

## 030- Morphometrics tests for significance and correlation

### Directory and doc rules

```
knitr::opts_chunk$set(  
  echo = TRUE,      # Display code chunks  
  eval = TRUE,      # Evaluate code chunks  
  warning = FALSE,  # Hide warnings  
  message = FALSE,  # Hide messages  
  fig.width = 20,    # Set plot width in inches  
  fig.height = 9,    # Set plot height in inches  
  fig.align = "center" # Align plots to the center  
)
```

### Load packages

```
library(tinytex)  
library(tidyr)  
library(tidyverse)  
library(vegan)
```

### Load data

```
#Port Angeles Yacht Club has been removed due to being an abnormally high outlier in comparison to all  
#getwd()  
mdata<- read.csv("/Users/cmantegna/Documents/WDFWmussels/data/morphometricdata.csv")
```

### Check data

```
summary(mdata)
```

```
##      latitude      longitude  reporting_area  site_number  
## Min.   :47.05   Min.   : -123.0   Min.    : 6.00   Min.    : 2.00  
## 1st Qu.:47.33   1st Qu.: -122.7   1st Qu. : 9.00   1st Qu. :22.00  
## Median :47.60   Median : -122.6   Median  :10.00   Median  :40.50  
## Mean   :47.70   Mean   : -122.6   Mean    :10.09   Mean    :40.42  
## 3rd Qu.:48.02   3rd Qu.: -122.4   3rd Qu. :11.00   3rd Qu. :59.00  
## Max.   :48.82   Max.   : -122.2   Max.    :13.00   Max.    :77.00  
## site_name      sample_id      at      cf  
## Length:306     Min.    : 1.00   Min.    :0.3550   Min.    :0.0430  
## Class :character 1st Qu.: 77.25   1st Qu.:0.6813   1st Qu.:0.1539  
## Mode  :character Median :153.50   Median :0.7950   Median :0.1739  
##              Mean   :154.75   Mean   :0.7831   Mean    :0.1776  
##              3rd Qu.:229.75   3rd Qu.:0.8750   3rd Qu.:0.1914
```

```
##           Max.      :312.00   Max.      :1.2600   Max.      :1.5799
##   mercury      arsenic      cadmium      copper
##   Min.      :-0.02570   Min.      : 7.246   Min.      :1.537   Min.      : 4.771
##   1st Qu.: 0.03128   1st Qu.: 8.119   1st Qu.:1.743   1st Qu.: 5.795
##   Median : 0.03396   Median : 8.466   Median :1.873   Median : 6.507
##   Mean      : 0.03374   Mean      : 8.512   Mean      :1.872   Mean      : 7.098
##   3rd Qu.: 0.03925   3rd Qu.: 8.851   3rd Qu.:1.969   3rd Qu.: 7.556
##   Max.      : 0.05195   Max.      :10.284   Max.      :2.312   Max.      :30.471
##   lead      zinc      lmwPAH      PAH16
##   Min.      :0.06993   Min.      : 67.97   Min.      : 79.14   Min.      : 24.59
##   1st Qu.:0.19825   1st Qu.: 79.28   1st Qu.:112.89   1st Qu.: 70.78
##   Median :0.24807   Median : 85.38   Median :182.21   Median :144.14
##   Mean      :0.28351   Mean      : 85.64   Mean      :404.46   Mean      :535.66
##   3rd Qu.:0.32995   3rd Qu.: 90.81   3rd Qu.:304.57   3rd Qu.:268.93
##   Max.      :0.88554   Max.      :110.78   Max.      :6125.29   Max.      :9800.46
##   sumPCB      hmwPAH      sumPAH      PAHgroup3
##   Min.      : 16.95   Min.      : 11.61   Min.      : 97.4   Min.      :1.000
##   1st Qu.: 35.82   1st Qu.: 74.60   1st Qu.:176.7   1st Qu.:1.000
##   Median : 48.69   Median :150.92   Median : 356.9   Median :2.000
##   Mean      : 58.05   Mean      :566.64   Mean      :967.8   Mean      :1.967
##   3rd Qu.: 64.79   3rd Qu.:280.54   3rd Qu.:599.0   3rd Qu.:3.000
##   Max.      :175.58   Max.      :9394.33   Max.      :14700.7   Max.      :3.000
##   PAHgroup4      PAHgroup5      PAHgroup6
##   Min.      :1.000   Min.      :0.00   Min.      :0.00
##   1st Qu.:1.000   1st Qu.:1.00   1st Qu.:1.00
##   Median :2.000   Median :2.00   Median :3.00
##   Mean      :2.464   Mean      :1.98   Mean      :2.49
##   3rd Qu.:3.000   3rd Qu.:3.00   3rd Qu.:4.00
##   Max.      :4.000   Max.      :4.00   Max.      :5.00
```

## Shapiro-Wilkes

```
#test for normality.
#Condition factor (cf) is not normally distributed.
#Average shell thickness (at) is normally distributed.
# *All analytes were determined not normally distributed in 010-p450.Rmd*
```

```
shapiro.test(mdata$cf)
```

```
##
## Shapiro-Wilk normality test
##
## data:  mdata$cf
## W = 0.2347, p-value < 2.2e-16
```

```
shapiro.test(mdata$at)
```

```
##
## Shapiro-Wilk normality test
##
## data:  mdata$at
## W = 0.99665, p-value = 0.7728
```

## Significant Differences

### cf- reporting area & site - Kruskal-Wallis (non-parametric data)

```
#test for significant differences - cf

# Change to character for the kw test AFTER keeping as numeric for the correlation tests - if necessary
#apdata$PAHgroup <- as.character(apdata$PAHgroup)
#apdata$PAHgroup2 <- as.character(apdata$PAHgroup2)
#apdata$PAHgroup3 <- as.character(apdata$PAHgroup3)

kruskal.test(cf ~ site_name, data = mdata)

##
## Kruskal-Wallis rank sum test
##
## data: cf by site_name
## Kruskal-Wallis chi-squared = 103.77, df = 72, p-value = 0.008454

kruskal.test(cf ~ reporting_area, data = mdata)

##
## Kruskal-Wallis rank sum test
##
## data: cf by reporting_area
## Kruskal-Wallis chi-squared = 15.747, df = 8, p-value = 0.04615
```

### cf- PAH groups - Kruskal-Wallis (non-parametric data)

```
kruskal.test(cf ~ PAHgroup3, data = mdata)

##
## Kruskal-Wallis rank sum test
##
## data: cf by PAHgroup3
## Kruskal-Wallis chi-squared = 4.2684, df = 2, p-value = 0.1183

kruskal.test(cf ~ PAHgroup4, data = mdata)

##
## Kruskal-Wallis rank sum test
##
## data: cf by PAHgroup4
## Kruskal-Wallis chi-squared = 4.2766, df = 3, p-value = 0.2331

kruskal.test(cf ~ PAHgroup5, data = mdata)

##
## Kruskal-Wallis rank sum test
##
## data: cf by PAHgroup5
## Kruskal-Wallis chi-squared = 4.8777, df = 4, p-value = 0.3001

kruskal.test(cf ~ PAHgroup6, data = mdata)

##
## Kruskal-Wallis rank sum test
```

```
##
## data:  cf by PAHgroup6
## Kruskal-Wallis chi-squared = 3.332, df = 5, p-value = 0.649

##cf- Kruskal-Wallis Multiple Comparisons (post hoc) Reporting Areas Are:
6 - East Juan de Fuca Strait
7 - San Juan Islands
8.1 - Deception Pass, Hope Island, and Skagit Bay
8.2 - Port Susan and Port Gardner
9 - Admiralty Inlet
10 - Seattle-Bremerton
11 - Tacoma-Vashon
12 - Hood Canal
13 - South Puget Sound

library(pgirmess)

mdata$reporting_area <- as.character(mdata$reporting_area)

# no significant differences across site.
# no significant differences across reporting area

mc_site<- as.data.frame(kruskalmc(cf ~ site_name, data = mdata, method = "bonferroni"))
mc_reporting<- as.data.frame(kruskalmc(cf ~ reporting_area, data = mdata, method = "bonferroni"))

head(mc_site)
```

```
##
## Aiston Preserve-Arroyo Beach Multiple comparison test after Kruskal-Wallis
## Aiston Preserve-Blair Waterway Multiple comparison test after Kruskal-Wallis
## Aiston Preserve-Blair Waterway #2 Multiple comparison test after Kruskal-Wallis
## Aiston Preserve-Brackenwood Ln Multiple comparison test after Kruskal-Wallis
## Aiston Preserve-Broad Spit (Fisherman's Point) Multiple comparison test after Kruskal-Wallis
## Aiston Preserve-Browns Point Lighthouse Multiple comparison test after Kruskal-Wallis
## alpha dif.com.obs.dif
## Aiston Preserve-Arroyo Beach 0.05 71.000
## Aiston Preserve-Blair Waterway 0.05 112.375
## Aiston Preserve-Blair Waterway #2 0.05 49.875
## Aiston Preserve-Brackenwood Ln 0.05 125.625
## Aiston Preserve-Broad Spit (Fisherman's Point) 0.05 61.000
## Aiston Preserve-Browns Point Lighthouse 0.05 111.000
## dif.com.critical.dif
## Aiston Preserve-Arroyo Beach 244.2160
## Aiston Preserve-Blair Waterway 267.5252
## Aiston Preserve-Blair Waterway #2 267.5252
## Aiston Preserve-Brackenwood Ln 267.5252
## Aiston Preserve-Broad Spit (Fisherman's Point) 267.5252
## Aiston Preserve-Browns Point Lighthouse 267.5252
## dif.com.stat.signif
## Aiston Preserve-Arroyo Beach FALSE
## Aiston Preserve-Blair Waterway FALSE
## Aiston Preserve-Blair Waterway #2 FALSE
## Aiston Preserve-Brackenwood Ln FALSE
## Aiston Preserve-Broad Spit (Fisherman's Point) FALSE
## Aiston Preserve-Browns Point Lighthouse FALSE
```

```
head(mc_reporting)
```

```
##                                statistic alpha dif.com.obs.dif
## 10-11 Multiple comparison test after Kruskal-Wallis 0.05      6.175325
## 10-12 Multiple comparison test after Kruskal-Wallis 0.05     39.124675
## 10-13 Multiple comparison test after Kruskal-Wallis 0.05     2.038961
## 10-6  Multiple comparison test after Kruskal-Wallis 0.05     20.774675
## 10-7  Multiple comparison test after Kruskal-Wallis 0.05     39.553703
## 10-8.1 Multiple comparison test after Kruskal-Wallis 0.05     49.449675
##      dif.com.critical.dif dif.com.stat.signif
## 10-11          47.84641          FALSE
## 10-12          95.08005          FALSE
## 10-13          49.67771          FALSE
## 10-6           95.08005          FALSE
## 10-7           56.58240          FALSE
## 10-8.1        105.07376          FALSE
```

## at- ANOVA (parametric data)

```
#test for significant differences - at
mdata$reporting_area <- as.character(mdata$reporting_area)
mdata$PAHgroup3 <- as.character(mdata$PAHgroup3)
mdata$PAHgroup4 <- as.character(mdata$PAHgroup4)
mdata$PAHgroup5 <- as.character(mdata$PAHgroup5)
mdata$PAHgroup6 <- as.character(mdata$PAHgroup6)
```

```
anova_site <- aov(at ~ site_name, data = mdata)
summary(anova_site)
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)
## site_name    72  3.441  0.04779    4.16 <2e-16 ***
## Residuals   233  2.677  0.01149
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova_ra <- aov(at ~ reporting_area, data = mdata)
summary(anova_ra)
```

```
##              Df Sum Sq Mean Sq F value    Pr(>F)
## reporting_area  8  0.884  0.11051    6.271 1.66e-07 ***
## Residuals     297  5.233  0.01762
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova_group3 <- aov(at ~ PAHgroup3, data = mdata)
summary(anova_group3)
```

```
##              Df Sum Sq Mean Sq F value    Pr(>F)
## PAHgroup3      2  0.024  0.01218    0.606  0.546
## Residuals     303  6.093  0.02011
```

```
anova_group4 <- aov(at ~ PAHgroup4, data = mdata)
summary(anova_group4)
```

```
##              Df Sum Sq Mean Sq F value    Pr(>F)
## PAHgroup4      3  0.255  0.08515    4.387 0.00485 **
```

```
## Residuals    302  5.862 0.01941
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova_group5 <- aov(at ~ PAHgroup5, data = mdata)
summary(anova_group5)
```

```
##              Df Sum Sq Mean Sq F value    Pr(>F)
## PAHgroup5      4  0.342  0.08554    4.458 0.00163 **
## Residuals    301  5.775  0.01919
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova_group6 <- aov(at ~ PAHgroup6, data = mdata)
summary(anova_group6)
```

```
##              Df Sum Sq Mean Sq F value    Pr(>F)
## PAHgroup6      5  0.473  0.09462    5.029 0.000193 ***
## Residuals    300  5.644  0.01881
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

## at- TukeyHSD (post hoc)

```
library(broom)
library(readr)
```

```
mdata$reporting_area <- as.character(mdata$reporting_area)
mdata$PAHgroup4 <- as.character(mdata$PAHgroup4)
mdata$PAHgroup5 <- as.character(mdata$PAHgroup5)
mdata$PAHgroup6 <- as.character(mdata$PAHgroup6)
```

*#significant differences between 112 pairwise comparisons. Table written to GH repo.*

```
tukey_site<- TukeyHSD(anova_site)
ttable_site<- tidy(tukey_site)
sigtable_site <- ttable_site %>% filter(adj.p.value < 0.05)
write.csv(sigtable_site, "/Users/cmantegna/Documents/WDFWmussels/output/tables/SignificantThicknessSite.csv")
```

*# significant differences between reporting area comparisons: 11-10, 12-11, 6-11, 7-11, 8.1-11, 13-12,*

```
tukey_ra<- TukeyHSD(anova_ra)
ttable_ra<- tidy(tukey_ra)
sigtable_ra <- ttable_ra %>% filter(adj.p.value < 0.05)
write.csv(sigtable_ra, "/Users/cmantegna/Documents/WDFWmussels/output/tables/SignificantThicknessRA.csv")
```

*# significant differences between Low(1) and Mid(2) as well as Low(1) and Very High(4). Table written*

```
tukey_group4<- TukeyHSD(anova_group4)
ttable_group4<- tidy(tukey_group4)
sigtable_group4 <- ttable_group4 %>% filter(adj.p.value < 0.05)
write.csv(sigtable_group4, "/Users/cmantegna/Documents/WDFWmussels/output/tables/SignificantThicknessGroup4.csv")
```

*# significant differences between Extremely Low(0) and Low(1) as well as Extremely Low(0) and Very High(4).*

```
tukey_group5<- TukeyHSD(anova_group5)
ttable_group5<- tidy(tukey_group5)
sigtable_group5 <- ttable_group5 %>% filter(adj.p.value < 0.05)
write.csv(sigtable_group5, "/Users/cmantegna/Documents/WDFWmussels/output/tables/SignificantThicknessGroup5.csv")
```

```
# significant differences between 15 pairwise comparisons. Table written to GH repo.
tukey_group6<- TukeyHSD(anova_group6)
ttable_group6<- tidy(tukey_group6)
sigtable_group6 <- ttable_group6 %>% filter(adj.p.value < 0.05)
write.csv(sigtable_group6, "/Users/cmantegna/Documents/WDFWmussels/output/tables/SignificantThicknessG
```

## Correlations

```
##cf- PAHgroup3, PAHgroup4, PAHgroup5 and PAHgroup6 0= VLow
1= Low
2= Mid
3= High
4= VHigh
5= EHigh PAH groups determined by set quantiles found in grouping.rmd.
Group3= 1-3 | Group4= 1-4 | Group5= 0-4 | Group6= 0-5
```

```
mdata$PAHgroup3 <- as.numeric(mdata$PAHgroup3)
mdata$PAHgroup4 <- as.numeric(mdata$PAHgroup4)
mdata$PAHgroup5 <- as.numeric(mdata$PAHgroup5)
mdata$PAHgroup6 <- as.numeric(mdata$PAHgroup6)
```

```
# no correlation
correlation_result <- cor.test(mdata$cf, mdata$PAHgroup3, method = "pearson")
print(correlation_result)
```

```
##
## Pearson's product-moment correlation
##
## data: mdata$cf and mdata$PAHgroup3
## t = -1.7752, df = 304, p-value = 0.07687
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.21101661 0.01095844
## sample estimates:
## cor
## -0.1012896
```

```
# no correlation
correlation_result <- cor.test(mdata$cf, mdata$PAHgroup4, method = "pearson")
print(correlation_result)
```

```
##
## Pearson's product-moment correlation
##
## data: mdata$cf and mdata$PAHgroup4
## t = -1.7389, df = 304, p-value = 0.08306
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.20903794 0.01302813
## sample estimates:
## cor
## -0.09924039
```

```
# no correlation
correlation_result <- cor.test(mdata$cf, mdata$PAHgroup5, method = "pearson")
print(correlation_result)
```

```
##
## Pearson's product-moment correlation
##
## data: mdata$cf and mdata$PAHgroup5
## t = -1.8167, df = 304, p-value = 0.07024
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.213281046 0.008587515
## sample estimates:
## cor
## -0.1036358
```

```
# no correlation
correlation_result <- cor.test(mdata$cf, mdata$PAHgroup6, method = "pearson")
print(correlation_result)
```

```
##
## Pearson's product-moment correlation
##
## data: mdata$cf and mdata$PAHgroup6
## t = -1.8948, df = 304, p-value = 0.05907
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.217526786 0.004135372
## sample estimates:
## cor
## -0.1080383
```

## cf- sumPAH, lmwPAH, hmwPAH and PAH16

```
# no correlation
correlation_result <- cor.test(mdata$cf, mdata$sumPAH, method = "pearson")
print(correlation_result)
```

```
##
## Pearson's product-moment correlation
##
## data: mdata$cf and mdata$sumPAH
## t = -0.30181, df = 304, p-value = 0.763
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.12918033 0.09500045
## sample estimates:
## cor
## -0.01730746
```

```
# no correlation
correlation_result <- cor.test(mdata$cf, mdata$lmwPAH, method = "pearson")
print(correlation_result)
```

```
##
```



```
## Pearson's product-moment correlation
##
## data: mdata$cf and mdata$lmwPAH
## t = -0.4515, df = 304, p-value = 0.652
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.13761081 0.08648791
## sample estimates:
## cor
## -0.02588668

# no correlation
correlation_result <- cor.test(mdata$cf, mdata$hmwPAH, method = "pearson")
print(correlation_result)
```

```
##
## Pearson's product-moment correlation
##
## data: mdata$cf and mdata$hmwPAH
## t = -0.19958, df = 304, p-value = 0.8419
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.1234112 0.1008069
## sample estimates:
## cor
## -0.01144602
```

```
# no correlation
correlation_result <- cor.test(mdata$cf, mdata$PAH16, method = "pearson")
print(correlation_result)
```

```
##
## Pearson's product-moment correlation
##
## data: mdata$cf and mdata$PAH16
## t = -0.24871, df = 304, p-value = 0.8038
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.12618457 0.09801749
## sample estimates:
## cor
## -0.01426281
```

## cf- sumPCB

```
# no correlation
correlation_result <- cor.test(mdata$cf, mdata$sumPCB, method = "pearson")
print(correlation_result)
```

```
##
## Pearson's product-moment correlation
##
## data: mdata$cf and mdata$sumPCB
## t = -0.31472, df = 304, p-value = 0.7532
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
```

```
## -0.12990826 0.09426672
## sample estimates:
##      cor
## -0.01804759
```

cf- mercury, arsenic, cadmium, copper, lead, zinc

```
# no correlation
correlation_result <- cor.test(mdata$cf, mdata$mercury, method = "pearson")
print(correlation_result)
```

```
##
## Pearson's product-moment correlation
##
## data: mdata$cf and mdata$mercury
## t = 0.89978, df = 304, p-value = 0.3689
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.06093819 0.16272076
## sample estimates:
##      cor
## 0.0515375
```

```
# no correlation
correlation_result <- cor.test(mdata$cf, mdata$arsenic, method = "pearson")
print(correlation_result)
```

```
##
## Pearson's product-moment correlation
##
## data: mdata$cf and mdata$arsenic
## t = 0.56631, df = 304, p-value = 0.5716
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.0799516 0.1440621
## sample estimates:
##      cor
## 0.03246296
```

```
# no correlation
correlation_result <- cor.test(mdata$cf, mdata$cadmium, method = "pearson")
print(correlation_result)
```

```
##
## Pearson's product-moment correlation
##
## data: mdata$cf and mdata$cadmium
## t = 1.7909, df = 304, p-value = 0.0743
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.01005861 0.21187631
## sample estimates:
##      cor
## 0.1021802
```

```
# no correlation
correlation_result <- cor.test(mdata$cf, mdata$copper, method = "pearson")
print(correlation_result)
```

```
##
## Pearson's product-moment correlation
##
## data: mdata$cf and mdata$copper
## t = -0.8421, df = 304, p-value = 0.4004
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.15950233 0.06422944
## sample estimates:
## cor
## -0.04824153
```

```
# no correlation
correlation_result <- cor.test(mdata$cf, mdata$lead, method = "pearson")
print(correlation_result)
```

```
##
## Pearson's product-moment correlation
##
## data: mdata$cf and mdata$lead
## t = -0.87638, df = 304, p-value = 0.3815
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.16141548 0.06227359
## sample estimates:
## cor
## -0.05020048
```

```
# no correlation
correlation_result <- cor.test(mdata$cf, mdata$zinc, method = "pearson")
print(correlation_result)
```

```
##
## Pearson's product-moment correlation
##
## data: mdata$cf and mdata$zinc
## t = 0.31175, df = 304, p-value = 0.7554
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.09443539 0.12974095
## sample estimates:
## cor
## 0.01787746
```

#Correlations

##at- PAHgroup3, PAHgroup4, PAHgroup5 and PAHgroup6 0= VLow  
 1= Low  
 2= Mid  
 3= High  
 4= VHigh  
 5= EHigh PAH groups determined by set quantiles found in grouping.rmd.

Group3= 1-3 | Group4= 1-4 | Group5= 0-4 | Group6= 0-5

```
mdata$PAHgroup3 <- as.numeric(mdata$PAHgroup3)
mdata$PAHgroup4 <- as.numeric(mdata$PAHgroup4)
mdata$PAHgroup5 <- as.numeric(mdata$PAHgroup5)
mdata$PAHgroup6 <- as.numeric(mdata$PAHgroup6)

# no correlation
correlation_result <- cor.test(mdata$at, mdata$PAHgroup3, method = "pearson")
print(correlation_result)

##
## Pearson's product-moment correlation
##
## data: mdata$at and mdata$PAHgroup3
## t = 0.84056, df = 304, p-value = 0.4013
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.06431723 0.15941642
## sample estimates:
## cor
## 0.04815358

# correlation= 0.1205069 with a p-value= 0.03511 indicates a weak positive correlation.
correlation_result <- cor.test(mdata$at, mdata$PAHgroup4, method = "pearson")
print(correlation_result)

##
## Pearson's product-moment correlation
##
## data: mdata$at and mdata$PAHgroup4
## t = 2.1165, df = 304, p-value = 0.03511
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.008498124 0.229529086
## sample estimates:
## cor
## 0.1205069

# correlation= 0.1382479 with a p-value= 0.01552 indicates a weak positive correlation.
correlation_result <- cor.test(mdata$at, mdata$PAHgroup5, method = "pearson")
print(correlation_result)

##
## Pearson's product-moment correlation
##
## data: mdata$at and mdata$PAHgroup5
## t = 2.4338, df = 304, p-value = 0.01552
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.02653572 0.24654976
## sample estimates:
## cor
## 0.1382479

# no correlation
correlation_result <- cor.test(mdata$at, mdata$PAHgroup6, method = "pearson")
```

```
print(correlation_result)
```

```
##
## Pearson's product-moment correlation
##
## data: mdata$at and mdata$PAHgroup6
## t = 1.6836, df = 304, p-value = 0.09329
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.01618568 0.20601573
## sample estimates:
## cor
## 0.09611229
```

at- sumPAH, lmwPAH, hmwPAH and PAH16

```
# correlation= 0.1459292 with a p-value= 0.01059 indicates a weak positive correlation.
correlation_result <- cor.test(mdata$at, mdata$sumPAH, method = "pearson")
print(correlation_result)
```

```
##
## Pearson's product-moment correlation
##
## data: mdata$at and mdata$sumPAH
## t = 2.5719, df = 304, p-value = 0.01059
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.03436797 0.25389843
## sample estimates:
## cor
## 0.1459292
```

```
# correlation= 0.1698226 with a p-value= 0.002881 indicates a weak positive correlation.
correlation_result <- cor.test(mdata$at, mdata$lmwPAH, method = "pearson")
print(correlation_result)
```

```
##
## Pearson's product-moment correlation
##
## data: mdata$at and mdata$lmwPAH
## t = 3.0046, df = 304, p-value = 0.002881
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.05881899 0.27667786
## sample estimates:
## cor
## 0.1698226
```

```
# correlation= 0.1306227 with a p-value= 0.02229 indicates a weak positive correlation.
correlation_result <- cor.test(mdata$at, mdata$hmwPAH, method = "pearson")
print(correlation_result)
```

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

```
## data: mdata$at and mdata$hwmPAH
## t = 2.2972, df = 304, p-value = 0.02229
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.01877409 0.23924232
## sample estimates:
## cor
## 0.1306227

# correlation= 0.1457735 with a p-value= 0.01067 indicates a weak positive correlation.
correlation_result <- cor.test(mdata$at, mdata$PAH16, method = "pearson")
print(correlation_result)
```

```
##
## Pearson's product-moment correlation
##
## data: mdata$at and mdata$PAH16
## t = 2.5691, df = 304, p-value = 0.01067
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.03420911 0.25374963
## sample estimates:
## cor
## 0.1457735
```

#### at- sumPCB

```
# no correlation
correlation_result <- cor.test(mdata$at, mdata$sumPCB, method = "pearson")
print(correlation_result)

##
## Pearson's product-moment correlation
##
## data: mdata$at and mdata$sumPCB
## t = 1.485, df = 304, p-value = 0.1386
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.02752252 0.19512978
## sample estimates:
## cor
## 0.08486291
```

#### at- mercury, arsenic, cadmium, copper, lead, zinc

```
# no correlation
correlation_result <- cor.test(mdata$at, mdata$mercury, method = "pearson")
print(correlation_result)

##
## Pearson's product-moment correlation
##
## data: mdata$at and mdata$mercury
## t = 0.44832, df = 304, p-value = 0.6542
## alternative hypothesis: true correlation is not equal to 0
```

```

## 95 percent confidence interval:
## -0.08666918 0.13743163
## sample estimates:
##      cor
## 0.02570416

# no correlation
correlation_result <- cor.test(mdata$at, mdata$arsenic, method = "pearson")
print(correlation_result)

##
## Pearson's product-moment correlation
##
## data: mdata$at and mdata$arsenic
## t = -1.8726, df = 304, p-value = 0.06208
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.216321993 0.005399629
## sample estimates:
##      cor
## -0.1067886

# no correlation
correlation_result <- cor.test(mdata$at, mdata$cadmium, method = "pearson")
print(correlation_result)

##
## Pearson's product-moment correlation
##
## data: mdata$at and mdata$cadmium
## t = -0.31745, df = 304, p-value = 0.7511
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.13006219 0.09411153
## sample estimates:
##      cor
## -0.01820411

# no correlation
correlation_result <- cor.test(mdata$at, mdata$copper, method = "pearson")
print(correlation_result)

##
## Pearson's product-moment correlation
##
## data: mdata$at and mdata$copper
## t = 1.2958, df = 304, p-value = 0.196
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.03832716 0.18470355
## sample estimates:
##      cor
## 0.07411489

# no correlation
correlation_result <- cor.test(mdata$at, mdata$lead, method = "pearson")
print(correlation_result)

```

```
##
## Pearson's product-moment correlation
##
## data:  mdata$at and mdata$lead
## t = 0.87778, df = 304, p-value = 0.3808
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.06219345  0.16149383
## sample estimates:
##          cor
## 0.05028073

# no correlation
correlation_result <- cor.test(mdata$at, mdata$zinc, method = "pearson")
print(correlation_result)

##
## Pearson's product-moment correlation
##
## data:  mdata$at and mdata$zinc
## t = 0.80358, df = 304, p-value = 0.4223
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.06642664  0.15735110
## sample estimates:
##          cor
## 0.04603982
```