Envr_Performance_Mantel_Tests

2025-01-23

This code analyzes the effect of pairwise environmental distance between conditions at the environments-of-origin on pairwise differences in survival and shell length for oysters in the hatchery and nursery at VIMS ABC.

```
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
```

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

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

#read in necessary files

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

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

#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_

#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_la
```

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

```r
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
```

```r
#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

```r
#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")
```

3

```r
#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

```r
#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
```

```r
#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/Sur
```

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 =
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, n
##
## Mantel statistic r: 0.3054
##       Significance: 0.072793
##
```

```
## Upper quantiles of permutations (null model):
##   90%   95% 97.5%   99%
## 0.266 0.364 0.476 0.574
## Permutation: free
## Number of permutations: 10000
```

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

```
length78_envr = mantel(day78_len_dist, envr_dist_mat, method = "spearman", permutations = 10000, na.rm =
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, r
##
## Mantel statistic r: -0.1653
##       Significance: 0.74143
##
## Upper quantiles of permutations (null model):
##   90%   95% 97.5%   99%
## 0.351 0.452 0.516 0.576
## 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: 0.50245
##
## Upper quantiles of permutations (null model):
##   90%   95% 97.5%   99%
## 0.279 0.362 0.432 0.508
## Permutation: free
## Number of permutations: 10000
```

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

#Correct Mantel p-values

```r
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
```

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

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

#Plot Mantel test results

```r
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_di

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_bl

length21_envr_dist
```
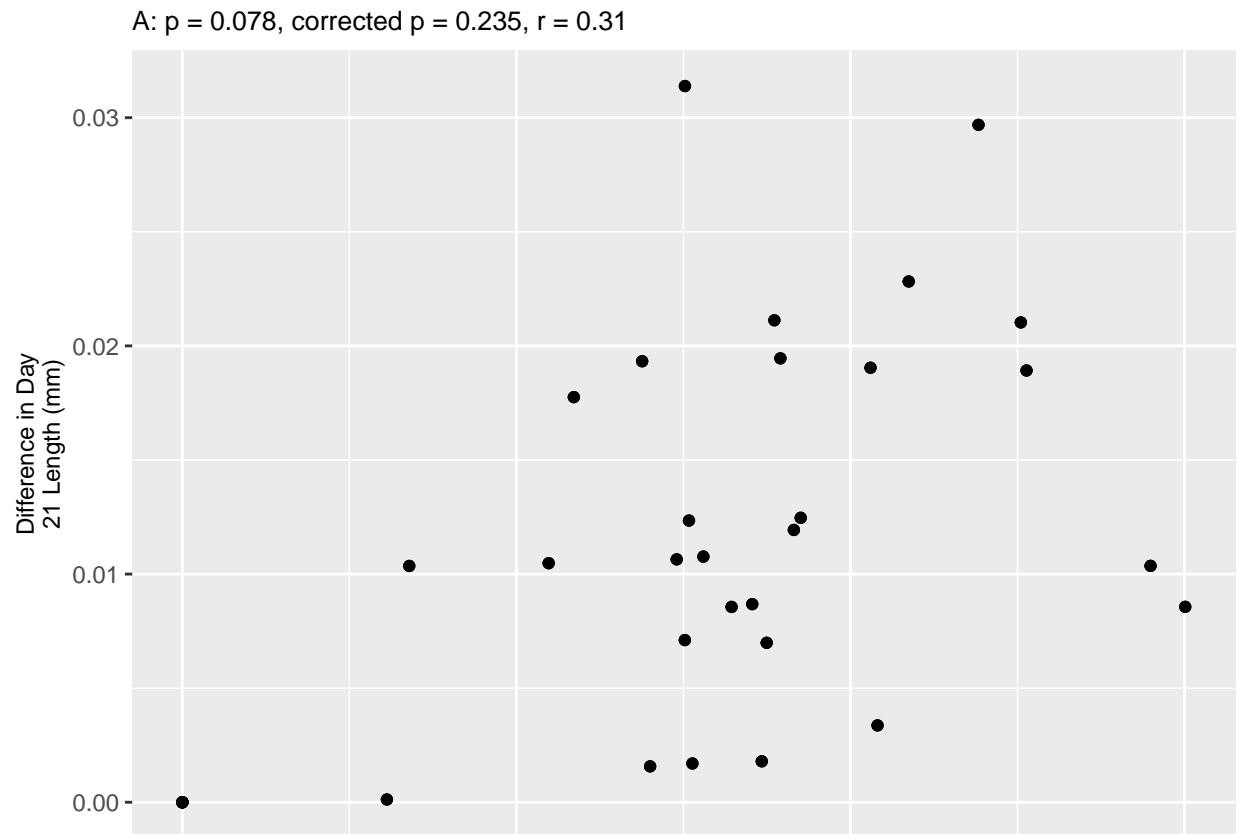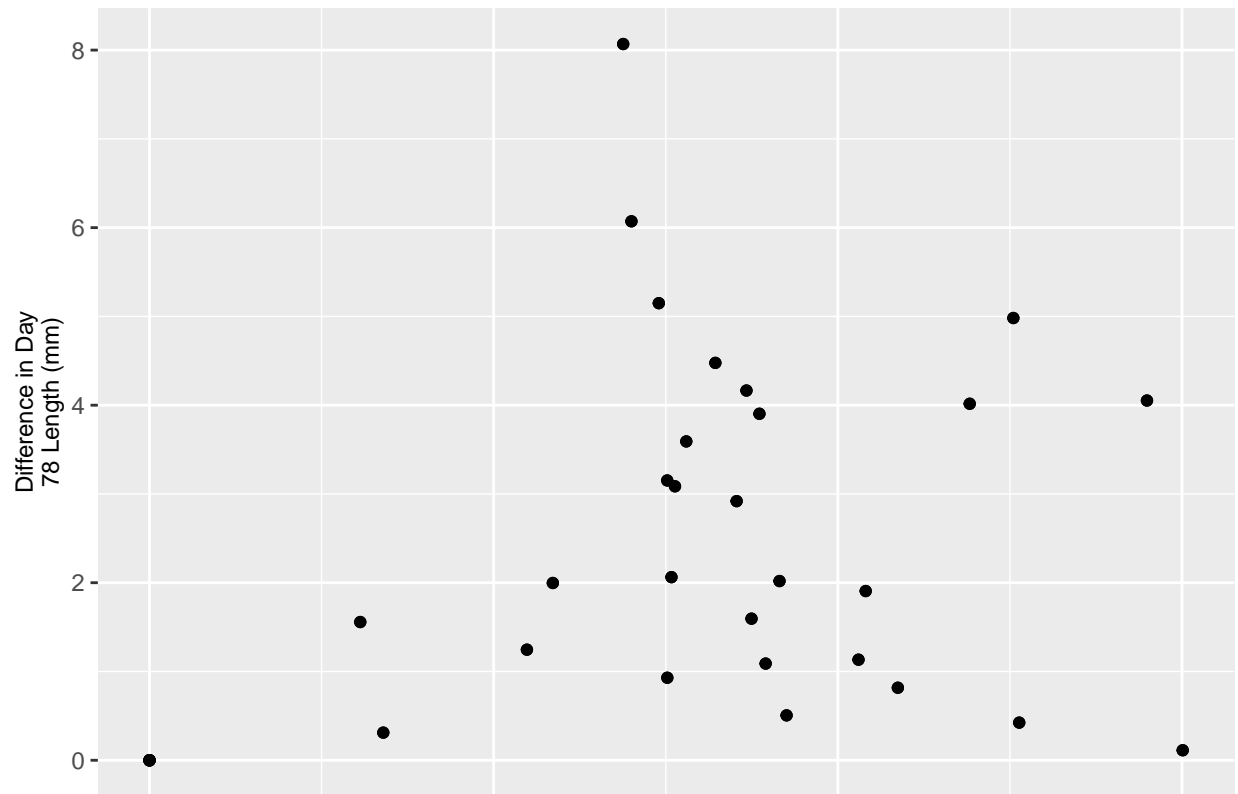
A: p = 0.078, corrected p = 0.235, r = 0.31


```
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_bla

length78_envr_dist
```

B: p = 0.738, corrected p = 0.738, r = −0.17



```r
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 = el

surv_envr_dist
```

C: p = 0.505, corrected p = 0.738, r = −0.23
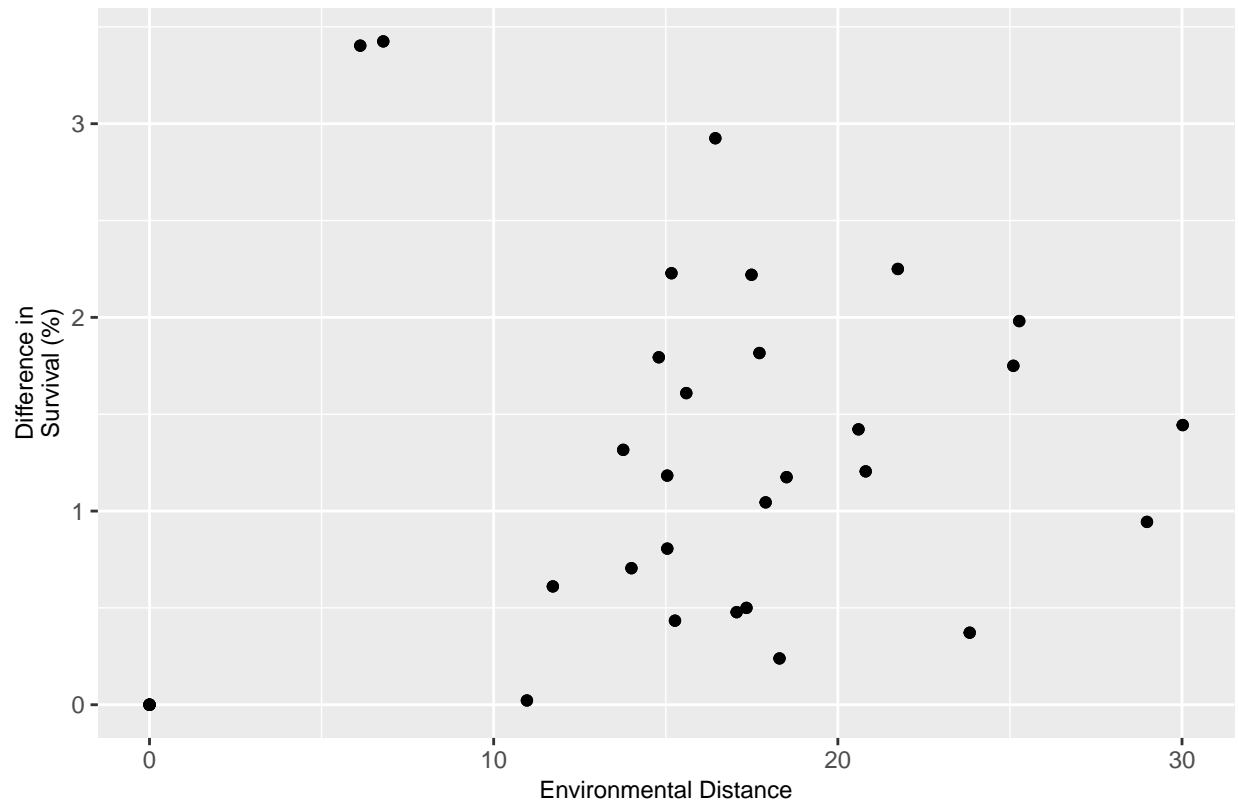

```
mantel_plots <- plot_grid(length21_envr_dist, length78_envr_dist, surv_envr_dist, ncol = 1, align = "v")

mantel_plots
```

A: p = 0.078, corrected p = 0.235, r = 0.31

B: p = 0.738, corrected p = 0.738, r = −0.17

C: p = 0.505, corrected p = 0.738, r = −0.23
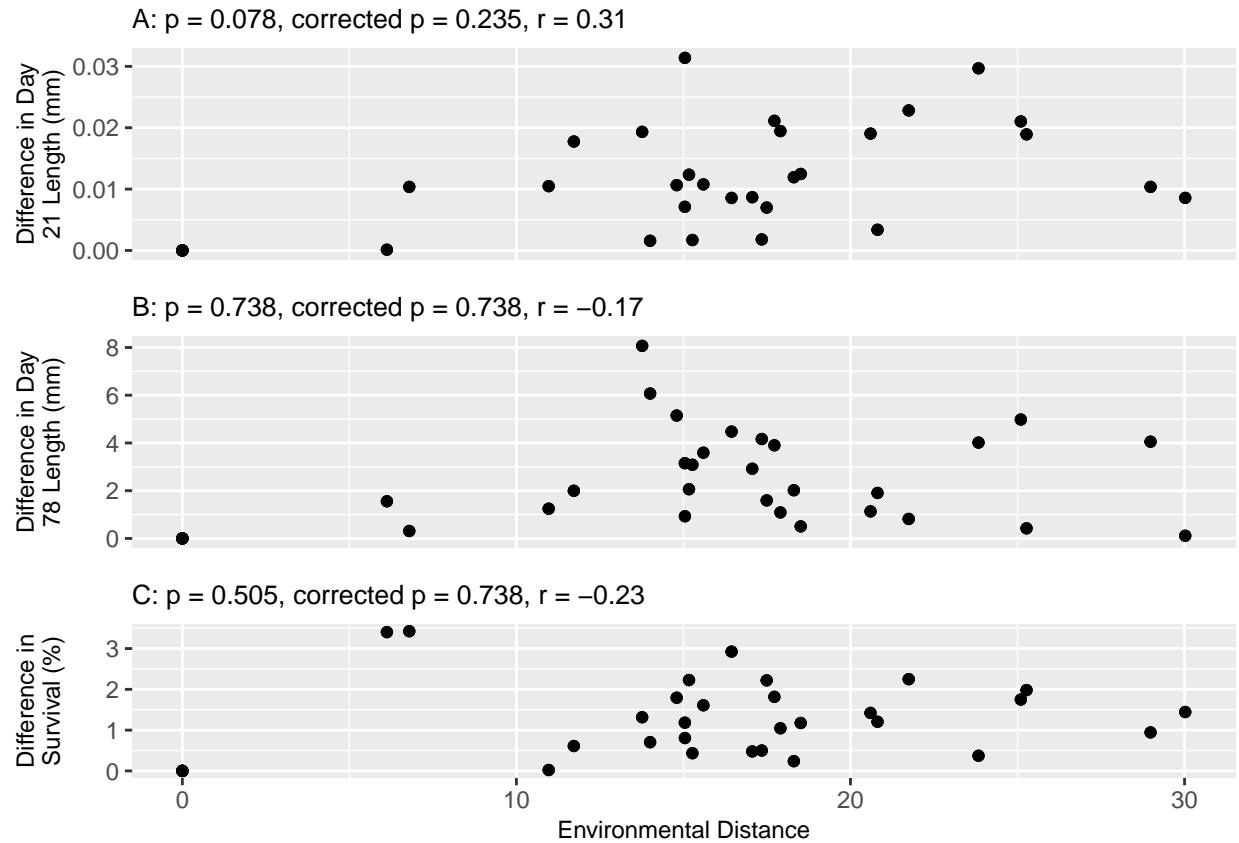
```
ggsave("mantel_plots.png",
       plot = mantel_plots,
       device = png,
       path = "/Users/nicolemongillo/Desktop/GitHub/MVP_Chesapeake_VIMS_hatchery/results/NM_results/Res
```

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