

Anova for the duckweed experiment at 27 C - autocorrelated temperatures

Goal: to determine if there is a significant relationship between duckweed offspring (dependent variable) and different autocorrelated temperature regimes (independent variable)

Library

```
library(ggplot2)
```

Load metafile data (.csv) and attribute columns 1 and 2 as factors, and 3 as numeric

```
duckweed.offspring <- read.csv(  
  "C:/Users/user/Desktop/uWaterloo/experiments/expdata_metafile_01062021-4anova.csv",  
  header = TRUE, colClasses = c("factor", "factor", "numeric"))  
summary(duckweed.offspring)
```

```
##   Experiment_Number      Autocorrelation Total_Offspring  
## 14          : 4          0 autocorr       : 8     Min.   : 3.00  
## 15          : 4          High autocorr cold: 6    1st Qu.: 36.00  
## 18          : 4          High autocorr warm:12   Median : 54.00  
## 19          : 4          Middle autocorr    : 8    Mean    : 57.94  
## 20          : 4          Middle autocorr    : 8    3rd Qu.: 77.00  
## 21          : 4          Middle autocorr    : 8    Max.    :124.00  
## (Other):10
```

Run an analysis of variance

```
res.aov <- aov(Total_Offspring ~ Autocorrelation, data = duckweed.offspring)  
summary(res.aov)
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)  
## Autocorrelation  3  5413   1804.3     2.1  0.121  
## Residuals       30 25777    859.2
```

Boxplots

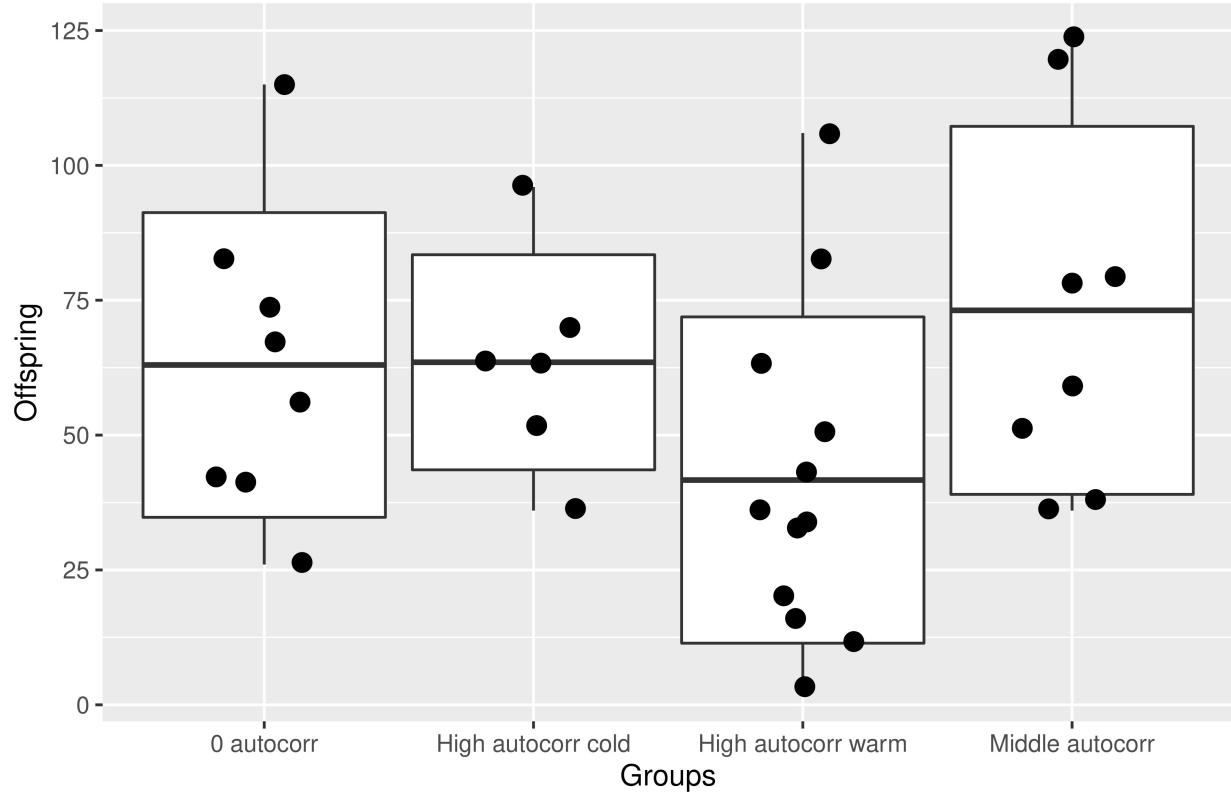
```
min.mean.sd.max <- function(x) {  
  r <- c(min(x), mean(x) - sd(x), mean(x), mean(x) + sd(x), max(x))  
  names(r) <- c("ymin", "lower", "middle", "upper", "ymax")  
  r  
}  
boxplots <- ggplot(aes(y = Total_Offspring, x = factor(Autocorrelation)),  
  data = duckweed.offspring)  
boxplots <- boxplots + stat_summary(fun.data = min.mean.sd.max,
```

```

geom = "boxplot") +
geom_jitter(position=position_jitter(width=.2), size=3) +
ggtitle("Boxplots: Autocorrelation Treatments and Offspring") +
xlab("Groups") + ylab("Offspring")
boxplots

```

Boxplots: Autocorrelation Treatments and Offspring



Linear model (0 autocorrelation vs. other groups)

```

lm.duckweed <- lm(Total_Offspring ~ Autocorrelation, data = duckweed.offspring)
summary(lm.duckweed)

```

```

##
## Call:
## lm(formula = Total_Offspring ~ Autocorrelation, data = duckweed.offspring)
##
## Residuals:
##     Min      1Q  Median      3Q     Max 
## -38.667 -21.917 -3.083  10.583  64.333 
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept)   63.00     10.36   6.079 1.12e-06 ***
## AutocorrelationHigh autocorr cold    0.50     15.83   0.032    0.975  
## AutocorrelationHigh autocorr warm   -21.33     13.38  -1.594    0.121  
## AutocorrelationMiddle autocorr     10.12     14.66   0.691    0.495  
## ---
## 
```

```

## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 29.31 on 30 degrees of freedom
## Multiple R-squared:  0.1735, Adjusted R-squared:  0.0909
## F-statistic:   2.1 on 3 and 30 DF,  p-value: 0.1212

```

Linear model (high autocorrelation cold vs. other groups)

```

changelevel <- relevel(duckweed.offspring$Autocorrelation, "High autocorr cold")
fit_changelevel <- lm(duckweed.offspring$Total_Offspring ~ changelevel)
summary(fit_changelevel)

##
## Call:
## lm(formula = duckweed.offspring$Total_Offspring ~ changelevel)
##
## Residuals:
##    Min     1Q Median     3Q    Max 
## -38.667 -21.917 -3.083 10.583 64.333 
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 63.500    11.967   5.306 9.81e-06 ***
## changelevel0 autocorr -0.500    15.831  -0.032   0.975  
## changelevelHigh autocorr warm -21.833   14.656  -1.490   0.147  
## changelevelMiddle autocorr    9.625    15.831   0.608   0.548  
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 29.31 on 30 degrees of freedom
## Multiple R-squared:  0.1735, Adjusted R-squared:  0.0909
## F-statistic:   2.1 on 3 and 30 DF,  p-value: 0.1212

```

Linear model (high autocorrelation warm vs. other groups)

```

changelevel2 <- relevel(duckweed.offspring$Autocorrelation,
                         "High autocorr warm")
fit_changelevel2 <- lm(duckweed.offspring$Total_Offspring ~ changelevel2)
summary(fit_changelevel2)

##
## Call:
## lm(formula = duckweed.offspring$Total_Offspring ~ changelevel2)
##
## Residuals:
##    Min     1Q Median     3Q    Max 
## -38.667 -21.917 -3.083 10.583 64.333 
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 41.667    8.462   4.924 2.89e-05 ***
## changelevel20 autocorr 21.333   13.379   1.594   0.1213  
## changelevel2High autocorr cold 21.833   14.656   1.490   0.1467  
## changelevel2Middle autocorr 31.458   13.379   2.351   0.0255 *  

```

```

## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 29.31 on 30 degrees of freedom
## Multiple R-squared: 0.1735, Adjusted R-squared: 0.0909
## F-statistic: 2.1 on 3 and 30 DF, p-value: 0.1212

```

Linear model (middle autocorrelation vs. other groups)

```

changelevel3 <- relevel(duckweed.offspring$Autocorrelation, "Middle autocorr")
fit_changelevel3 <- lm(duckweed.offspring$Total_Offspring ~ changelevel3)
summary(fit_changelevel3)

```

```

##
## Call:
## lm(formula = duckweed.offspring$Total_Offspring ~ changelevel3)
##
## Residuals:
##     Min      1Q  Median      3Q     Max 
## -38.667 -21.917 - 3.083 10.583 64.333
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)    
## (Intercept)                73.125    10.364   7.056 7.62e-08 ***
## changelevel30 autocorr     -10.125    14.656  -0.691  0.4950    
## changelevel3High autocorr cold   -9.625    15.831  -0.608  0.5478    
## changelevel3High autocorr warm  -31.458    13.379  -2.351  0.0255 *  
## ---                        
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 29.31 on 30 degrees of freedom
## Multiple R-squared: 0.1735, Adjusted R-squared: 0.0909
## F-statistic: 2.1 on 3 and 30 DF, p-value: 0.1212

```