

Lymphatic Graphs

```
library(tidyverse)
```

```
## -- Attaching packages ----- tidyverse 1.3.1 --
```

```
## v ggplot2 3.3.3    v purrr  0.3.4
## v tibble  3.1.0    v dplyr  1.0.5
## v tidyr   1.1.3    v stringr 1.4.0
## v readr   1.4.0    v forcats 0.5.1
```

```
## -- Conflicts ----- tidyverse_conflicts() --
```

```
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
library(car)
```

```
## Loading required package: carData
```

```
##
```

```
## Attaching package: 'car'
```

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

```
##
```

```
##      recode
```

```
## The following object is masked from 'package:purrr':
```

```
##
```

```
##      some
```

```
summ4.df = readRDS("TEST.rds")
```

```
summ5.df = readRDS("TEST_sum.rds")
```

```
make_graph = function(all_data, summ_data, ylab, variable_name)
{
```

```
  all_data$variable = all_data[[variable_name]]
```

```
  summ_data$variable = summ_data[[variable_name]]
```

```
  summ_data$std = summ_data[[paste(variable_name, "_std", sep = "")]]
```

```
  print(summ_data %>% dplyr::select(`treatment`, `n`))
```

```
  plot(ggplot(all_data) + geom_boxplot(aes(y = variable, x = treatment)) +
```

```
    geom_point(aes(y = variable, x = treatment), color = "blue", shape = 16, size = 3, alpha = 0.5) +
```

```

scale_y_continuous(limits = c(NA,NA)) +
labs(y = ylab, x = "")

plot(ggplot(summ_data) + geom_col(aes(y = variable, x = treatment)) +
  geom_errorbar(aes(y = variable, x = treatment, ymax = (variable + std), ymin = (variable-std))) +
  labs(y = ylab, x = ""))

plot(ggplot(summ_data) + geom_col(aes(y = variable, x = treatment)) +
  geom_errorbar(aes(y = variable, x = treatment, ymax = (variable + std), ymin = (variable-std))) +
  labs(y = ylab, x = "")+
  geom_point(aes(y = variable, x = treatment), data = all_data, color = "blue", shape = 16, size = 3))

# Compute the analysis of variance
res.aov <- aov(variable ~ treatment, data = all_data)
print(summary(res.aov))
print(TukeyHSD(res.aov))

print(leveneTest(variable ~ treatment, data = all_data))
aov_residuals <- residuals(object = res.aov)
print(shapiro.test(x = aov_residuals))
print(kruskal.test(variable ~ treatment, data = all_data))

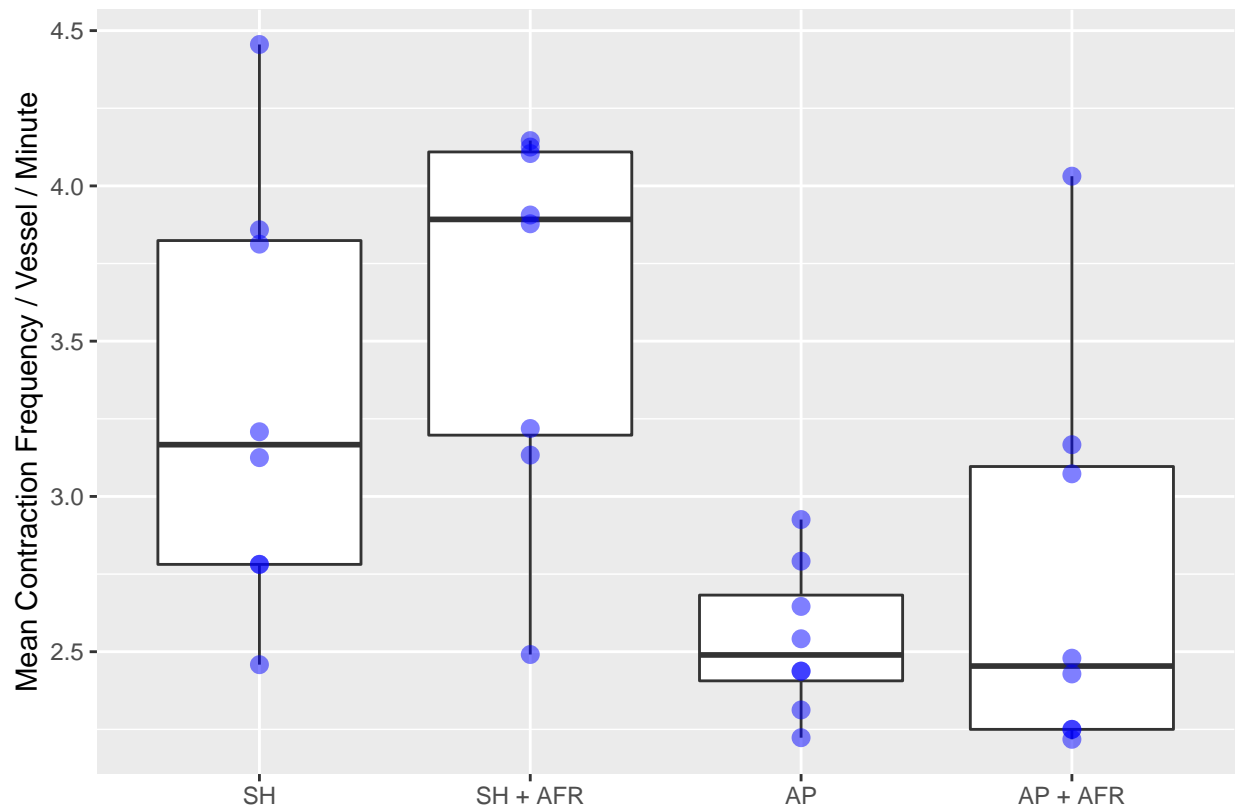
print(pairwise.wilcox.test(all_data$variable, all_data$treatment,
  p.adjust.method = "fdr"))
}

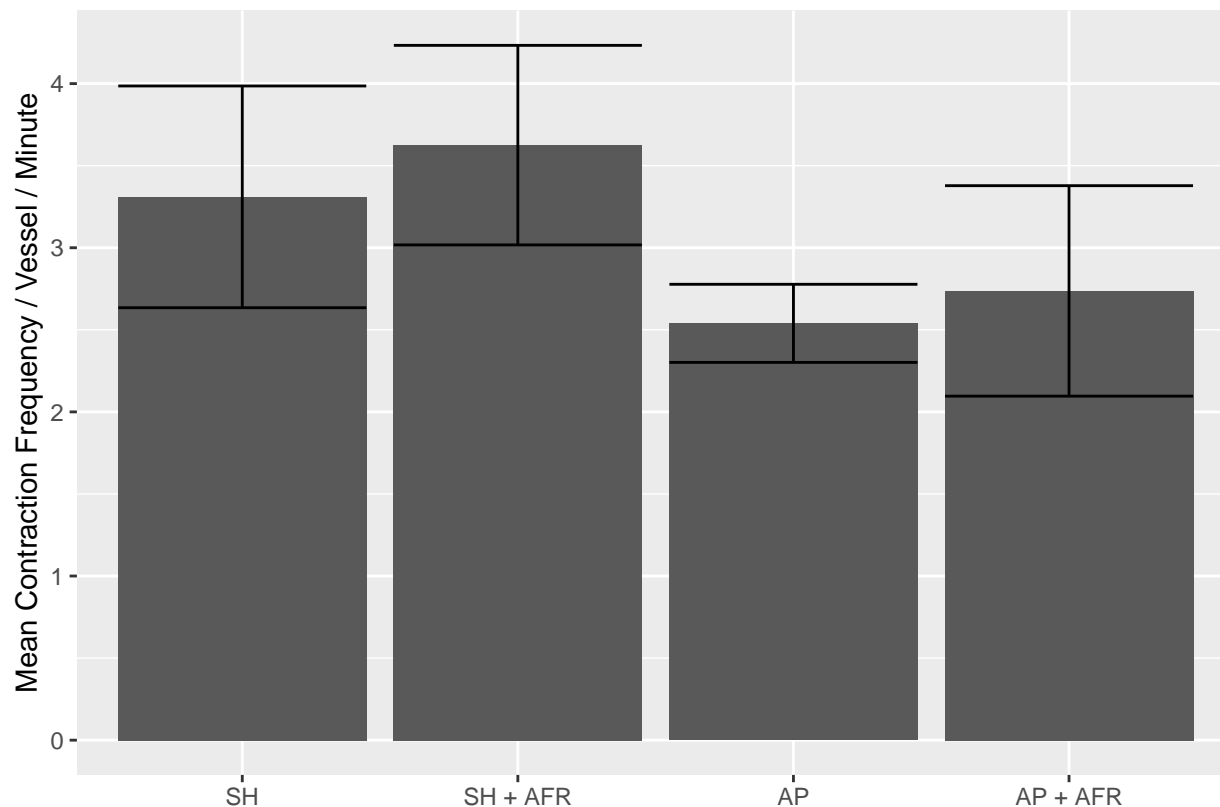
```

Mean Contraction Frequency

```
make_graph(summ4.df, summ5.df, "Mean Contraction Frequency / Vessel / Minute", "max_n_cont")
```

```
## # A tibble: 4 x 2
##   treatment      n
##   <fct>         <int>
## 1 SH             8
## 2 SH + AFR       8
## 3 AP             8
## 4 AP + AFR       8
```





```
##           Df Sum Sq Mean Sq F value    Pr(>F)
## treatment   3  6.057   2.0191    6.243 0.00221 **
## Residuals  28  9.055   0.3234
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = variable ~ treatment, data = all_data)
##
## $treatment
##           diff          lwr          upr      p adj
## SH + AFR-SH    0.3151972 -0.4611457  1.091539998 0.6873725
## AP-SH         -0.7706473 -1.5469901  0.005695504 0.0522466
## AP + AFR-SH   -0.5730097 -1.3493525  0.203333152 0.2065822
## AP-SH + AFR   -1.0858445 -1.8621873 -0.309501669 0.0035968
## AP + AFR-SH + AFR -0.8882068 -1.6645497 -0.111864020 0.0202919
## AP + AFR-AP    0.1976376 -0.5787052  0.973980474 0.8981059
##
## Levene's Test for Homogeneity of Variance (center = median)
##           Df F value Pr(>F)
## group    3  1.0223 0.3977
##          28
##
## Shapiro-Wilk normality test
##
```

```
## data: aov_residuals
## W = 0.96709, p-value = 0.4233
##
##
## Kruskal-Wallis rank sum test
##
## data: variable by treatment
## Kruskal-Wallis chi-squared = 13.351, df = 3, p-value = 0.003936

## Warning in wilcox.test.default(xi, xj, paired = paired, ...): cannot compute
## exact p-value with ties

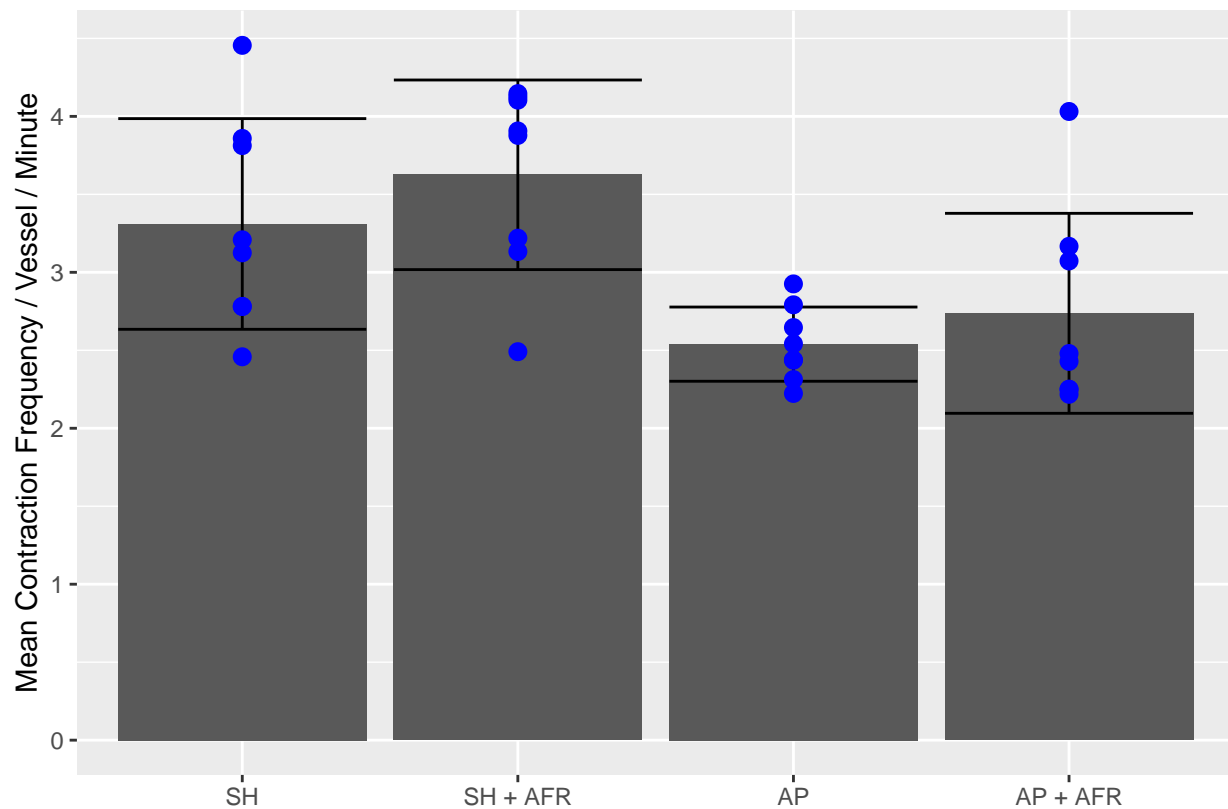
## Warning in wilcox.test.default(xi, xj, paired = paired, ...): cannot compute
## exact p-value with ties

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## exact p-value with ties
```

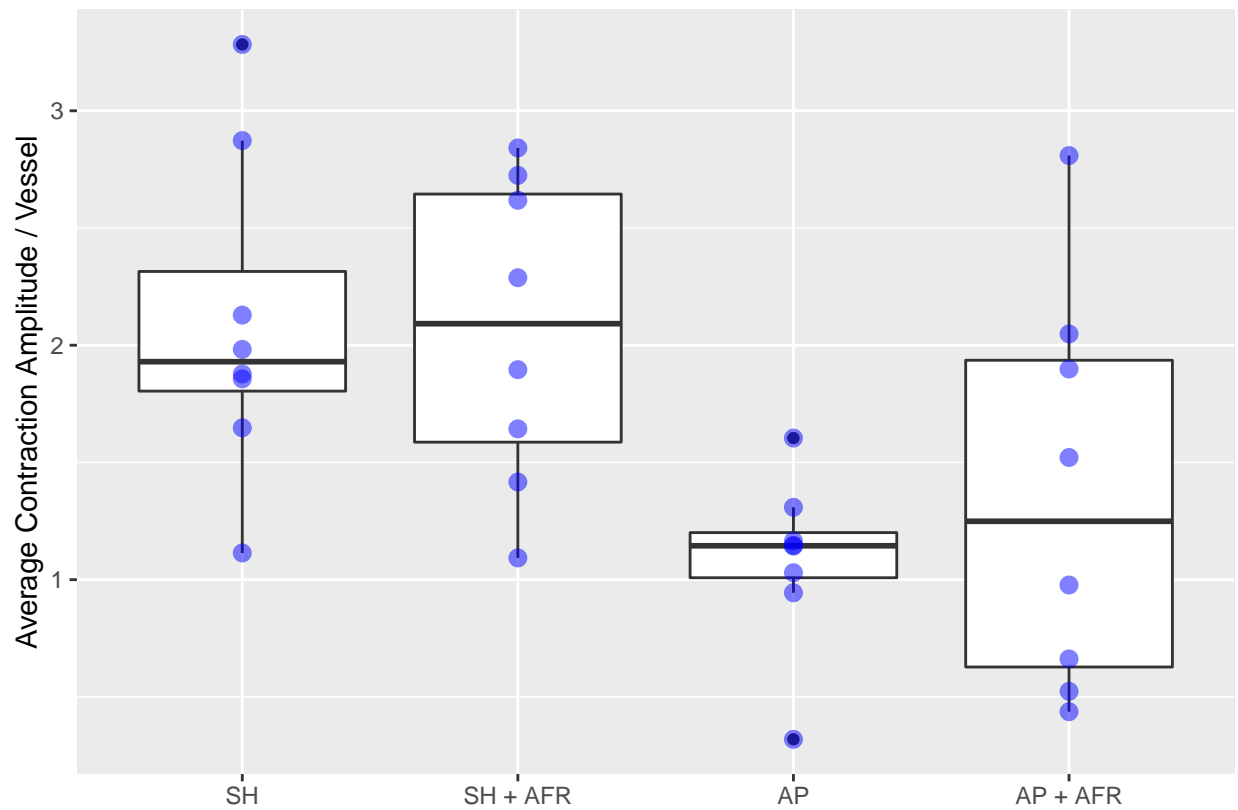


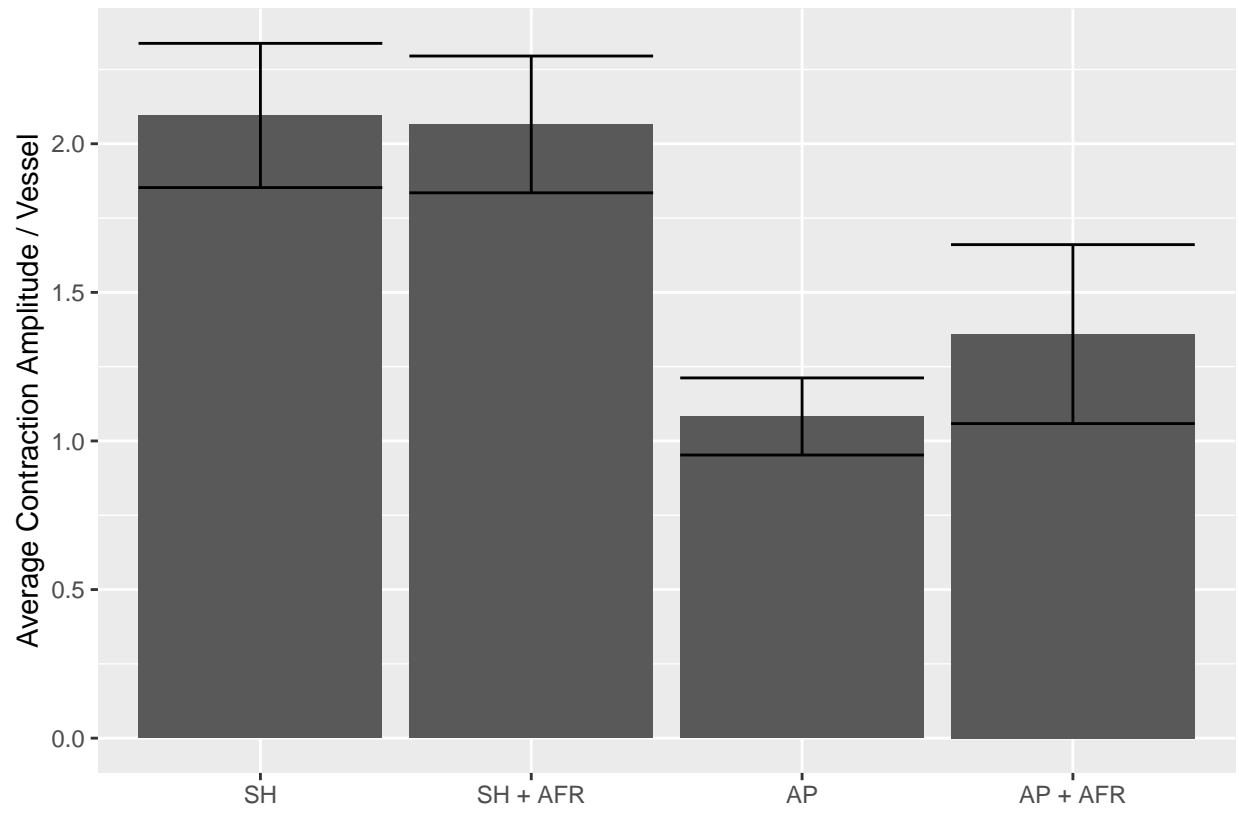
```
##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: all_data$variable and all_data$treatment
##
##          SH      SH + AFR AP
## SH + AFR 0.227 -          -
## AP       0.027 0.023      -
## AP + AFR 0.124 0.027      1.000
##
## P value adjustment method: fdr
```

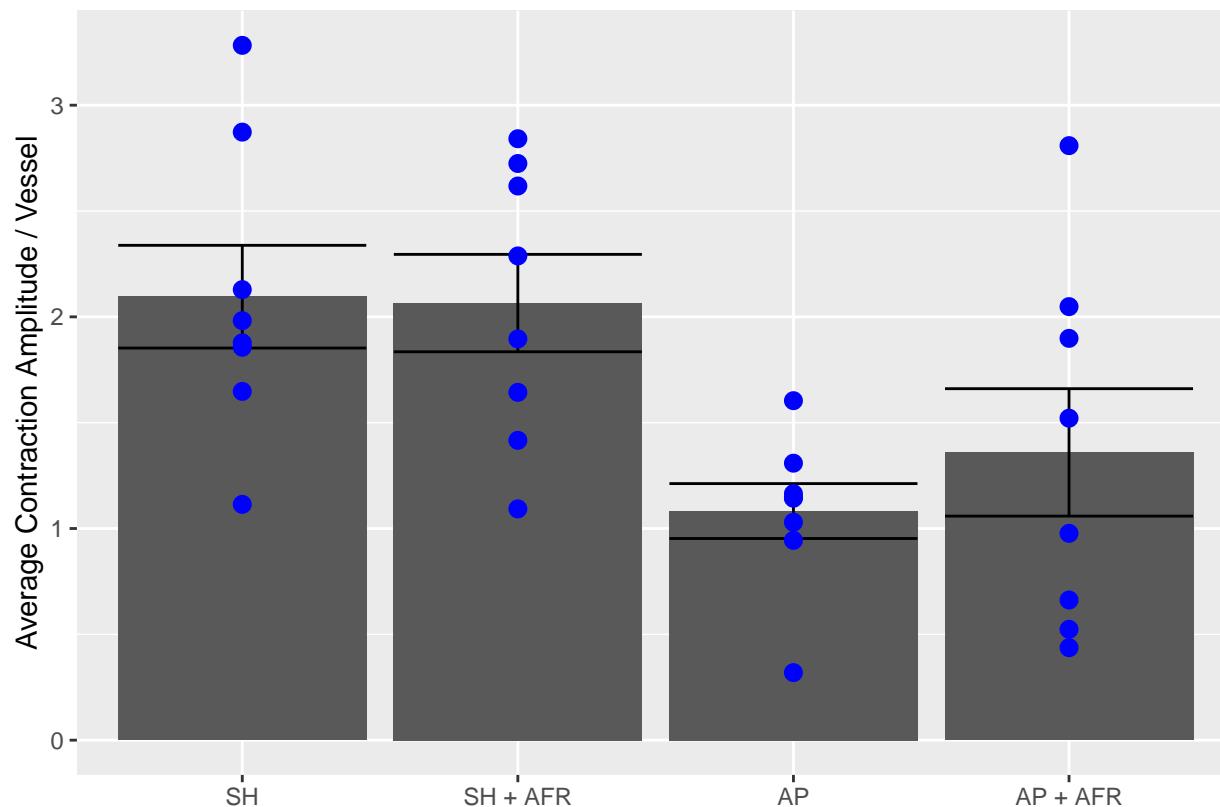
Average contraction amplitude

```
make_graph(summ4.df, summ5.df, "Average Contraction Amplitude / Vessel", "mean_mag")
```

```
## # A tibble: 4 x 2
##   treatment    n
##   <fct>      <int>
## 1 SH          8
## 2 SH + AFR    8
## 3 AP          8
## 4 AP + AFR    8
```







```
##           Df Sum Sq Mean Sq F value    Pr(>F)
## treatment    3  6.216    2.0720     4.725 0.00863 **
## Residuals   28 12.279    0.4385
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = variable ~ treatment, data = all_data)
##
## $treatment
##           diff          lwr          upr      p adj
## SH + AFR-SH   -0.03018752 -0.9342112   0.87383612 0.9997215
## AP-SH         -1.01280563 -1.9168293  -0.10878198 0.0236550
## AP + AFR-SH   -0.73566186 -1.6396855   0.16836179 0.1420010
## AP-SH + AFR   -0.98261810 -1.8866418  -0.07859446 0.0292584
## AP + AFR-SH + AFR -0.70547433 -1.6094980   0.19854931 0.1682023
## AP + AFR-AP    0.27714377 -0.6268799   1.18116742 0.8364023
##
## Levene's Test for Homogeneity of Variance (center = median)
##           Df F value Pr(>F)
## group    3    2.318 0.0971 .
##          28
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```

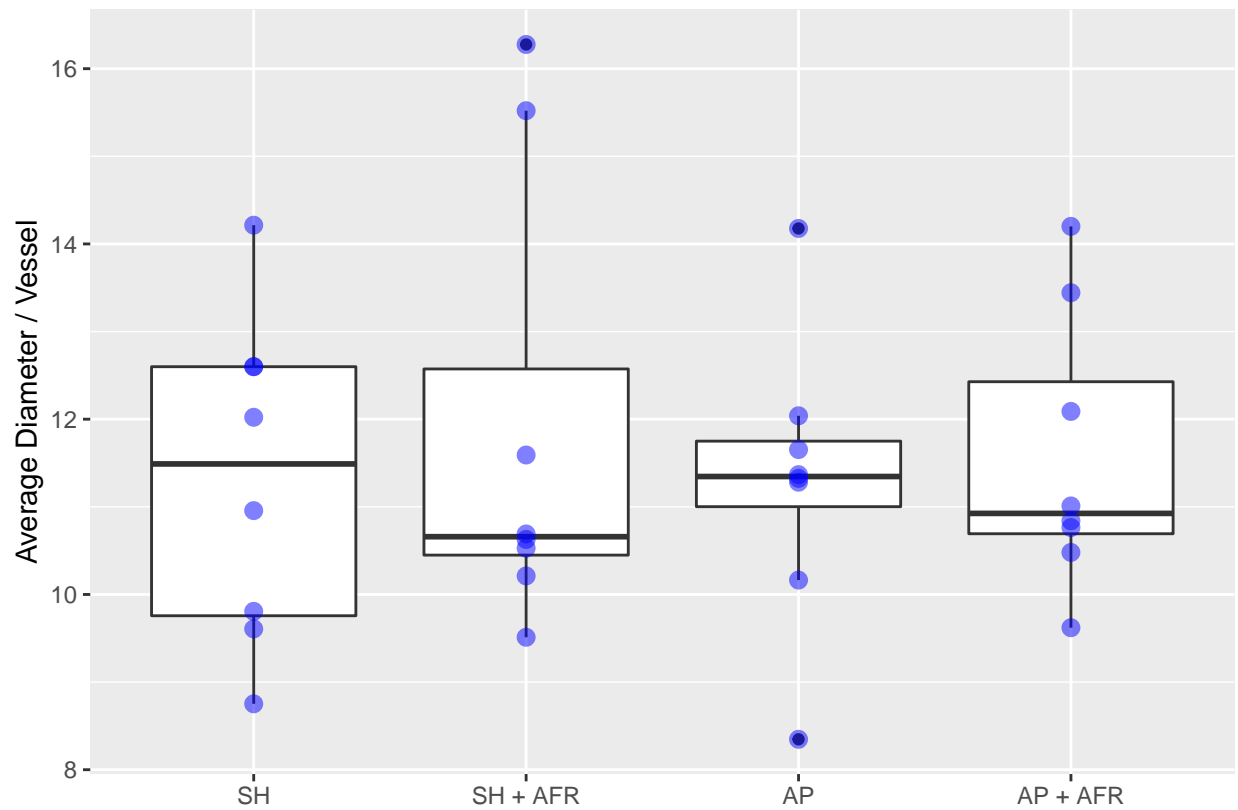
## Shapiro-Wilk normality test
##
## data:  aov_residuals
## W = 0.9711, p-value = 0.5304
##
##
## Kruskal-Wallis rank sum test
##
## data:  variable by treatment
## Kruskal-Wallis chi-squared = 10.688, df = 3, p-value = 0.01354
##
##
## Pairwise comparisons using Wilcoxon rank sum exact test
##
## data:  all_data$variable and all_data$treatment
##
##           SH      SH + AFR AP
## SH + AFR 0.878 -          -
## AP       0.014 0.014      -
## AP + AFR 0.196 0.196      0.865
##
## P value adjustment method: fdr

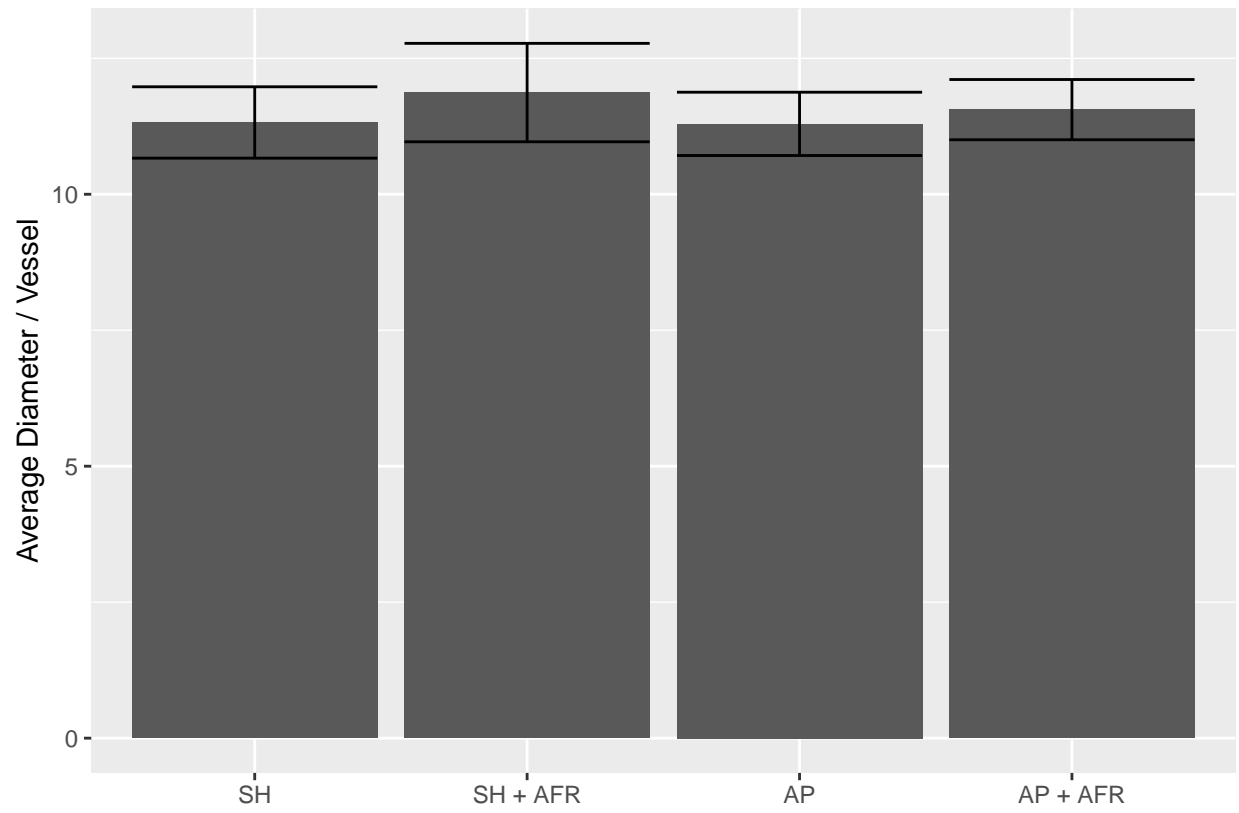
```

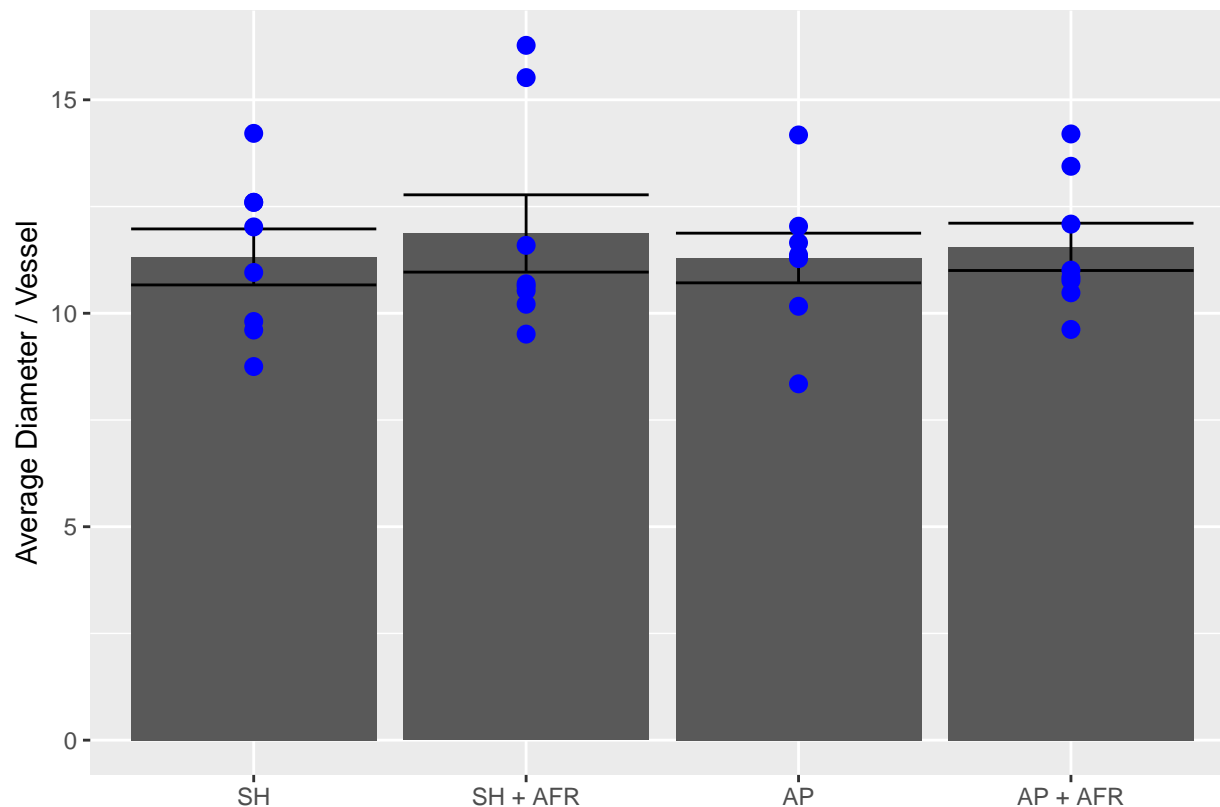
Average Diameter

```
make_graph(all_data = summ4.df, summ_data = summ5.df, ylab = "Average Diameter / Vessel", variable_name
```

```
## # A tibble: 4 x 2
##   treatment      n
##   <fct>         <int>
## 1 SH             8
## 2 SH + AFR       8
## 3 AP             8
## 4 AP + AFR       8
```







```
##           Df Sum Sq Mean Sq F value Pr(>F)
## treatment   3   1.71   0.571   0.151  0.928
## Residuals  28 106.10   3.789
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = variable ~ treatment, data = all_data)
##
## $treatment
##           diff          lwr          upr          p adj
## SH + AFR-SH      0.54991001 -2.107482  3.207302  0.9416076
## AP-SH           -0.02553014 -2.682922  2.631862  0.9999933
## AP + AFR-SH      0.23621883 -2.421173  2.893611  0.9948560
## AP-SH + AFR     -0.57544014 -3.232832  2.081952  0.9338955
## AP + AFR-SH + AFR -0.31369118 -2.971083  2.343701  0.9881741
## AP + AFR-AP      0.26174897 -2.395643  2.919141  0.9930400
##
## Levene's Test for Homogeneity of Variance (center = median)
##           Df F value Pr(>F)
## group     3   0.343 0.7944
##          28
##
## Shapiro-Wilk normality test
##
## data:  aov_residuals
## W = 0.95254, p-value = 0.1701
```

```

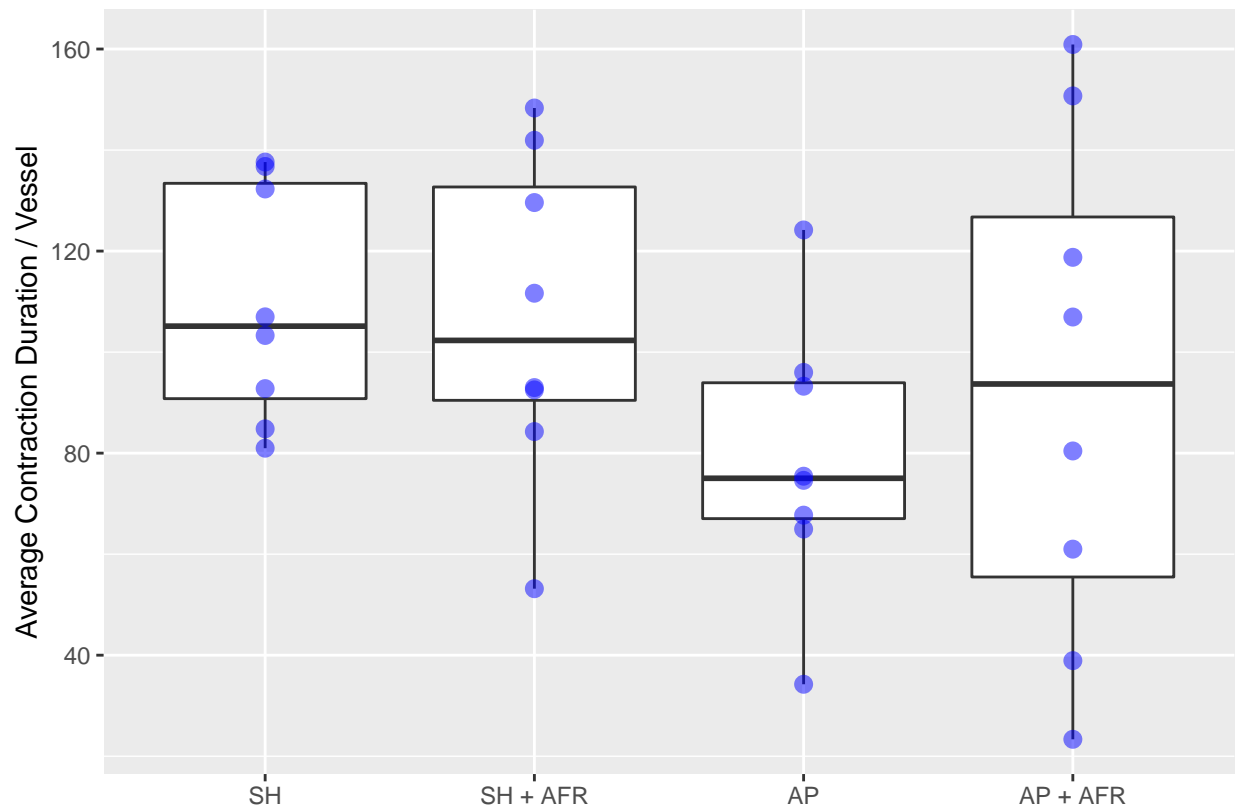
##
##
## Kruskal-Wallis rank sum test
##
## data:  variable by treatment
## Kruskal-Wallis chi-squared = 0.082386, df = 3, p-value = 0.9939
##
##
## Pairwise comparisons using Wilcoxon rank sum exact test
##
## data:  all_data$variable and all_data$treatment
##
##          SH    SH + AFR AP
## SH + AFR 0.96 -          -
## AP       0.96 0.96      -
## AP + AFR 0.96 0.96      0.96
##
## P value adjustment method: fdr

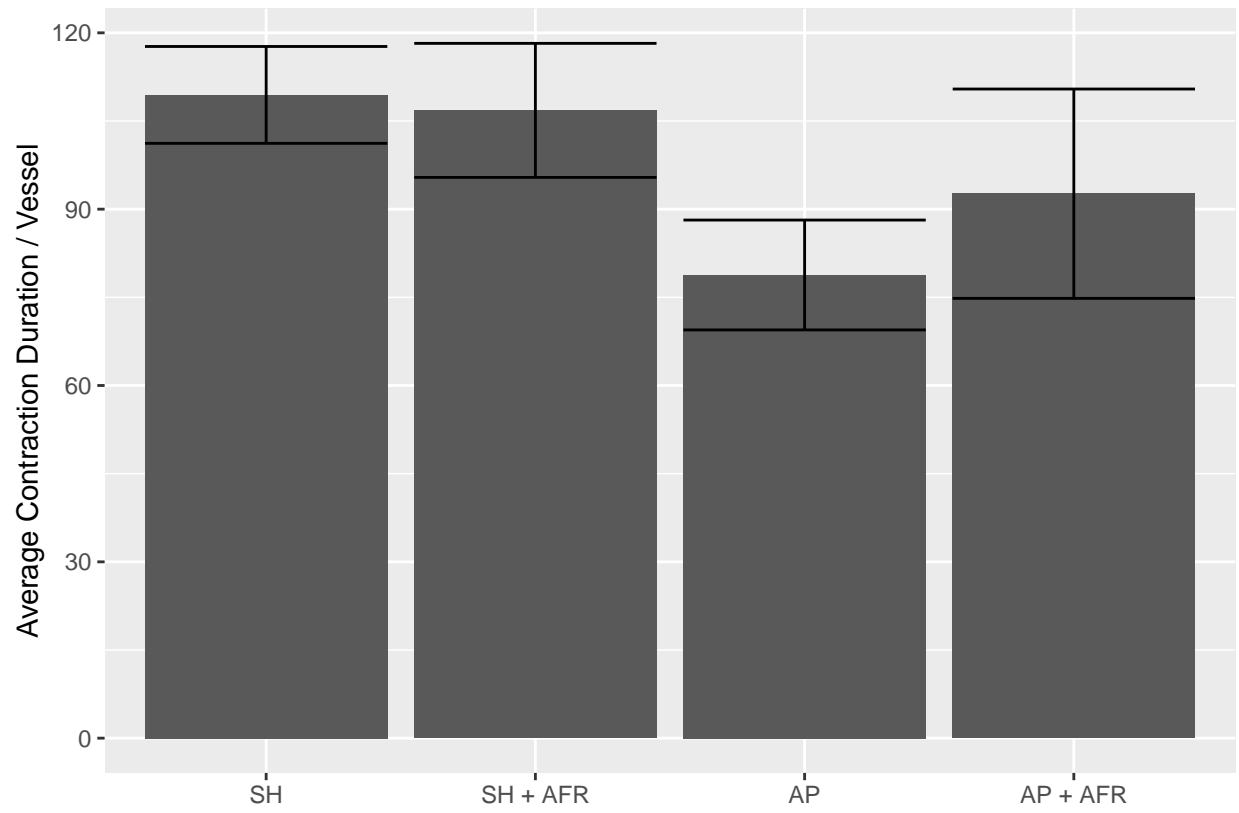
```

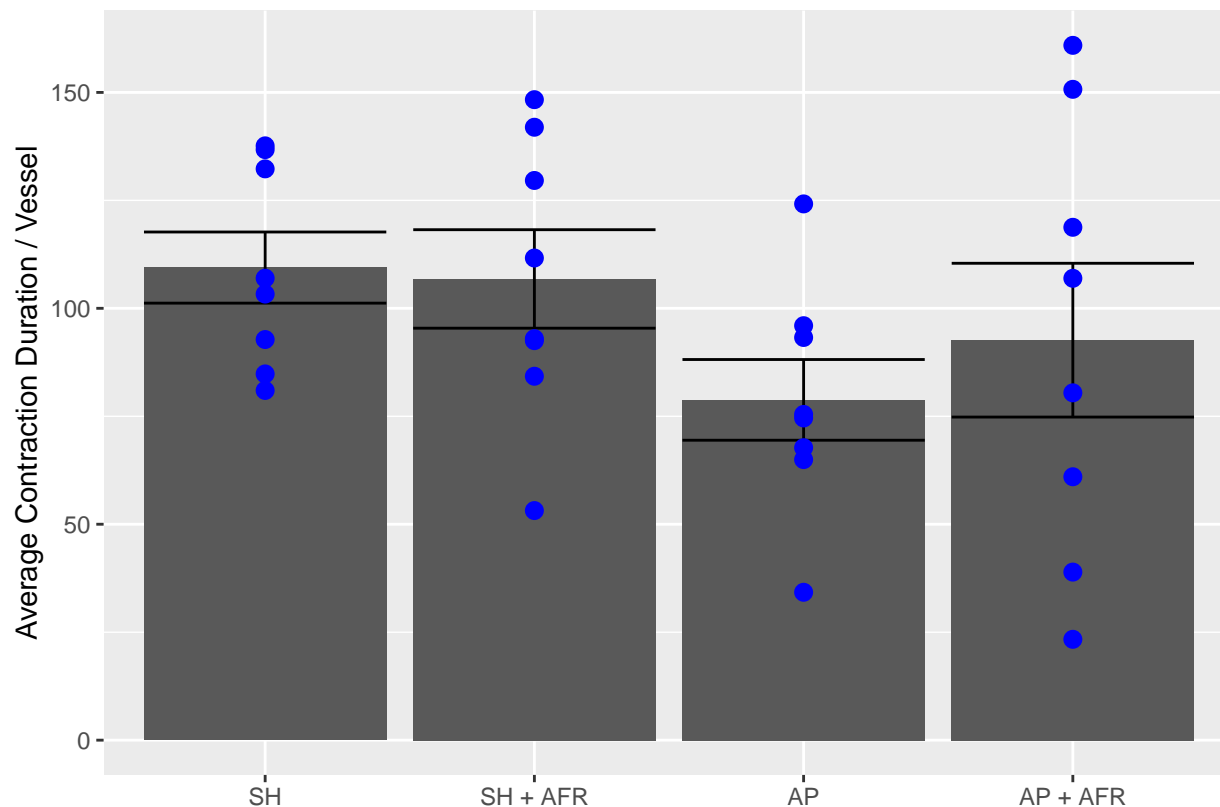
Average contraction duration

```
make_graph(all_data = summ4.df, summ_data = summ5.df, ylab = "Average Contraction Duration / Vessel", v
```

```
## # A tibble: 4 x 2
##   treatment      n
##   <fct>         <int>
## 1 SH              8
## 2 SH + AFR        8
## 3 AP              8
## 4 AP + AFR        8
```







```
##           Df Sum Sq Mean Sq F value Pr(>F)
## treatment    3   4810    1603   1.331  0.284
## Residuals   28  33730    1205
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = variable ~ treatment, data = all_data)
##
## $treatment
##           diff      lwr      upr    p adj
## SH + AFR-SH    -2.633452 -50.01539  44.74848 0.9987239
## AP-SH          -30.639102 -78.02104  16.74283 0.3105873
## AP + AFR-SH    -16.810861 -64.19280  30.57107 0.7680952
## AP-SH + AFR    -28.005650 -75.38758  19.37628 0.3874764
## AP + AFR-SH + AFR -14.177410 -61.55934  33.20453 0.8459495
## AP + AFR-AP     13.828241 -33.55369  61.21018 0.8552618
##
## Levene's Test for Homogeneity of Variance (center = median)
##           Df F value Pr(>F)
## group    3   2.8611 0.05466 .
##          28
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Shapiro-Wilk normality test
##
```

```

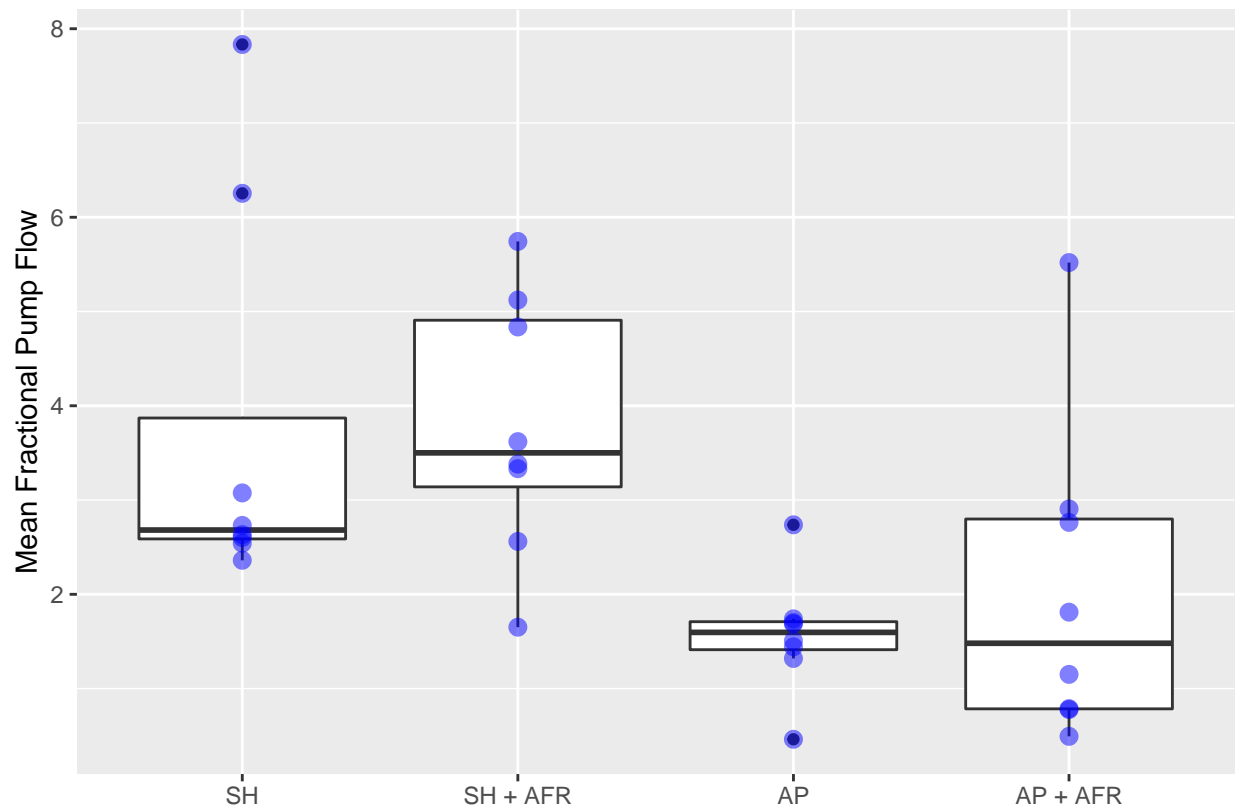
## data:  aov_residuals
## W = 0.98725, p-value = 0.962
##
##
## Kruskal-Wallis rank sum test
##
## data:  variable by treatment
## Kruskal-Wallis chi-squared = 4.1392, df = 3, p-value = 0.2468
##
##
## Pairwise comparisons using Wilcoxon rank sum exact test
##
## data:  all_data$variable and all_data$treatment
##
##          SH    SH + AFR AP
## SH + AFR 1.00  -        -
## AP        0.17 0.39     -
## AP + AFR 0.77 0.77     0.77
##
## P value adjustment method: fdr

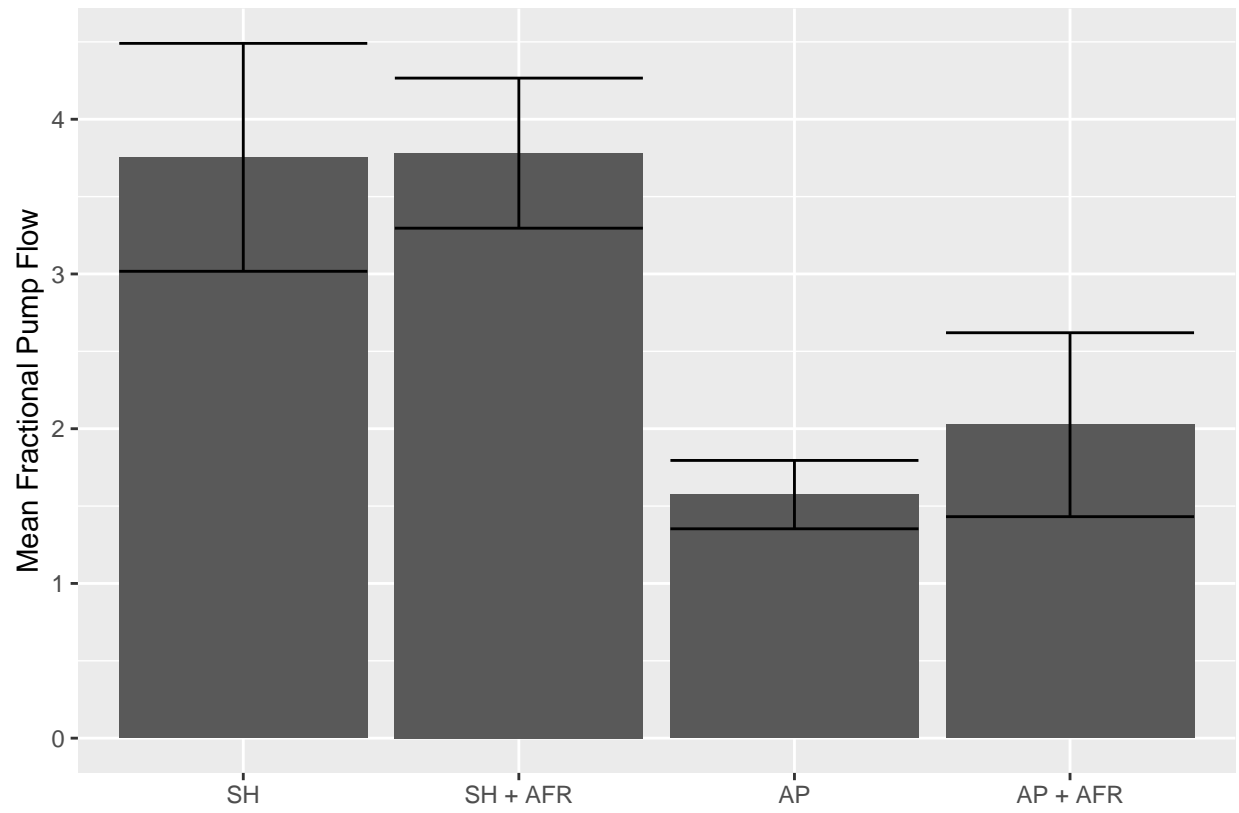
```

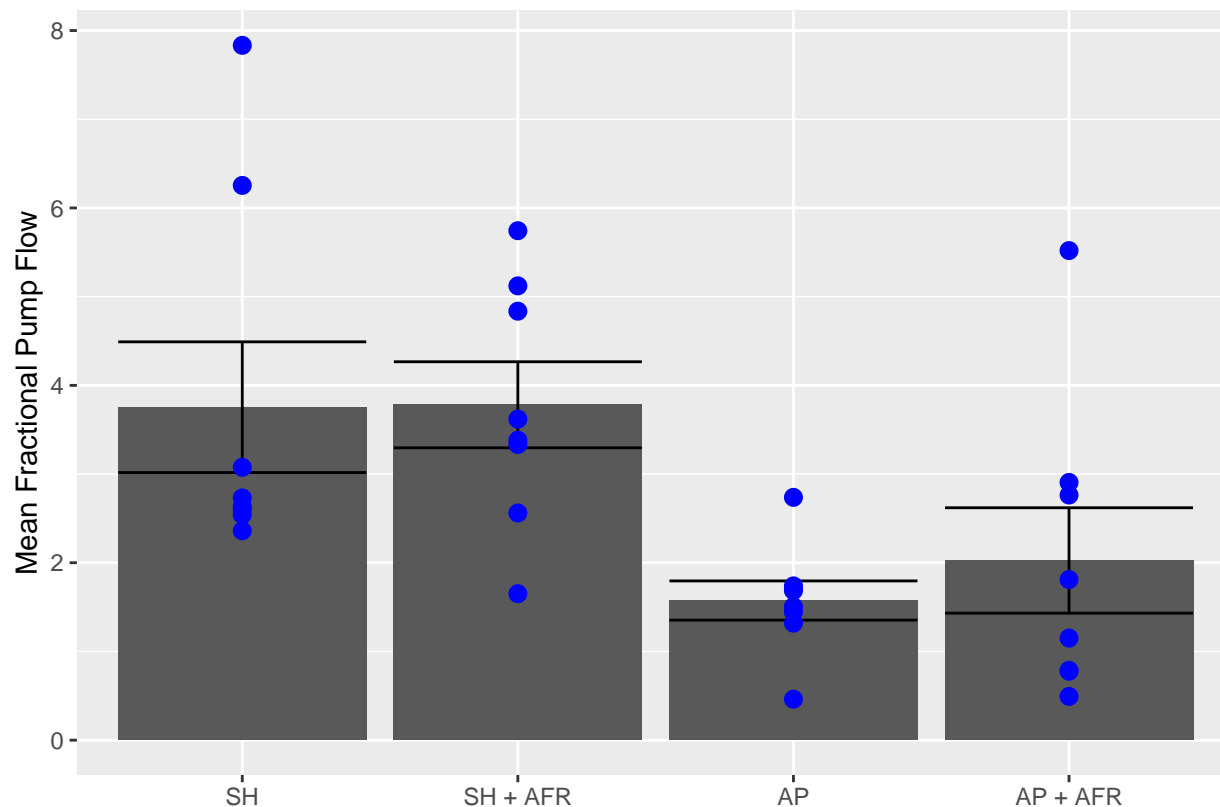
Mean Fractional Pump Flow

```
make_graph(all_data = summ4.df, summ_data = summ5.df, ylab = "Mean Fractional Pump Flow", variable_name
```

```
## # A tibble: 4 x 2
##   treatment    n
##   <fct>      <int>
## 1 SH          8
## 2 SH + AFR    8
## 3 AP          8
## 4 AP + AFR    8
```







```
##           Df Sum Sq Mean Sq F value Pr(>F)
## treatment   3  31.79   10.60    4.49 0.0108 *
## Residuals  28  66.07    2.36
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = variable ~ treatment, data = all_data)
##
## $treatment
##           diff          lwr          upr      p adj
## SH + AFR-SH    0.02709538 -2.070004   2.12419484 0.9999838
## AP-SH         -2.17981591 -4.276915  -0.08271645 0.0393399
## AP + AFR-SH   -1.72805775 -3.825157   0.36904170 0.1346421
## AP-SH + AFR   -2.20691129 -4.304011  -0.10981183 0.0363235
## AP + AFR-SH + AFR -1.75515314 -3.852253   0.34194632 0.1258166
## AP + AFR-AP    0.45175815 -1.645341   2.54885761 0.9348247
##
## Levene's Test for Homogeneity of Variance (center = median)
##           Df F value Pr(>F)
## group     3  0.7871 0.5112
##           28
##
## Shapiro-Wilk normality test
##
```

```

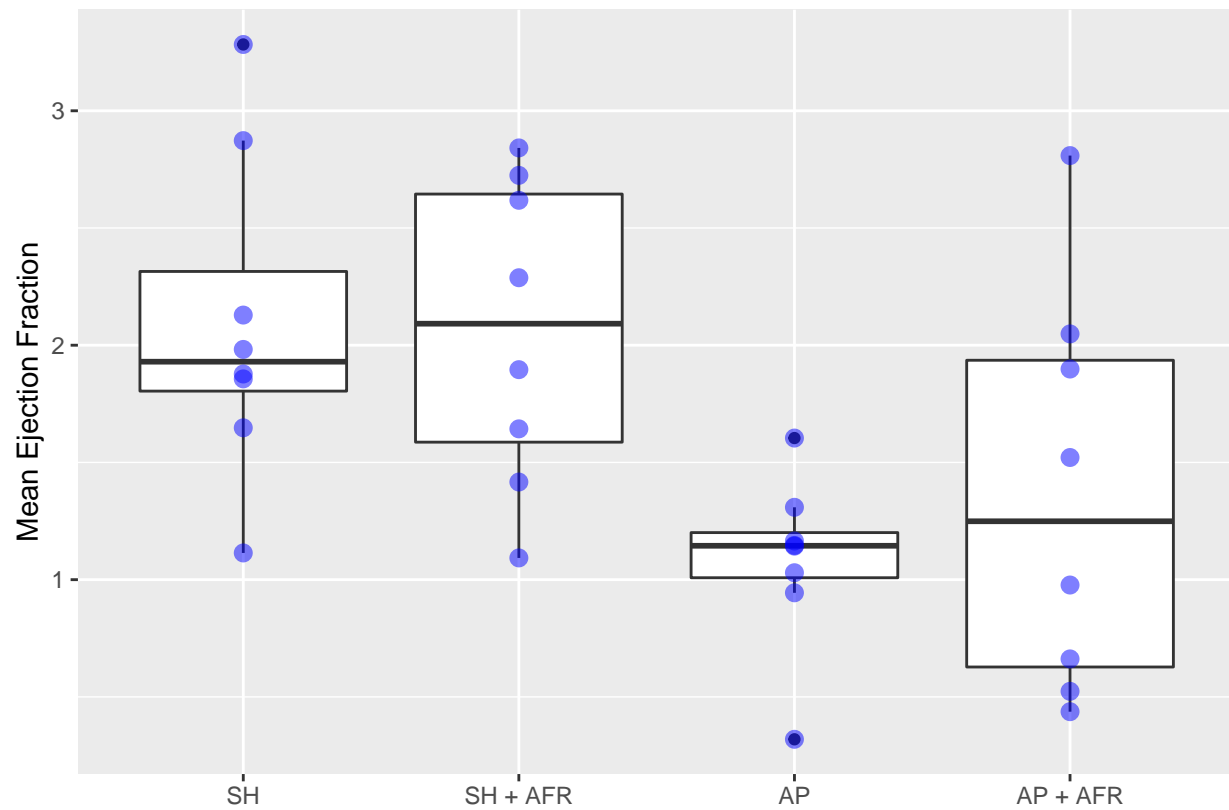
## data:  aov_residuals
## W = 0.89491, p-value = 0.004608
##
##
## Kruskal-Wallis rank sum test
##
## data:  variable by treatment
## Kruskal-Wallis chi-squared = 12.097, df = 3, p-value = 0.007059
##
##
## Pairwise comparisons using Wilcoxon rank sum exact test
##
## data:  all_data$variable and all_data$treatment
##
##          SH      SH + AFR AP
## SH + AFR 0.6885 -      -
## AP       0.0089 0.0089 -
## AP + AFR 0.1573 0.0758 0.7984
##
## P value adjustment method: fdr

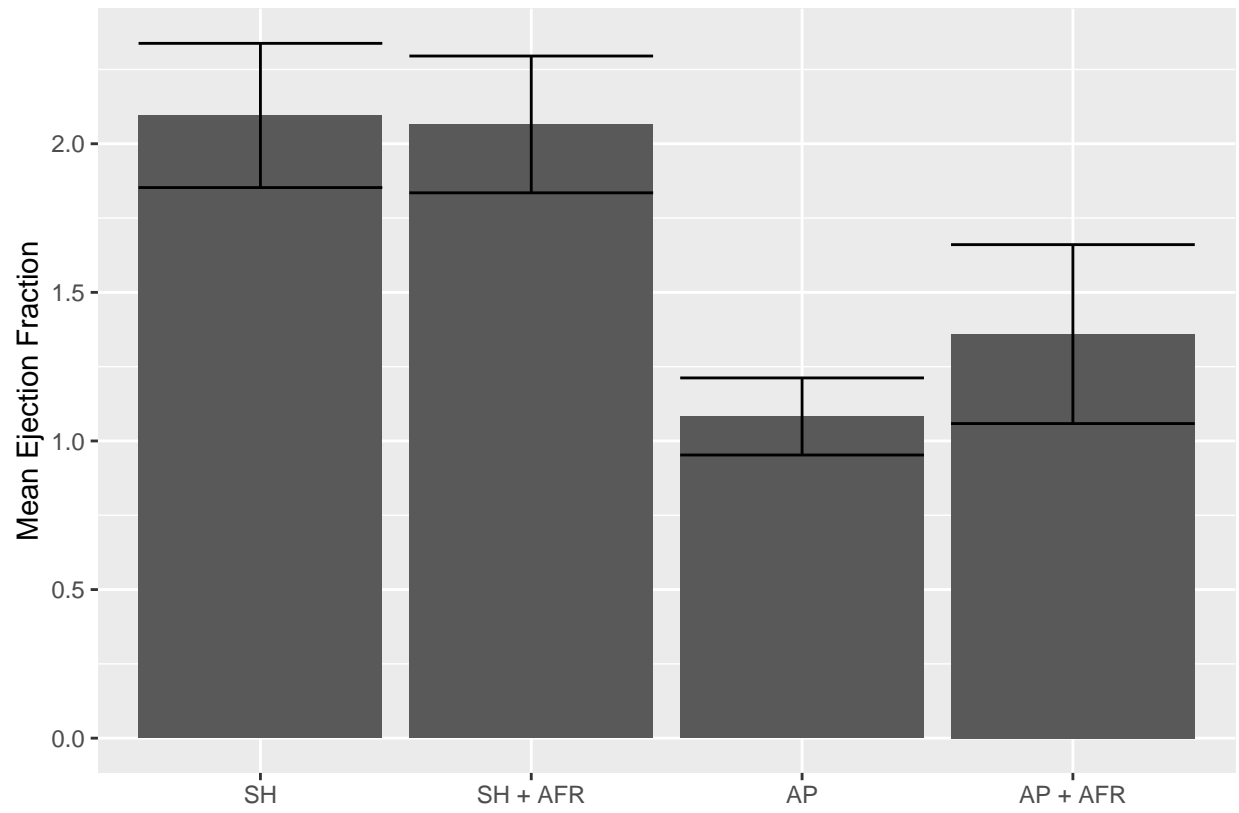
```

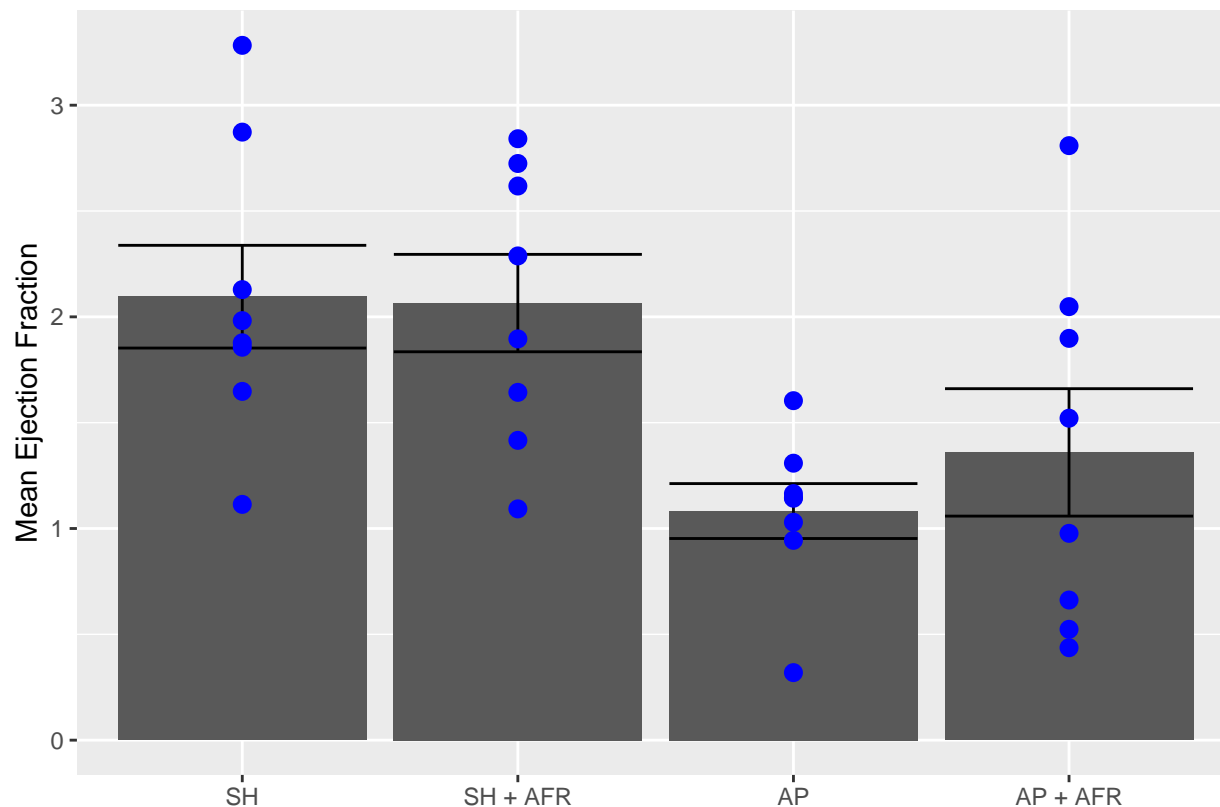
Mean ejection fraction

```
make_graph(all_data = summ4.df, summ_data = summ5.df, ylab = "Mean Ejection Fraction", variable_name =
```

```
## # A tibble: 4 x 2
##   treatment    n
##   <fct>      <int>
## 1 SH          8
## 2 SH + AFR    8
## 3 AP          8
## 4 AP + AFR    8
```







```
##           Df Sum Sq Mean Sq F value    Pr(>F)
## treatment    3  6.216    2.0720     4.725 0.00863 **
## Residuals   28 12.279    0.4385
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = variable ~ treatment, data = all_data)
##
## $treatment
##           diff          lwr          upr      p adj
## SH + AFR-SH   -0.03018752 -0.9342112   0.87383612 0.9997215
## AP-SH         -1.01280563 -1.9168293  -0.10878198 0.0236550
## AP + AFR-SH   -0.73566186 -1.6396855   0.16836179 0.1420010
## AP-SH + AFR   -0.98261810 -1.8866418  -0.07859446 0.0292584
## AP + AFR-SH + AFR -0.70547433 -1.6094980   0.19854931 0.1682023
## AP + AFR-AP    0.27714377 -0.6268799   1.18116742 0.8364023
##
## Levene's Test for Homogeneity of Variance (center = median)
##           Df F value Pr(>F)
## group    3    2.318 0.0971 .
##          28
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```

## Shapiro-Wilk normality test
##
## data:  aov_residuals
## W = 0.9711, p-value = 0.5304
##
##
## Kruskal-Wallis rank sum test
##
## data:  variable by treatment
## Kruskal-Wallis chi-squared = 10.688, df = 3, p-value = 0.01354
##
##
## Pairwise comparisons using Wilcoxon rank sum exact test
##
## data:  all_data$variable and all_data$treatment
##
##           SH      SH + AFR AP
## SH + AFR 0.878 -          -
## AP       0.014 0.014      -
## AP + AFR 0.196 0.196      0.865
##
## P value adjustment method: fdr

```