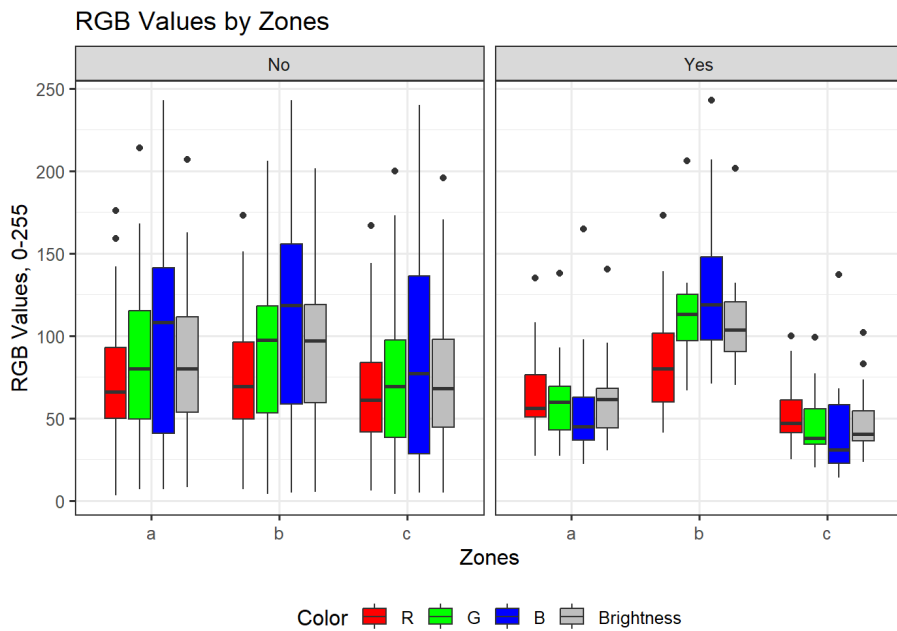
▼ Code

```
# Boxplot based on zones
data1 %>%
  pivot_longer(cols = c(R, G, B, Brightness),
               names_to = "Color",
               values_to = "Value")%>%
  mutate(Color = factor(Color, levels = c("R", "G", "B", "Brightness"))) %>%
  ggplot(aes(x = zone, y = Value, fill = Color)) +
  geom_boxplot() +
  scale_fill_manual(values = c("R" = "red", "G" = "green", "B" = "blue", "Brightness" = "gray")) +
  labs(title = "RGB Values by Zones",
       x = "Zones",
       y = "RGB Values, 0-255") +
  theme_bw() +
  theme(legend.position = "bottom")
```



▼ Code

```
# Boxplot based on zones & Disruptive
data1 %>%
  pivot_longer(cols = c(R, G, B, Brightness),
               names_to = "Color",
               values_to = "Value")%>%
  mutate(Color = factor(Color, levels = c("R", "G", "B", "Brightness"))) %>%
  ggplot(aes(x = zone, y = Value, fill = Color)) +
  geom_boxplot() +
  scale_fill_manual(values = c("R" = "red", "G" = "green", "B" = "blue", "Brightness" = "gray")) +
  facet_wrap("Disruptive") +
  labs(title = "RGB Values by Zones",
       x = "Zones",
       y = "RGB Values, 0-255") +
  theme_bw() +
  theme(legend.position = "bottom")
```



BEHAVIOR

BEHAVIOUR VS ARMS

▼ Code

```
BA=table(behav$Behaviour, behav$Arms)
BA
```

	curled	No	raised
Hovering	0	21	1
Sitting	94	94	6

▼ Code

```
#barplot(BA,beside = T,legend=T, main = "Arm Behaviour", xlab = "Arm Behaviour")
## Chi Square
chisq.test(BA,correct=T)
```

Pearson's Chi-squared test

data: BA
X-squared = 18.987, df = 2, p-value = 7.534e-05

▼ Code

```
## Post-hoc
sigAdj=0.05/6#number of categories of VAR1*VAR2
qnorm(sigAdj/2)#get the residual as post-hoc for chi-square, bonferonni adjustment
```

[1] -2.638257

▼ Code

```
chisq.test(BA,correct=T)$stdres # any value exceed or less than AdjSig will be known as
```

	curled	No	raised
Hovering	-4.3443155	4.1873185	0.3646567
Sitting	4.3443155	-4.1873185	-0.3646567

BEHAVIOUR VS DISRUPTION

▼ Code

```
BD=table(behav$Behaviour, behav$Disruptive)
BD
```

	No	Yes
Hovering	22	0
Sitting	171	23

▼ Code

```
#barplot(BD,beside = T,legend=T, main = "Disruptive with Behaviour", xlab = "Behaviour")
## Chi Square
chisq.test(BD,correct=T)
```

Pearson's Chi-squared test with Yates' continuity correction

data: BD
X-squared = 1.806, df = 1, p-value = 0.179

▼ Code

```
## Post-hoc
sigAdj=0.05/4#number of categories of VAR1*VAR2
qnorm(sigAdj/2)#get the residual as post-hoc for chi-square, bonferonni adjustment
```

[1] -2.497705

▼ Code

```
chisq.test(BD,correct=T)$stdres # any value exceed or less than AdjSig will be known as significant
```

	No	Yes
Hovering	1.70853	-1.70853
Sitting	-1.70853	1.70853

ARMS VS DISRUPTION

▼ Code

```
AD=table(behav$Arms, behav$Disruptive)
AD
```

	No	Yes
curled	83	11
No	103	12
raised	7	0

▼ Code

```
#barplot(AD,beside = T,legend=T, main = "Disruptive with Arm Behaviour", xlab = "Arm Behaviour")
## Chi Square
chisq.test(AD,correct=T)
```

Pearson's Chi-squared test

data: AD
X-squared = 0.94945, df = 2, p-value = 0.6221

▼ Code

```
## Post-hoc
sigAdj=0.05/4#number of categories of VAR1*VAR2
qnorm(sigAdj/2)#get the residual as post-hoc for chi-square, bonferonni adjustment
```

[1] -2.497705

▼ Code

```
chisq.test(AD,correct=T)$stdres # any value exceed or less than AdjSig will be known as significant
```

	No	Yes
curled	-0.4408128	0.4408128
No	0.1084802	-0.1084802
raised	0.9285131	-0.9285131

ZONE:

BLUE PROC

ZONE A

▼ Code

```
data1_a=data1 %>%  
  filter(zone %in% c("a"))  
  
wilcox.test(B~Disruptive,data1_a,conf.int=T)
```

Wilcoxon rank sum test with continuity correction

```
data: B by Disruptive  
W = 624, p-value = 0.02153  
alternative hypothesis: true location shift is not equal to 0  
95 percent confidence interval:  
 6.000049 80.000010  
sample estimates:  
difference in location  
 43.99999
```

▼ Code

```
data1_a_roc_B <- roc(data1_a$Disruptive, data1_a$B)  
data1_a_roc_B$auc
```

Area under the curve: 0.6933

▼ Code

```
data1_a_roc_B.y = coords(data1_a_roc_B, x="best", best.method="youden")  
data1_a_roc_B.y
```

	threshold	specificity	sensitivity
1	99.5	0.5333333	0.9333333
2	75.5	0.6000000	0.8666667

▼ Code

```
data1_a_roc_B.y$sensitivity+data1_a_roc_B.y$specificity-1
```

```
[1] 0.4666667 0.4666667
```

ZONE B

▼ Code

```
data1_b=data1 %>%  
  filter(zone %in% c("b"))  
  
wilcox.test(B~Disruptive,data1_b,conf.int=T)
```

Wilcoxon rank sum test with continuity correction

```
data: B by Disruptive  
W = 395.5, p-value = 0.4744  
alternative hypothesis: true location shift is not equal to 0  
95 percent confidence interval:  
 -57.00006 24.99999  
sample estimates:  
difference in location  
 -12.00006
```

▼ Code

```
data1_b_roc_B <- roc(data1_b$Disruptive, data1_b$B)  
data1_b_roc_B$auc
```

Area under the curve: 0.5606

▼ Code

```
data1_b_roc_B.y = coords(data1_b_roc_B, x="best", best.method="youden")
data1_b_roc_B.y
```

```
threshold specificity sensitivity
1      69.5      0.2833333      1
```

▼ Code

```
data1_b_roc_B.y$sensitivity+data1_b_roc_B.y$specificity-1
```

```
[1] 0.2833333
```

ZONE C

▼ Code

```
data1_c=data1 %>%
  filter(zone %in% c("c"))

wilcox.test(B~Disruptive,data1_c,conf.int=T)
```

Wilcoxon rank sum test with continuity correction

```
data: B by Disruptive
W = 623, p-value = 0.02231
alternative hypothesis: true location shift is not equal to 0
95 percent confidence interval:
 3.000065 77.999997
sample estimates:
difference in location
      40.99995
```

▼ Code

```
data1_c_roc_B <- roc(data1_c$Disruptive, data1_c$B)
data1_c_roc_B$auc
```

Area under the curve: 0.6922

▼ Code

```
data1_c_roc_B.y = coords(data1_c_roc_B, x="best", best.method="youden")
data1_c_roc_B.y
```

```
threshold specificity sensitivity
1      69.5      0.55      0.9333333
```

▼ Code

```
data1_c_roc_B.y$sensitivity+data1_c_roc_B.y$specificity-1
```

```
[1] 0.4833333
```

BRIGHTNESS PROC

ZONE A

▼ Code

```
wilcox.test(Brightness~Disruptive,data1_a,conf.int=T)
```

Wilcoxon rank sum test with continuity correction

```
data: Brightness by Disruptive
W = 610, p-value = 0.03463
alternative hypothesis: true location shift is not equal to 0
95 percent confidence interval:
 1.597214 40.830235
sample estimates:
difference in location
      19.74039
```

▼ Code

```
data1_a_roc_I <- roc(data1_a$Disruptive, data1_a$Brightness)
data1_a_roc_I$auc
```

Area under the curve: 0.6778

▼ Code

```
data1_a_roc_I.y = coords(data1_a_roc_I, x="best", best.method="youden")
data1_a_roc_I.y
```

```
threshold specificity sensitivity
1 70.30714          0.65    0.8666667
```

▼ Code

```
data1_a_roc_I.y$sensitivity+data1_a_roc_I.y$specificity-1
```

```
[1] 0.5166667
```

ZONE B

▼ Code

```
wilcox.test(Brightness~Disruptive,data1_b,conf.int=T)
```

Wilcoxon rank sum test with continuity correction

```
data: Brightness by Disruptive
W = 350.5, p-value = 0.1898
alternative hypothesis: true location shift is not equal to 0
95 percent confidence interval:
 -36.43391   5.73014
sample estimates:
difference in location
      -14.82684
```

▼ Code

```
data1_b_roc_I <- roc(data1_b$Disruptive, data1_b$Brightness)
data1_b_roc_I$auc
```

Area under the curve: 0.6106

▼ Code

```
data1_b_roc_I.y = coords(data1_b_roc_I, x="best", best.method="youden")
data1_b_roc_I.y
```

```
threshold specificity sensitivity
1 70.02904    0.2833333          1
```

▼ Code

```
data1_b_roc_I.y$sensitivity+data1_b_roc_I.y$specificity-1
```

```
[1] 0.2833333
```

ZONE C

▼ Code

```
wilcox.test(Brightness~Disruptive,data1_c,conf.int=T)
```

Wilcoxon rank sum test with continuity correction

```
data: Brightness by Disruptive
W = 629, p-value = 0.01806
alternative hypothesis: true location shift is not equal to 0
95 percent confidence interval:
  3.709275 39.044348
sample estimates:
difference in location
      21.69738
```

▼ Code

```
data1_c_roc_I <- roc(data1_c$Disruptive, data1_c$Brightness)
data1_c_roc_I$auc
```

Area under the curve: 0.6989

▼ Code

```
data1_c_roc_I.y = coords(data1_c_roc_I, x="best", best.method="youden")
data1_c_roc_I.y
```

```
threshold specificity sensitivity
1 60.69699 0.6000000 0.8000000
2 48.80283 0.6666667 0.7333333
```

▼ Code

```
data1_c_roc_I.y$sensitivity+data1_c_roc_I.y$specificity-1
```

```
[1] 0.4 0.4
```

ZONE DIFFERENCES

BRIGHTNESS PROC

DISRUPTIVE_ZONE AB

▼ Code

```
data1_ab=data1%>%filter((zone %in% c("a", "b")))%>%
  select(Animal,Disruptive, zone, Brightness)%>%
  pivot_wider(
    names_from = zone,
    values_from = Brightness)%>%
  mutate(AB= b-a)%>%
  mutate(AB.per=(b-a)*100/mean(b+a))%>%
  mutate(AB.rat=b/a)
```

AB

▼ Code

```
wilcox.test(AB~Disruptive,data1_ab,conf.int=T)
```

Wilcoxon rank sum test with continuity correction

```
data: AB by Disruptive
W = 37, p-value = 4.663e-08
alternative hypothesis: true location shift is not equal to 0
95 percent confidence interval:
 -48.35916 -31.35009
sample estimates:
difference in location
 -39.38569
```

▼ Code

```
# ROC Curve
## Empirical
data1_ab_roc_AB <- roc(data1_ab$Disruptive, data1_ab$AB)
data1_ab_roc_AB$auc
```

Area under the curve: 0.9589

▼ Code

```
# 1.0: Perfect classification,
# 0.9-0.99: Excellent discrimination,
# 0.8-0.89: Good discrimination,
# 0.7-0.79: Fair discrimination,
# 0.6-0.69: Poor discrimination,
# 0.5: No discrimination,
# <0.5: Something is wrong

data1_ab_roc_AB.y = coords(data1_ab_roc_AB, x="best", best.method="youden")
data1_ab_roc_AB.y
```

```
threshold specificity sensitivity
1 21.4173 0.8666667 1
```

▼ Code

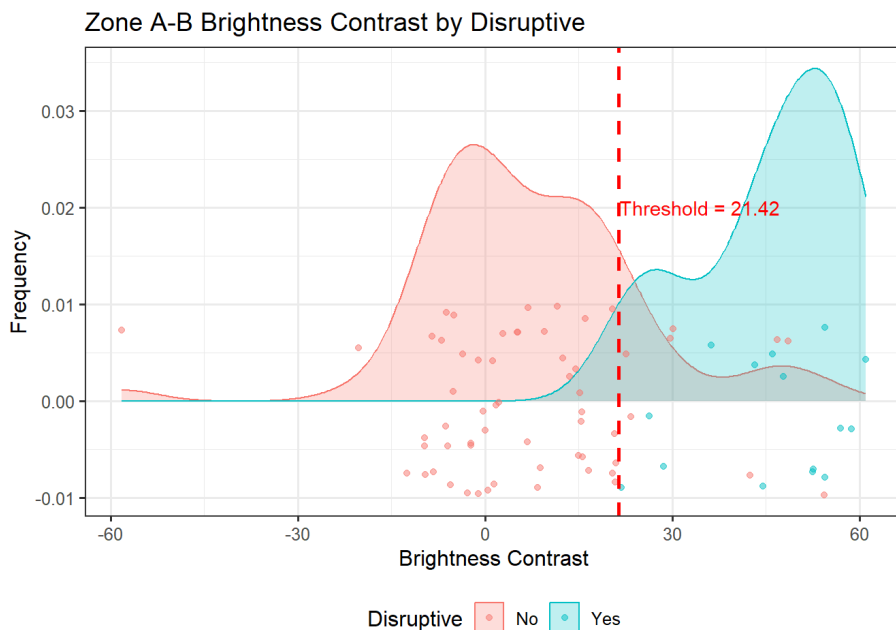
```
# Sensitivity = Correctly identifies % of the positive cases
# Specificity = Correctly identifies % of the negative cases

# Youden Index
data1_ab_roc_AB.y$sensitivity+data1_ab_roc_AB.y$specificity-1
```

```
[1] 0.8666667
```

▼ Code

```
ggplot(data1_ab, aes(x = AB, fill=Disruptive, color=Disruptive)) +
  geom_density(alpha = 0.25) +
  geom_point(aes(y = 0), position = position_jitter(height = 0.01), alpha = 0.5) +
  geom_vline(xintercept = data1_ab_roc_AB.y$threshold, linetype = "dashed", color = "red") +
  annotate("text",
    x = data1_ab_roc_AB.y$threshold + 0.1, # offset the text slightly to the right
    y = 0.02, # adjust this value to position the text at your desired height
    label = paste("Threshold =", round(data1_ab_roc_AB.y$threshold, 2)),
    color = "red",
    hjust = 0) +
  labs(title = "Zone A-B Brightness Contrast by Disruptive",
    x = "Brightness Contrast",
    y = "Frequency") +
  theme_bw() +
  theme(legend.position = "bottom")
```



AB %

▼ Code

```
wilcox.test(AB.per~Disruptive,data1_ab,conf.int=T)
```

Wilcoxon rank sum test with continuity correction

```
data: AB.per by Disruptive
W = 37, p-value = 4.663e-08
alternative hypothesis: true location shift is not equal to 0
95 percent confidence interval:
-27.51187 -17.83527
sample estimates:
difference in location
-22.40458
```

▼ Code

```
# Percentage
data1_ab_roc_AB.per <- roc(data1_ab$Disruptive, data1_ab$AB.per)
data1_ab_roc_AB.per$auc
```

Area under the curve: 0.9589

▼ Code

```
data1_ab_roc_AB.per.y = coords(data1_ab_roc_AB.per, x="best", best.method="youden")
data1_ab_roc_AB.per.y
```

```
threshold specificity sensitivity
1 12.18445 0.8666667 1
```

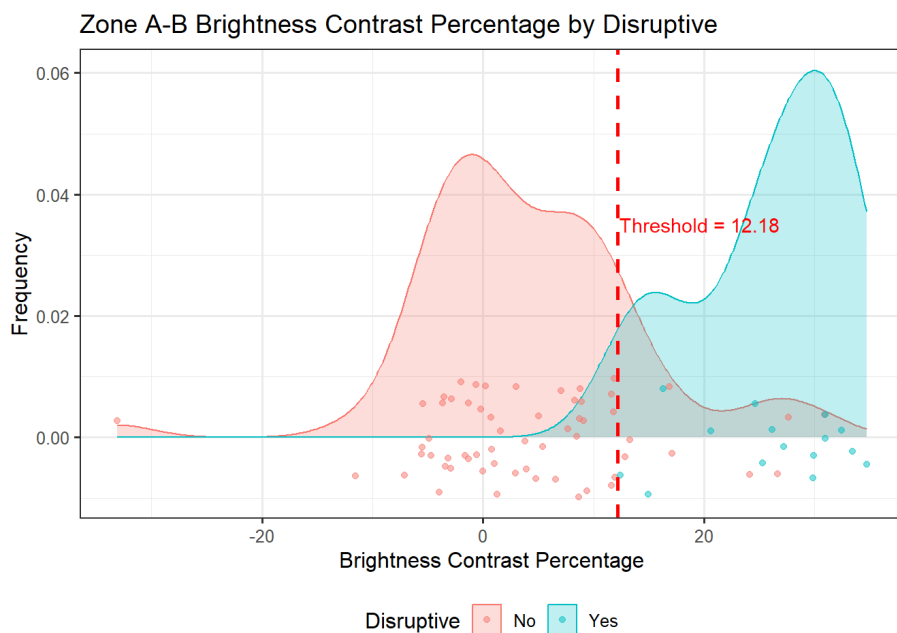
▼ Code

```
data1_ab_roc_AB.per.y$sensitivity+data1_ab_roc_AB.per.y$specificity-1
```

```
[1] 0.8666667
```

▼ Code

```
ggplot(data1_ab, aes(x = AB.per, fill=Disruptive,color=Disruptive)) +
  geom_density(alpha = 0.25) +
  geom_point(aes(y = 0), position = position_jitter(height = 0.01), alpha = 0.5) +
  geom_vline(xintercept = data1_ab_roc_AB.per.y$threshold, linetype = "dashed", color = "red",
    annotate("text",
      x = data1_ab_roc_AB.per.y$threshold + 0.1, # offset the text slightly to the right
      y = 0.035, # adjust this value to position the text at your desired height
      label = paste("Threshold =", round(data1_ab_roc_AB.per.y$threshold, 2)),
      color = "red",
      hjust = 0) +
  labs(title = "Zone A-B Brightness Contrast Percentage by Disruptive",
    x = "Brightness Contrast Percentage",
    y = "Frequency") +
  theme_bw() +
  theme(legend.position = "bottom")
```



AB RATIO

▼ Code

```
wilcox.test(AB.rat~Disruptive,data1_ab,conf.int=T)
```

Wilcoxon rank sum test with continuity correction

```
data: AB.rat by Disruptive
W = 33, p-value = 3.455e-08
alternative hypothesis: true location shift is not equal to 0
95 percent confidence interval:
 -0.8426198 -0.4919721
sample estimates:
difference in location
 -0.6912148
```

▼ Code

```
# Ratio
data1_ab_roc_AB.rat <- roc(data1_ab$Disruptive, data1_ab$AB.rat)
data1_ab_roc_AB.rat$auc
```

Area under the curve: 0.9633

▼ Code

```
data1_ab_roc_AB.rat.y = coords(data1_ab_roc_AB.rat, x="best", best.method="youden")
data1_ab_roc_AB.rat.y
```

```
threshold specificity sensitivity
1 1.360975 0.8666667 1
```

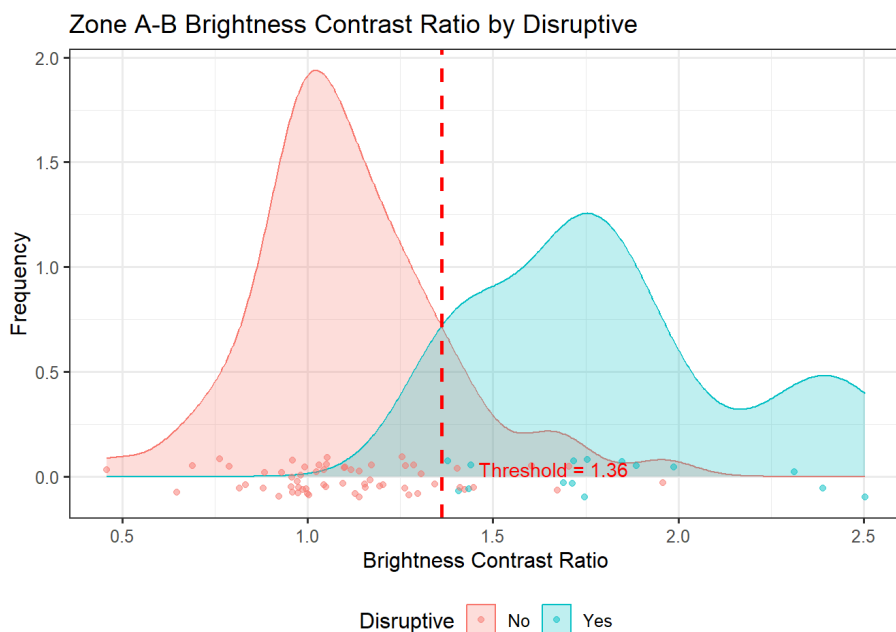
▼ Code

```
data1_ab_roc_AB.rat.y$sensitivity+data1_ab_roc_AB.rat.y$specificity-1
```

```
[1] 0.8666667
```

▼ Code

```
ggplot(data1_ab, aes(x = AB.rat, fill=Disruptive, color=Disruptive)) +
  geom_density(alpha = 0.25) +
  geom_point(aes(y = 0), position = position_jitter(height = 0.1), alpha = 0.5) +
  geom_vline(xintercept = data1_ab_roc_AB.rat.y$threshold, linetype = "dashed", color = "red",
    annotate("text",
      x = data1_ab_roc_AB.rat.y$threshold + 0.1, # offset the text slightly to the right
      y = 0.035, # adjust this value to position the text at your desired height
      label = paste("Threshold =", round(data1_ab_roc_AB.rat.y$threshold, 2)),
      color = "red",
      hjust = 0) +
  labs(title = "Zone A-B Brightness Contrast Ratio by Disruptive",
    x = "Brightness Contrast Ratio",
    y = "Frequency") +
  theme_bw() +
  theme(legend.position = "bottom")
```



DISRUPTIVE_ZONE BC

▼ Code

```
data1_bc=data1%>%filter((zone %in% c("c", "b")))%>%
  select(animal,Disruptive, zone, Brightness)%>%
  pivot_wider(
    names_from = zone,
    values_from = Brightness)%>%
  mutate(BC= b-c)%>%
  mutate(BC.per=(b-c)*100/mean(b+c))%>%
  mutate(BC.rat=b/c)
```

BC

▼ Code

```
wilcox.test(BC~Disruptive,data1_bc,conf.int=T)
```

Wilcoxon rank sum test with continuity correction

```
data: BC by Disruptive
W = 60, p-value = 2.482e-07
alternative hypothesis: true location shift is not equal to 0
95 percent confidence interval:
 -52.13545 -31.66160
sample estimates:
difference in location
 -43.36277
```

▼ Code

```
# ROC Curve
## Empirical
data1_bc_roc_BC <- roc(data1_bc$Disruptive, data1_bc$BC)
data1_bc_roc_BC$auc
```

Area under the curve: 0.9333

▼ Code

```
data1_bc_roc_BC.y = coords(data1_bc_roc_BC, x="best", best.method="youden")
data1_bc_roc_BC.y
```

```
threshold specificity sensitivity
1 35.22663 0.8166667 1
```

▼ Code

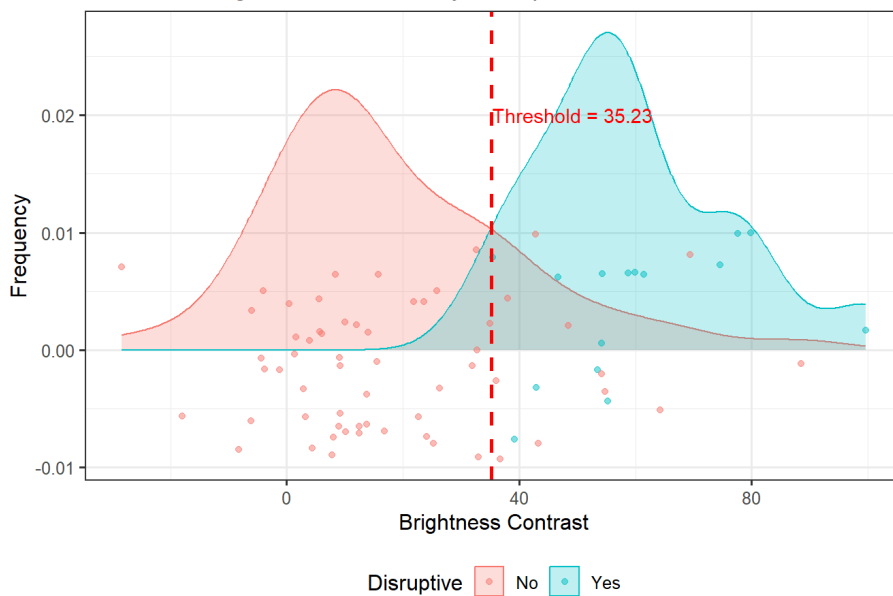
```
data1_bc_roc_BC.y$sensitivity+data1_bc_roc_BC.y$specificity-1
```

```
[1] 0.8166667
```

▼ Code

```
ggplot(data1_bc, aes(x = BC, fill=Disruptive, color=Disruptive)) +
  geom_density(alpha = 0.25) +
  geom_point(aes(y = 0), position = position_jitter(height = 0.01), alpha = 0.5) +
  geom_vline(xintercept = data1_bc_roc_BC.y$threshold, linetype = "dashed", color = "red",
    annotate("text",
      x = data1_bc_roc_BC.y$threshold + 0.1, # offset the text slightly to the right
      y = 0.02, # adjust this value to position the text at your desired height
      label = paste("Threshold =", round(data1_bc_roc_BC.y$threshold, 2)),
      color = "red",
      hjust = 0) +
  labs(title = "Zone B-C Brightness Contrast by Disruptive",
    x = "Brightness Contrast",
    y = "Frequency") +
  theme_bw()+
  theme(legend.position = "bottom")
```

Zone B-C Brightness Contrast by Disruptive



BC %

▼ Code

```
wilcox.test(BC.per~Disruptive,data1_bc,conf.int=T)
```

Wilcoxon rank sum test with continuity correction

```
data: BC.per by Disruptive
W = 60, p-value = 2.482e-07
alternative hypothesis: true location shift is not equal to 0
95 percent confidence interval:
 -31.70583 -19.25481
sample estimates:
difference in location
 -26.33077
```

▼ Code

```
# Percentage
data1_bc_roc_BC.per <- roc(data1_bc$Disruptive, data1_bc$BC.per)
data1_bc_roc_BC.per$auc
```

Area under the curve: 0.9333

▼ Code

```
data1_bc_roc_BC.per.y = coords(data1_bc_roc_BC.per, x="best", best.method="youden")
data1_bc_roc_BC.per.y
```

```
threshold specificity sensitivity
1 21.42287 0.8166667 1
```

▼ Code

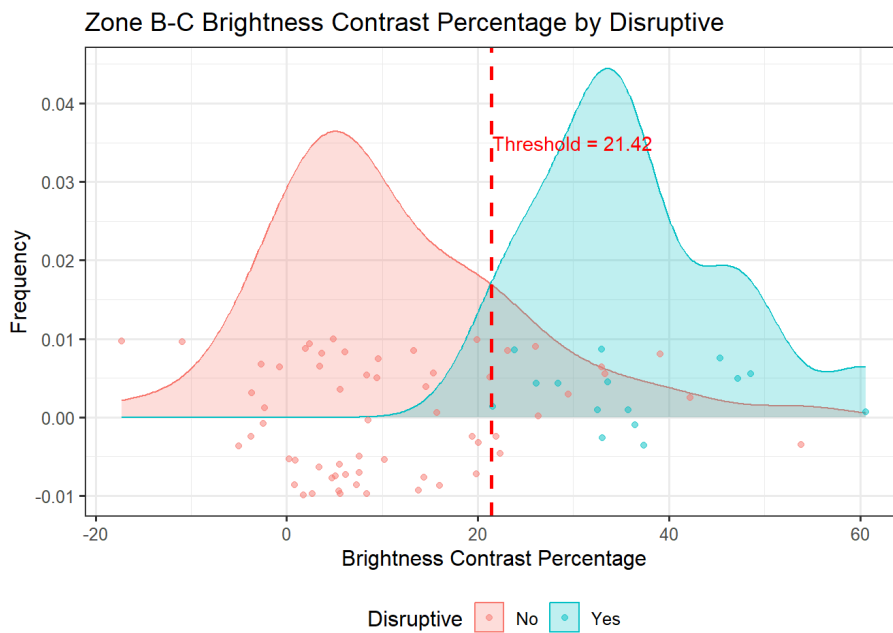
```
data1_bc_roc_BC.per.y$sensitivity+data1_bc_roc_BC.per.y$specificity-1
```

```
[1] 0.8166667
```

▼ Code

```
ggplot(data1_bc, aes(x = BC.per, fill=Disruptive,color=Disruptive)) +
  geom_density(alpha = 0.25) +
  geom_point(aes(y = 0), position = position_jitter(height = 0.01), alpha = 0.5) +
  geom_vline(xintercept = data1_bc_roc_BC.per.y$threshold, linetype = "dashed", color = "red",
    annotate("text",
      x = data1_bc_roc_BC.per.y$threshold + 0.1, # offset the text slightly to the right
      y = 0.035, # adjust this value to position the text at your desired height
      label = paste("Threshold =", round(data1_bc_roc_BC.per.y$threshold, 2)),
      color = "red",
      hjust = 0) +
  labs(title = "Zone B-C Brightness Contrast Percentage by Disruptive",
    x = "Brightness Contrast Percentage",
```

```
y = "Frequency") +
theme_bw()+
theme(legend.position = "bottom")
```



BC RATIO

▼ Code

```
wilcox.test(BC.rat~Disruptive,data1_bc,conf.int=T)
```

Wilcoxon rank sum test with continuity correction

```
data: BC.rat by Disruptive
W = 72, p-value = 5.73e-07
alternative hypothesis: true location shift is not equal to 0
95 percent confidence interval:
 -1.3509031 -0.8411773
sample estimates:
difference in location
 -1.095581
```

▼ Code

```
# Ratio
data1_bc_roc_BC.rat <- roc(data1_bc$Disruptive, data1_bc$BC.rat)
data1_bc_roc_BC.rat$auc
```

Area under the curve: 0.92

▼ Code

```
data1_bc_roc_BC.rat.y = coords(data1_bc_roc_BC.rat, x="best", best.method="youden")
data1_bc_roc_BC.rat.y
```

```
threshold specificity sensitivity
1 1.769653 0.9 0.9333333
```

▼ Code

```
data1_bc_roc_BC.rat.y$sensitivity+data1_bc_roc_BC.rat.y$specificity-1
```

```
[1] 0.8333333
```

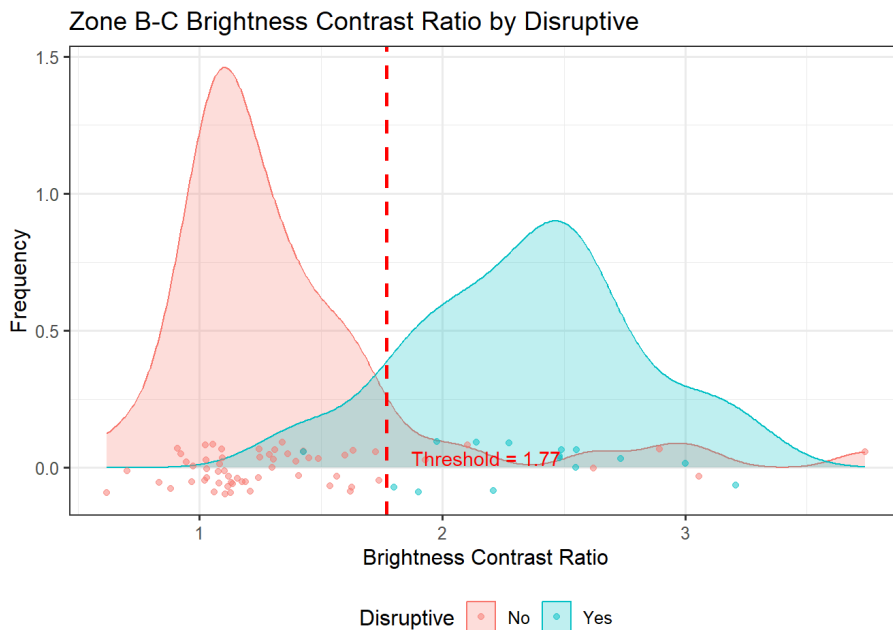
▼ Code

```
ggplot(data1_bc, aes(x = BC.rat, fill=Disruptive, color=Disruptive)) +
  geom_density(alpha = 0.25) +
  geom_point(aes(y = 0), position = position_jitter(height = 0.1), alpha = 0.5) +
  geom_vline(xintercept = data1_bc_roc_BC.rat.y$threshold, linetype = "dashed", color = "red",
    annotate("text",
      x = data1_bc_roc_BC.rat.y$threshold + 0.1, # offset the text slightly to the right
      y = 0.035, # adjust this value to position the text at your desired height
```

```

label = paste("Threshold =", round(data1_bc_roc_BC.rat.y$threshold, 2)),
color = "red",
hjust = 0) +
labs(title = "Zone B-C Brightness Contrast Ratio by Disruptive",
x = "Brightness Contrast Ratio",
y = "Frequency") +
theme_bw()+
theme(legend.position = "bottom")

```



BLUE PROC

DISRUPTIVE_ZONE AB

▼ Code

```

data1_ab=data1%>%filter((zone %in% c("a", "b")))%>%
  select(animal,Disruptive, zone, B)%>%
  pivot_wider(
    names_from = zone,
    values_from = B)%>%
  mutate(AB= b-a)%>%
  mutate(AB.per=(b-a)*100/mean(b+a))%>%
  mutate(AB.rat=b/a)

```

AB

▼ Code

```
wilcox.test(AB~Disruptive,data1_ab,conf.int=T)
```

Wilcoxon rank sum test with continuity correction

```

data: AB by Disruptive
W = 40, p-value = 5.775e-08
alternative hypothesis: true location shift is not equal to 0
95 percent confidence interval:
 -78.00005 -45.99994
sample estimates:
difference in location
 -58.99997

```

▼ Code

```

# ROC Curve
## Empirical
data1_ab_roc_AB <- roc(data1_ab$Disruptive, data1_ab$AB)
data1_ab_roc_AB$auc

```

Area under the curve: 0.9556

▼ Code

```
# 1.0: Perfect classification,
# 0.9-0.99: Excellent discrimination,
# 0.8-0.89: Good discrimination,
# 0.7-0.79: Fair discrimination,
# 0.6-0.69: Poor discrimination,
# 0.5: No discrimination,
# <0.5: Something is wrong

data1_ab_roc_AB.y = coords(data1_ab_roc_AB, x="best", best.method="youden")
data1_ab_roc_AB.y
```

```
threshold specificity sensitivity
1          44  0.9166667  0.9333333
```

▼ Code

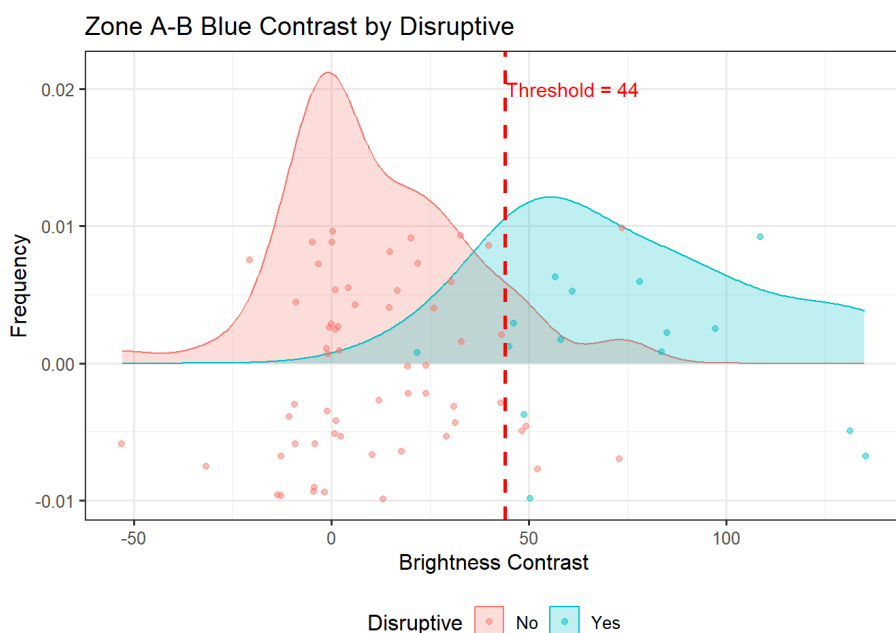
```
# Sensitivity = Correctly identifies % of the positive cases
# Specificity = Correctly identifies % of the negative cases
```

```
#Youden Index
data1_ab_roc_AB.y$sensitivity+data1_ab_roc_AB.y$specificity-1
```

```
[1] 0.85
```

▼ Code

```
ggplot(data1_ab, aes(x = AB, fill=Disruptive, color=Disruptive)) +
  geom_density(alpha = 0.25) +
  geom_point(aes(y = 0), position = position_jitter(height = 0.01), alpha = 0.5) +
  geom_vline(xintercept = data1_ab_roc_AB.y$threshold, linetype = "dashed", color = "red",
    annotate("text",
      x = data1_ab_roc_AB.y$threshold + 0.1, # offset the text slightly to the right
      y = 0.02, # adjust this value to position the text at your desired height
      label = paste("Threshold =", round(data1_ab_roc_AB.y$threshold, 2)),
      color = "red",
      hjust = 0) +
  labs(title = "Zone A-B Blue Contrast by Disruptive",
    x = "Brightness Contrast",
    y = "Frequency") +
  theme_bw() +
  theme(legend.position = "bottom")
```



AB %

▼ Code

```
wilcox.test(AB.per~Disruptive,data1_ab,conf.int=T)
```

Wilcoxon rank sum test with continuity correction

```
data: AB.per by Disruptive
W = 40, p-value = 5.775e-08
alternative hypothesis: true location shift is not equal to 0
```

95 percent confidence interval:
-38.02414 -22.42444
sample estimates:
difference in location
-28.76176

▼ Code

```
# Percentage  
data1_ab_roc_AB.per <- roc(data1_ab$Disruptive, data1_ab$AB.per)  
data1_ab_roc_AB.per$auc
```

Area under the curve: 0.9556

▼ Code

```
data1_ab_roc_AB.per.y = coords(data1_ab_roc_AB.per, x="best", best.method="youden")  
data1_ab_roc_AB.per.y
```

```
threshold specificity sensitivity  
1 21.44946 0.9166667 0.9333333
```

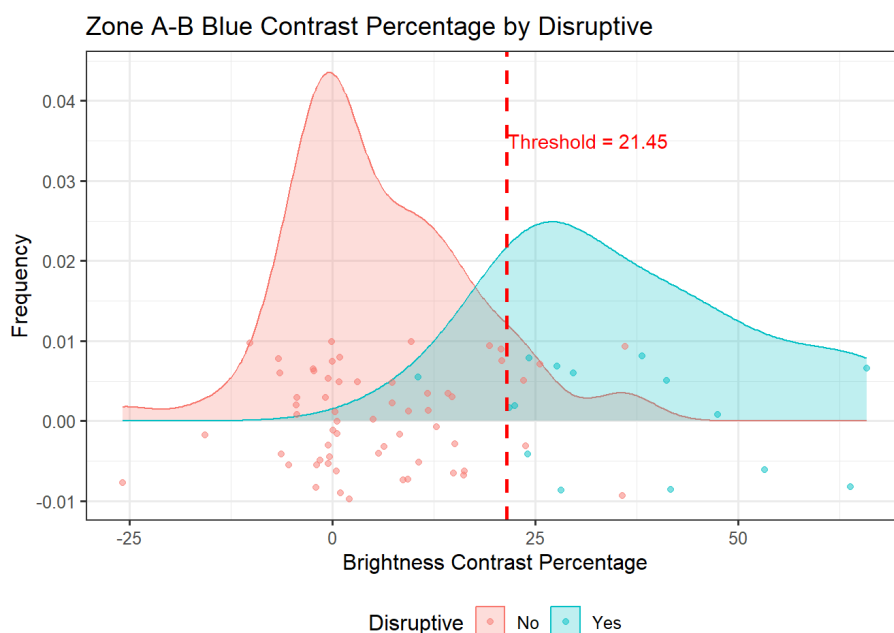
▼ Code

```
data1_ab_roc_AB.per.y$sensitivity+data1_ab_roc_AB.per.y$specificity-1
```

[1] 0.85

▼ Code

```
ggplot(data1_ab, aes(x = AB.per, fill=Disruptive,color=Disruptive)) +  
  geom_density(alpha = 0.25) +  
  geom_point(aes(y = 0), position = position_jitter(height = 0.01), alpha = 0.5) +  
  geom_vline(xintercept = data1_ab_roc_AB.per.y$threshold, linetype = "dashed", color =  
    annotate("text",  
      x = data1_ab_roc_AB.per.y$threshold + 0.1, # offset the text slightly to the  
      y = 0.035, # adjust this value to position the text at your desired height  
      label = paste("Threshold =", round(data1_ab_roc_AB.per.y$threshold, 2)),  
      color = "red",  
      hjust = 0) +  
  labs(title = "Zone A-B Blue Contrast Percentage by Disruptive",  
    x = "Brightness Contrast Percentage",  
    y = "Frequency") +  
  theme_bw() +  
  theme(legend.position = "bottom")
```



AB RATIO

▼ Code

```
wilcox.test(AB.rat~Disruptive,data1_ab,conf.int=T)
```

Wilcoxon rank sum test with continuity correction

```
data: AB.rat by Disruptive
W = 34, p-value = 3.719e-08
alternative hypothesis: true location shift is not equal to 0
95 percent confidence interval:
 -2.0193138 -0.9025919
sample estimates:
difference in location
 -1.281965
```

▼ Code

```
# Ratio
data1_ab_roc_AB.rat <- roc(data1_ab$Disruptive, data1_ab$AB.rat)
data1_ab_roc_AB.rat$auc
```

Area under the curve: 0.9622

▼ Code

```
data1_ab_roc_AB.rat.y = coords(data1_ab_roc_AB.rat, x="best", best.method="youden")
data1_ab_roc_AB.rat.y
```

```
threshold specificity sensitivity
1 1.447463 0.85 1
```

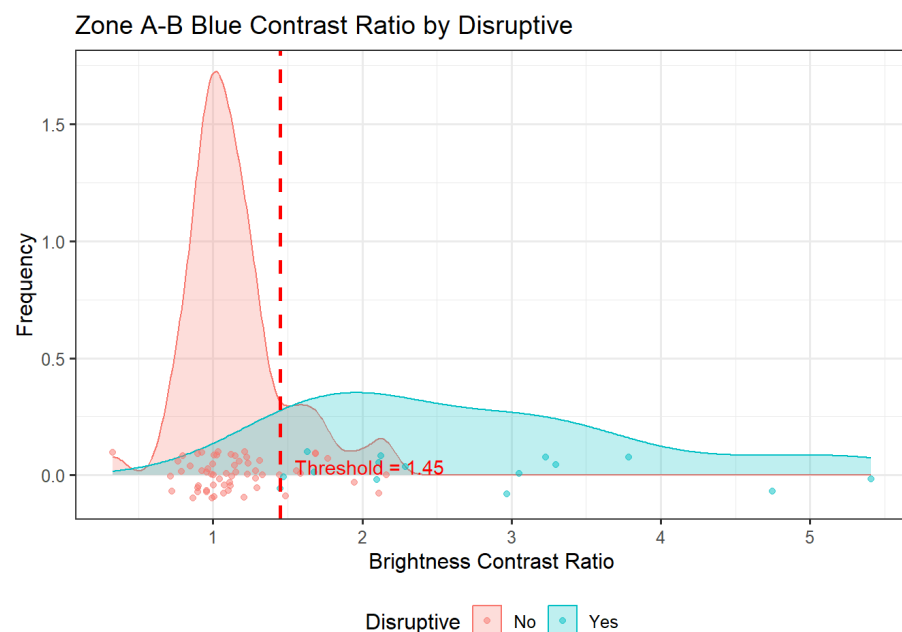
▼ Code

```
data1_ab_roc_AB.rat.y$sensitivity+data1_ab_roc_AB.rat.y$specificity-1
```

```
[1] 0.85
```

▼ Code

```
ggplot(data1_ab, aes(x = AB.rat, fill=Disruptive, color=Disruptive)) +
  geom_density(alpha = 0.25) +
  geom_point(aes(y = 0), position = position_jitter(height = 0.1), alpha = 0.5) +
  geom_vline(xintercept = data1_ab_roc_AB.rat.y$threshold, linetype = "dashed", color = "red",
    annotate("text",
      x = data1_ab_roc_AB.rat.y$threshold + 0.1, # offset the text slightly to the right
      y = 0.035, # adjust this value to position the text at your desired height
      label = paste("Threshold =", round(data1_ab_roc_AB.rat.y$threshold, 2)),
      color = "red",
      hjust = 0) +
  labs(title = "Zone A-B Blue Contrast Ratio by Disruptive",
    x = "Brightness Contrast Ratio",
    y = "Frequency") +
  theme_bw() +
  theme(legend.position = "bottom")
```



DISRUPTIVE_ZONE BC

▼ Code

```
data1_bc=data1%>%filter((zone %in% c("c", "b")))%>%
  select(animal,Disruptive, zone, B)%>%
  pivot_wider(
    names_from = zone,
    values_from = B)%>%
  mutate(BC= b-c)%>%
  mutate(BC.per=(b-c)*100/mean(b+c))%>%
  mutate(BC.rat=b/c)
```

BC

▼ Code

```
wilcox.test(BC~Disruptive,data1_bc,conf.int=T)
```

Wilcoxon rank sum test with continuity correction

```
data: BC by Disruptive
W = 71, p-value = 5.288e-07
alternative hypothesis: true location shift is not equal to 0
95 percent confidence interval:
 -80.00003 -44.00007
sample estimates:
difference in location
 -59.00005
```

▼ Code

```
# ROC Curve
## Empirical
data1_bc_roc_BC <- roc(data1_bc$Disruptive, data1_bc$BC)
data1_bc_roc_BC$auc
```

Area under the curve: 0.9211

▼ Code

```
data1_bc_roc_BC.y = coords(data1_bc_roc_BC, x="best", best.method="youden")
data1_bc_roc_BC.y
```

```
threshold specificity sensitivity
1      44.5    0.8166667    0.9333333
```

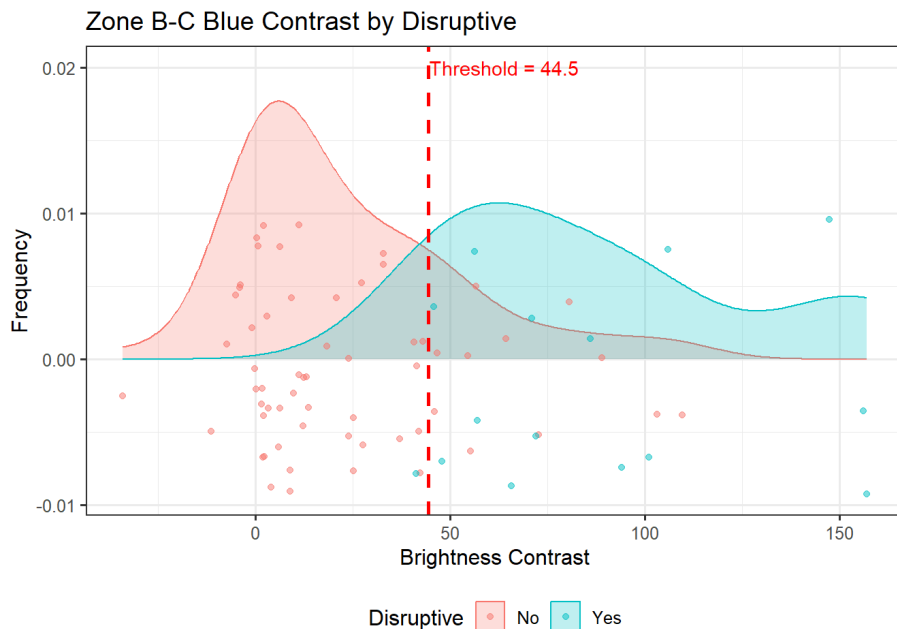
▼ Code

```
data1_bc_roc_BC.y$sensitivity+data1_bc_roc_BC.y$specificity-1
```

```
[1] 0.75
```

▼ Code

```
ggplot(data1_bc, aes(x = BC, fill=Disruptive, color=Disruptive)) +
  geom_density(alpha = 0.25) +
  geom_point(aes(y = 0), position = position_jitter(height = 0.01), alpha = 0.5) +
  geom_vline(xintercept = data1_bc_roc_BC.y$threshold, linetype = "dashed", color = "red",
    annotate("text",
      x = data1_bc_roc_BC.y$threshold + 0.1, # offset the text slightly to the right
      y = 0.02, # adjust this value to position the text at your desired height
      label = paste("Threshold =", round(data1_bc_roc_BC.y$threshold, 2)),
      color = "red",
      hjust = 0) +
  labs(title = "Zone B-C Blue Contrast by Disruptive",
    x = "Brightness Contrast",
    y = "Frequency") +
  theme_bw()+
  theme(legend.position = "bottom")
```



BC %

▼ Code

```
wilcox.test(BC.per~Disruptive,data1_bc,conf.int=T)
```

Wilcoxon rank sum test with continuity correction

```
data: BC.per by Disruptive
W = 71, p-value = 5.288e-07
alternative hypothesis: true location shift is not equal to 0
95 percent confidence interval:
 -41.40502 -22.77282
sample estimates:
difference in location
 -30.53621
```

▼ Code

```
# Percentage
data1_bc_roc_BC.per <- roc(data1_bc$Disruptive, data1_bc$BC.per)
data1_bc_roc_BC.per$auc
```

Area under the curve: 0.9211

▼ Code

```
data1_bc_roc_BC.per.y <- coords(data1_bc_roc_BC.per, x="best", best.method="youden")
data1_bc_roc_BC.per.y
```

```
threshold specificity sensitivity
1 23.03154 0.8166667 0.9333333
```

▼ Code

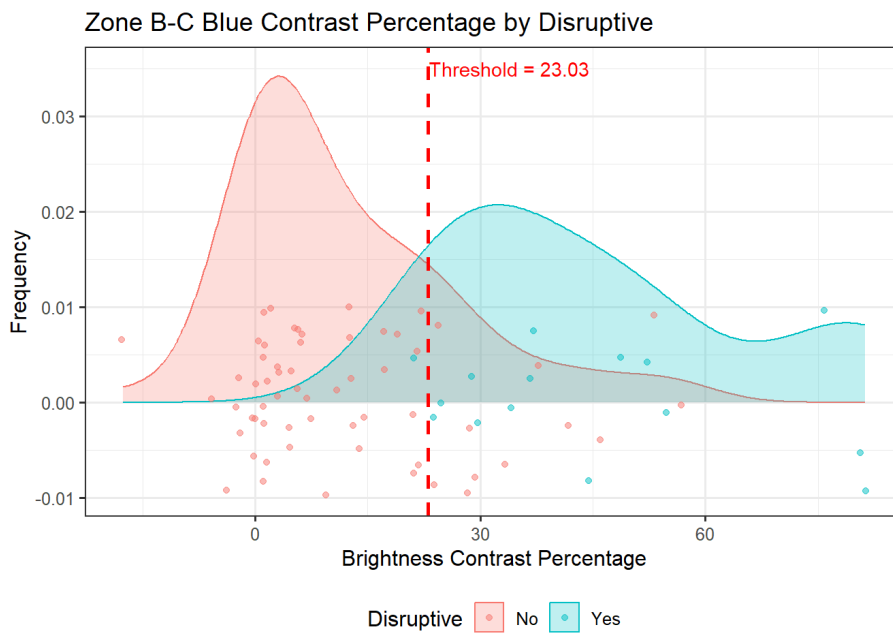
```
data1_bc_roc_BC.per.y$sensitivity+data1_bc_roc_BC.per.y$specificity-1
```

```
[1] 0.75
```

▼ Code

```
ggplot(data1_bc, aes(x = BC.per, fill=Disruptive,color=Disruptive)) +
  geom_density(alpha = 0.25) +
  geom_point(aes(y = 0), position = position_jitter(height = 0.01), alpha = 0.5) +
  geom_vline(xintercept = data1_bc_roc_BC.per.y$threshold, linetype = "dashed", color = "red",
    annotate("text",
      x = data1_bc_roc_BC.per.y$threshold + 0.1, # offset the text slightly to the right
      y = 0.035, # adjust this value to position the text at your desired height
      label = paste("Threshold =", round(data1_bc_roc_BC.per.y$threshold, 2)),
      color = "red",
      hjust = 0) +
  labs(title = "Zone B-C Blue Contrast Percentage by Disruptive",
    x = "Brightness Contrast Percentage",
```

```
y = "Frequency") +
theme_bw()+
theme(legend.position = "bottom")
```



BC RATIO

▼ Code

```
wilcox.test(BC.rat~Disruptive,data1_bc,conf.int=T)
```

Wilcoxon rank sum test with continuity correction

```
data: BC.rat by Disruptive
W = 52, p-value = 1.401e-07
alternative hypothesis: true location shift is not equal to 0
95 percent confidence interval:
 -2.530977 -1.355086
sample estimates:
difference in location
 -1.90538
```

▼ Code

```
# Ratio
data1_bc_roc_BC.rat <- roc(data1_bc$Disruptive, data1_bc$BC.rat)
data1_bc_roc_BC.rat$auc
```

Area under the curve: 0.9422

▼ Code

```
data1_bc_roc_BC.rat.y = coords(data1_bc_roc_BC.rat, x="best", best.method="youden")
data1_bc_roc_BC.rat.y
```

```
threshold specificity sensitivity
1 1.590139 0.8166667 1
```

▼ Code

```
data1_bc_roc_BC.rat.y$sensitivity+data1_bc_roc_BC.rat.y$specificity-1
```

```
[1] 0.8166667
```

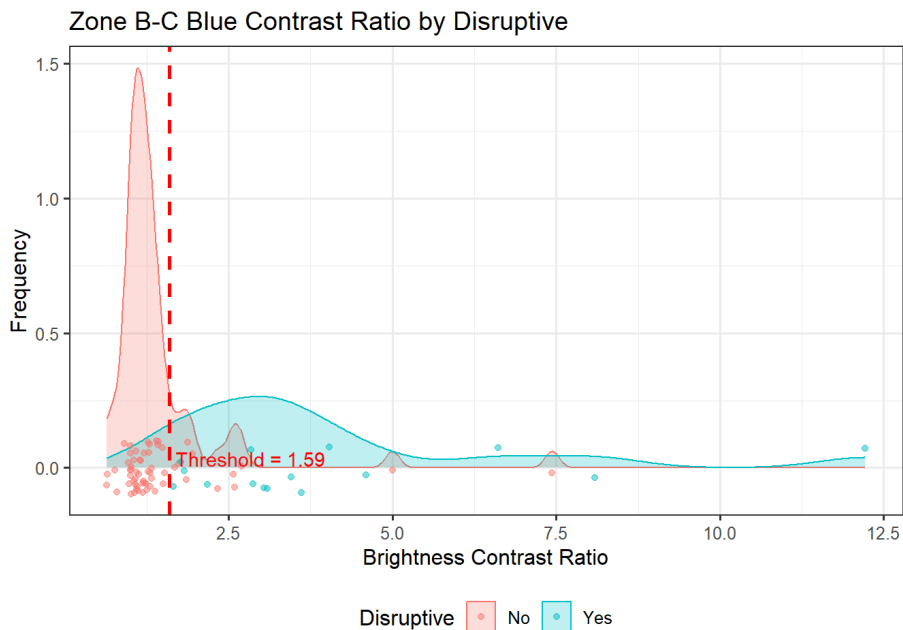
▼ Code

```
ggplot(data1_bc, aes(x = BC.rat, fill=Disruptive, color=Disruptive)) +
  geom_density(alpha = 0.25) +
  geom_point(aes(y = 0), position = position_jitter(height = 0.1), alpha = 0.5) +
  geom_vline(xintercept = data1_bc_roc_BC.rat.y$threshold, linetype = "dashed", color = "red",
    annotate("text",
      x = data1_bc_roc_BC.rat.y$threshold + 0.1, # offset the text slightly to the right
      y = 0.035, # adjust this value to position the text at your desired height
```

```

label = paste("Threshold =", round(data1_bc_roc_BC.rat.y$threshold, 2)),
color = "red",
hjust = 0) +
labs(title = "Zone B-C Blue Contrast Ratio by Disruptive",
x = "Brightness Contrast Ratio",
y = "Frequency") +
theme_bw()+
theme(legend.position = "bottom")

```



REFERENCES

▼ Code

```
report(sessionInfo())
```

Analyses were conducted using the R Statistical language (version 4.4.3; R Core Team, 2025) on Windows 11 x64 (build 26100), using the packages lubridate (version 1.9.4; Grolemund G, Wickham H, 2011), ggtern (version 3.5.0; Hamilton NE, Ferry M, 2018), gt (version 1.0.0; Iannone R et al., 2025), moments (version 0.14.1; Komsta L, Novomestky F, 2022), report (version 0.6.1; Makowski D et al., 2023), rcompanion (version 2.5.0; Mangiafico SS, 2025), tibble (version 3.2.1; Müller K, Wickham H, 2023), FSA (version 0.9.6; Ogle DH et al., 2025), PerformanceAnalytics (version 2.0.8; Peterson BG, Carl P, 2024), PMCMRplus (version 1.9.12; Pohlert T, 2024), pROC (version 1.18.5; Robin X et al., 2011), xts (version 0.14.1; Ryan JA, Ulrich JM, 2024), gtsummary (version 2.2.0; Sjöberg D et al., 2021), skimr (version 2.1.5; Waring E et al., 2022), ggplot2 (version 3.5.2; Wickham H, 2016), forcats (version 1.0.0; Wickham H, 2023), stringr (version 1.5.1; Wickham H, 2023), tidyverse (version 2.0.0; Wickham H et al., 2019), readxl (version 1.4.5; Wickham H, Bryan J, 2025), dplyr (version 1.1.4; Wickham H et al., 2023), purrr (version 1.0.4; Wickham H, Henry L, 2025), readr (version 2.1.5; Wickham H et al., 2024), tidyr (version 1.3.1; Wickham H et al., 2024) and zoo (version 1.8.14; Zeileis A, Grothendieck G, 2005).

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