

rupertreach

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Rupert reaching data for PA grant

Let's recreate one of our python box plots to show we've loaded the data.

Testlink <http://spencelab.com>.

Get started

```
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(tidyr)  
library(readr)  
library(ggplot2)  
library(ggpubr)  
library(car)
```

```
## Loading required package: carData  
##  
## Attaching package: 'car'  
## The following object is masked from 'package:dplyr':  
##  
##   recode
```

```
library(Hmisc)
```

```
## Loading required package: lattice  
## Loading required package: survival  
## Loading required package: Formula  
##  
## Attaching package: 'Hmisc'
```

```
## The following objects are masked from 'package:dplyr':
##
##   src, summarize

## The following objects are masked from 'package:base':
##
##   format.pval, units

library(rstatix)

##
## Attaching package: 'rstatix'

## The following object is masked from 'package:stats':
##
##   filter

library(emmeans)
library(nlme)

##
## Attaching package: 'nlme'

## The following object is masked from 'package:dplyr':
##
##   collapse

library(stringr)
library(ggforce)

theme_update(plot.title = element_text(hjust = 0.5))
# maybe the plain BW background looks better than the grey stuff
# https://www.datanovia.com/en/lessons/combine-multiple-ggplots-into-a-figure/
#
theme_set(theme_bw())
#+
#   theme(legend.position = "top")
# )
dfx <- read.csv("alldata_x.csv")
dfy <- read.csv("alldata_y.csv")
```

prepare data, aggregate and stats

```
dfx$treatment <- factor(dfx$treatment)
dfx$treatment <- relevel(dfx$treatment, 'excite')
dfxt <- dfx %>% filter(time==0.4)
dfxt %>% group_by(treatment) %>%
  summarise(
    count = n(),
    mean = mean(x, na.rm = TRUE),
    sd = sd(x, na.rm = TRUE),
    median = median(x, na.rm = TRUE),
    IQR = IQR(x, na.rm = TRUE)
  )

## # A tibble: 3 x 6
```

```
##   treatment count  mean    sd median   IQR
##   <fct>      <int> <dbl> <dbl> <dbl> <dbl>
## 1 excite      11 12.4   4.51 12.4   3.79
## 2 control      7 -5.20  4.21 -3.31  3.13
## 3 inhib       4 -7.92  4.21 -8.51  4.42

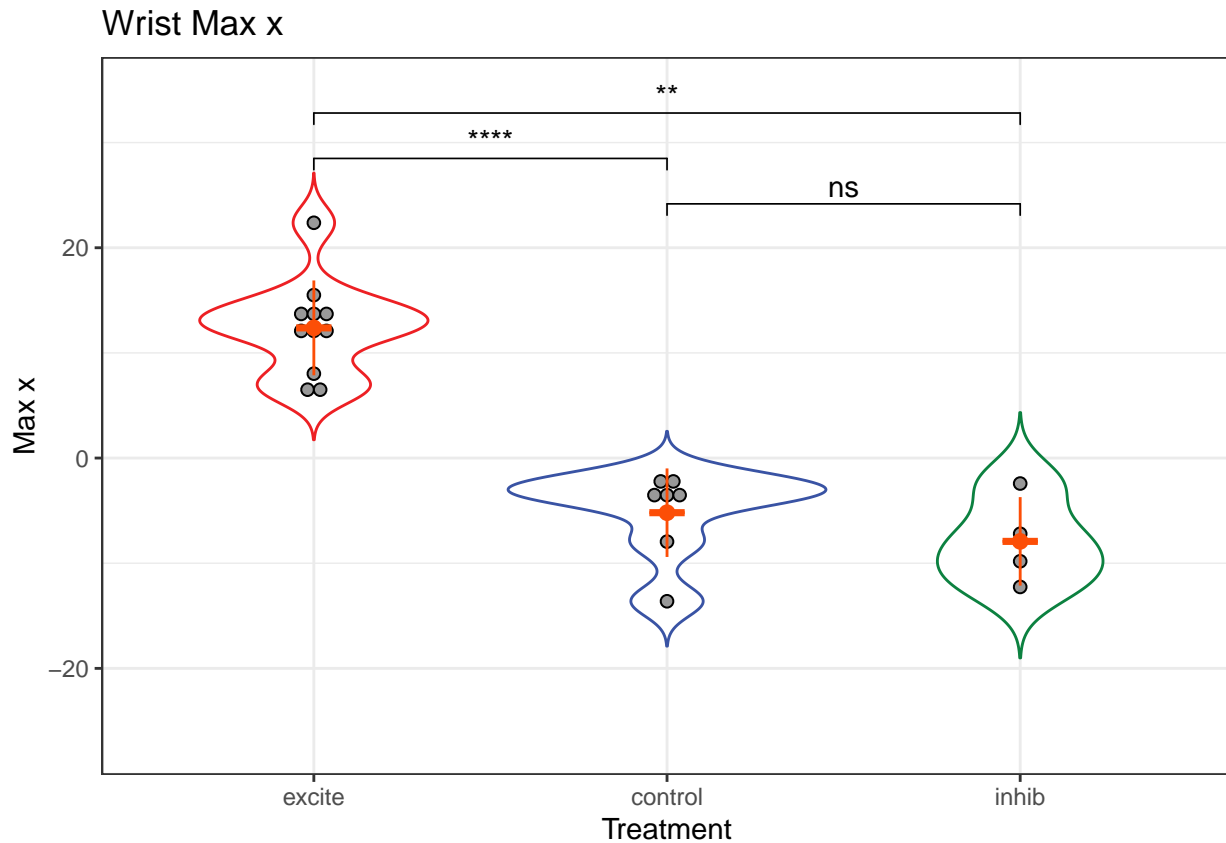
# Plot it:
# choose comparisons to plot
# http://www.sthda.com/english/articles/32-r-graphics-essentials/132-plot-grouped-data-box-plot-bar-plot
my_comps <- list( c("control","inhib"),c("excite","control"),
                  c("excite","inhib") )
dfxt %>% ggplot(aes(x = treatment, y = x,color = treatment))+
  #geom_boxplot(aes(color = treatment), show.legend = FALSE)+
  geom_violin(trim = FALSE,show.legend=FALSE) +
  geom_dotplot(
    binaxis='y', stackdir='center',
    color = "black", fill = "#999999",
  ) +
  stat_summary(
    fun.data="mean_sdl", fun.args = list(mult=1),
    geom = "pointrange", color = "#FC4E07", size = 0.4
  )+
  stat_summary(fun.y= mean, fun.ymin=mean, fun.ymax=mean, geom="crossbar", width=0.1, color = "#FC4E07")
  #geom_sina(aes(color = treatment), show.legend = FALSE)+
  ylab("Max x") +
  xlab("Treatment") +
  coord_cartesian(ylim = c(-27, 35)) +
  scale_color_manual(values = c("#ED2024","#3953A4","#0C8140"))+
  ggtitle("Wrist Max x")+
  stat_compare_means(comparisons=my_comps, label="p.signif") # + # default is Wilcoxon

## Warning: The `fun.y` argument of `stat_summary()` is deprecated as of ggplot2 3.3.0.
## i Please use the `fun` argument instead.

## Warning: The `fun.ymin` argument of `stat_summary()` is deprecated as of ggplot2 3.3.0.
## i Please use the `fun.min` argument instead.

## Warning: The `fun.ymax` argument of `stat_summary()` is deprecated as of ggplot2 3.3.0.
## i Please use the `fun.max` argument instead.

## Bin width defaults to 1/30 of the range of the data. Pick better value with
## `binwidth`.
```



```
# take out the global comparison, because it's implied that significant
# since we are doing post hoc tests
#stat_compare_means(aes(group = treatment), label = "p.signif", label.y=30,
#                      method='kruskal.test' ) # actually default is kruskal
```

```
# stat_compare_means(aes(group = treatment),
#                      method='kruskal.test' )
```

```
ggsave('xbox.pdf',width=2.5,height=3,units='in')
```

```
## Bin width defaults to 1/30 of the range of the data. Pick better value with
## `binwidth`.
```

```
kruskal.test(x ~ treatment, data = dfxt)
```

```
##
## Kruskal-Wallis rank sum test
##
## data: x by treatment
## Kruskal-Wallis chi-squared = 15.932, df = 2, p-value = 0.0003471
```

```
pairwise.wilcox.test(dfxt$x, dfxt$treatment,
                      p.adjust.method = "BH")
```

```
##
## Pairwise comparisons using Wilcoxon rank sum exact test
##
## data: dfxt$x and dfxt$treatment
##
```

```
##          excite  control
## control 0.00019 -
## inhib   0.00220 0.52727
##
## P value adjustment method: BH
```

y coord box plot

```
dfy$treatment <- factor(dfy$treatment)
dfy$treatment <- relevel(dfy$treatment, 'excite')
dfyt <- dfy %>% filter(time==0.4)
dfyt %>% group_by(treatment) %>%
  summarise(
    count = n(),
    mean = mean(y, na.rm = TRUE),
    sd = sd(y, na.rm = TRUE),
    median = median(y, na.rm = TRUE),
    IQR = IQR(y, na.rm = TRUE)
  )
```

```
## # A tibble: 3 x 6
##   treatment count  mean    sd median  IQR
##   <fct>      <int> <dbl> <dbl> <dbl> <dbl>
## 1 excite         11 20.7   8.79  19.5  12.9
## 2 control         7 -3.94  6.35  -3.37  7.02
## 3 inhib          4 -6.22  4.52  -6.40  5.78
```

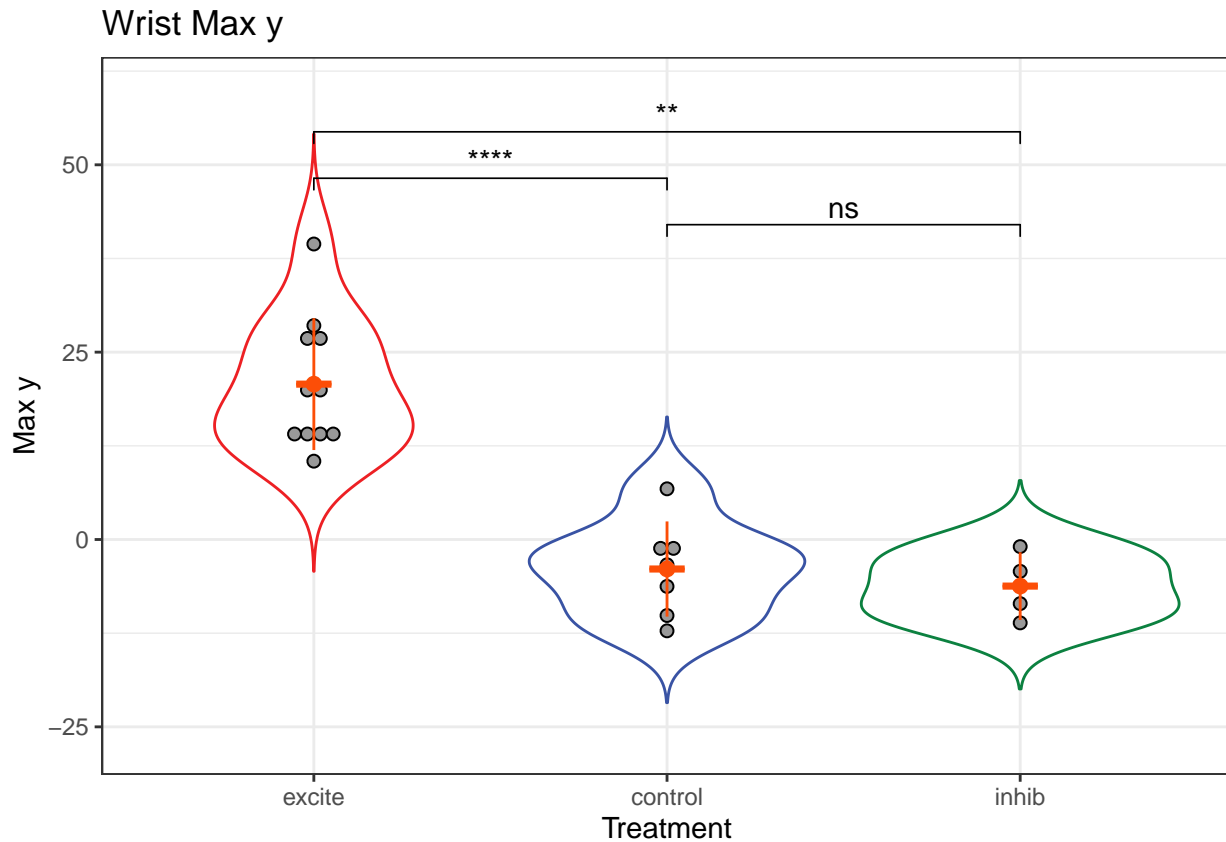
```
# let's try to add the overbars and stars
# Statistical test
stat.test <- dfyt %>%
  kruskal.test(x=.$y, g=.$treatment) %>%
  add_significance()
stat.test
```

```
##
## Kruskal-Wallis rank sum test
##
## data:  .$y and .$treatment
## Kruskal-Wallis chi-squared = 15.82, df = 2, p-value = 0.0003671
```

```
#stat.test <- tidy(stat.test) %>% add_xy_position(x = "treatment")
dfyt %>% ggplot(aes(x = treatment, y = y, color=treatment))+
  #geom_boxplot(aes(color = treatment), show.legend = FALSE)+
  geom_violin(trim = FALSE, show.legend=FALSE) +
  geom_dotplot(
    binaxis='y', stackdir='center',
    color = "black", fill = "#999999",
  ) +
  stat_summary(
    fun.data="mean_sdl", fun.args = list(mult=1),
    geom = "pointrange", color = "#FC4E07", size = 0.4
  )+
  stat_summary(fun.y= mean, fun.ymin=mean, fun.ymax=mean, geom="crossbar", width=0.1, color = "#FC4E07"
)
ylab("Max y") +
  xlab("Treatment") +
```

```
coord_cartesian(ylim = c(-27, 60)) +
scale_color_manual(values = c("#ED2024", "#3953A4", "#0C8140")) +
ggtitle("Wrist Max y") +
stat_compare_means(comparisons=my_comps, label="p.signif") # + # default is Wilcoxon
```

```
## Bin width defaults to 1/30 of the range of the data. Pick better value with
## `binwidth`.
```



```
#stat_compare_means(aes(group = treatment), label = "p.signif",
#                    method='kruskal.test', hide.ns = TRUE )
ggsave('ybox.pdf',width=2.5,height=3,units='in')
```

```
## Bin width defaults to 1/30 of the range of the data. Pick better value with
## `binwidth`.
```

```
kruskal.test(y ~ treatment, data = dfyt)
```

```
##
## Kruskal-Wallis rank sum test
##
## data: y by treatment
## Kruskal-Wallis chi-squared = 15.82, df = 2, p-value = 0.0003671
```

```
pairwise.wilcox.test(dfyt$y, dfyt$treatment,
                     p.adjust.method = "BH")
```

```
##
## Pairwise comparisons using Wilcoxon rank sum exact test
##
```

```
## data: dfyt$y and dfyt$treatment
##
##      excite  control
## control 0.00019 -
## inhib   0.00220 0.78788
##
## P value adjustment method: BH
```

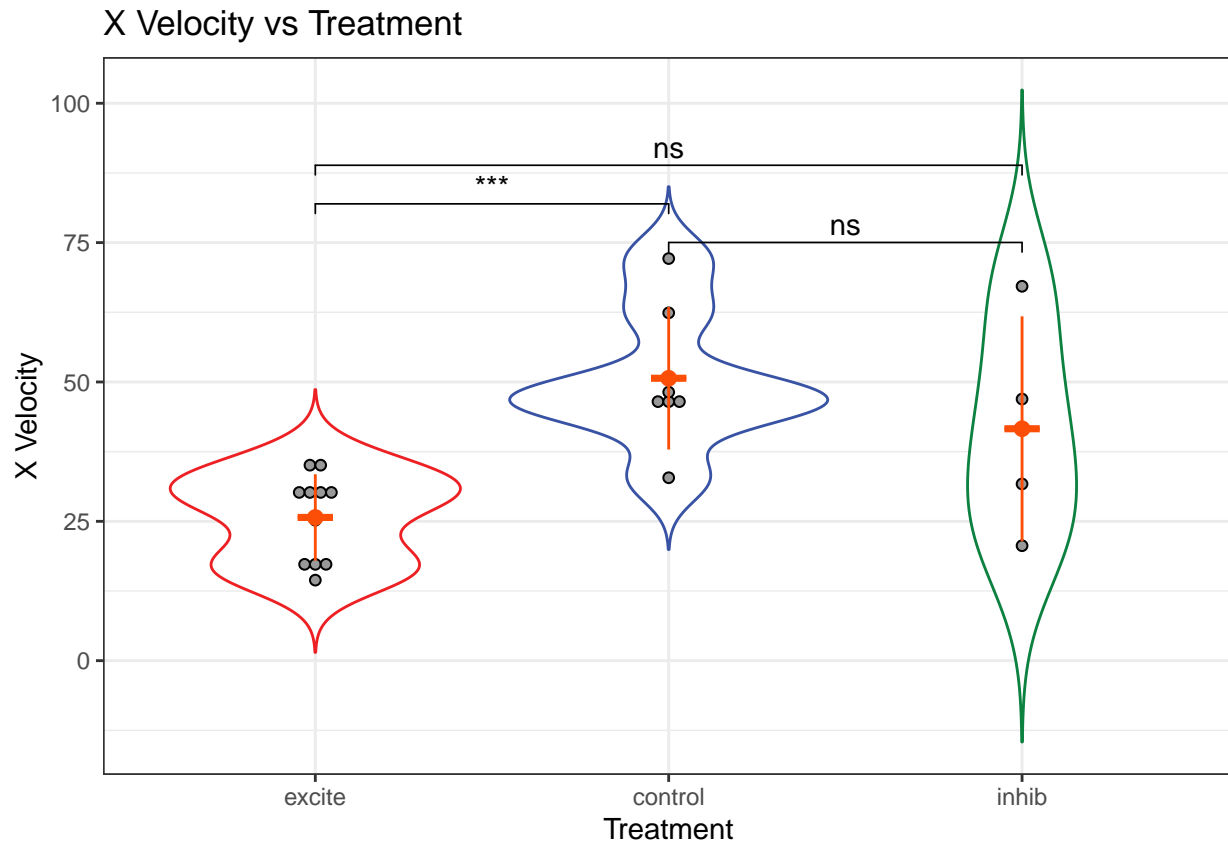
Ok let's update with velocities, reach duration, deltaX, deltaY plots.

```
md<-read_csv("reachfiles_generated_wvelocities.csv",col_types = cols(type=col_factor())) %>% filter(good)
```

```
## New names:
## * `` -> `...1`
```

```
md$type <- relevel(md$type,'control')
md$type <- relevel(md$type,'excite')
my_comps <- list( c("control","inhib"),c("excite","control"),
                  c("excite","inhib") )
md %>% ggplot(aes(x = type, y = velx, color=type))+
  #geom_boxplot(aes(color = treatment), show.legend = FALSE)+
  geom_violin(trim = FALSE,show.legend=FALSE) +
  geom_dotplot(
    binaxis='y', stackdir='center',
    color = "black", fill = "#999999",
  ) +
  stat_summary(
    fun.data="mean_sdl", fun.args = list(mult=1),
    geom = "pointrange", color = "#FC4E07", size = 0.4
  )+
  stat_summary(fun.y= mean, fun.ymin=mean, fun.ymax=mean, geom="crossbar", width=0.1, color = "#FC4E07")
ylab("X Velocity") +
  xlab("Treatment") +
  #coord_cartesian(ylim = c(-27, 60)) +
  scale_color_manual(values = c("#ED2024","#3953A4","#0C8140"))+
  ggtitle("X Velocity vs Treatment") +
  stat_compare_means(comparisons=my_comps, label="p.signif") # + # default is Wilcoxon
```

```
## Bin width defaults to 1/30 of the range of the data. Pick better value with
## `binwidth`.
```



```
#stat_compare_means(aes(group = treatment), label = "p.signif",
#                    method='kruskal.test', hide.ns = TRUE )
ggsave('xvel.pdf',width=2.5,height=3,units='in')
```

```
## Bin width defaults to 1/30 of the range of the data. Pick better value with
## `binwidth`.
```

and now y

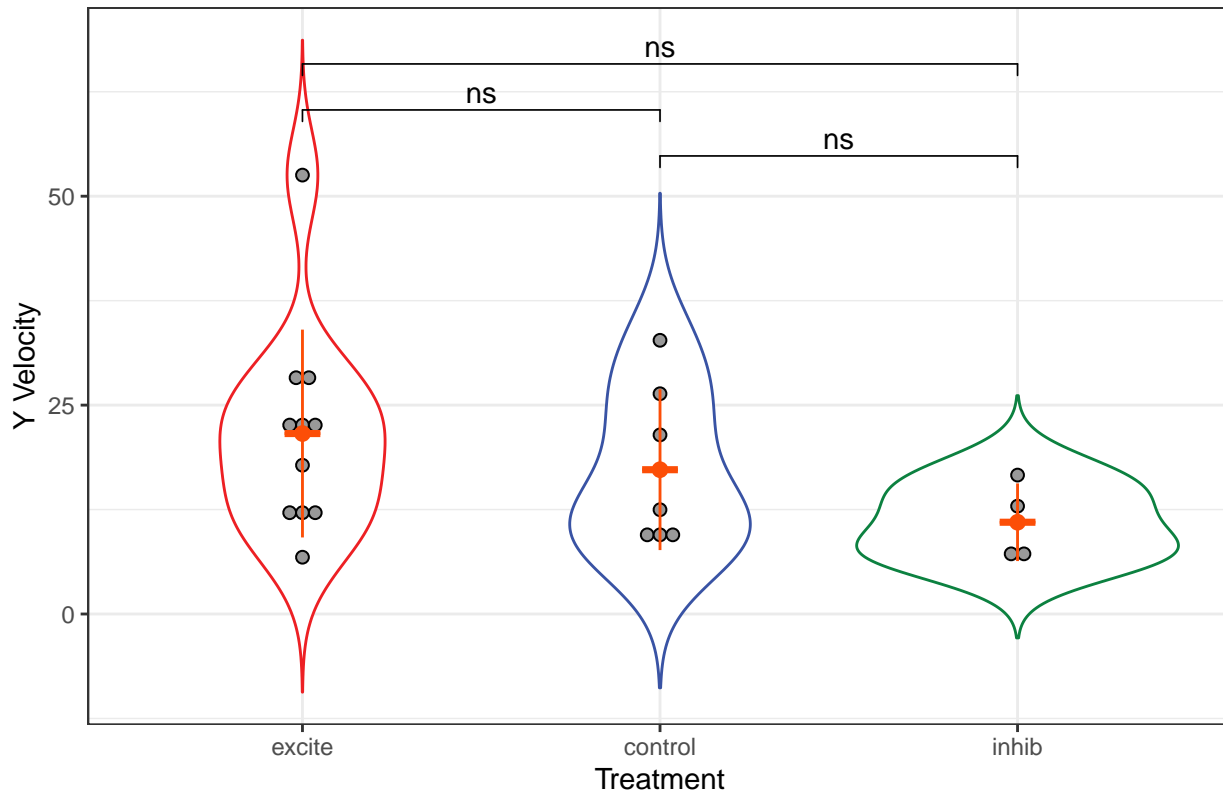
```
md %>% ggplot(aes(x = type, y = -vely, color=type))+
  #geom_boxplot(aes(color = treatment), show.legend = FALSE)+
  geom_violin(trim = FALSE,show.legend=FALSE) +
  geom_dotplot(
    binaxis='y', stackdir='center',
    color = "black", fill = "#999999",
  ) +
  stat_summary(
    fun.data="mean_sdl", fun.args = list(mult=1),
    geom = "pointrange", color = "#FC4E07", size = 0.4
  )+
  stat_summary(fun.y= mean, fun.ymin=mean, fun.ymax=mean, geom="crossbar", width=0.1, color = "#FC4E07")
ylab("Y Velocity") +
  xlab("Treatment") +
  #coord_cartesian(ylim = c(-27, 60)) +
  scale_color_manual(values = c("#ED2024", "#3953A4", "#0C8140"))+
  ggtitle("Y Velocity vs Treatment") +
  stat_compare_means(comparisons=my_comps, label="p.signif") # + # default is Wilcoxon
```

```
## Bin width defaults to 1/30 of the range of the data. Pick better value with
```



```
## `binwidth`.
```

Y Velocity vs Treatment



```
#stat_compare_means(aes(group = treatment), label = "p.signif",
#                     method='kruskal.test', hide.ns = TRUE )
ggsave('yvel.pdf',width=2.5,height=3,units='in')
```

```
## Bin width defaults to 1/30 of the range of the data. Pick better value with
## `binwidth`.
```

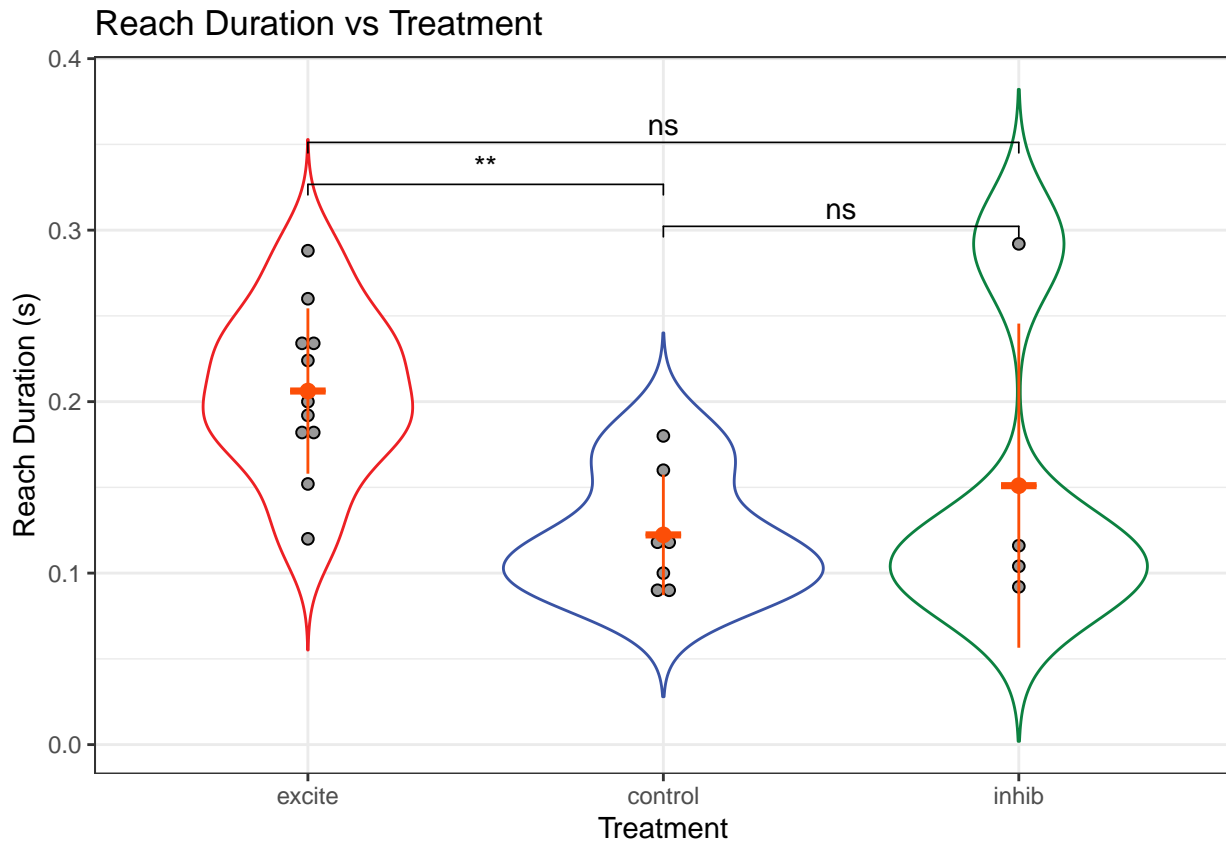
and now dur

```
md %>% ggplot(aes(x = type, y = rchdur, color=type))+
  #geom_boxplot(aes(color = treatment), show.legend = FALSE)+
  geom_violin(trim = FALSE,show.legend=FALSE) +
  geom_dotplot(
    binaxis='y', stackdir='center',
    color = "black", fill = "#999999",
  ) +
  stat_summary(
    fun.data="mean_sdl", fun.args = list(mult=1),
    geom = "pointrange", color = "#FC4E07", size = 0.4
  )+
  stat_summary(fun.y= mean, fun.ymin=mean, fun.ymax=mean, geom="crossbar", width=0.1, color = "#FC4E07")
ylab("Reach Duration (s)") +
  xlab("Treatment") +
  #coord_cartesian(ylim = c(-27, 60)) +
  scale_color_manual(values = c("#ED2024", "#3953A4", "#0C8140"))+
  ggtitle("Reach Duration vs Treatment") +
  stat_compare_means(comparisons=my_comps, label="p.signif") # + # default is Wilcoxon
```

```
## Bin width defaults to 1/30 of the range of the data. Pick better value with
## `binwidth`.

## Warning in wilcox.test.default(c(0.152, 0.26, 0.2, 0.232, 0.192, 0.18, 0.12, :
## cannot compute exact p-value with ties

## Warning in wilcox.test.default(c(0.16, 0.116, 0.18, 0.092, 0.12, 0.1, 0.088:
## cannot compute exact p-value with ties
```



```
#stat_compare_means(aes(group = treatment), label = "p.signif",
#                    method='kruskal.test', hide.ns = TRUE )
ggsave('reachdur.pdf',width=2.5,height=3,units='in')
```

```
## Bin width defaults to 1/30 of the range of the data. Pick better value with
## `binwidth`.

## Warning in wilcox.test.default(c(0.152, 0.26, 0.2, 0.232, 0.192, 0.18, 0.12, :
## cannot compute exact p-value with ties
```

```
## Warning in wilcox.test.default(c(0.152, 0.26, 0.2, 0.232, 0.192, 0.18, 0.12, :
## cannot compute exact p-value with ties
```

and now deltax

```
md %>% ggplot(aes(x = type, y = dx, color=type))+
  #geom_boxplot(aes(color = treatment), show.legend = FALSE)+
  geom_violin(trim = FALSE,show.legend=FALSE) +
  geom_dotplot(
    binaxis='y', stackdir='center',
    color = "black", fill = "#999999",
```

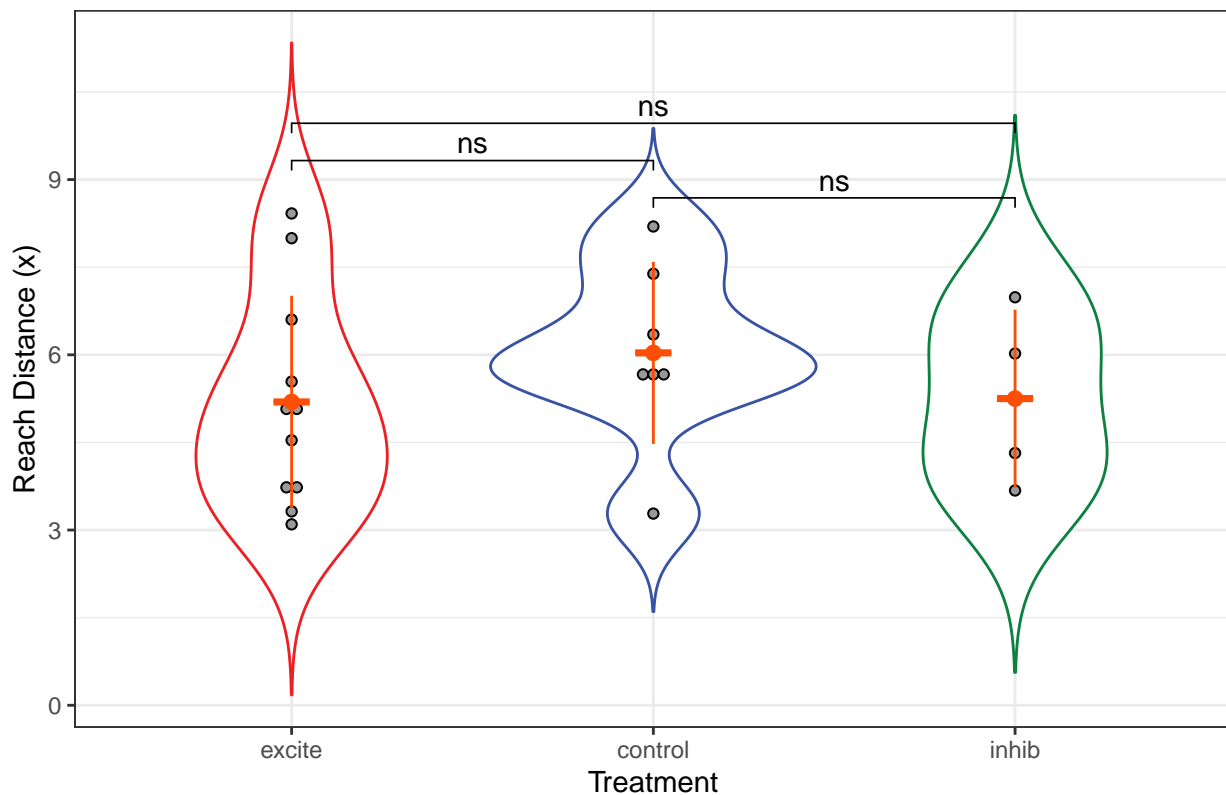
```

) +
stat_summary(
  fun.data="mean_sdl", fun.args = list(mult=1),
  geom = "pointrange", color = "#FC4E07", size = 0.4
)+
stat_summary(fun.y= mean, fun.ymin=mean, fun.ymax=mean, geom="crossbar", width=0.1, color = "#FC4E07"
ylab("Reach Distance (x)") +
xlab("Treatment") +
#coord_cartesian(ylim = c(-27, 60)) +
scale_color_manual(values = c("#ED2024", "#3953A4", "#0C8140"))+
ggtitle("Reach X Distance vs Treatment") +
stat_compare_means(comparisons=my_comps, label="p.signif") # + # default is Wilcoxon

```

Bin width defaults to 1/30 of the range of the data. Pick better value with
`binwidth`.

Reach X Distance vs Treatment



```

#stat_compare_means(aes(group = treatment), label = "p.signif",
#                    method='kruskal.test', hide.ns = TRUE )
ggsave('xdistance.pdf',width=2.5,height=3,units='in')

```

Bin width defaults to 1/30 of the range of the data. Pick better value with
`binwidth`.

and now deltat

```

md %>% ggplot(aes(x = type, y = dy, color=type))+
  #geom_boxplot(aes(color = treatment), show.legend = FALSE)+
  geom_violin(trim = FALSE,show.legend=FALSE) +
  geom_dotplot(

```

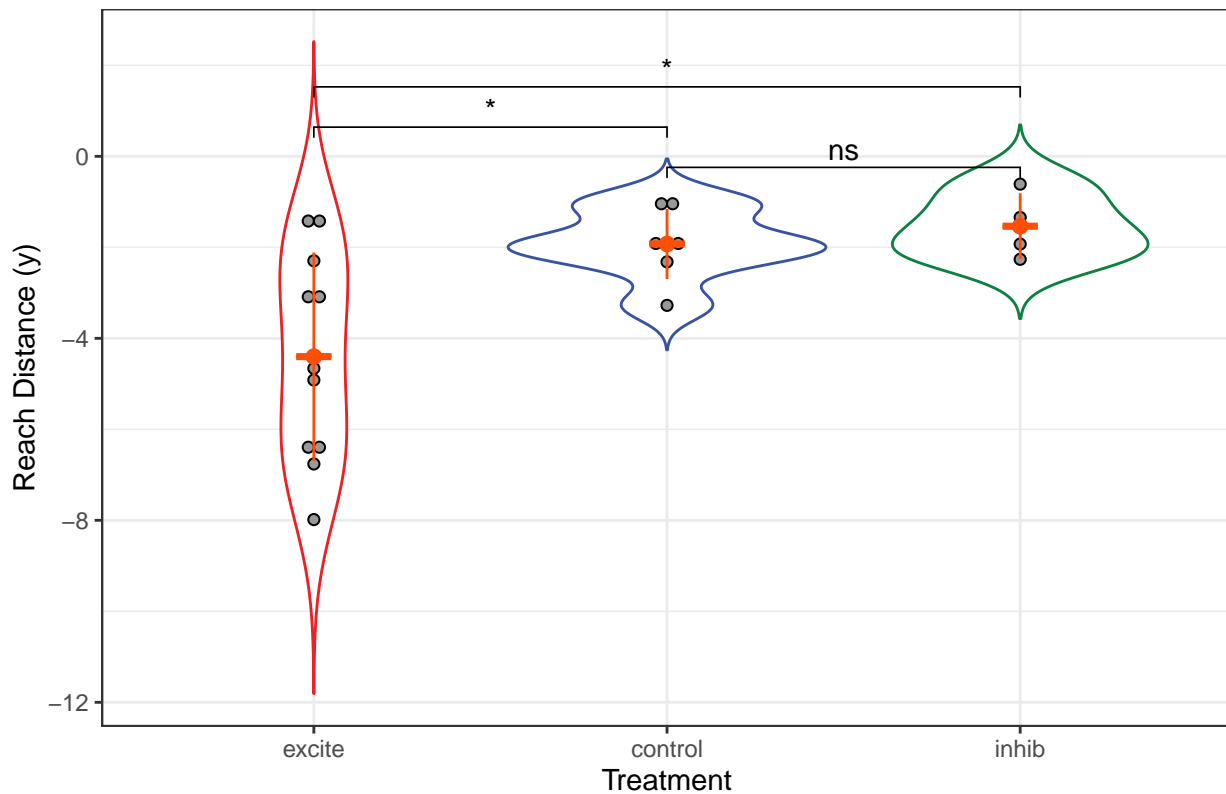
```

    binaxis='y', stackdir='center',
    color = "black", fill = "#999999",
  ) +
  stat_summary(
    fun.data="mean_sdl", fun.args = list(mult=1),
    geom = "pointrange", color = "#FC4E07", size = 0.4
  ) +
  stat_summary(fun.y= mean, fun.ymin=mean, fun.ymax=mean, geom="crossbar", width=0.1, color = "#FC4E07")
  ylab("Reach Distance (y)") +
  xlab("Treatment") +
  #coord_cartesian(ylim = c(-27, 60)) +
  scale_color_manual(values = c("#ED2024", "#3953A4", "#0C8140")) +
  ggtitle("Reach Y Distance vs Treatment") +
  stat_compare_means(comparisons=my_comps, label="p.signif") # + # default is Wilcoxon

```

Bin width defaults to 1/30 of the range of the data. Pick better value with
`binwidth`.

Reach Y Distance vs Treatment



```

  #stat_compare_means(aes(group = treatment), label = "p.signif",
  #                    method='kruskal.test', hide.ns = TRUE )
  ggsave('ydistance.pdf', width=2.5, height=3, units='in')

```

Bin width defaults to 1/30 of the range of the data. Pick better value with
`binwidth`.