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 = 0.3) +
```

```r
    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, a

# 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"))
}
```
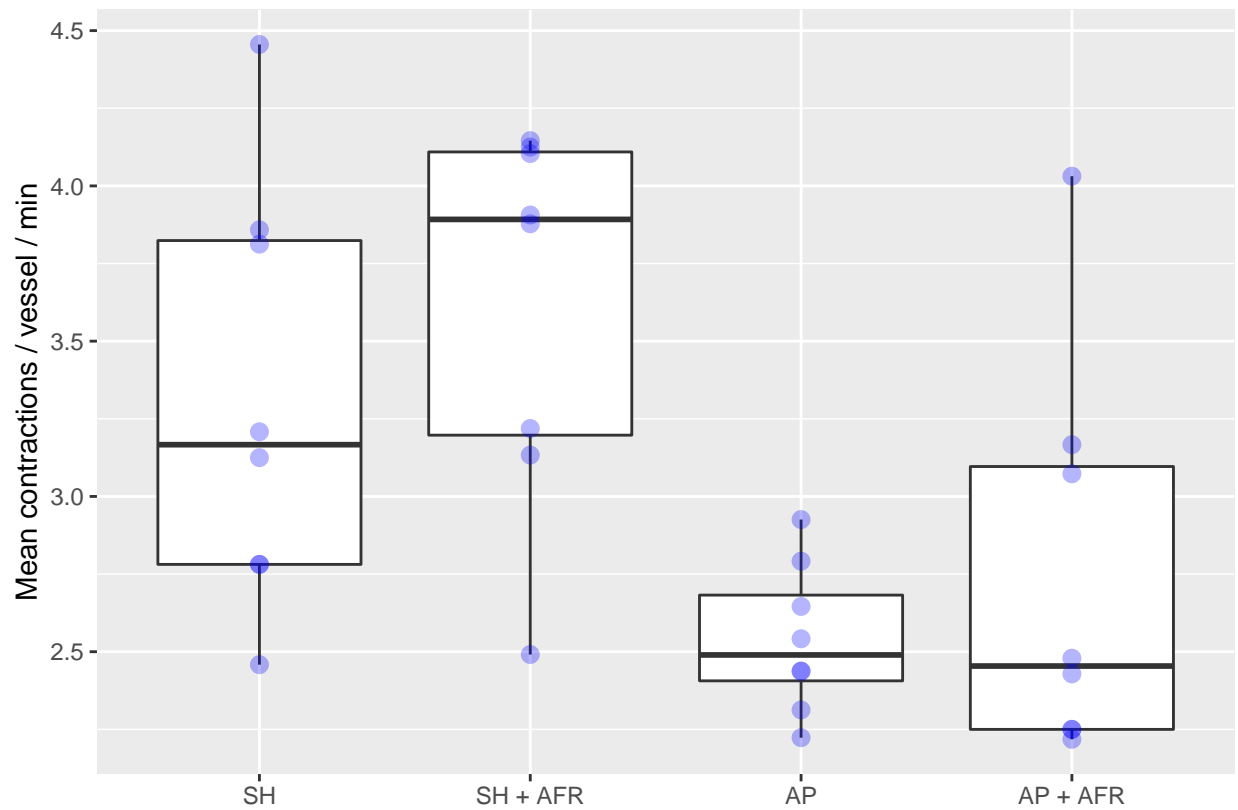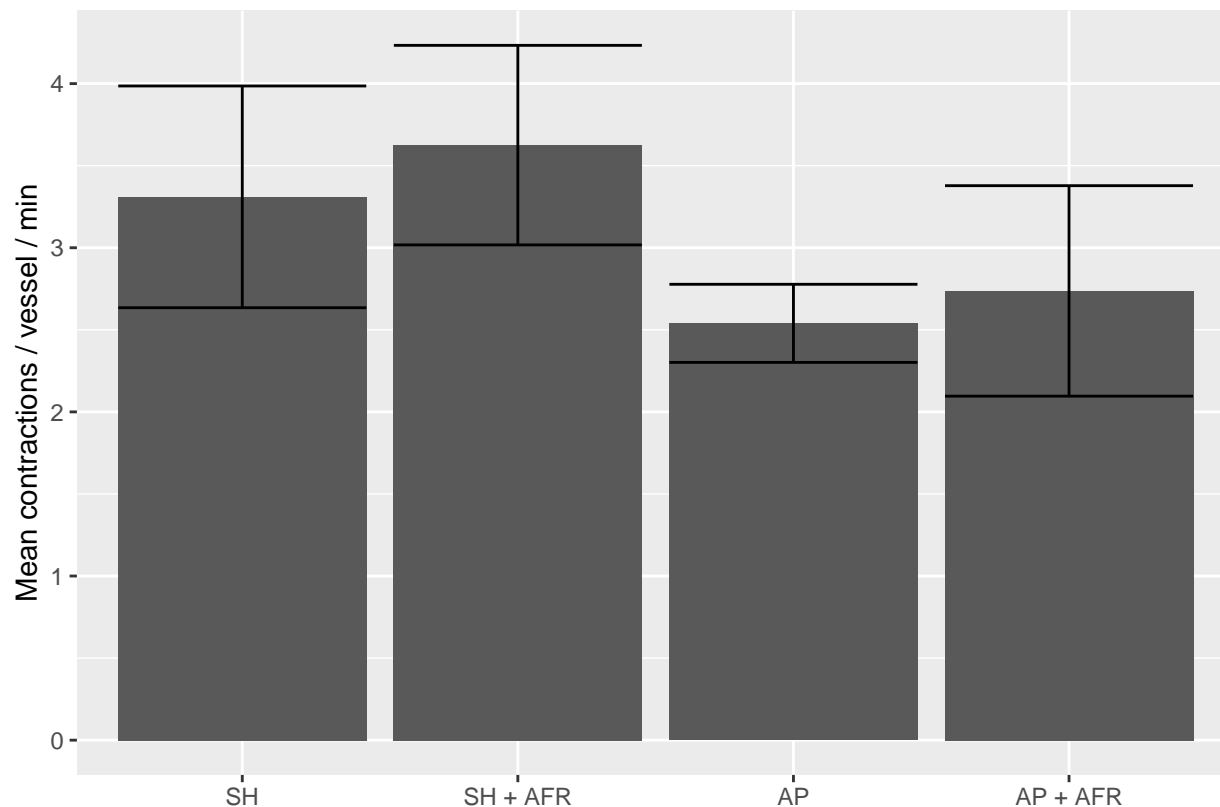
Mean Contraction Frequency

```
make_graph(summ4.df, summ5.df, "Mean contractions / vessel / min", "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

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## exact p-value with ties

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## exact p-value with ties

## Warning in wilcox.test.default(xi, xj, paired = paired, ...): cannot compute
## exact p-value with ties
```
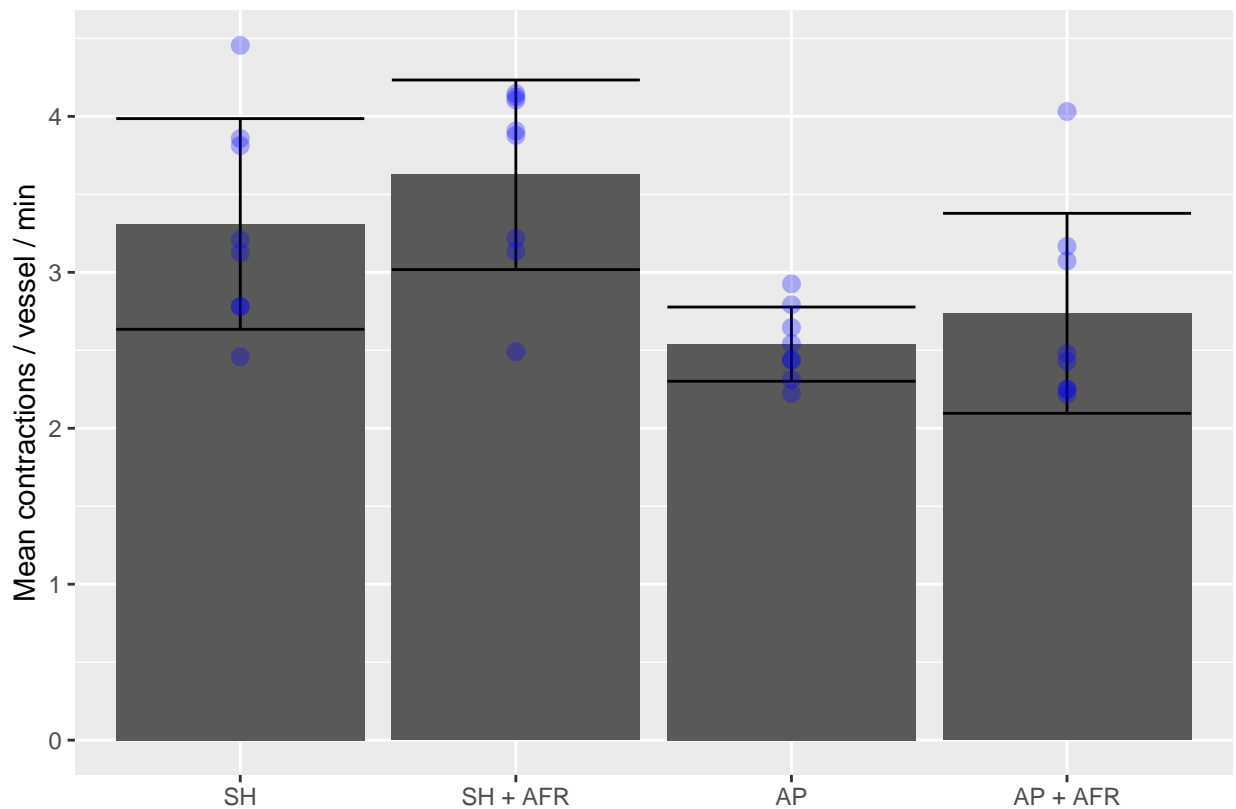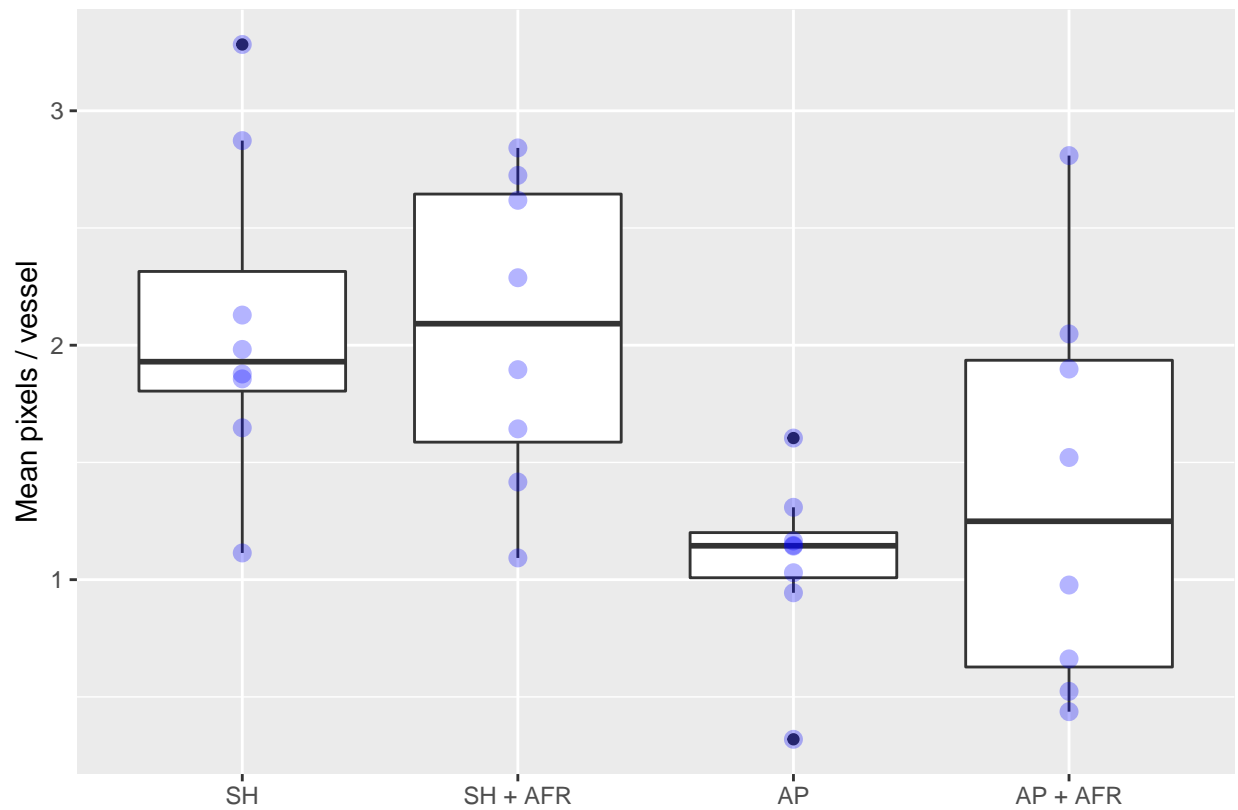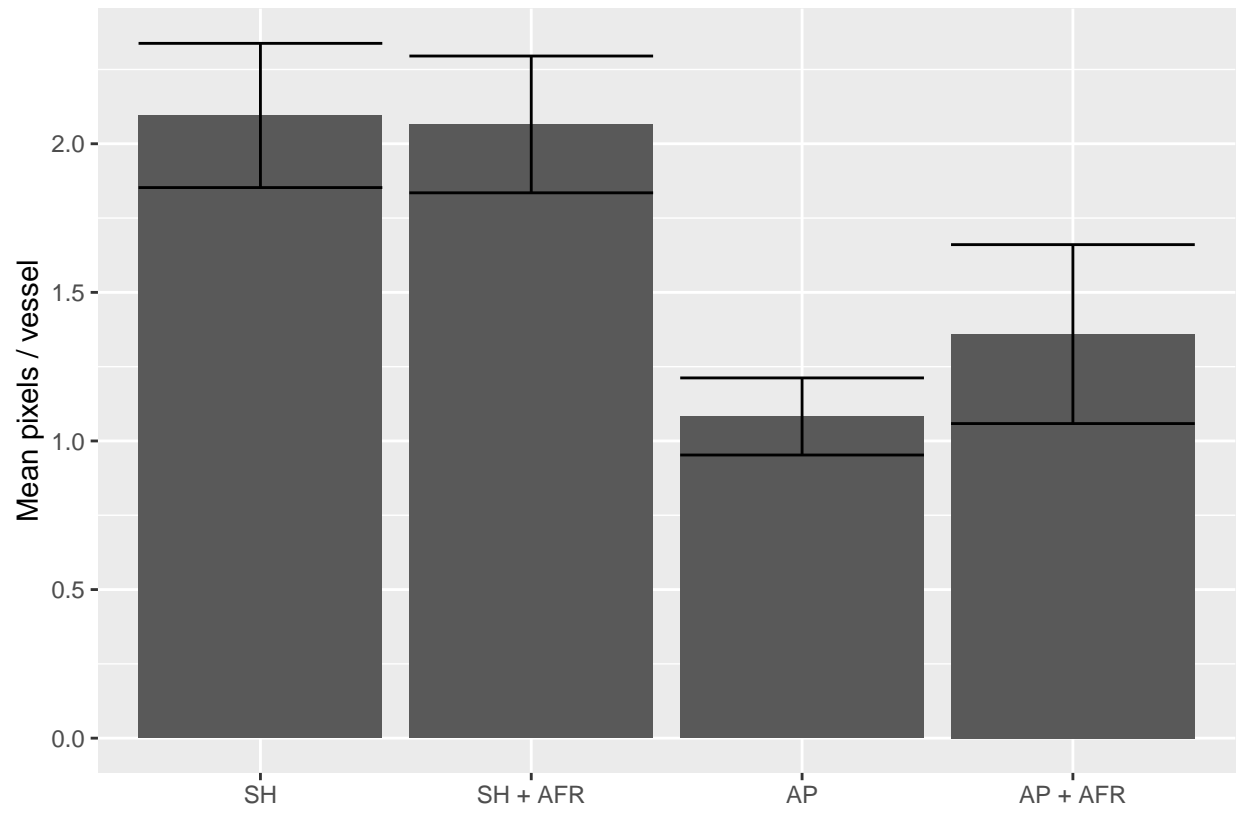
```
## 
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
## 
## data:  all_data$variable and all_data$treatment
## 
##          SH    SH + AFR AP
## SH + AFR 0.227 -        -
## AP       0.027 0.023    -
## AP + AFR 0.124 0.027    1.000
## 
## P value adjustment method: fdr
```
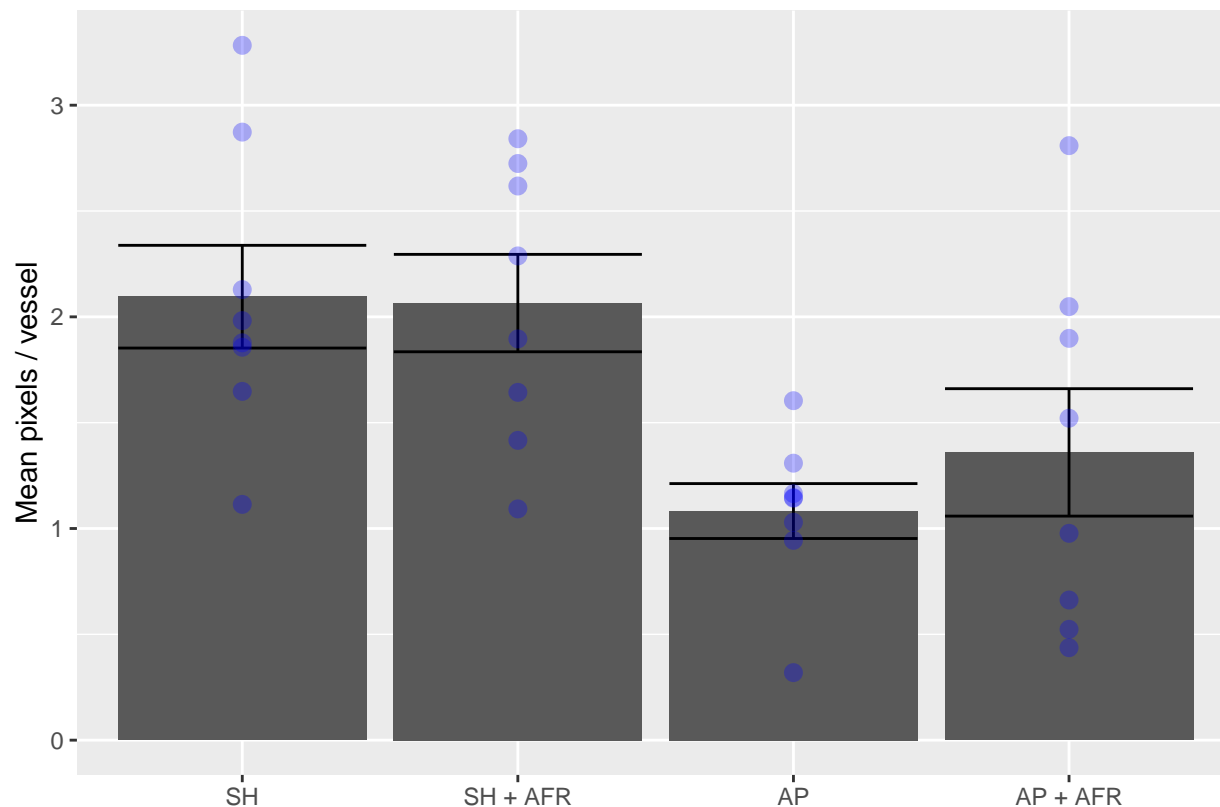
Average contraction amplitude

```
make_graph(summ4.df, summ5.df, "Mean pixels / 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
```
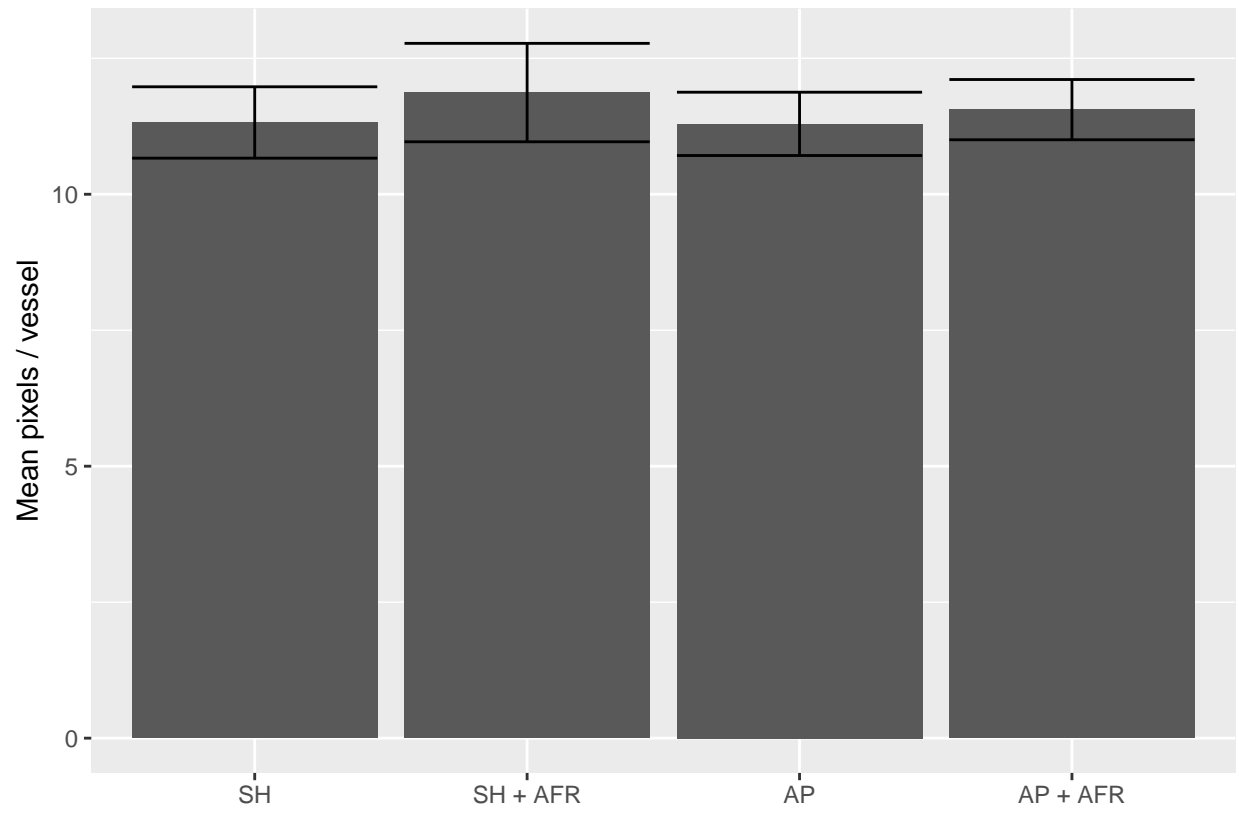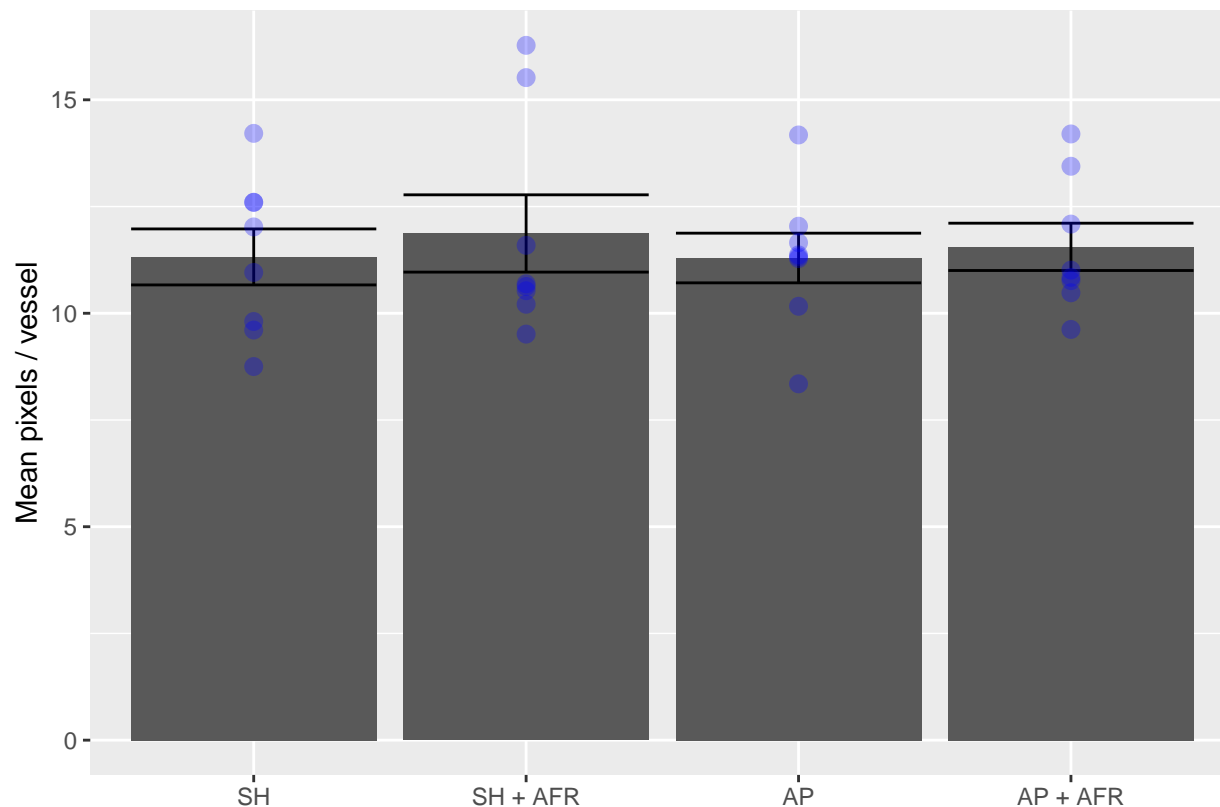
Average Diameter

```
make_graph(all_data = summ4.df, summ_data = summ5.df, ylab = "Mean pixels / vessel", variable_name = "w
```

```
## # A tibble: 4 x 2
##   treatment      n
##   <fct>      <int>
## 1 SH             8
## 2 SH + AFR       8
## 3 AP             8
## 4 AP + AFR       8
```
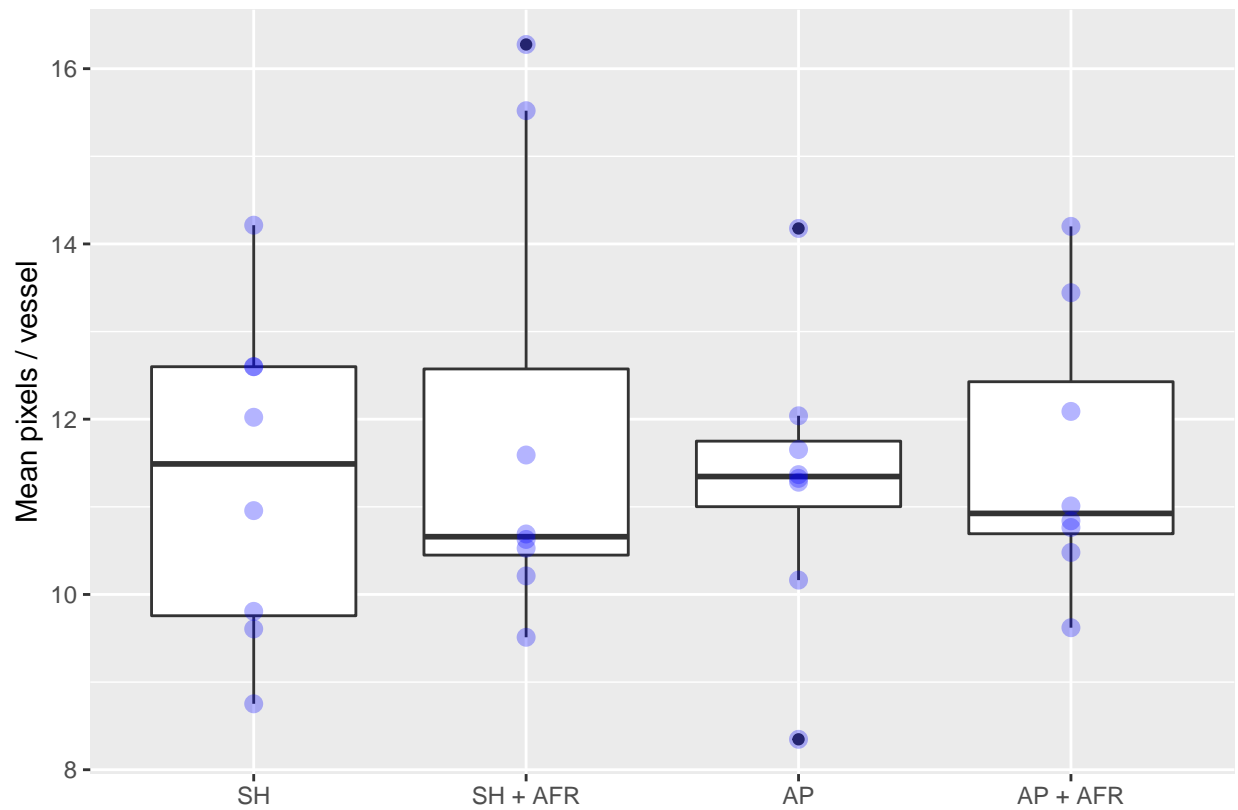
```
##              Df Sum Sq Mean Sq F value Pr(>F)
## treatment    3   1.71   0.571   0.151  0.928
## Residuals   28 106.10   3.789
##    Tukey multiple comparisons of means
##      95% family-wise confidence level
##
## Fit: aov(formula = variable ~ treatment, data = all_data)
##
## $treatment
##                        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
```
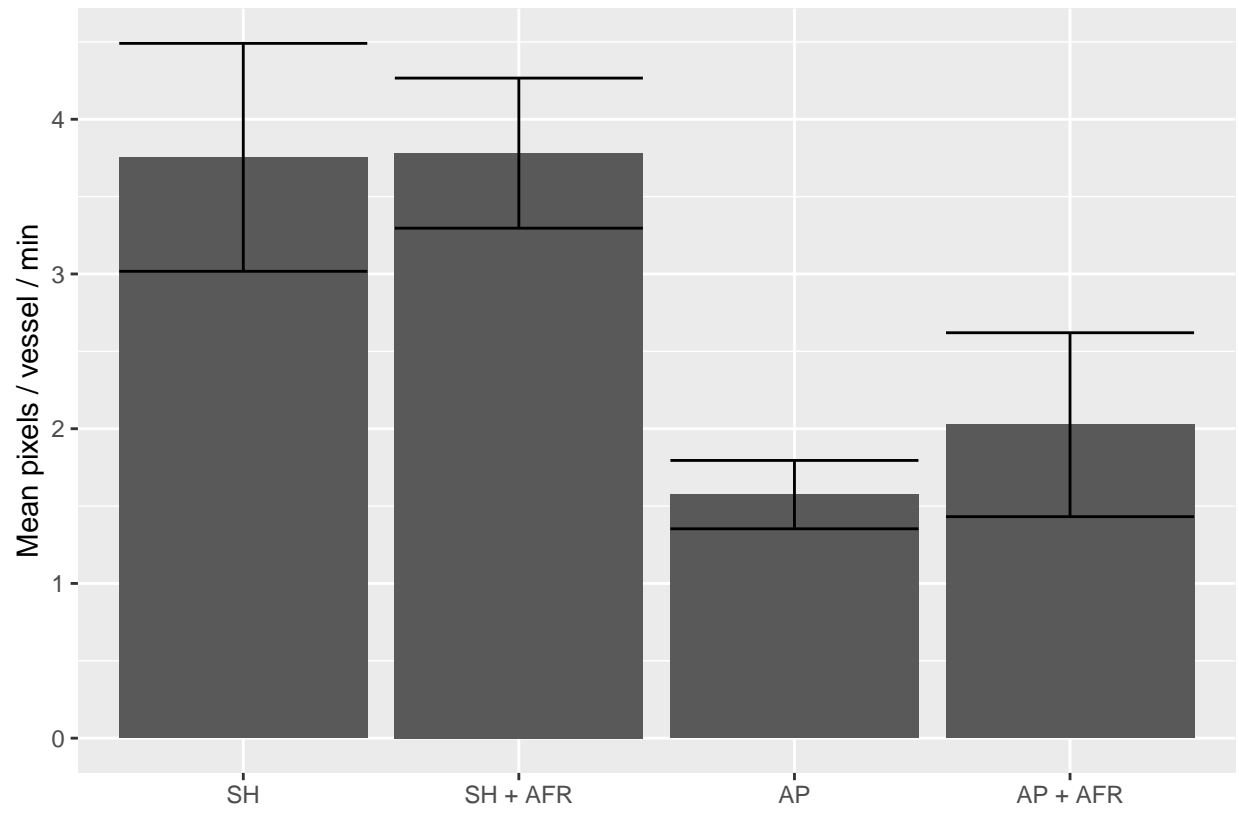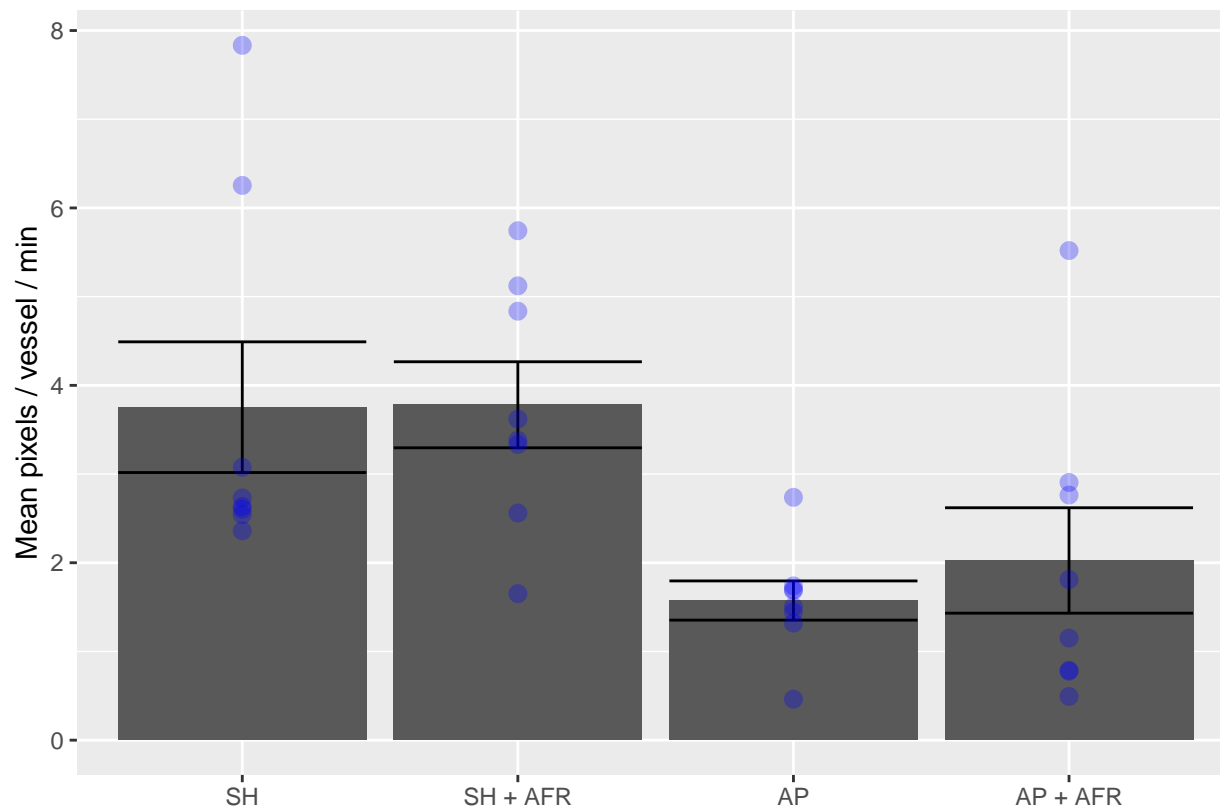
Mean Fractional Pump Flow

```
make_graph(all_data = summ4.df, summ_data = summ5.df, ylab = "Mean pixels / vessel / min", 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
```
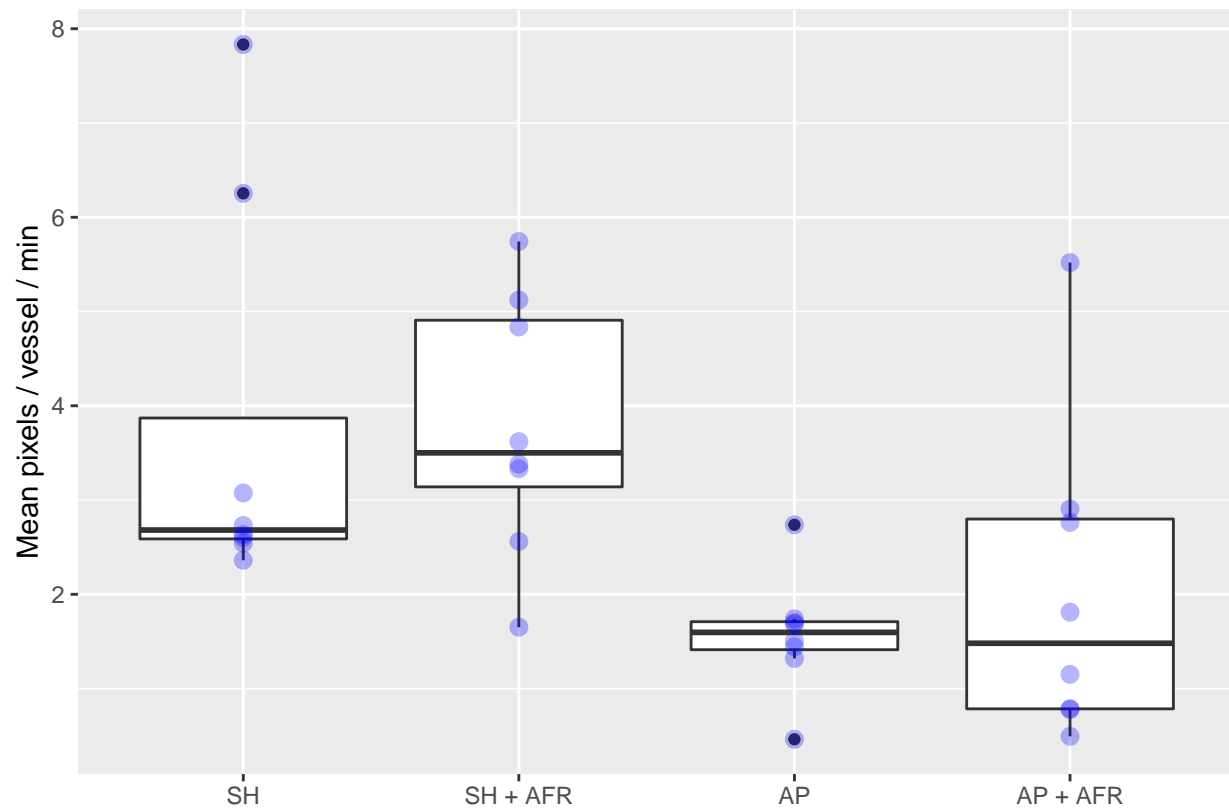
```
##             Df Sum Sq Mean Sq F value Pr(>F)
## treatment    3  31.79   10.60    4.49 0.0108 *
## Residuals   28  66.07    2.36
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = variable ~ treatment, data = all_data)
##
## $treatment
##                        diff        lwr         upr      p adj
## SH + AFR-SH      0.02709538 -2.070004  2.12419484 0.9999838
## AP-SH           -2.17981591 -4.276915 -0.08271645 0.0393399
## AP + AFR-SH     -1.72805775 -3.825157  0.36904170 0.1346421
## AP-SH + AFR     -2.20691129 -4.304011 -0.10981183 0.0363235
## AP + AFR-SH + AFR -1.75515314 -3.852253  0.34194632 0.1258166
## AP + AFR-AP      0.45175815 -1.645341  2.54885761 0.9348247
##
## Levene's Test for Homogeneity of Variance (center = median)
##       Df F value Pr(>F)
## group  3  0.7871 0.5112
##       28
##
##  Shapiro-Wilk normality test
##
```
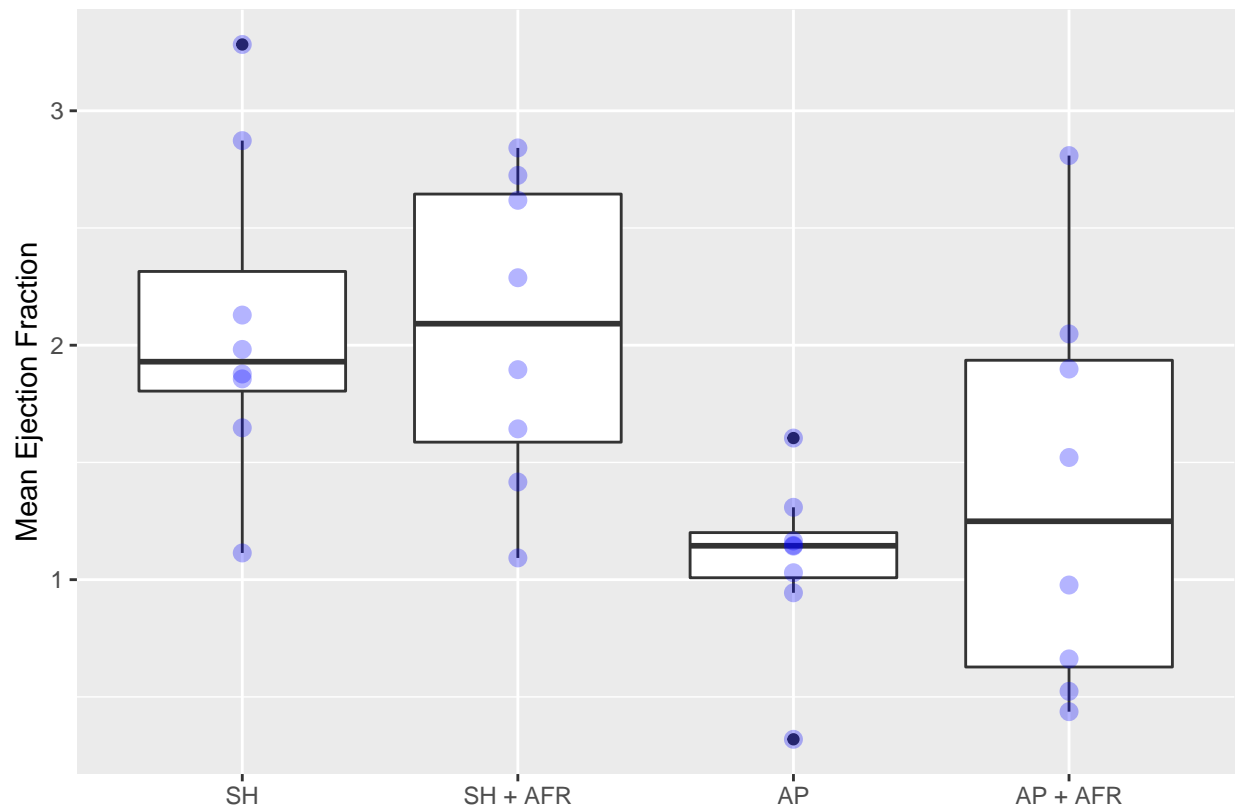
```
## data:  aov_residuals
## W = 0.89491, p-value = 0.004608
##
##
##  Kruskal-Wallis rank sum test
##
## data:  variable by treatment
## Kruskal-Wallis chi-squared = 12.097, df = 3, p-value = 0.007059
##
##
##  Pairwise comparisons using Wilcoxon rank sum exact test
##
## data:  all_data$variable 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
```
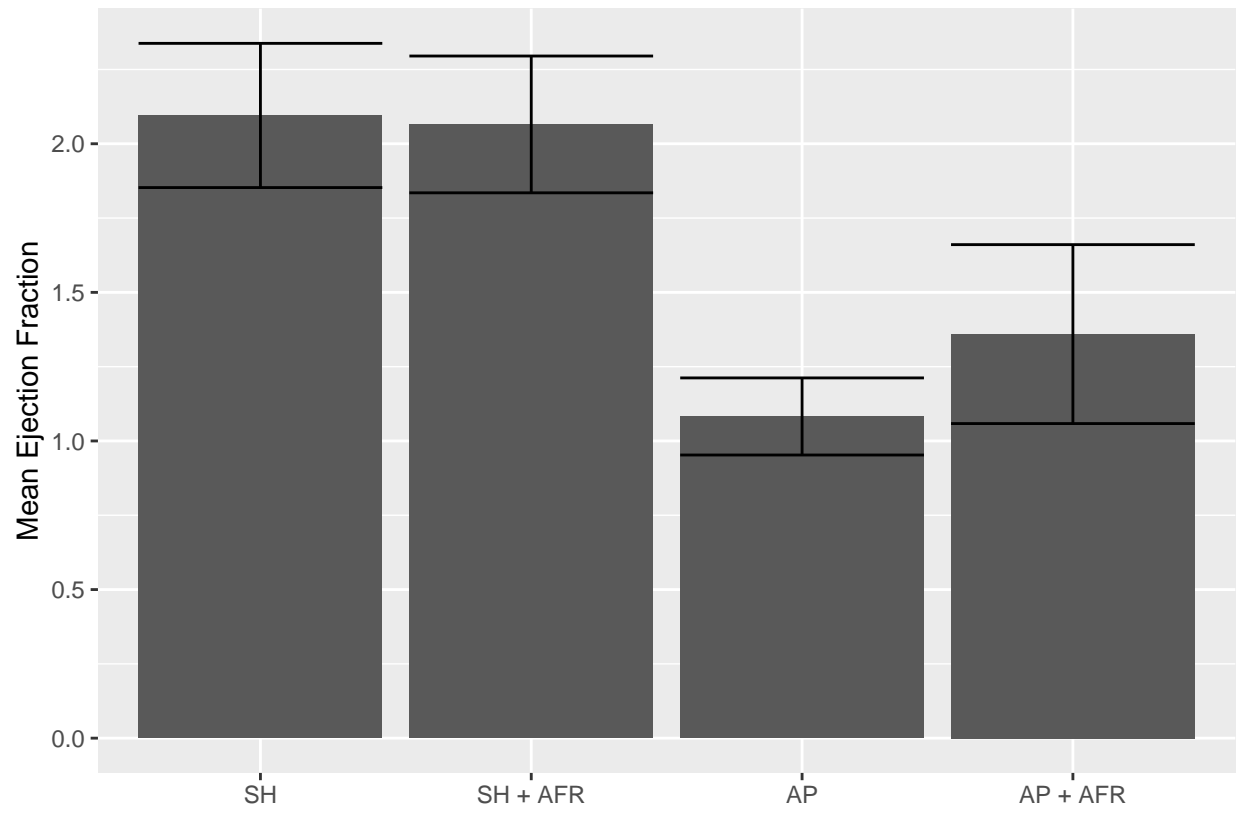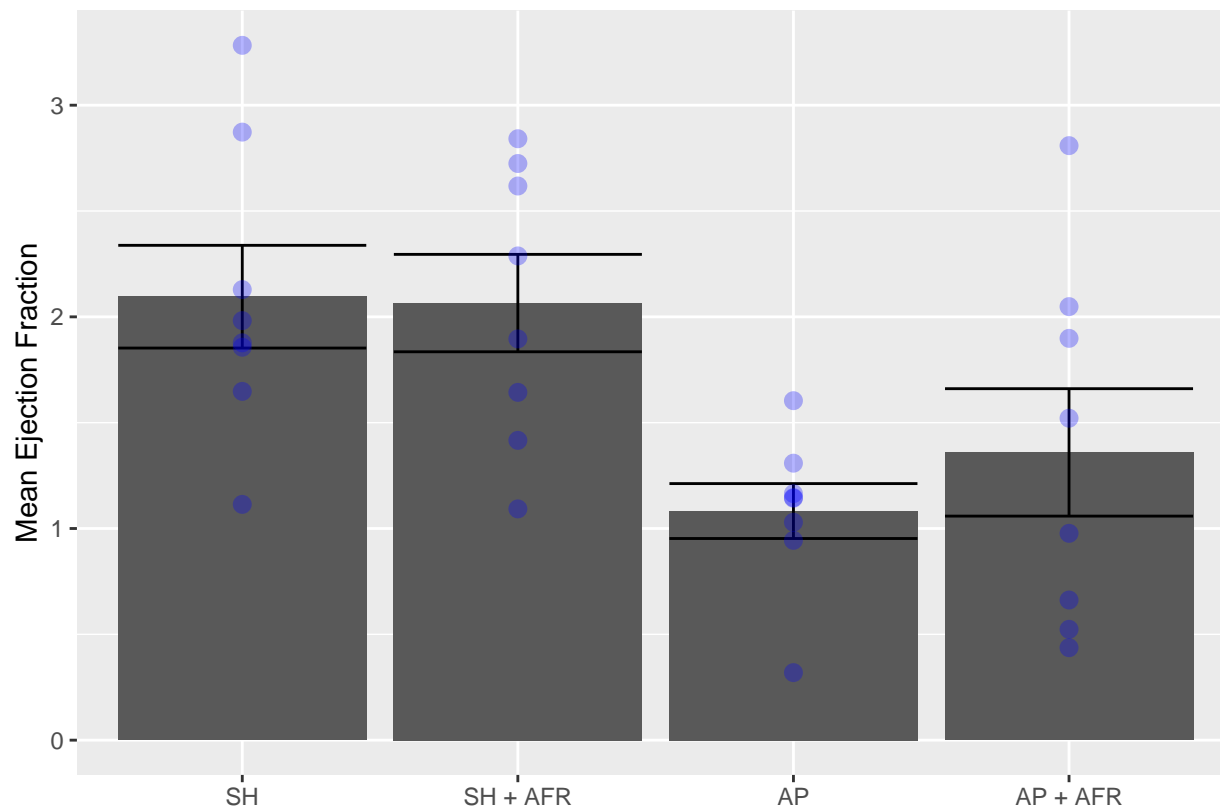
Mean ejection fraction

```
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
```
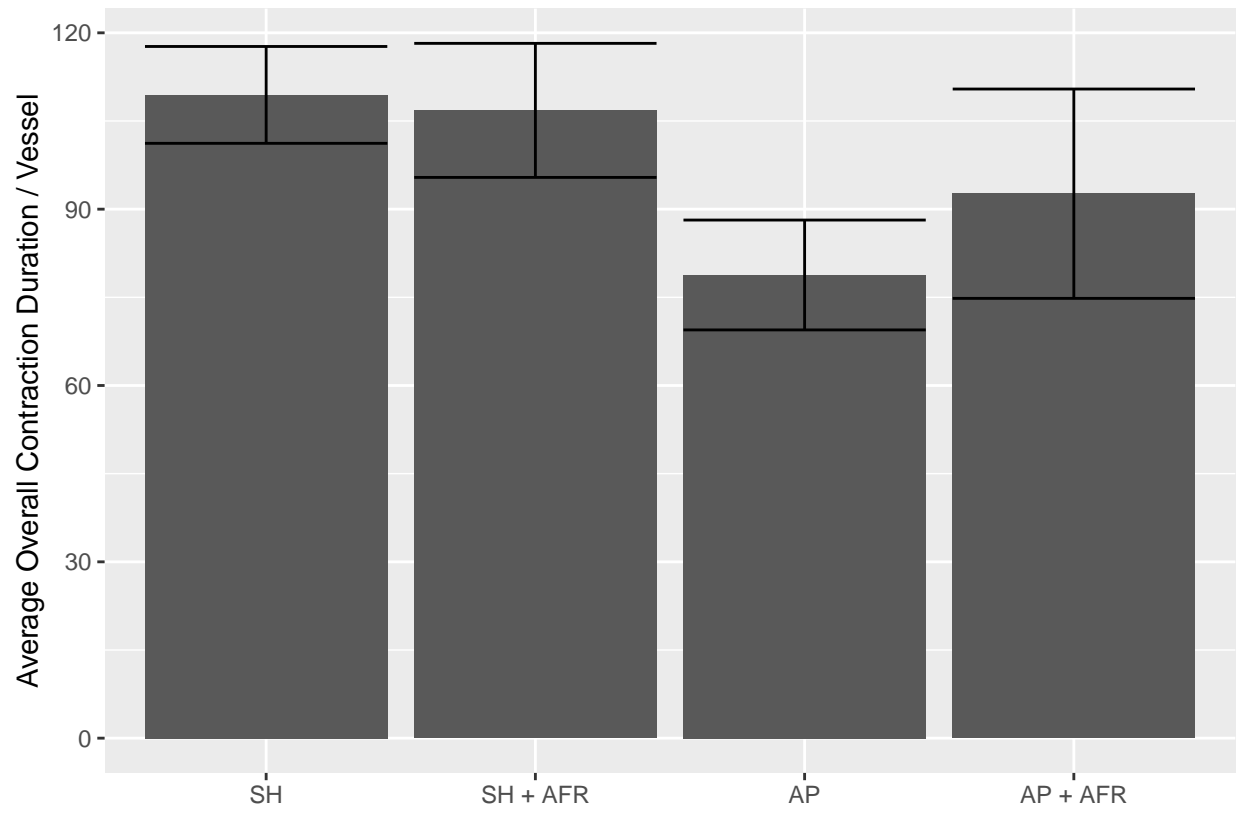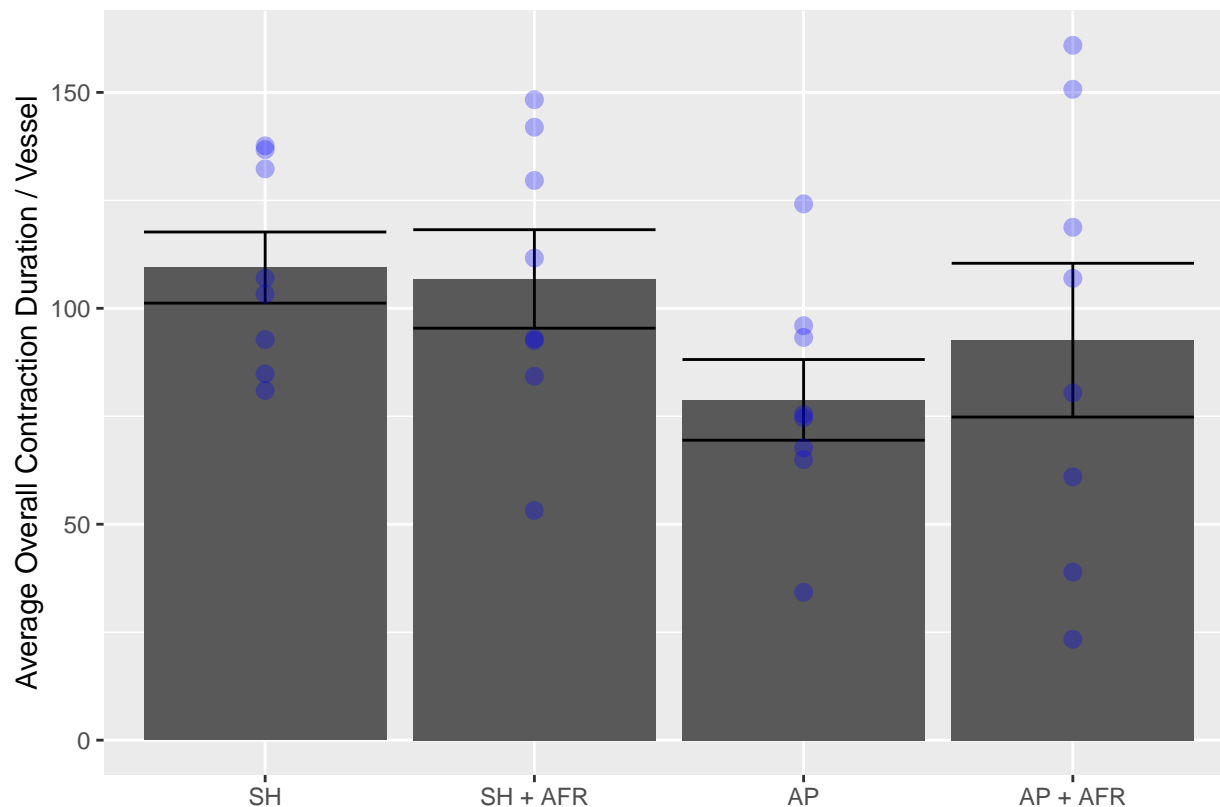
Average overall contraction duration

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

```
## # A tibble: 4 x 2
##   treatment      n
##   <fct>      <int>
## 1 SH             8
## 2 SH + AFR       8
## 3 AP             8
## 4 AP + AFR       8
```
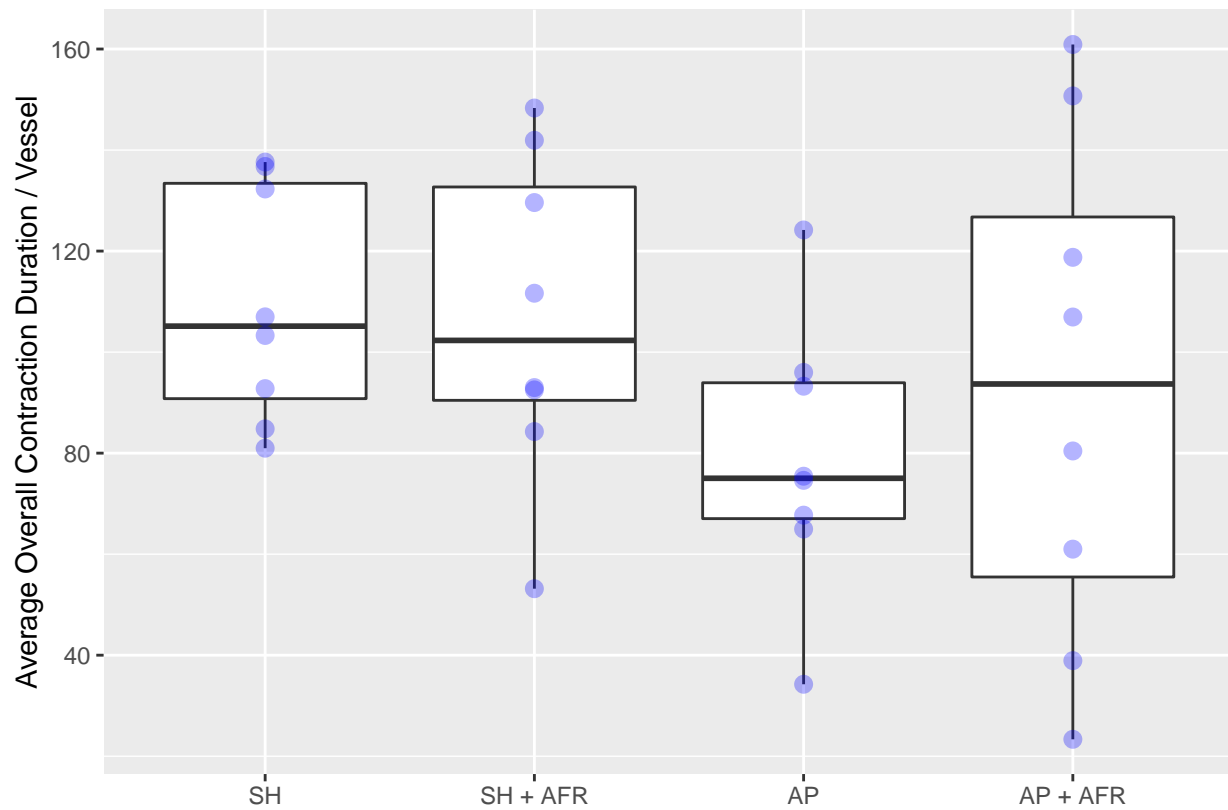
```
##             Df Sum Sq Mean Sq F value Pr(>F)
## treatment    3   4810    1603   1.331  0.284
## Residuals   28  33730    1205
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = variable ~ treatment, data = all_data)
##
## $treatment
##                      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
```
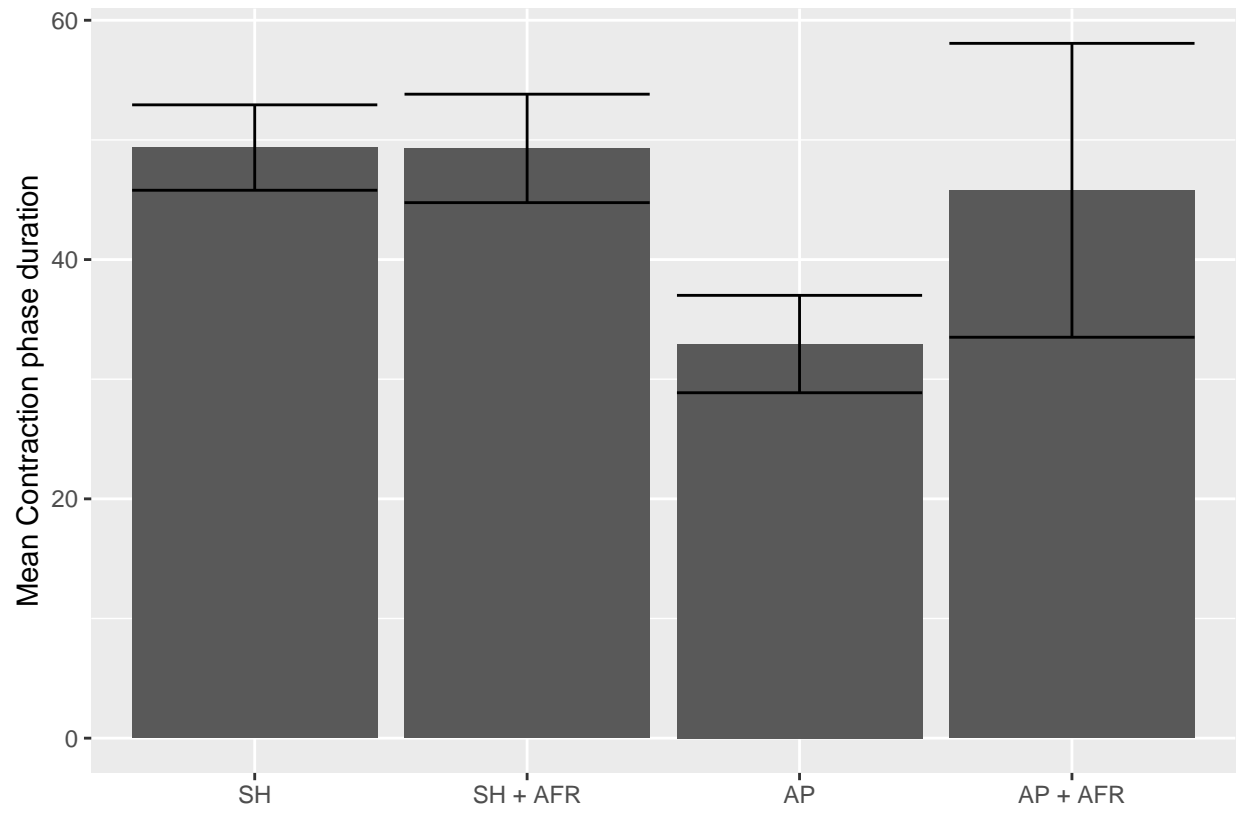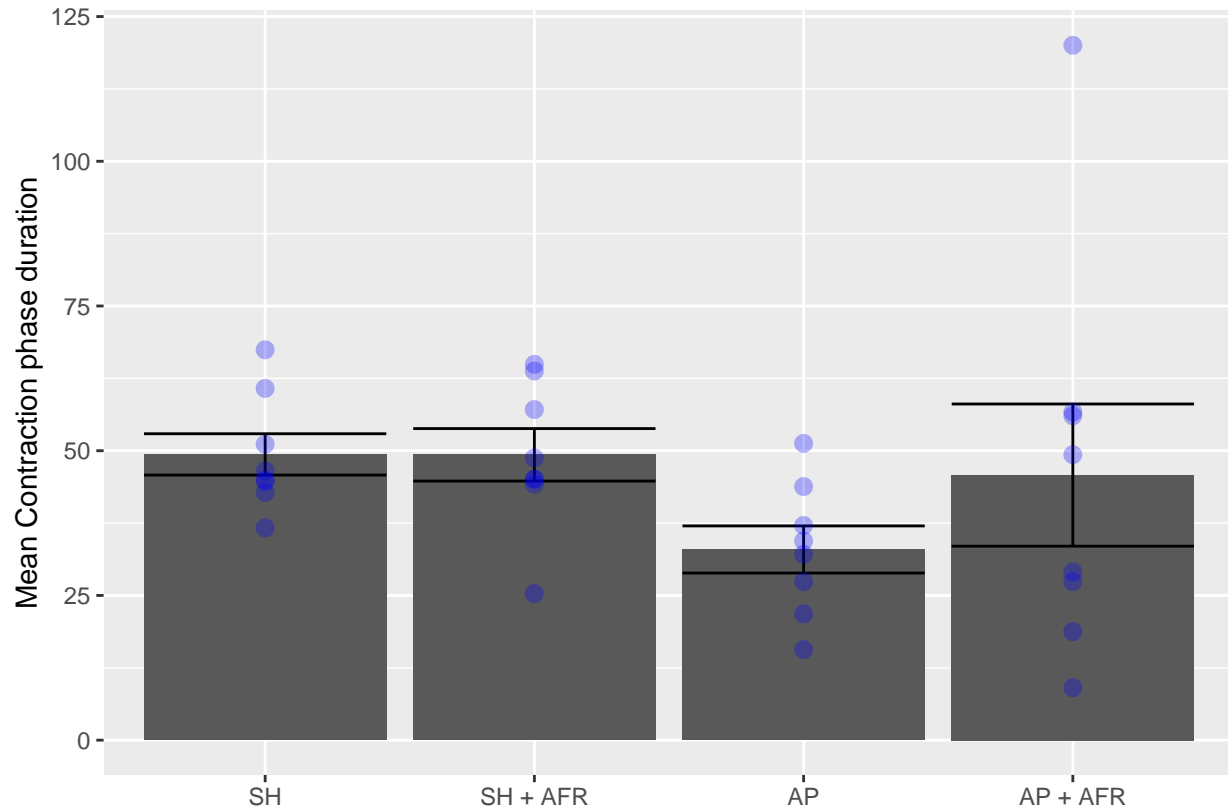
Average contraction phase duration

```
make_graph(all_data = summ4.df, summ_data = summ5.df, ylab = "Mean Contraction phase duration", variable
```

```
## # A tibble: 4 x 2
##    treatment       n
##    <fct>       <int>
## 1 SH              8
## 2 SH + AFR        8
## 3 AP              8
## 4 AP + AFR        8
```
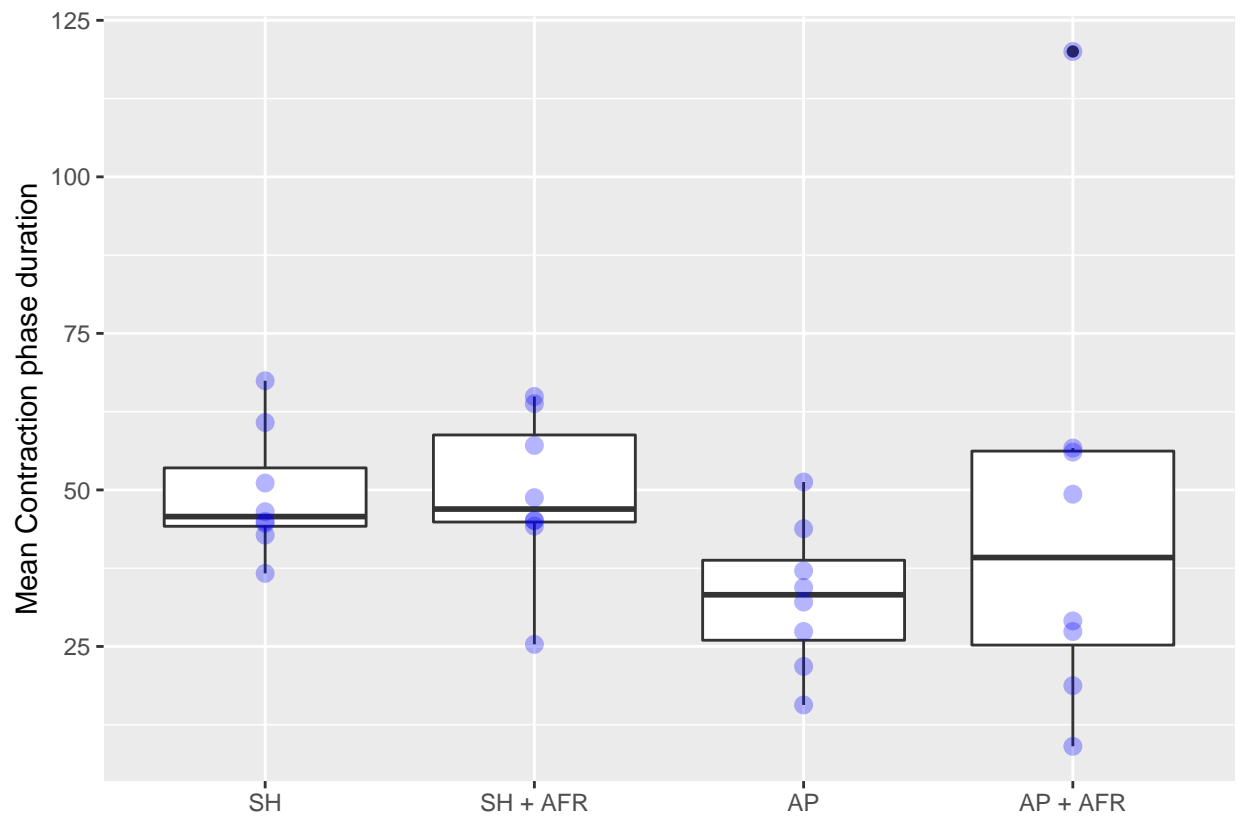
```
##             Df Sum Sq Mean Sq F value Pr(>F)
## treatment    3   1454   484.8   1.208  0.325
## Residuals   28  11237   401.3
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = variable ~ treatment, data = all_data)
##
## $treatment
##                        diff        lwr      upr      p adj
## SH + AFR-SH       -0.07147984 -27.41999 27.27703 0.9999999
## AP-SH            -16.42194172 -43.77045 10.92657 0.3737960
## AP + AFR-SH       -3.57258169 -30.92109 23.77593 0.9841259
## AP-SH + AFR      -16.35046188 -43.69897 10.99805 0.3775710
## AP + AFR-SH + AFR -3.50110185 -30.84961 23.84741 0.9850289
## AP + AFR-AP       12.84936003 -14.49915 40.19787 0.5811190
##
## Levene's Test for Homogeneity of Variance (center = median)
##       Df F value Pr(>F)
## group  3  2.9526 0.0497 *
##       28
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##   Shapiro-Wilk normality test
##
```

```
## data:  aov_residuals
## W = 0.86301, p-value = 0.0008044
##
##
##  Kruskal-Wallis rank sum test
##
## data:  variable by treatment
## Kruskal-Wallis chi-squared = 6.1562, df = 3, p-value = 0.1043
##
##
##  Pairwise comparisons using Wilcoxon rank sum exact test
##
## data:  all_data$variable and all_data$treatment
##
##           SH     SH + AFR AP
## SH + AFR 0.798 -        -
## AP       0.062 0.062    -
## AP + AFR 0.758 0.758    0.774
##
## P value adjustment method: fdr
```
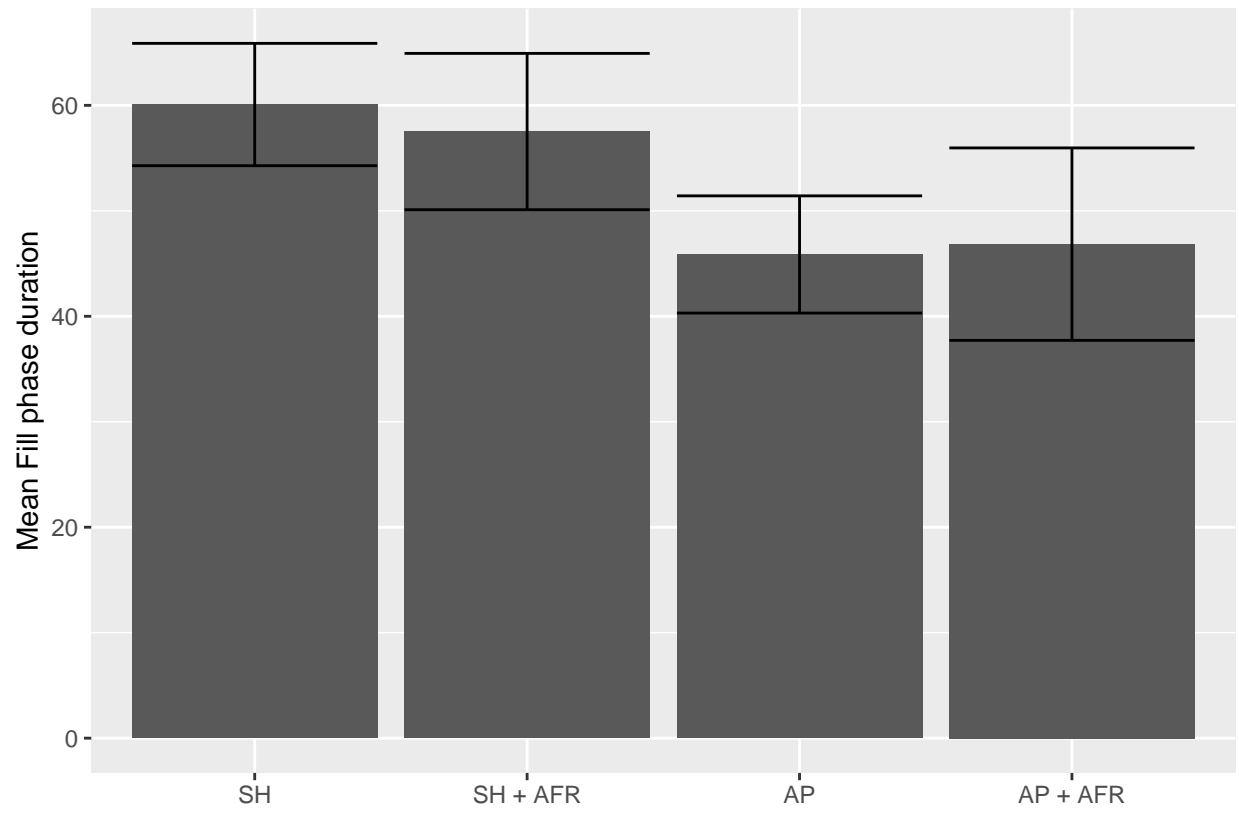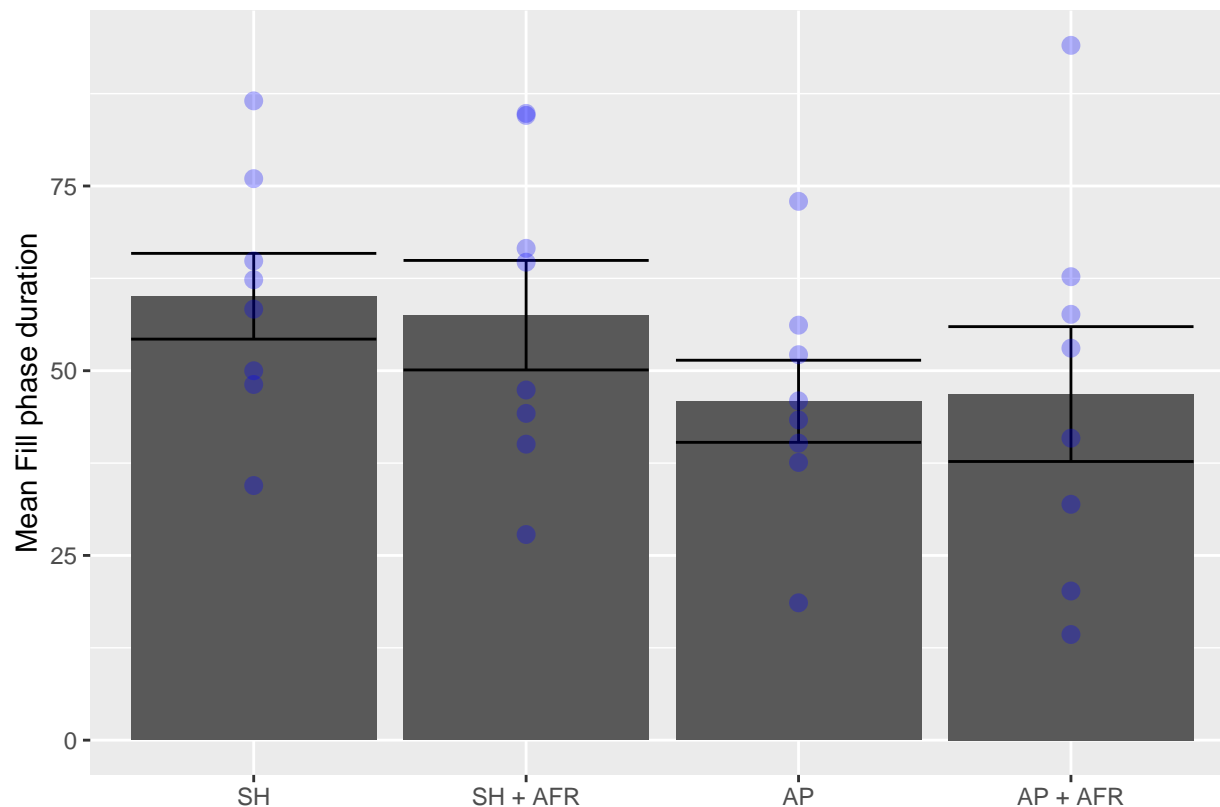
Average fill phase duration

```
make_graph(all_data = summ4.df, summ_data = summ5.df, ylab = "Mean Fill phase duration", 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
```
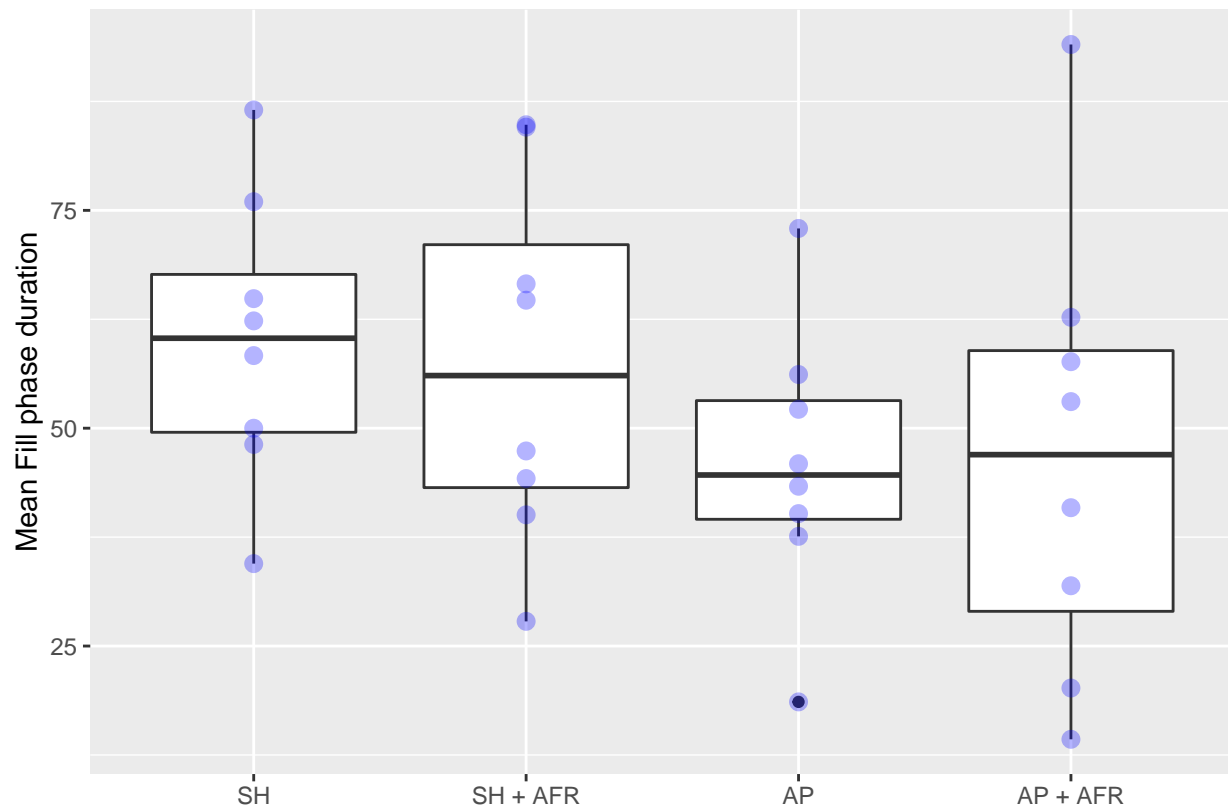
```
##             Df Sum Sq Mean Sq F value Pr(>F)
## treatment    3   1269   423.2   1.044  0.389
## Residuals   28  11351   405.4
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = variable ~ treatment, data = all_data)
##
## $treatment
##                        diff       lwr      upr     p adj
## SH + AFR-SH      -2.5619718 -30.04812 24.92418 0.9940836
## AP-SH           -14.2171600 -41.70331 13.26899 0.5024823
## AP + AFR-SH     -13.2382795 -40.72443 14.24787 0.5613808
## AP-SH + AFR     -11.6551882 -39.14134 15.83096 0.6576849
## AP + AFR-SH + AFR -10.6763077 -38.16246 16.80984 0.7157870
## AP + AFR-AP       0.9788805 -26.50727 28.46503 0.9996624
##
## Levene's Test for Homogeneity of Variance (center = median)
##       Df F value Pr(>F)
## group  3  1.1821 0.3344
##       28
##
##  Shapiro-Wilk normality test
##
## data:  aov_residuals
## W = 0.97521, p-value = 0.6535
```

```
##
##
##  Kruskal-Wallis rank sum test
##
## data:  variable by treatment
## Kruskal-Wallis chi-squared = 3.3778, df = 3, p-value = 0.337
##
##
##  Pairwise comparisons using Wilcoxon rank sum exact test
##
## data:  all_data$variable and all_data$treatment
##
##          SH   SH + AFR AP
## SH + AFR 0.87 -        -
## AP       0.57 0.57     -
## AP + AFR 0.57 0.57     0.96
##
## P value adjustment method: fdr
```