HC Subjects: BL vs SWD

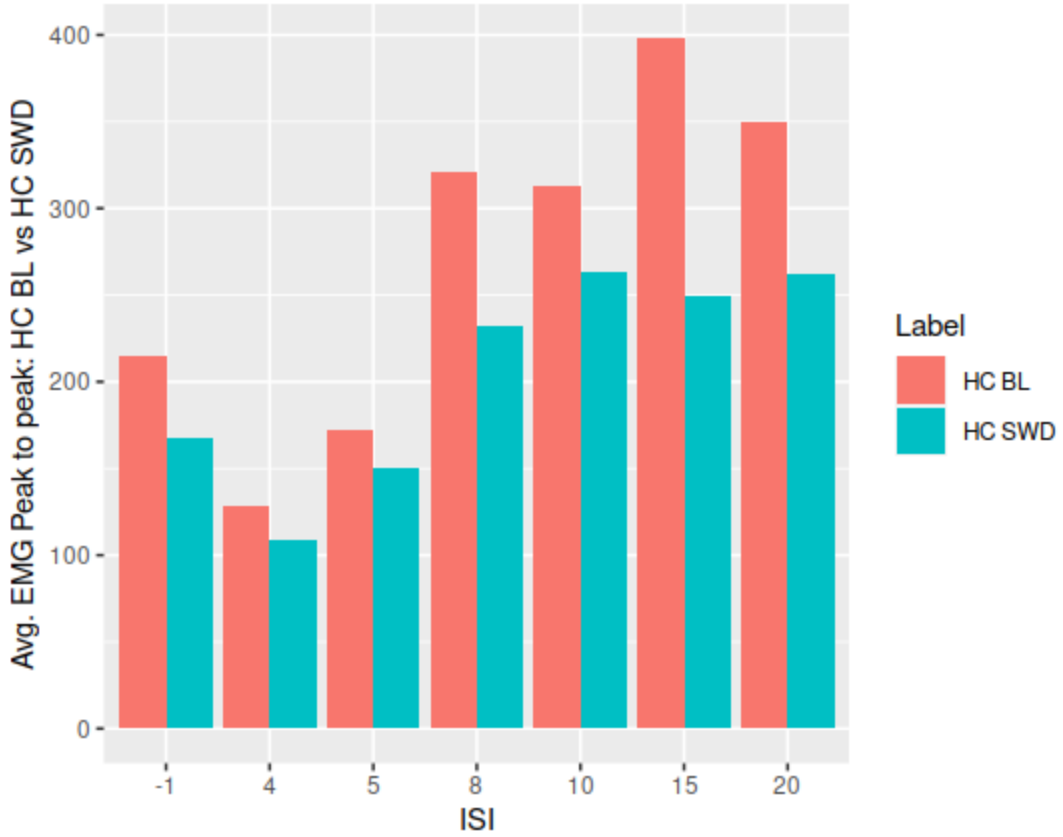
One-way ANOVA:

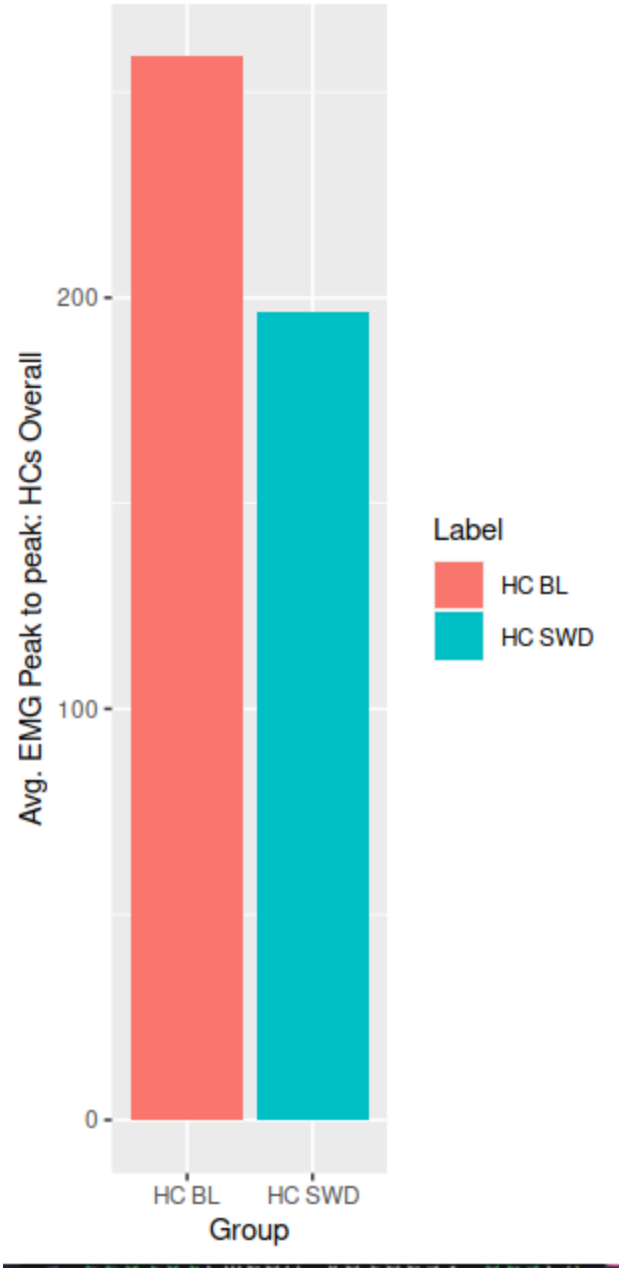
```
> res <- aov(EMGPeakToPeak ~ Label, df %>% filter(Group == 1))
> summary(res)
              Df   Sum Sq Mean Sq F value   Pr(>F)
Label          1  2136677 2136677   51.99 7.59e-13 ***
Residuals   2230 91639832   41094
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

# Robust tests

> X <- filter(df, Group == 1)
> a <- X %>% filter(Type == "SWD")
> b <- X %>% filter(Type == "BL")

# Wilcox (median) : Differences found

> wilcox.test(a$EMGPeakToPeak, b$EMGPeakToPeak)

        Wilcoxon rank sum test with continuity correction

data:  a$EMGPeakToPeak and b$EMGPeakToPeak
W = 491658, p-value < 2.2e-16
alternative hypothesis: true location shift is not equal to 0

# Permutation test: Differences found

> summary(lmp(EMGPeakToPeak~Label,data=X))
[1] "Settings:  unique SS "

Call:
lmp(formula = EMGPeakToPeak ~ Label, data = X)

Residuals:
    Min      1Q  Median      3Q     Max
-254.11 -146.68  -59.14   82.86 1049.09

Coefficients:
       Estimate Iter Pr(Prob)
Label1    30.96 5000   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 202.7 on 2230 degrees of freedom
```

```
Multiple R-Squared: 0.02278,    Adjusted R-squared: 0.02235
F-statistic: 51.99 on 1 and 2230 DF,  p-value: 7.586e-13
```

Two-way ANOVA:

```
> res <- aov(EMGPeakToPeak ~ Label * ISI, df %>% filter(Group == 1))
> summary(res)
              Df   Sum Sq Mean Sq F value   Pr(>F)
Label          1  2136677 2136677  55.895 1.09e-13 ***
ISI            1  6124357 6124357 160.211  < 2e-16 ***
Label:ISI      1   346375  346375   9.061  0.00264 **
Residuals   2228 85169100   38227
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```




Avg. EMG Peak to peak: HCs Overall
200
100
0
HC BL
HC SWD
Group
Label
HC BL
HC SWD