violin-plots

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Violin plots

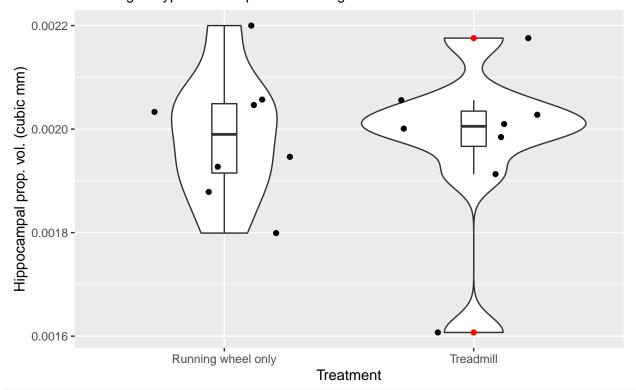
```
graph <- data %>%
 filter(! is.na(Proportional.Volume)) %>%
 filter(! is.na(genotype)) %>%
 filter(genotype != "") %>%
 filter(genotype != "HN") %>%
 mutate(geno = case_when(
   genotype == "APOE2" | genotype == "APOE22" ~ "APOE2",
   genotype == "APOE3" | genotype == "APOE33" ~ "APOE3",
   genotype == "CVN" ~ "CVN"
  )) %>%
  group_by(geno) %>%
  select(Proportional.Volume, geno)
ggplot(data = graph, aes(factor(geno), Proportional.Volume)) +
 geom_violin() +
  geom_boxplot(width = 0.1, outlier.color = "red") +
 geom_jitter(height = 0, width = 0.3) +
 labs(x = "Genotype",
      y = "Hippocampal prop. vol. (cubic mm)",
      title = "Distributions of hippocampal proportional volumes by genotype",
      subtitle = "Red points denoting outliers")
```

Distributions of hippocampal proportional volumes by genotype Red points denoting outliers



```
cvn_graph <- cvn_data %>%
  filter(! is.na(Proportional.Volume)) %>%
  mutate(treat = case_when(
    Treatment == "runningwheel_only" ~ "Running wheel only",
    Treatment == "treadmill" ~ "Treadmill"
  )) %>%
  group_by(treat) %>%
  select(Proportional.Volume, treat)
rw <- cvn_data %>%
  filter(! is.na(Proportional.Volume)) %>%
  filter(Treatment == "runningwheel_only") %>%
  pull(Proportional.Volume)
tm <- cvn_data %>%
  filter(! is.na(Proportional.Volume)) %>%
  filter(Treatment == "treadmill") %>%
  pull(Proportional.Volume)
ggplot(data = cvn_graph, aes(factor(treat), Proportional.Volume)) +
  geom_violin() +
  geom_boxplot(width = 0.1, outlier.color = "red") +
  geom_jitter(height = 0, width = 0.3) +
  labs(x = "Treatment",
       y = "Hippocampal prop. vol. (cubic mm)",
       title = "Distributions of hippocampal proportional volumes by treatment",
       subtitle = "In CVN genotype with red points denoting outliers")
```

Distributions of hippocampal proportional volumes by treatment In CVN genotype with red points denoting outliers



t.test(rw, tm)

```
##
## Welch Two Sample t-test
##
## data: rw and tm
## t = 0.19398, df = 13.009, p-value = 0.8492
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.0001436222 0.0001719597
## sample estimates:
## mean of x mean of y
## 0.001986000 0.001971831
```