Deslorelin SICB paper

R Markdown

This is an R Markdown document. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS Word documents. For more details on using R Markdown see http://rmarkdown.rstudio.com.

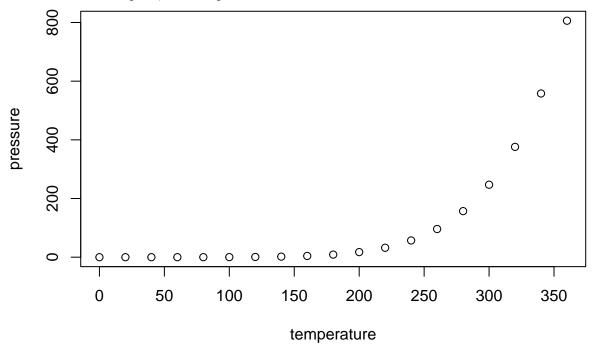
When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:

summary(cars)

```
##
                          dist
        speed
##
            : 4.0
                    Min.
                               2.00
                    1st Qu.: 26.00
##
    1st Qu.:12.0
##
    Median:15.0
                    Median: 36.00
##
    Mean
            :15.4
                    Mean
                            : 42.98
    3rd Qu.:19.0
                    3rd Qu.: 56.00
            :25.0
                            :120.00
    Max.
                    Max.
```

Including Plots

You can also embed plots, for example:

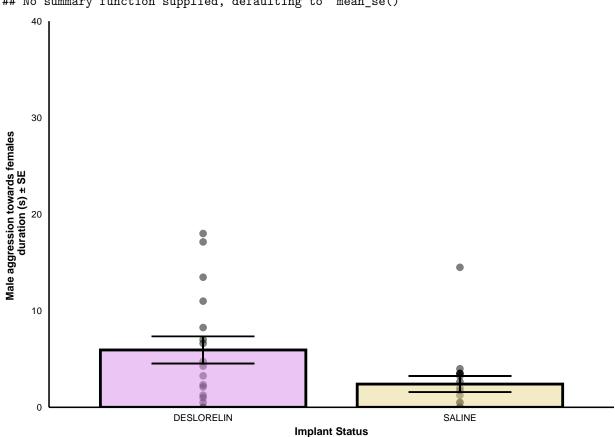


Note that the echo = FALSE parameter was added to the code chunk to prevent printing of the R code that generated the plot.

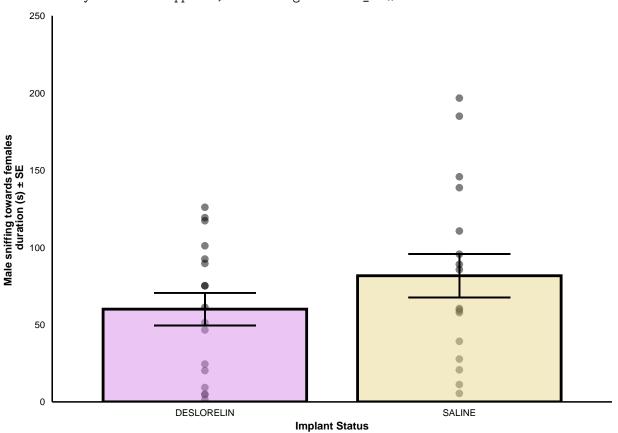
```
AMITdata <-read.csv("BEVdata.csv")
summary(AMITdata)
```

```
##
        Date
                         Trial
                                            ID
                                                              Sex
## Min.
          :2142020
                     Min.
                            :1502020
                                       Length:72
                                                          Length:72
                                                          Class : character
  1st Qu.:2292020
                     1st Qu.:1509355
                                       Class : character
                                                          Mode :character
## Median :3162020
                     Median :1510726
                                       Mode :character
## Mean
          :4092020
                     Mean
                           :1510331
## 3rd Qu.:6302020
                     3rd Qu.:1512013
##
  Max.
          :7102020 Max.
                           :1513924
      Status
                      Aggression.dur
##
                                         Aggression.n
                                                           Sniff.dur
## Length:72
                      Min. : 0.0000
                                       Min. : 0.000
                                                         Min.
                                                                : 1.50
## Class :character
                     1st Qu.: 0.5008 1st Qu.: 1.000
                                                         1st Qu.: 36.19
## Mode :character Median : 3.2555
                                       Median : 3.500
                                                         Median : 60.88
##
                            : 6.3406
                                              : 7.972
                                                               : 71.30
                      Mean
                                        Mean
                                                         Mean
                      3rd Qu.:11.0610
##
                                        3rd Qu.:12.000
                                                         3rd Qu.: 96.96
                             :36.1730
                                        Max. :50.000
##
                      Max.
                                                         Max.
                                                                :246.49
##
                   Total.time.w.male
      Sniff.n
                                        X
                                                        X.1
##
   Min. : 1.00
                   Min. : 2.252
                                     Mode:logical
                                                    Length:72
                                     NA's:72
## 1st Qu.:10.25
                   1st Qu.:123.369
                                                    Class : character
## Median :18.00
                  Median :209.984
                                                    Mode :character
## Mean
         :21.32
                  Mean
                         :239.998
## 3rd Qu.:32.00
                   3rd Qu.:295.865
## Max.
          :70.00 Max.
                          :951.217
AMITdata$Trial <- as.factor(AMITdata$Trial)</pre>
AMITdata$Sex <- as.factor(AMITdata$Sex)</pre>
AMITdata$ID <- as.factor(AMITdata$ID)</pre>
AMITdata$Status <- as.factor(AMITdata$Status)</pre>
AMITdata$PercentAGG <- AMITdata$Aggression.dur/AMITdata$Total.time.w.male*100
AMITdata$PercentPOS <- AMITdata$Sniff.dur/AMITdata$Total.time.w.male*100
#Remove one trial where both females were saline-treated (human error)
AMITdata <-AMITdata[!(AMITdata$Trial=="1510959"),]</pre>
### First plot, Male aggression towards females ###
plotdata <- AMITdata %>% filter(ID=="Male") %>% group_by(Status) %>% mutate(meanagg = mean(Aggression.d
aggplot1 <- ggplot(plotdata, aes(x=Status, y=Aggression.dur, fill= Status)) +
 scale_y = c(0,0), limits = c(0,40) +
 \#coord\_cartesian(ylim = c(0, 10)) +
 geom_jitter(aes(color = (as.factor(Status))), size = 2, position=position_dodge(width=0.9), alpha=0.5
 geom_bar(aes(color = as.factor(Status)), alpha = .5,
          width=0.8,
          stat="summary", size = 1, position="dodge") +
 geom_errorbar(aes(ymin=meanagg-stanaggerr, ymax=meanagg+stanaggerr, color = as.factor(Status)), width
               position=position_dodge(.9)) +
 labs(x = "Implant Status", y="Male aggression towards females \n duration (s) ± SE")+ #Axes labels
 theme alex() +
 scale_fill_manual(values=c(COLOR1, COLOR2)) + #colors in hexadecimal
 scale_color_manual(values=c("Black", "Black")) + #colors in hexadecimal
 # annotate("segment", x = 1, xend = 4, y = 40, yend = 40, colour = "black", size=1, alpha=1) +
 \#annotate("text", x = 2.5, y = 41.5, size = 6, label = "**") +
  \#annotate("segment", x = 1, xend = 3, y = 35, yend = 35, colour = "black", size=1, alpha=1) +
  \#annotate("text", x = 2, y = 36.5, size = 6, label = "*") +
 guides(fill="none", color = "none") +
 theme(legend.title=element_text(size=8, face="bold"),
```

```
legend.text = element_text(size=8),
        axis.text = element_text(size=7, colour="black"),
        axis.title=element_text(size=8,face="bold"),
        axis.line = element_line(colour = "black"),
        panel.border = element_blank(),
        legend.position = "right"
aggplot1 #show plot
```



How much did males spend sniffing females ### plotdata2 <- AMITdata %>% filter(ID=="Male") %% group_by(Status) %>% mutate(meansniff = mean(Sniff.dur sniffplot1 <- ggplot(plotdata2, aes(x=Status, y=Sniff.dur, fill= Status)) +</pre> $scale_y = continuous(expand = c(0,0), limits = c(0, 250)) +$ $\#coord_cartesian(ylim = c(0, 10)) +$ geom_jitter(aes(color = (as.factor(Status))), size = 2, position=position_dodge(width=0.9), alpha=0.5 geom_bar(aes(color = as.factor(Status)), alpha = .5, width=0.8, stat="summary", size = 1, position="dodge") + geom_errorbar(aes(ymin=meansniff-stanSnifferr, ymax=meansniff+stanSnifferr, color = as.factor(Status) position=position_dodge(.9)) + labs(x = "Implant Status", y="Male sniffing towards females \n duration (s) ± SE")+ #Axes labels theme_alex() + scale_fill_manual(values=c(COLOR1, COLOR2)) + #colors in hexadecimal

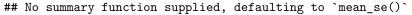


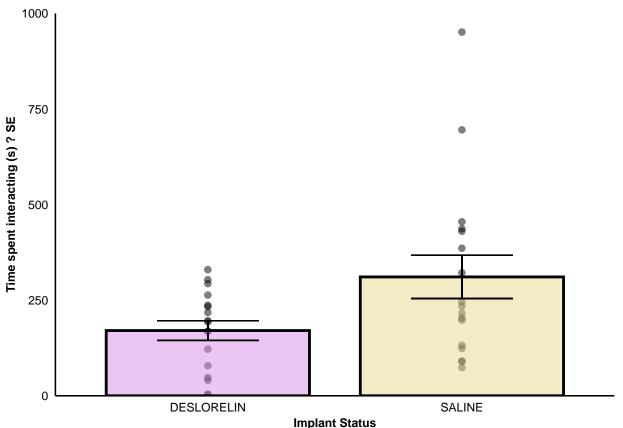
```
### Association time ###

plotdataINTERACT <- AMITdata %>% filter(ID=="Male") %>% group_by(Status) %>% mutate(meaninteract = mean

INTERACTplot <- ggplot(plotdataINTERACT, aes(x=Status, y=Total.time.w.male, fill= Status)) +
    scale_y_continuous(expand= c(0,0), limits = c(0, 1000)) +
    #coord_cartesian(ylim = c(0, 10)) +
    geom_jitter(aes(color = (as.factor(Status))), size = 2, position=position_dodge(width=0.9), alpha=0.5
    geom_bar(aes(color = as.factor(Status)), alpha = .5,</pre>
```

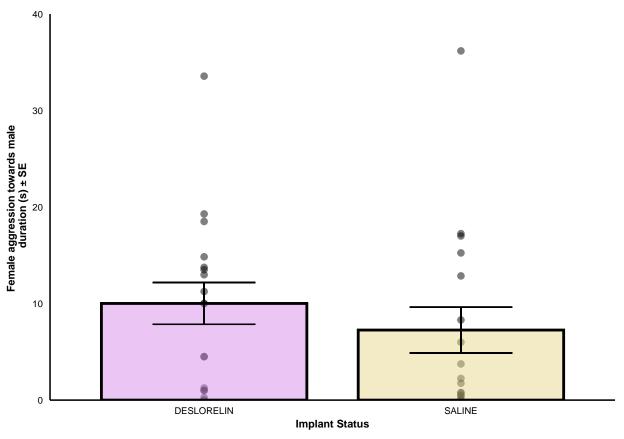
```
width=0.8,
                                      stat="summary", size = 1, position="dodge") +
       geom errorbar(aes(ymin=meaninteract-stanInteracterr, ymax=meaninteract+stanInteracterr, color = as.fa
                                                       position=position_dodge(.9)) +
       labs(x = "Implant Status", y="Time spent interacting (s) ? SE")+ #Axes labels
       theme_alex() +
       scale_fill_manual(values=c(COLOR1, COLOR2)) + #colors in hexadecimal
       scale_color_manual(values=c("Black", "Black")) + #colors in hexadecimal
       \# annotate("segment", x = 1, xend = 4, y = 40, yend = 40, xcolour = "black", xsize=1, x2, x3, x4, y5, y6, y7, y8, y8, y9, y9, y1, y1, y1, y2, y3, y4, y5, y6, y7, y8, y8, y8, y9, y9, y1, y1, y1, y1, y1, y2, y3, y3, y4, y5, y6, y8, y8, y9, y9, y1, y1, y1, y1, y1, y1, y2, y3, y3, y4, y4, y4, y4, y5, y4, y4, y5, y5, y6, y7, y8, 
       \#annotate("text", x = 2.5, y = 41.5, size = 6, label = "**") +
       \#annotate("segment", x = 1, xend = 3, y = 35, yend = 35, xcolour = "black", xsize=1, x2, x3, y4 + x5, y6 + y7 + y8 + y
       \#annotate("text", x = 2, y = 36.5, size = 6, label = "*") +
       guides(fill="none", color = "none") +
       theme(legend.title=element_text(size=8, face="bold"),
                            legend.text = element_text(size=8),
                            axis.text = element_text(size=9, colour="black"),
                           axis.title=element_text(size=9,face="bold"),
                            axis.line = element_line(colour = "black"),
                           panel.border = element_blank(),
                            legend.position = "right"
       )
INTERACTplot #show plot
```





ggsave("Interaction Plot.png", width=4, height=4, dpi=600)

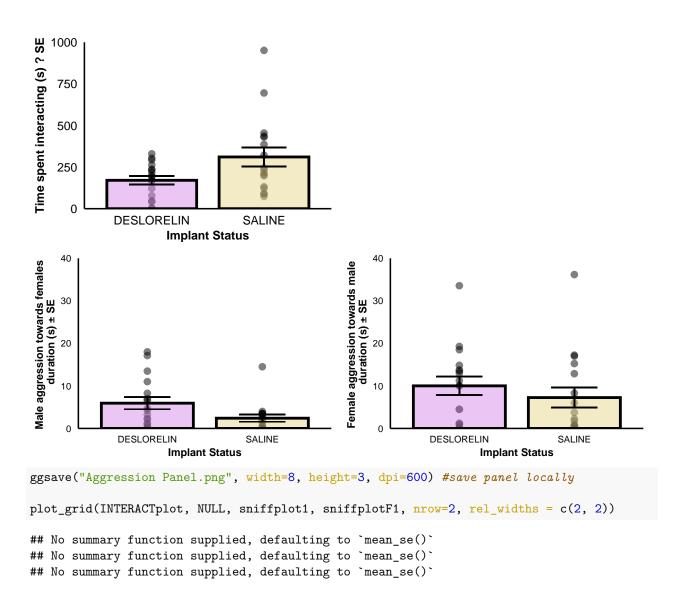
```
## No summary function supplied, defaulting to `mean_se()`
### Female Aggression ####
plotdataF1 <- AMITdata %>% filter(Sex=="F") %>% group by(Status) %>% mutate(meanagg = mean(Aggression.d
aggplot2 <- ggplot(plotdataF1, aes(x=Status, y=Aggression.dur, fill= Status)) +
  scale_y = c(0,0), limits = c(0,40) +
  \#coord\_cartesian(ylim = c(0, 10)) +
  geom_jitter(aes(color = (as.factor(Status))), size = 2, position=position_dodge(width=0.9), alpha=0.5
  geom_bar(aes(color = as.factor(Status)), alpha = .5,
          width=0.8,
          stat="summary", size = 1, position="dodge") +
  geom_errorbar(aes(ymin=meanagg-stanaggerr, ymax=meanagg+stanaggerr, color = as.factor(Status)), width
                position=position_dodge(.9)) +
  labs(x = "Implant Status", y="Female aggression towards male \n duration (s) ± SE")+ #Axes labels
  theme_alex() +
  scale_fill_manual(values=c(COLOR1, COLOR2)) + #colors in hexadecimal
  scale_color_manual(values=c("Black", "Black")) + #colors in hexadecimal
  \# annotate("segment", x = 1, xend = 4, y = 40, yend = 40, colour = "black", size=1, alpha=1) +
  \#annotate("text", x = 2.5, y = 41.5, size = 6, label = "**") +
  \#annotate("segment", x = 1, xend = 3, y = 35, yend = 35, xcolour = "black", xsize=1, xlpha=1) +
  \#annotate("text", x = 2, y = 36.5, size = 6, label = "*") +
  guides(fill="none", color = "none") +
  theme(legend.title=element_text(size=8, face="bold"),
       legend.text = element_text(size=8),
       axis.text = element_text(size=7, colour="black"),
       axis.title=element_text(size=8,face="bold"),
       axis.line = element_line(colour = "black"),
       panel.border = element_blank(),
        legend.position = "right"
aggplot2 #show plot
```

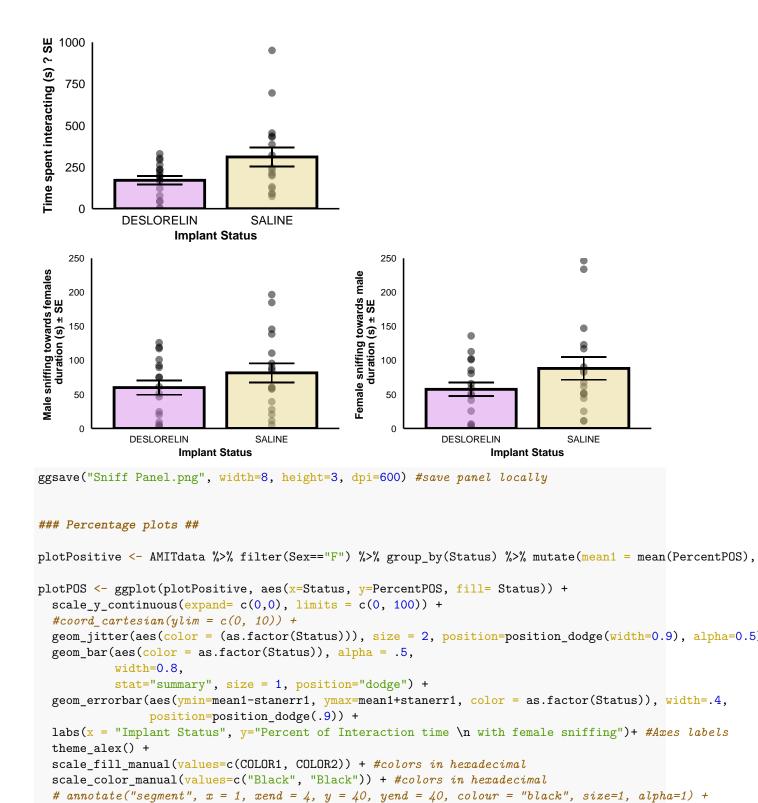


```
##Female Sniffing###
plotdataF2 <- AMITdata %>% filter(Sex=="F") %>% group_by(Status) %>% mutate(meansniff = mean(Sniff.dur)
sniffplotF1 <- ggplot(plotdataF2, aes(x=Status, y=Sniff.dur, fill= Status)) +</pre>
   scale_y_continuous(expand= c(0,0), limits = c(0, 250)) +
   \#coord\_cartesian(ylim = c(0, 10)) +
   geom_jitter(aes(color = (as.factor(Status))), size = 2, position=position_dodge(width=0.9), alpha=0.5
   geom_bar(aes(color = as.factor(Status)), alpha = .5,
                    width=0.8,
                    stat="summary", size = 1, position="dodge") +
   geom_errorbar(aes(ymin=meansniff-stanSnifferr, ymax=meansniff+stanSnifferr, color = as.factor(Status)
                              position=position_dodge(.9)) +
   labs(x = "Implant Status", y="Female sniffing towards male \n duration (s) ± SE")+ #Axes labels
   theme_alex() +
   scale_fill_manual(values=c(COLOR1, COLOR2)) + #colors in hexadecimal
   scale_color_manual(values=c("Black", "Black")) + #colors in hexadecimal
   \# annotate("segment", x = 1, xend = 4, y = 40, yend = 40, xcolour = "black", xsize=1, x2, x3, x4, y5, y6, y7, y8, y8, y9, y9, y9, y1, y1, y1, y2, y3, y3, y4, y5, y6, y7, y8, y8, y9, y9, y9, y1, y1, y1, y1, y1, y2, y3, y3, y4, y4, y4, y5, y6, y7, y8, y8, y8, y9, y9, y1, y1, y1, y1, y1, y1, y2, y3, y3, y4, 
   \#annotate("text", x = 2.5, y = 41.5, size = 6, label = "**") +
   \#annotate("segment", x = 1, xend = 3, y = 35, yend = 35, xcolour = "black", xsize=1, xlpha=1) +
    \#annotate("text", x = 2, y = 36.5, size = 6, label = "*") +
   guides(fill="none", color = "none") +
   theme(legend.title=element_text(size=8, face="bold"),
               legend.text = element_text(size=8),
               axis.text = element_text(size=7, colour="black"),
               axis.title=element_text(size=8,face="bold"),
               axis.line = element_line(colour = "black"),
```

```
panel.border = element_blank(),
          legend.position = "right"
sniffplotF1 #show plot
## No summary function supplied, defaulting to `mean_se()`
     200
Female sniffing towards male duration (s) ± SE
     150
     100
      50
                                 DESLORELIN
                                                                                    SALINE
                                                        Implant Status
```

```
##
plot_grid(INTERACTplot, NULL, aggplot1, aggplot2, nrow=2, rel_widths = c(2, 2))
## No summary function supplied, defaulting to `mean_se()`
## No summary function supplied, defaulting to `mean_se()`
```





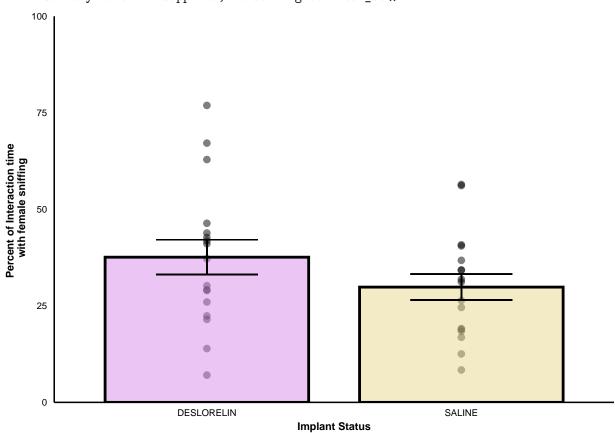
#annotate("segment", x = 1, xend = 3, y = 35, yend = 35, colour = "black", size=1, alpha=1) +

#annotate("text", x = 2.5, y = 41.5, size = 6, label = "**") +

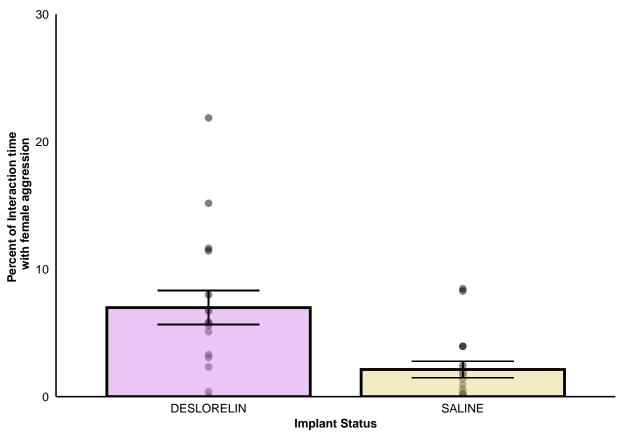
#annotate("text", x = 2, y = 36.5, size = 6, label = "*") +

guides(fill="none", color = "none") +

```
axis.text = element_text(size=7, colour="black"),
    axis.title=element_text(size=8,face="bold"),
    axis.line = element_line(colour = "black"),
    panel.border = element_blank(),
    legend.position = "right"
)
plotPOS #show plot
```



plotAggressive <- AMITdata %>% filter(Sex=="F") %>% group_by(Status) %>% mutate(mean1 = mean(PercentAGG plotAGG <- ggplot(plotAggressive, aes(x=Status, y=PercentAGG, fill= Status)) +</pre> $scale_y_continuous(expand= c(0,0), limits = c(0, 30)) +$ $\#coord_cartesian(ylim = c(0, 10)) +$ geom_jitter(aes(color = (as.factor(Status))), size = 2, position=position_dodge(width=0.9), alpha=0.5 geom_bar(aes(color = as.factor(Status)), alpha = .5, width=0.8, stat="summary", size = 1, position="dodge") + geom_errorbar(aes(ymin=mean1-stanerr1, ymax=mean1+stanerr1, color = as.factor(Status)), width=.4, position=position_dodge(.9)) + labs(x = "Implant Status", y="Percent of Interaction time <math>n with female aggression")+ #Axes labels theme alex() + scale_fill_manual(values=c(COLOR1, COLOR2)) + #colors in hexadecimal scale_color_manual(values=c("Black", "Black")) + #colors in hexadecimal # annotate("segment", x = 1, xend = 4, y = 40, yend = 40, colour = "black", size=1, alpha=1) + #annotate("text", x = 2.5, y = 41.5, size = 6, label = "**") +



ggsave("Aggression Plot2.png", width=4, height=4, dpi=600) #save panel locally

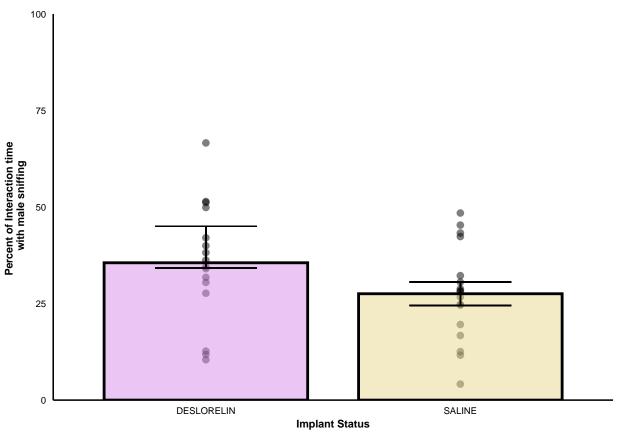
```
## No summary function supplied, defaulting to `mean_se()`
```

```
### Percentage plots male ##

plotPositiveM <- AMITdata %>% filter(Sex=="M") %>% group_by(Status) %>% mutate(mean1 = mean(PercentPOS)

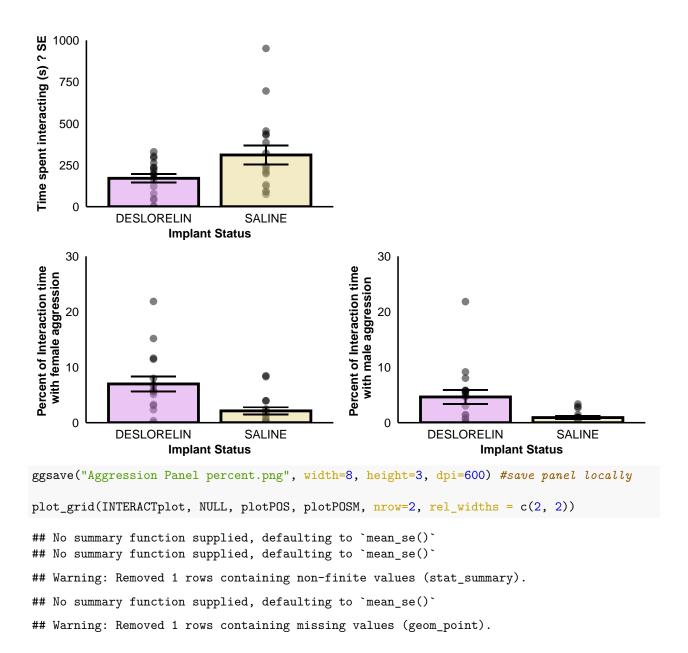
plotPOSM <- ggplot(plotPositiveM, aes(x=Status, y=PercentPOS, fill= Status)) +
    scale_y_continuous(expand= c(0,0), limits = c(0, 100)) +
    #coord_cartesian(ylim = c(0, 10)) +
    geom_jitter(aes(color = (as.factor(Status))), size = 2, position=position_dodge(width=0.9), alpha=0.5</pre>
```

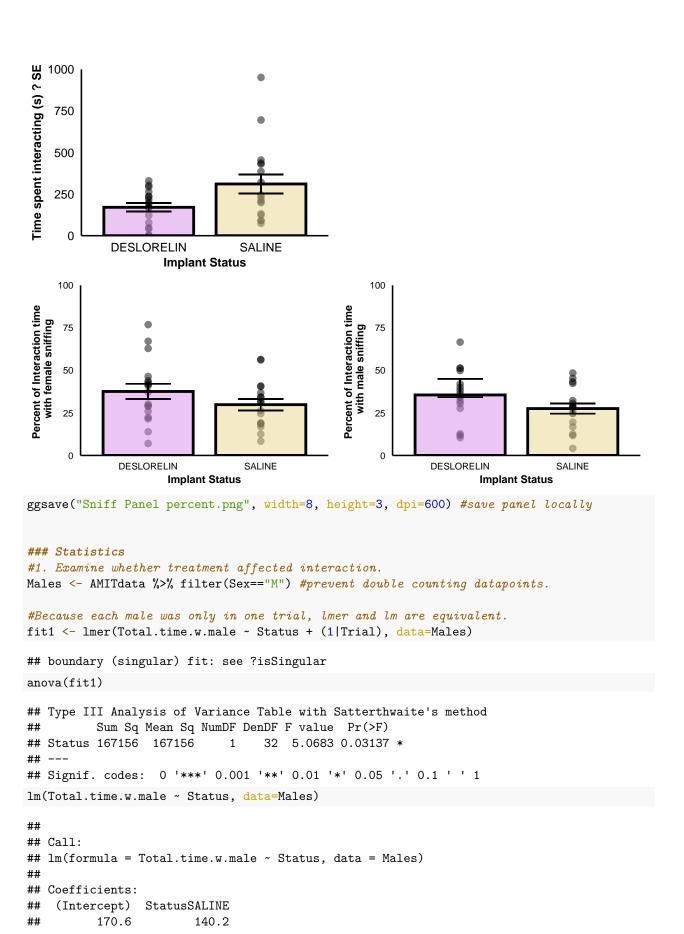
```
geom_bar(aes(color = as.factor(Status)), alpha = .5,
                       width=0.8,
                       stat="summary", size = 1, position="dodge") +
    geom_errorbar(aes(ymin=mean1-stanerr1, ymax=mean1+stanerr1, color = as.factor(Status)), width=.4,
                                  position=position_dodge(.9)) +
    labs(x = "Implant Status", y="Percent of Interaction time \n with male sniffing")+ #Axes labels
    theme_alex() +
    scale fill manual(values=c(COLOR1, COLOR2)) + #colors in hexadecimal
    scale_color_manual(values=c("Black", "Black")) + #colors in hexadecimal
    \# annotate("segment", x = 1, x = 4, y = 40, y 
    \#annotate("text", x = 2.5, y = 41.5, size = 6, label = "**") +
    \#annotate("segment", x = 1, xend = 3, y = 35, yend = 35, colour = "black", size=1, alpha=1) +
    \#annotate("text", x = 2, y = 36.5, size = 6, label = "*") +
    guides(fill="none", color = "none") +
    theme(legend.title=element_text(size=8, face="bold"),
                 legend.text = element_text(size=8),
                 axis.text = element_text(size=7, colour="black"),
                 axis.title=element_text(size=8,face="bold"),
                 axis.line = element_line(colour = "black"),
                 panel.border = element_blank(),
                 legend.position = "right"
plotPOSM #show plot
## Warning: Removed 1 rows containing non-finite values (stat_summary).
## No summary function supplied, defaulting to `mean_se()`
## Warning: Removed 1 rows containing missing values (geom_point).
```



```
plotAggressiveM <- AMITdata %>% filter(Sex=="M") %>% group_by(Status) %>% mutate(mean1 = mean(PercentAG
plotAGGM <- ggplot(plotAggressiveM, aes(x=Status, y=PercentAGG, fill= Status)) +</pre>
   scale_y = continuous(expand = c(0,0), limits = c(0,30)) +
   \#coord\_cartesian(ylim = c(0, 10)) +
   geom_jitter(aes(color = (as.factor(Status))), size = 2, position=position_dodge(width=0.9), alpha=0.5
   geom_bar(aes(color = as.factor(Status)), alpha = .5,
                    width=0.8,
                    stat="summary", size = 1, position="dodge") +
   geom_errorbar(aes(ymin=mean1-stanerr1, ymax=mean1+stanerr1, color = as.factor(Status)), width=.4,
                              position=position_dodge(.9)) +
   labs(x = "Implant Status", y="Percent of Interaction time \n with male aggression")+ #Axes labels
   theme_alex() +
   scale_fill_manual(values=c(COLOR1, COLOR2)) + #colors in hexadecimal
   scale_color_manual(values=c("Black", "Black")) + #colors in hexadecimal
   \# annotate("segment", x = 1, xend = 4, y = 40, yend = 40, xcolour = "black", xsize=1, x2, x3, x4, y5, y6, y7, y8, y8, y9, y9, y1, y1, y1, y2, y3, y4, y5, y6, y7, y8, y8, y8, y9, y9, y1, y1, y1, y1, y1, y2, y3, y3, y4, y4, y5, y6, y8, y8, y8, y9, y9, y1, y1, y1, y1, y1, y1, y2, y3, y3, y4, y4, y4, y5, y4, y4, y5, y5, y6, y8, 
   \#annotate("text", x = 2.5, y = 41.5, size = 6, label = "**") +
    \#annotate("segment", x = 1, xend = 3, y = 35, yend = 35, colour = "black", size=1, alpha=1) +
    \#annotate("text", x = 2, y = 36.5, size = 6, label = "*") +
   guides(fill="none", color = "none") +
   theme(legend.title=element_text(size=8, face="bold"),
               legend.text = element_text(size=8),
               axis.text = element_text(size=9, colour="black"),
               axis.title=element_text(size=9,face="bold"),
              axis.line = element_line(colour = "black"),
              panel.border = element blank(),
               legend.position = "right"
```

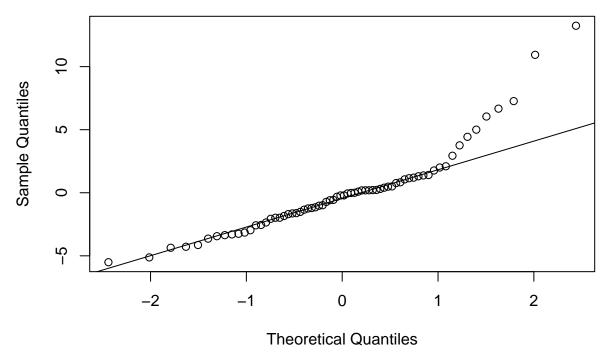
```
plotAGGM #show plot
## No summary function supplied, defaulting to `mean_se()`
     30
Percent of Interaction time with male aggression
     10
      0
                          DESLORELIN
                                                                      SALINE
                                              Implant Status
ggsave("Aggression Panel percent2.png", width=4, height=4, dpi=600)
## No summary function supplied, defaulting to `mean_se()`
plot_grid(INTERACTplot, NULL, plotAGG, plotAGGM, nrow=2, rel_widths = c(2, 2))
## No summary function supplied, defaulting to `mean_se()`
## No summary function supplied, defaulting to `mean_se()`
## No summary function supplied, defaulting to `mean_se()`
```





```
anova(lm(Total.time.w.male ~ Status, data=Males))
## Analysis of Variance Table
##
## Response: Total.time.w.male
            Df Sum Sq Mean Sq F value Pr(>F)
##
             1 167156 167156 5.0683 0.03137 *
## Residuals 32 1055375
                        32980
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
#2. Does status predict aggression time?
fit2 <- lmer(PercentAGG ~ Status * Sex + (1|Trial), data=AMITdata)</pre>
anova(fit2)
## Type III Analysis of Variance Table with Satterthwaite's method
              Sum Sq Mean Sq NumDF DenDF F value
## Status
             312.077 312.077
                                 1
                                      48 23.0820 1.564e-05 ***
## Sex
              53.790 53.790
                                 1
                                      48 3.9784
                                                   0.05178 .
               5.527
                       5.527
                                 1
                                      48 0.4088
                                                   0.52561
## Status:Sex
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
fit2.emm <- emmeans(fit2, ~ Status*Sex)</pre>
qqnorm(resid(fit2))
qqline(resid(fit2))
```

Normal Q-Q Plot



```
#3. Does status predict sniffing time?
fit3 <- lmer(PercentPOS ~ Status * Sex + (1|Trial), data=AMITdata)
anova(fit3)</pre>
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##
              Sum Sq Mean Sq NumDF DenDF F value
                                                  Pr(>F)
## Status
             1667.23 1667.23
                                 1
                                      48 9.2288 0.003847 **
## Sex
                0.38
                        0.38
                                 1
                                      48 0.0021 0.963730
## Status:Sex
               79.17
                       79.17
                                      48 0.4382 0.511143
                                 1
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
fit3.emm <- emmeans(fit3, ~ Status*Sex)</pre>
qqnorm(resid(fit3))
qqline(resid(fit3))
```

Normal Q-Q Plot

