

# Environment\_Length\_Survival\_Hatchery

2024-10-26

```
setwd("/Users/nicolemongillo/Desktop/GitHub/MVP_Chesapeake_VIMS_hatchery/src/NM")
```

```
library(tidyverse)
```

```
## -- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
## v dplyr      1.1.4      v readr      2.1.5
## v forcats    1.0.0      v stringr   1.5.1
## v ggplot2    3.5.1      v tibble    3.2.1
## v lubridate  1.9.3      v tidyr     1.3.1
## v purrr      1.0.2
## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()     masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

```
library(ggplot2)
library(gridExtra)
```

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

```
library(multcompView) #extract significance letters from Tukey-Kramer test
library(tidyverse)
library(grid)#for ggplot arranging
library(cowplot) #arrange ggplots
```

```
##
## Attaching package: 'cowplot'
##
## The following object is masked from 'package:lubridate':
##
##      stamp
```

```
library(ggpmisc)
```

```
## Loading required package: ggpp
## Registered S3 methods overwritten by 'ggpp':
```

```
## method from
## heightDetails.titleGrob ggplot2
## widthDetails.titleGrob ggplot2
##
## Attaching package: 'ggpp'
##
## The following object is masked from 'package:ggplot2':
##
## annotate
```

```
library(vegan) #for Mantel tests
```

```
## Loading required package: permute
## Loading required package: lattice
## This is vegan 2.6-8
```

```
#read in necessary files
```

```
#this file contains raw lengths of all oysters aged 15-78 days
length <- read.csv("/Users/nicolemongillo/Desktop/GitHub/MVP_ChESApeake_VIMS_hatchery/data/lateststage_lengths.csv")

#this file has summary statistics on temperature and salinity for the 8 sites (DEBY, LOLA, JR, TX, LA, JR, TX, LA)
envr_summary <- read.csv("/Users/nicolemongillo/Desktop/GitHub/MVP_ChESApeake_VIMS_hatchery/data/envr_summary.csv")

#this file is a matrix of the environmental distances between each site
envr_dist <- read.csv("/Users/nicolemongillo/Desktop/GitHub/MVP_ChESApeake_VIMS_hatchery/data/envr_raw_distances.csv")

#this file contains survival rate data for larval oysters up to day 21 post hatching
survival <- read.csv("/Users/nicolemongillo/Desktop/GitHub/MVP_ChESApeake_VIMS_hatchery/data/CViMVP_larval_survival.csv")
```

Extract survival rates from survival data frame, and reorganize data frame

```
summary(survival)
```

```
## SpawnTrt_Key      Tank_naming      Group_Day_Key      Group_Day_Label
## Length:120        Length:120        Length:120        Length:120
## Class :character  Class :character  Class :character  Class :character
## Mode :character   Mode :character   Mode :character   Mode :character
##
##
##
##      Tank      Day_Treatment      Day_analysis      Day
## Length:120    Length:120        Length:120        Min.   : 0.00
## Class :character  Class :character  Class :character  1st Qu.: 0.00
## Mode :character   Mode :character   Mode :character   Median : 6.00
##                                     Mean    :15.31
##                                     3rd Qu.:19.00
##                                     Max.    :78.00
##                                     NA's    :9
##      Date      Filter_size_µm      Sample_count      Group_count
## Length:120     Min.   : 35.00      Min.   : 0        Min.   : 0
```

```
## Class :character 1st Qu.: 35.00 1st Qu.: 10000 1st Qu.: 287000
## Mode :character Median : 48.00 Median : 30000 Median : 602000
## Mean : 85.17 Mean :100309 Mean : 2726089
## 3rd Qu.: 75.00 3rd Qu.:161250 3rd Qu.: 2912500
## Max. :212.00 Max. :600000 Max. :15000000
## NA's :38 NA's :52 NA's :30
## Survival_rate_perc Vial_label Notes
## Min. : 0.000 Mode:logical Length:120
## 1st Qu.: 1.706 NA's:120 Class :character
## Median : 5.346 Mode :character
## Mean : 7.880
## 3rd Qu.:11.250
## Max. :50.000
## NA's :52
```

```
#For survival rates, we only care about survival from day 21 (marked as day_an 15-21), so filter for th
survival_day21 <- survival %>%
```

```
  filter(Day_analysis == "15-21") %>%
  filter(Tank_naming != "MVP-LARMIX")
```

```
#Exclude any groups with "small" in their label. The length data only considers the eyed oysters.
#use grep function to make a vector of all indices in latestage_len with the phrase "small" in them, ig
small <- grep("small", survival_day21$Group_Day_Label, ignore.case = TRUE)
```

```
#make new dataframe WITHOUT any indices saved in small, mean remaining data are everything except small
survival_day21_sub <- survival_day21[-small, ]
```

```
#exclude "MVP" from group names to shorten them
```

```
survival_day21_sub["Tank_naming"][survival_day21_sub["Tank_naming"] == "MVP-DEBY"] <- "DEBY"
survival_day21_sub["Tank_naming"][survival_day21_sub["Tank_naming"] == "MVP-FL"] <- "FL"
survival_day21_sub["Tank_naming"][survival_day21_sub["Tank_naming"] == "MVP-JR"] <- "JR"
survival_day21_sub["Tank_naming"][survival_day21_sub["Tank_naming"] == "MVP-LA"] <- "LA"
survival_day21_sub["Tank_naming"][survival_day21_sub["Tank_naming"] == "MVP-LOLA"] <- "LOLA"
survival_day21_sub["Tank_naming"][survival_day21_sub["Tank_naming"] == "MVP-ME"] <- "ME"
survival_day21_sub["Tank_naming"][survival_day21_sub["Tank_naming"] == "MVP-NH"] <- "NH"
survival_day21_sub["Tank_naming"][survival_day21_sub["Tank_naming"] == "MVP-TX"] <- "TX"
```

```
#select only tank naming and survival rate columns
```

```
survival_filter <- survival_day21_sub[, c("Tank_naming", "Survival_rate_perc")]
```

```
#rename columns
```

```
colnames(survival_filter) <- c("site_name", "percent_survival")
```

```
#length df organizing
```

```
#select columns with group, day, and shell length in mm
```

```
length <- length[,c("group", "day_an", "shell_length_mm")]
```

```
#filter out LARMIX from group
```

```
length_filter <- length %>%
  filter(group != "LARMIX")
```

```
#keep only data from days 15-21
```

```
length_21 <- length_filter %>%
  filter(day_an == "15-21")

length_78 <- length_filter %>%
  filter(day_an == "78")

#find mean shell lengths of each group on each day
means_mm_21 <- aggregate(shell_length_mm ~ group, FUN = mean, data = length_21)
colnames(means_mm_21) <- c("site_name", "mean_length_mm_21")

means_mm_78 <- aggregate(shell_length_mm ~ group, FUN = mean, data = length_78)
colnames(means_mm_78) <- c("site_name", "mean_length_mm_78")
```

```
#remove extra columns from environmental data frame
```

```
#remove extra site label and standard deviations from envr_summary
envr <- envr_summary[,-c(2,6,10)]

summary(envr)
```

```
##          X          Mean_Annual_Temperature_C Mean_max_temperature_C
## Length:8      Min.      :15.33              Min.      :23.46
## Class :character 1st Qu.:16.86              1st Qu.:26.35
## Mode  :character Median :17.83              Median :28.65
##          Mean      :19.09              Mean      :28.54
##          3rd Qu.:22.33              3rd Qu.:30.98
##          Max.      :23.11              Max.      :33.17
## Mean_min_temperature_C Mean_Annual_Salinity_ppt Mean_max_Salinity_ppt
## Min.      : 1.758      Min.      :10.46      Min.      :16.88
## 1st Qu.: 3.192      1st Qu.:14.87      1st Qu.:23.69
## Median : 3.784      Median :18.99      Median :27.90
## Mean      : 5.121      Mean      :20.02      Mean      :27.25
## 3rd Qu.: 7.481      3rd Qu.:23.01      3rd Qu.:30.54
## Max.      :10.387      Max.      :32.35      Max.      :37.20
## Mean_min_Salinity_ppt
## Min.      : 0.9688
## 1st Qu.: 5.0596
## Median : 9.3657
## Mean      : 8.5100
## 3rd Qu.:12.6328
## Max.      :15.4224
```

```
#rename cols
colnames(envr) <- c("site_name", "Mean_Annual_Temperature_C", "Mean_max_temperature_C", "Mean_min_temper

#add sampling site latitudes. Note that these latitudes ARE NOT the same as the latitudes of where envi
envr$lat <- c(37.249107, 37.98030, 37.1501163, 28.096000, 29.239925, 30.440030, 43.053746, 44.01330)
```

```
#Join data frames
```

```

surv_length_envr <- left_join(envr, means_mm_21, by = "site_name") %>%
  left_join(means_mm_78, by = "site_name") %>%
  left_join(survival_filter, by = "site_name")

write.csv(surv_length_envr, "/Users/nicolemongillo/Desktop/GitHub/MVP_Chesapeake_VIMS_hatchery/data/Surv")

```

```

#compare mean length on day 21 to mean annual temp, mean annual salinity, and latitude

```

```

length21_temp_lm <- lm(mean_length_mm_21 ~ Mean_Annual_Temperature_C, data = surv_length_envr)
summary(length21_temp_lm)

```

```

##
## Call:
## lm(formula = mean_length_mm_21 ~ Mean_Annual_Temperature_C, data = surv_length_envr)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.0153946 -0.0062781  0.0004731  0.0080888  0.0131565
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.3281427   0.0261835    12.532 1.58e-05 ***
## Mean_Annual_Temperature_C -0.0008187   0.0013556    -0.604   0.568
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.01122 on 6 degrees of freedom
## Multiple R-squared:  0.0573, Adjusted R-squared:  -0.09982
## F-statistic: 0.3647 on 1 and 6 DF,  p-value: 0.568

```

```

#extract p-value (.568)

```

```

length21_temp_pval <- summary(length21_temp_lm)$coefficients[,4]
length21_temp_pval <- unname(length21_temp_pval[2])

```

```

length21_sal_lm <- lm(mean_length_mm_21 ~ Mean_Annual_Salinity_ppt, data = surv_length_envr)

```

```

#extract p-value (.411)

```

```

length21_sal_pval <- summary(length21_sal_lm)$coefficients[,4]
length21_sal_pval <- unname(length21_sal_pval[2])

```

```

length21_lat_lm <- lm(mean_length_mm_21 ~ lat, data = surv_length_envr)
summary(length21_lat_lm)

```

```

##
## Call:
## lm(formula = mean_length_mm_21 ~ lat, data = surv_length_envr)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.015881 -0.005571  0.001032  0.007308  0.013481
##
## Coefficients:

```

```
##           Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.3003121  0.0255685  11.745  2.3e-05 ***
## lat         0.0003398  0.0007034   0.483   0.646
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.01134 on 6 degrees of freedom
## Multiple R-squared:  0.03745,    Adjusted R-squared:  -0.123
## F-statistic: 0.2334 on 1 and 6 DF,  p-value: 0.6461
```

```
#extract p-value (0.646)
```

```
length21_lat_pval <- summary(length21_lat_lm)$coefficients[,4]
length21_lat_pval <- unname(length21_lat_pval[2])
```

```
#compare percent survival to mean annual temp, mean annual salinity, and envr distance from DEBY
surv_temp_lm <- lm(percent_survival ~ Mean_Annual_Temperature_C, data = surv_length_envr)
summary(surv_temp_lm)
```

```
##
## Call:
## lm(formula = percent_survival ~ Mean_Annual_Temperature_C, data = surv_length_envr)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.0024 -0.5082  0.1592  0.3649  0.9948
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -3.04143     1.87564  -1.622  0.1560
## Mean_Annual_Temperature_C  0.29084     0.09711   2.995  0.0242 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.8037 on 6 degrees of freedom
## Multiple R-squared:  0.5992, Adjusted R-squared:  0.5324
## F-statistic: 8.97 on 1 and 6 DF,  p-value: 0.02416
```

```
#extract p-value (0.024)
```

```
surv_temp_pval <- summary(surv_temp_lm)$coefficients[,4]
surv_temp_pval <- unname(surv_temp_pval[2])
```

```
surv_sal_lm <- lm(percent_survival ~ Mean_Annual_Salinity_ppt, data = surv_length_envr)
summary(surv_sal_lm)
```

```
##
## Call:
## lm(formula = percent_survival ~ Mean_Annual_Salinity_ppt, data = surv_length_envr)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.3035 -0.9805  0.2219  0.6144  1.4024
##
## Coefficients:
```

```
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      4.18142    1.14239   3.66  0.0106 *
## Mean_Annual_Salinity_ppt -0.08341    0.05382  -1.55  0.1721
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.073 on 6 degrees of freedom
## Multiple R-squared:  0.2859, Adjusted R-squared:  0.1669
## F-statistic: 2.402 on 1 and 6 DF, p-value: 0.1721
```

```
#extract p-value (0.172)
surv_sal_pval <- summary(surv_sal_lm)$coefficients[,4]
surv_sal_pval <- unname(surv_sal_pval[2])

surv_lat_lm <- lm(percent_survival ~ lat, data = surv_length_envr)
summary(surv_lat_lm)
```

```
##
## Call:
## lm(formula = percent_survival ~ lat, data = surv_length_envr)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.97500 -0.76479  0.03013  0.54583  1.11282
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)   7.45699    2.00449   3.720  0.00985 **
## lat          -0.13775    0.05514  -2.498  0.04664 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.8887 on 6 degrees of freedom
## Multiple R-squared:  0.5098, Adjusted R-squared:  0.4282
## F-statistic: 6.241 on 1 and 6 DF, p-value: 0.04664
```

```
#extract p-value (0.0466)
surv_lat_pval <- summary(surv_lat_lm)$coefficients[,4]
surv_lat_pval <- unname(surv_lat_pval[2])

#compare length at day 78 to mean annual temp, mean annual salinity, and envr distance from DEBY
length78_temp_lm <- lm(mean_length_mm_78 ~ Mean_Annual_Temperature_C, data = surv_length_envr)
summary(length78_temp_lm)
```

```
##
## Call:
## lm(formula = mean_length_mm_78 ~ Mean_Annual_Temperature_C, data = surv_length_envr)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4.1777 -0.5723 -0.0590  0.8314  3.9262
##
## Coefficients:
```

```
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      17.1980     5.7027   3.016  0.0235 *
## Mean_Annual_Temperature_C -0.1900     0.2953  -0.644  0.5436
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.443 on 6 degrees of freedom
## Multiple R-squared:  0.06458,    Adjusted R-squared:  -0.09132
## F-statistic: 0.4142 on 1 and 6 DF,  p-value: 0.5436
```

```
#extract p-value (0.543)
```

```
length78_temp_pval <- summary(length78_temp_lm)$coefficients[,4]
```

```
length78_temp_pval <- unname(length78_temp_pval[2])
```

```
length78_sal_lm <- lm(mean_length_mm_78 ~ Mean_Annual_Salinity_ppt, data = surv_length_envr)
```

```
#extract p-value (0.983)
```

```
length78_sal_pval <- summary(length78_sal_lm)$coefficients[,4]
```

```
length78_sal_pval <- unname(length78_sal_pval[2])
```

```
length78_lat_lm <- lm(mean_length_mm_78 ~ lat, data = surv_length_envr)
```

```
#extract p-value (0.962)
```

```
length78_lat_pval <- summary(length78_lat_lm)$coefficients[,4]
```

```
length78_lat_pval <- unname(length78_lat_pval[2])
```

```
temp_lat_corr <- cor.test(surv_length_envr$Mean_Annual_Temperature_C, surv_length_envr$lat)
```

```
temp_lat_corr #significant correlation between temp and lat, cannot include both in multiple regression
```

```
##
```

```
## Pearson's product-moment correlation
```

```
##
```

```
## data: surv_length_envr$Mean_Annual_Temperature_C and surv_length_envr$lat
```

```
## t = -8.8851, df = 6, p-value = 0.0001132
```

```
## alternative hypothesis: true correlation is not equal to 0
```

```
## 95 percent confidence interval:
```

```
## -0.9936754 -0.8088184
```

```
## sample estimates:
```

```
## cor
```

```
## -0.9640364
```

```
#multiple regression
```

```
surv_temp_sal_lm <- lm(percent_survival ~ Mean_Annual_Temperature_C + Mean_Annual_Salinity_ppt, data = surv_length_envr)
```

```
summary(surv_temp_sal_lm) #both explanatory variables significant, whole model significant
```

```
##
```

```
## Call:
```

```
## lm(formula = percent_survival ~ Mean_Annual_Temperature_C + Mean_Annual_Salinity_ppt,
```

```
## data = surv_length_envr)
```

```
##
```

```
## Residuals:
```

```
##      1      2      3      4      5      6      7      8
```

```
## -0.41864 -0.34440  0.61996  0.27276 -0.47766 -0.02476  0.68693 -0.31417
```



```
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      -1.30130    1.44748  -0.899  0.40985
## Mean_Annual_Temperature_C  0.28004    0.06744   4.153  0.00889 **
## Mean_Annual_Salinity_ppt  -0.07660    0.02800  -2.736  0.04099 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5571 on 5 degrees of freedom
## Multiple R-squared:  0.8395, Adjusted R-squared:  0.7753
## F-statistic: 13.08 on 2 and 5 DF,  p-value: 0.01032

length21_temp_sal_lm <- lm(mean_length_mm_21 ~ Mean_Annual_Temperature_C + Mean_Annual_Salinity_ppt, data = surv_length_envr)
summary(length21_temp_sal_lm) #neither explanatory variable significant, model not significant

##
## Call:
## lm(formula = mean_length_mm_21 ~ Mean_Annual_Temperature_C +
##     Mean_Annual_Salinity_ppt, data = surv_length_envr)
##
## Residuals:
##      1      2      3      4      5      6      7
## -0.0039705  0.0070959 -0.0008724 -0.0125143  0.0115745  0.0042660 -0.0145993
##      8
##  0.0090201
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.3176148  0.0300787  10.559 0.000132 ***
## Mean_Annual_Temperature_C -0.0007533  0.0014013  -0.538 0.613937
## Mean_Annual_Salinity_ppt  0.0004635  0.0005818   0.797 0.461836
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.01158 on 5 degrees of freedom
## Multiple R-squared:  0.1635, Adjusted R-squared: -0.1712
## F-statistic: 0.4885 on 2 and 5 DF,  p-value: 0.6401

length78_temp_sal_lm <- lm(mean_length_mm_78 ~ Mean_Annual_Temperature_C + Mean_Annual_Salinity_ppt, data = surv_length_envr)
summary(length78_temp_sal_lm) #neither explanatory variable significant, model insignificant

##
## Call:
## lm(formula = mean_length_mm_78 ~ Mean_Annual_Temperature_C +
##     Mean_Annual_Salinity_ppt, data = surv_length_envr)
##
## Residuals:
##      1      2      3      4      5      6      7      8
##  1.0415  3.8777 -0.2769  0.1329 -1.0801  0.8543 -4.1905 -0.3589
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
```

```
## (Intercept)          17.367666    6.952154    2.498    0.0546 .
## Mean_Annual_Temperature_C -0.191080    0.323889   -0.590    0.5809
## Mean_Annual_Salinity_ppt  -0.007467    0.134480   -0.056    0.9579
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.676 on 5 degrees of freedom
## Multiple R-squared:  0.06516,    Adjusted R-squared:  -0.3088
## F-statistic: 0.1742 on 2 and 5 DF,  p-value: 0.845
```

```
#put multiple regression output table in results
```

```
#adjust p-values
```

```
p_values <- c(length21_temp_pval, length21_sal_pval, length21_lat_pval, surv_temp_pval, surv_sal_pval,
p_adj <- p.adjust(p_values, method = "BH")
p_values
```

```
## [1] 0.56802380 0.41097924 0.64610781 0.02416428 0.17214151 0.04664046 0.54362971
## [8] 0.98297176 0.96196115
```

```
p_adj
```

```
## [1] 0.8307100 0.8307100 0.8307100 0.2098821 0.5164245 0.2098821 0.8307100
## [8] 0.9829718 0.9829718
```

ADJUSTED P-VALUES - NICOLE YOU NEED TO UPDATE THESE - Mean annual temp is not a significant predictor of mean length at day 21 ( $p = 0.831$ ) - Mean annual salinity is not a significant predictor of mean length at day 21 ( $p = 0.831$ ). - Latitude is not a significant predictor of mean length at day 21 ( $p = 0.831$ ).

- Mean annual temp is no longer a significant predictor of percent survival at day 21 ( $p = 0.210$ ).
- Mean annual salinity is not a significant predictor of percent survival at day 21 ( $p = 0.516$ ).
- Latitude is not a significant predictor of percent survival at day 21 ( $p = 0.210$ ).
- Mean annual temp is not a significant predictor of mean length at day 78 ( $p = 0.831$ )
- Mean annual salinity is not a significant predictor of mean length at day 78 ( $p = 0.983$ ).
- Latitude is not a significant predictor of mean length at day 78 ( $p = 0.983$ ).

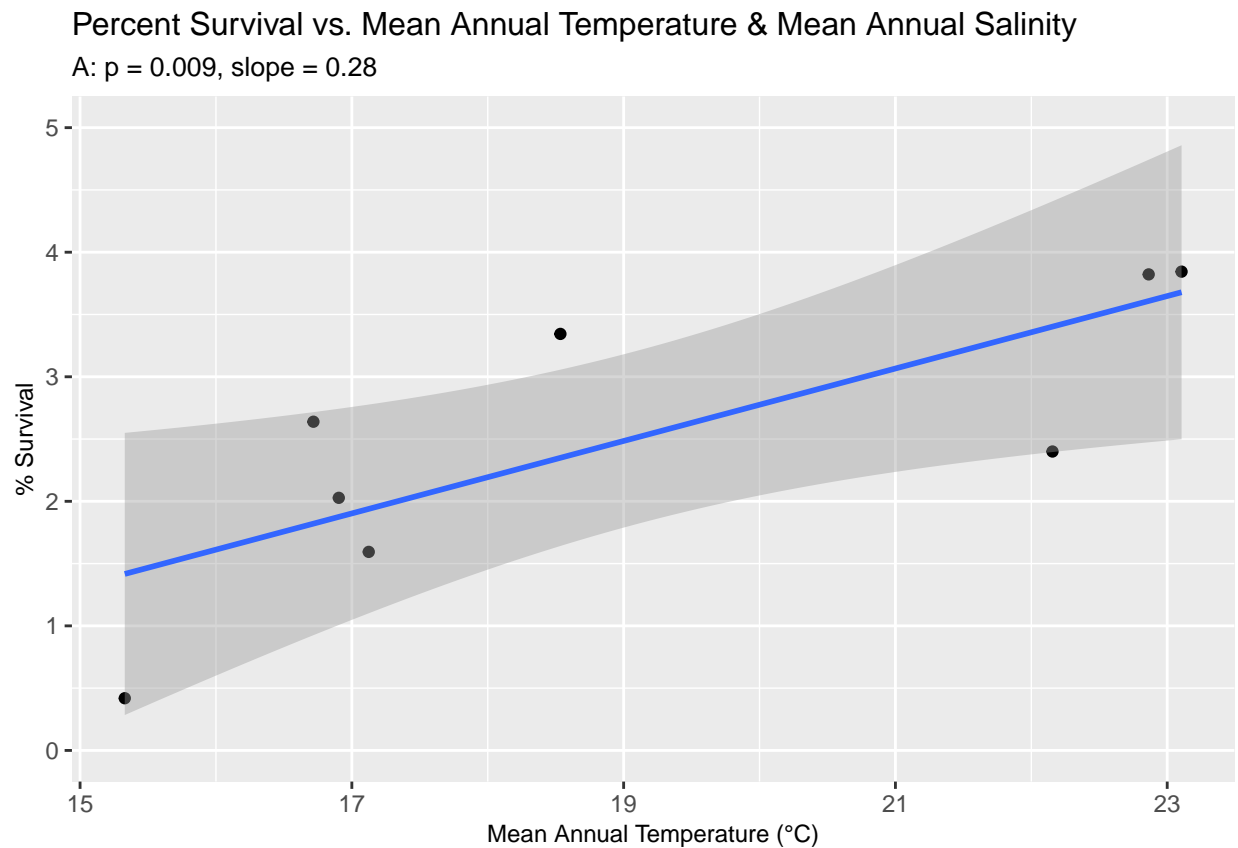
```
#make function to wrap title text
wrapper <- function(x, ...)
{
  paste(strwrap(x, ...), collapse = "\n")
}

surv_temp_plot <- surv_length_envr %>%
  ggplot(aes(x = Mean_Annual_Temperature_C, y = percent_survival))+
```

```
geom_point()+
labs(subtitle = "A: p = 0.009, slope = 0.28")+
ggtitle("Percent Survival vs. Mean Annual Temperature & Mean Annual Salinity")+
ylab("% Survival")+
xlab("Mean Annual Temperature (°C)")+
ylim(c(0,5))+
theme(axis.title.y = element_text(size = 9), axis.title.x = element_text(size = 9), axis.text.x = element_text(size = 9))+
geom_smooth(method = "lm", se = TRUE, fullrange = TRUE)
```

surv\_temp\_plot

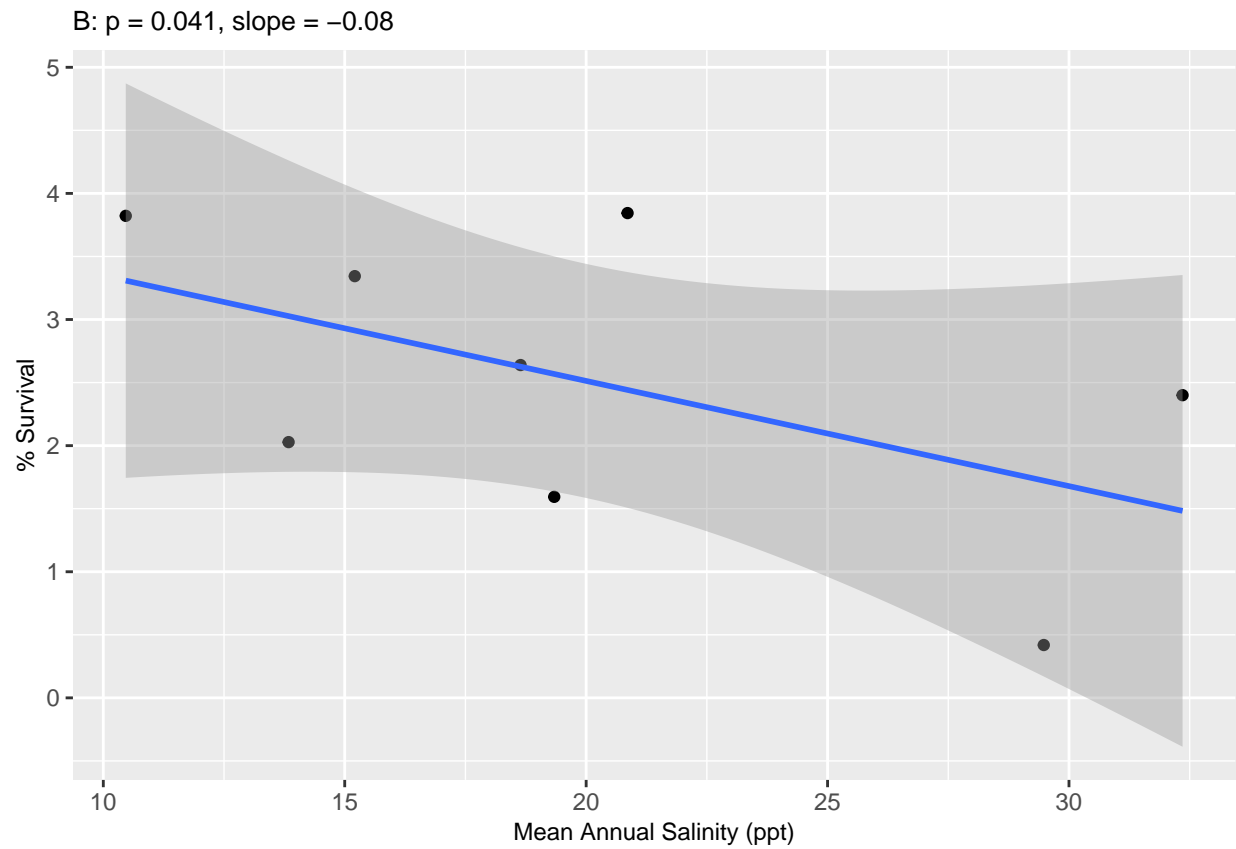
## 'geom\_smooth()' using formula = 'y ~ x'



```
surv_sal_plot <- surv_length_envr %>%
ggplot(aes(x = Mean_Annual_Salinity_ppt, y = percent_survival))+
geom_point()+
labs(subtitle = "B: p = 0.041, slope = -0.08")+
ylab("% Survival")+
xlab("Mean Annual Salinity (ppt)")+
theme(axis.title.x = element_text(size = 9), plot.title = element_blank(), plot.subtitle = element_text(size = 9))+
geom_smooth(method = "lm", se = TRUE, fullrange = TRUE)
```

surv\_sal\_plot

## 'geom\_smooth()' using formula = 'y ~ x'



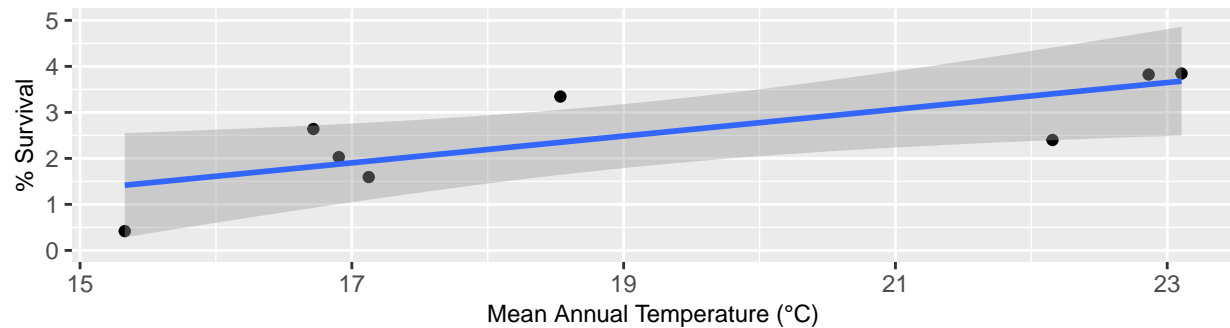
```
surv_plots <- plot_grid(surv_temp_plot, surv_sal_plot, ncol = 1, align = "v")
```

```
## 'geom_smooth()' using formula = 'y ~ x'
## 'geom_smooth()' using formula = 'y ~ x'
```

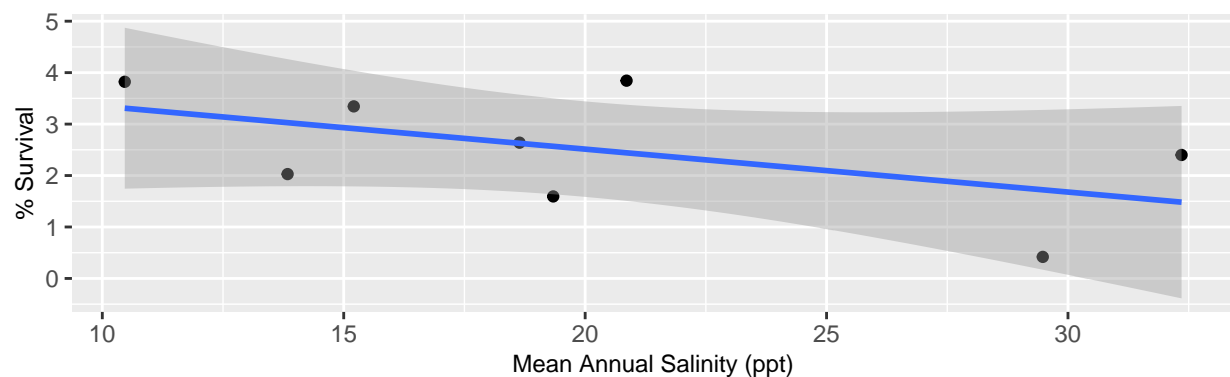
```
surv_plots
```

## Percent Survival vs. Mean Annual Temperature & Mean Annual Salinity

A:  $p = 0.009$ , slope = 0.28



B:  $p = 0.041$ , slope = -0.08



```
ggsave("surv_plots.png",
  plot = surv_plots,
  device = png,
  path = "/Users/nicolemongillo/Desktop/GitHub/MVP_Chesapeake_VIMS_hatchery/results/NM_results/Res")
```

## Saving 6.5 x 4.5 in image

Make distance matrices for difference in mean length across groups at days 21 and 78 and difference in survival across groups at day 21

```
#save vector of row and column names
rownames <- c("DEBY", "LOLA", "JR", "TX", "LA", "FL", "NH", "ME")
colnames <- c("DEBY", "LOLA", "JR", "TX", "LA", "FL", "NH", "ME")

means_mm_21 <- subset(means_mm_21, select = -c(site_name))

day21_len_dist <- as.matrix(dist(means_mm_21$mean_length_mm_21))
rownames(day21_len_dist) <- rownames
colnames(day21_len_dist) <- colnames

day78_len_dist <- as.matrix(dist(means_mm_78$mean_length_mm_78))
rownames(day78_len_dist) <- rownames
colnames(day78_len_dist) <- colnames

day21_surv_dist <- as.matrix(dist(survival_filter$percent_survival))
```

```

rownames(day21_surv_dist) <- rownames
colnames(day21_surv_dist) <- colnames

#remove site_name column from envr_dist, and make it a matrix
envr_dist <- subset(envr_dist, select = -c(X))
envr_dist_mat <- as.matrix(envr_dist)

```

I will run Mantel tests comparing days 21 and 78 length distance and day 21 survival distance to environmental distance. The goal is to see if more environmentally distant pairs of groups also have greater differences in length and survival.

H0: There is no correlation between the environmental distance matrix values and the length or survival matrix values. Environmental distance and length/survival do not vary with each other in any predictable way

#Mantel test

```

length21_envr = mantel(day21_len_dist, envr_dist_mat, method = "spearman", permutations = 10000, na.rm = TRUE)
length21_envr

```

```

##
## Mantel statistic based on Spearman's rank correlation rho
##
## Call:
## mantel(xdis = day21_len_dist, ydis = envr_dist_mat, method = "spearman",      permutations = 10000, na.rm = TRUE)
##
## Mantel statistic r: 0.3054
##      Significance: 0.081292
##
## Upper quantiles of permutations (null model):
##   90%   95% 97.5%   99%
## 0.274 0.384 0.500 0.589
## Permutation: free
## Number of permutations: 10000

```

*#mantel r = 0.3054, p = 0.078492. As environmental distance between a pair of sights increases, so does length21*

```

length78_envr = mantel(day78_len_dist, envr_dist_mat, method = "spearman", permutations = 10000, na.rm = TRUE)
length78_envr

```

```

##
## Mantel statistic based on Spearman's rank correlation rho
##
## Call:
## mantel(xdis = day78_len_dist, ydis = envr_dist_mat, method = "spearman",      permutations = 10000, na.rm = TRUE)
##
## Mantel statistic r: -0.1653
##      Significance: 0.72883
##
## Upper quantiles of permutations (null model):
##   90%   95% 97.5%   99%
## 0.352 0.443 0.504 0.560
## Permutation: free
## Number of permutations: 10000

```

```
#mantel r = -0.1653. p = 0.73843. As environmental distance between a pair of sights increases, the dis
surv21_envr = mantel(day21_surv_dist, envr_dist_mat, method = "spearman", permutations = 10000, na.rm =
surv21_envr
```

```
##
## Mantel statistic based on Spearman's rank correlation rho
##
## Call:
## mantel(xdis = day21_surv_dist, ydis = envr_dist_mat, method = "spearman",      permutations = 10000,
##
## Mantel statistic r: -0.02299
##      Significance: 0.51015
##
## Upper quantiles of permutations (null model):
##   90%   95% 97.5%   99%
## 0.292 0.379 0.448 0.522
## Permutation: free
## Number of permutations: 10000
```

```
#mantel r = -0.2299, p = 0.50545
```

```
#Correct Mantel p-values
```

```
mantel_p <- c(0.078492, 0.73843, 0.50545)
mantel_p_adj <- p.adjust(mantel_p, method = "BH")
mantel_p_adj
```

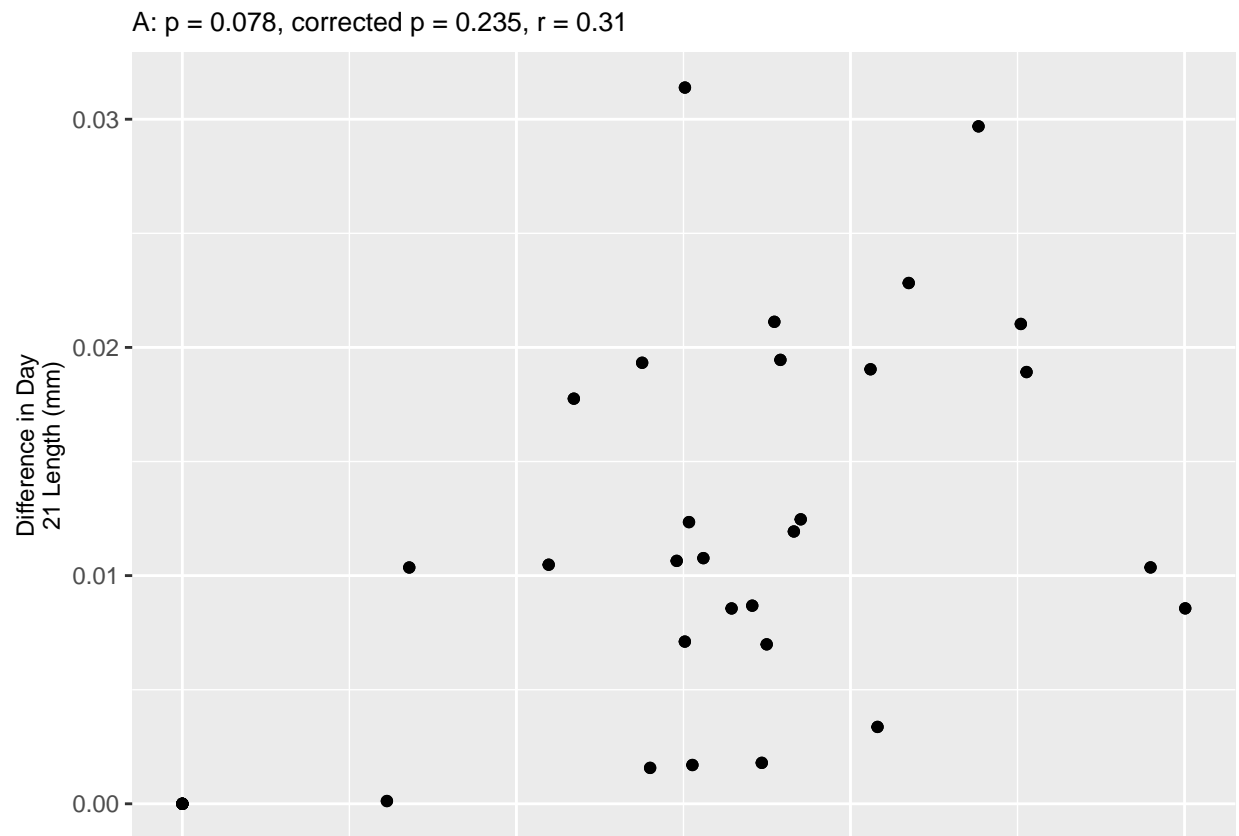
```
## [1] 0.235476 0.738430 0.738430
```

```
#length21_envr corrected p = 0.235476, length78_envr corrected p = 0.738430, surv21_envr corrected p =
```

```
#Plot Mantel test results
```

```
envr_pairwise_dist <- as.vector(envr_dist_mat)
day21_pairwise_len_dist <- as.vector(day21_len_dist)
day78_pairwise_len_dist <- as.vector(day78_len_dist)
day21_pairwise_surv_dist <- as.vector(day21_surv_dist)
pairwise_dist <- as.data.frame(cbind(envr_pairwise_dist, day21_pairwise_len_dist, day78_pairwise_len_dist,
day21_pairwise_surv_dist))
length21_envr_dist <- pairwise_dist %>%
  ggplot(aes(x = envr_pairwise_dist, y = day21_pairwise_len_dist))+
  geom_point()+
  labs(subtitle = "A: p = 0.078, corrected p = 0.235, r = 0.31")+
  ylab(wrapper("Difference in Day 21 Length (mm)", width = 20))+
```

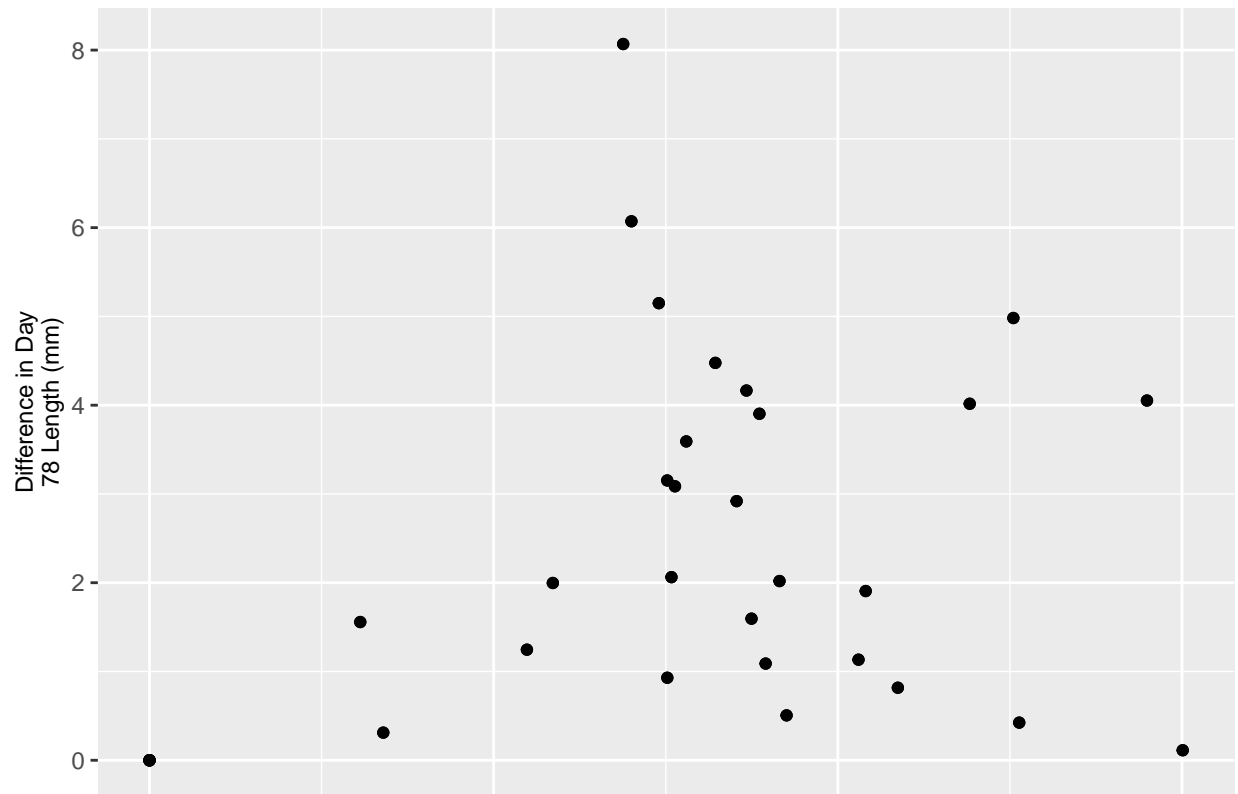
```
theme(axis.title.y = element_text(size = 9), axis.title.x = element_blank(), axis.text.x = element_blank(),
length21_envr_dist
```



```
length78_envr_dist <- pairwise_dist %>%
  ggplot(aes(x = envr_pairwise_dist, y = day78_pairwise_len_dist))+
  geom_point()+
  labs(subtitle = "B:  $p = 0.738$ , corrected  $p = 0.738$ ,  $r = -0.17$ ") +
  ylab(wrapper("Difference in Day 78 Length (mm)", width = 20)) +
  theme(axis.title.y = element_text(size = 9), axis.title.x = element_blank(), axis.text.x = element_blank(),
length78_envr_dist
```



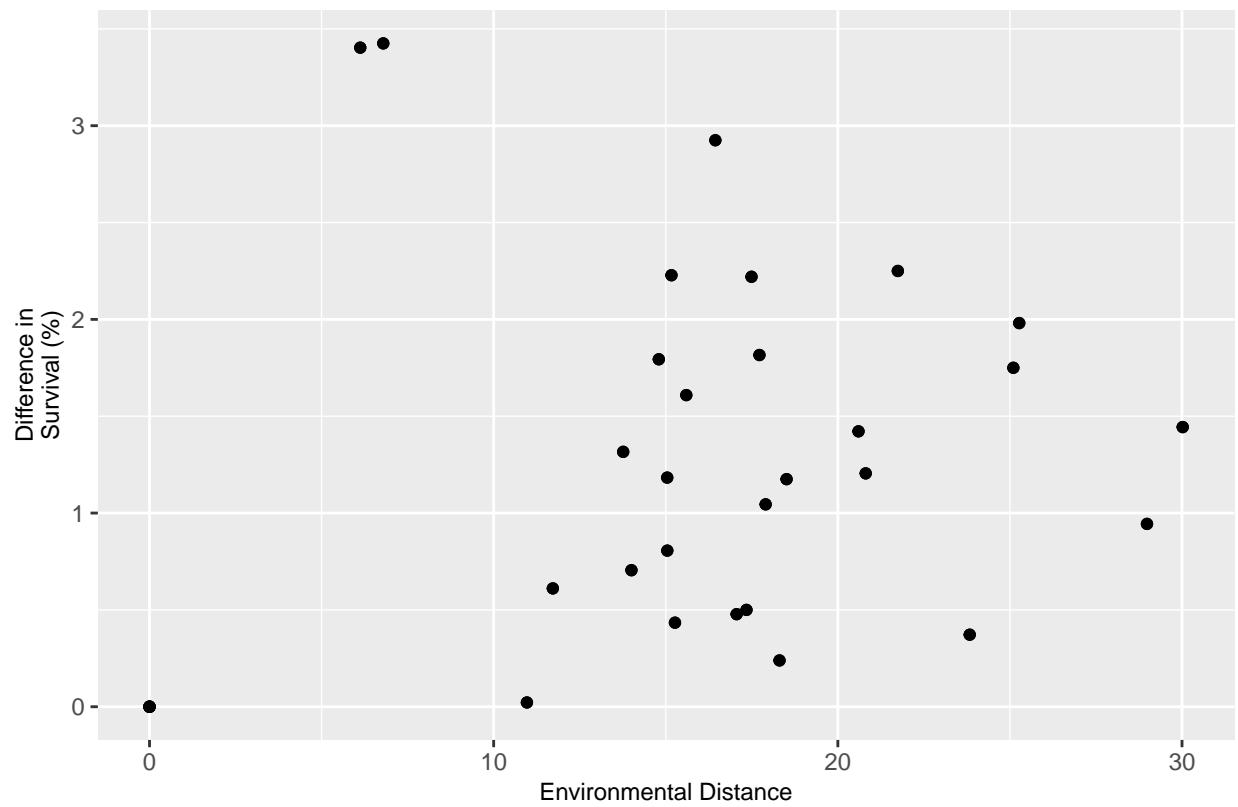
B:  $p = 0.738$ , corrected  $p = 0.738$ ,  $r = -0.17$



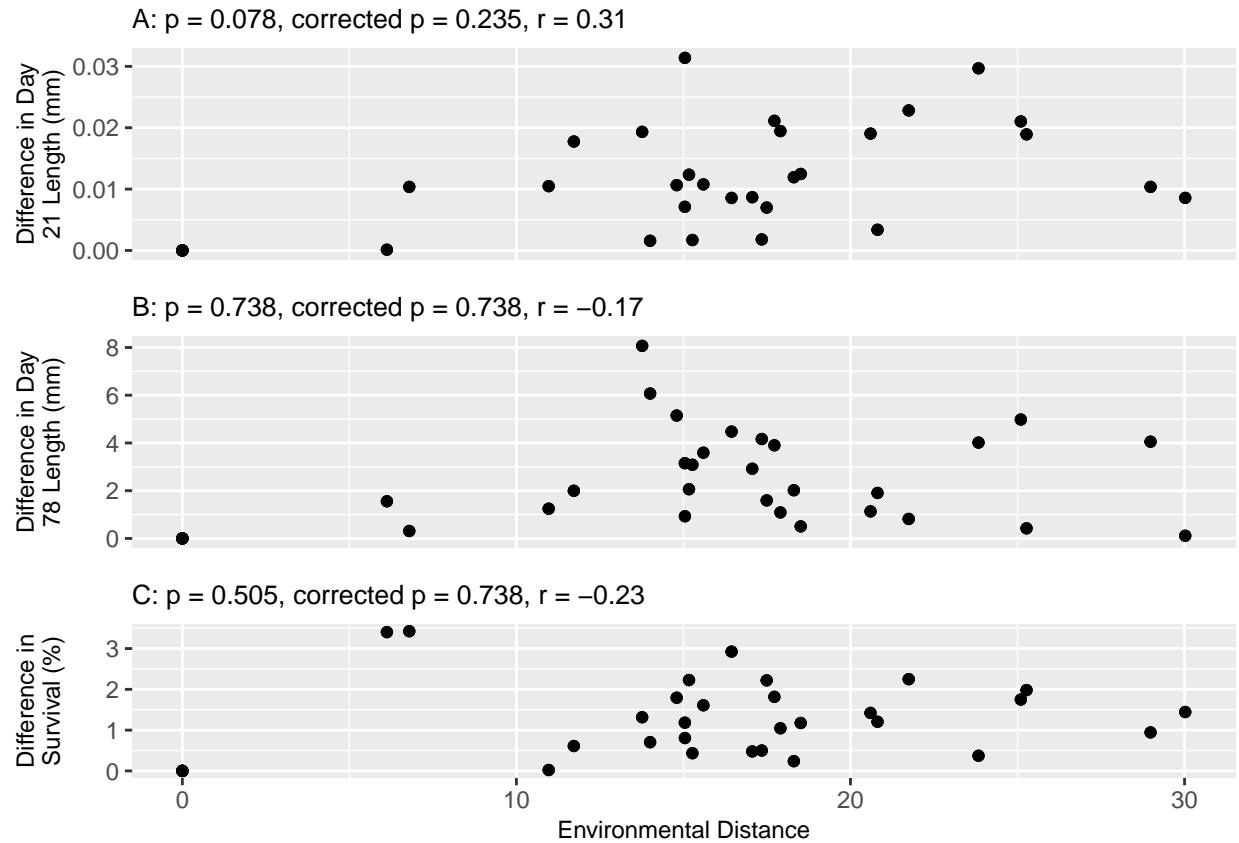
```
surv_envr_dist <- pairwise_dist %>%
  ggplot(aes(x = envr_pairwise_dist, y = day21_pairwise_surv_dist))+
  geom_point()+
  labs(subtitle = "C: p = 0.505, corrected p = 0.738, r = -0.23")+
  ylab(wrapper("Difference in Survival (%)", width = 20))+
  xlab("Environmental Distance")+
  theme(axis.title.y = element_text(size = 9), axis.title.x = element_text(size = 9), plot.subtitle = e

surv_envr_dist
```

C:  $p = 0.505$ , corrected  $p = 0.738$ ,  $r = -0.23$



```
mantel_plots <- plot_grid(length21_envr_dist, length78_envr_dist, surv_envr_dist, ncol = 1, align = "v")
mantel_plots
```



```
ggsave("mantel_plots.png",
  plot = mantel_plots,
  device = png,
  path = "/Users/nicolemongillo/Desktop/GitHub/MVP_Chesapeake_VIMS_hatchery/results/NM_results/Res")
```

```
## Saving 6.5 x 4.5 in image
```