

06- Explore(01) through Analytes(05) with one average value per site

Setup

```
knitr::opts_chunk$set(  
  echo = TRUE,      # Display code chunks  
  eval = TRUE,      # Evaluate code chunks  
  warning = FALSE,  # Hide warnings  
  message = FALSE,  # Hide messages  
  fig.width = 8,    # Set plot width in inches  
  fig.height = 5,   # Set plot height in inches  
  fig.align = "center" # Align plots to the center  
)
```

Load packages

```
#install.packages("/Users/cmantegna/Downloads/spdep_1.2-8.tar.gz", repos = NULL, type = "source")  
library(tidyr)  
library(tidyverse)  
library(ggplot2)  
library(vegan)  
library(tinytex)
```

Load data

Note:

For *data* the units are listed below. Weight = g
Length, width, height = mm
p450, SOD = activity/ (mg/protein)
Condition factor, economic factor = unitless
For *pah* and *indv* the units are ng/g

```
getwd()  
  
## [1] "/Users/cmantegna/Documents/WDFWmussels/code"  
  
#data has all sites, coordinates, p450, sod, condition factor, economic factor data  
data<- read.csv("/Users/cmantegna/Documents/WDFWmussels/data/biomarkerfull.csv")  
  
#pah has complete site values and different summed pah analyte whole tissue values  
pah<- read.csv("/Users/cmantegna/Documents/Biomarker Data Analysis/sum_analytes.csv")  
  
#indv has complete site values and individual named pah analyte whole tissue values  
indv<- read.csv("/Users/cmantegna/Documents/Biomarker Data Analysis/individual_analytes.csv")
```

```
# Review data frame structure
```

```
str(data)
```

```
## 'data.frame':    312 obs. of  16 variables:
## $ latitude      : num  48.7 48.7 48.7 48.7 47.5 ...
## $ longitude     : num -123 -123 -123 -123 -122 ...
## $ site_name     : chr   "Aiston Preserve" "Aiston Preserve" "Aiston Preserve" "Aiston Preserve" ..
## $ site_number   : int   77 77 77 77 13 13 13 13 13 13 ...
## $ sample        : int  239 240 241 242 281 282 283 284 285 286 ...
## $ p450          : int  5965780 1508156 4674882 2861653 3448794 6485447 3563340 1813227 1987132 95...
## $ SOD           : num    0 4.88 8.87 0.01 7.08 ...
## $ weight_initial : chr   "11.6884" "10.833" "14.7041" "14.6121" ...
## $ length        : chr   "53.9" "53.49" "55.99" "58.55" ...
## $ width         : chr   "22.73" "23.92" "27.79" "28.38" ...
## $ height        : chr   "18.59" "18.36" "19.57" "19.55" ...
## $ weight_final   : num    3.28 3.48 4.73 4.45 4.62 ...
## $ weight_change  : chr   "8.41" "7.35" "9.98" "10.17" ...
## $ condition_factor: chr   "0.1560" "0.1374" "0.1782" "0.1737" ...
## $ avg_thickness  : num    0.7 0.79 0.825 0.93 0.92 0.965 0.86 0.955 0.875 0.645 ...
## $ economic_index : chr   "0.0018" "0.002" "0.002" "0.0021" ...
```

```
str(pah)
```

```
## 'data.frame':    390 obs. of  10 variables:
## $ latitude      : num  48.2 48.7 48.2 48.2 47.6 ...
## $ longitude     : num -123 -123 -123 -123 -123 ...
## $ LabSampleID   : chr   "119-5763" "119-5753" "119-5764" "119-5765" ...
## $ SampleID      : chr   "22WB_PCB1-MTW01" "22SAM1115-MTW01" "22WB_PCB2-MTW01" "22WB_PCB3-MTW01" ...
## $ SiteName      : chr   "Penn Cove Baseline 1" "Aiston Preserve" "Penn Cove Baseline 2" "Penn Cove Base...
## $ Analyte       : chr   "SumPAHs" "SumPAHs" "SumPAHs" "SumPAHs" ...
## $ Units         : chr   "ng/g" "ng/g" "ng/g" "ng/g" ...
## $ PctSolids     : num    20 16.4 17.9 18.8 14.6 ...
## $ DryValue      : num    89.9 97.4 100.7 101.3 116.1 ...
## $ Comments      : chr    NA NA NA NA ...
```

```
str(indv)
```

```
## 'data.frame':    2886 obs. of  12 variables:
## $ Latitude      : num  47.5 47.5 47.5 47.5 47.5 ...
## $ Longitude     : num -122 -122 -122 -122 -122 ...
## $ LabSampleID   : chr   "119-5708" "119-5708" "119-5708" "119-5708" ...
## $ SampleID      : chr   "22SAM002-MTW01" "22SAM002-MTW01" "22SAM002-MTW01" "22SAM002-MTW01" ...
## $ SiteName      : chr   "Arroyo Beach" "Arroyo Beach" "Arroyo Beach" "Arroyo Beach" ...
## $ Analyte       : chr   "acenaphthene" "acenaphthylene" "anthracene" "benz[a]anthracene" ...
## $ Units         : chr   "ng/g" "ng/g" "ng/g" "ng/g" ...
## $ PctSolids     : num    16.7 16.7 16.7 16.7 16.7 ...
## $ DryValue      : num   -3.9 -3.9 -3.9 13.2 -3 ...
## $ Qualifier     : chr    "U" "U" "U" "D" ...
## $ LabMethodConcat: chr   "GC/MS_ASE_MeCl2" "GC/MS_ASE_MeCl2" "GC/MS_ASE_MeCl2" "GC/MS_ASE_MeCl2" ...
## $ Comments      : chr   "dNPH Surrogate recovery below minimum QA value (60%)" "dNPH Surrogate reco...
```

```
# Review basic data types and stats
```

```
summary(data)
```

```

##      latitude      longitude      site_name      site_number
## Min.      :47.05    Min.      :-123.5    Length:312    Min.      : 1.00
## 1st Qu.:47.33    1st Qu.: -122.7    Class :character    1st Qu.:21.00
## Median :47.61    Median : -122.6    Mode  :character    Median :40.00
## Mean      :47.71    Mean      :-122.6                Mean      :39.66
## 3rd Qu.:48.02    3rd Qu.: -122.4                3rd Qu.:59.00
## Max.      :48.82    Max.      :-122.2                Max.      :77.00
##      sample      p450      SOD      weight_initial
## Min.      : 1.00    Min.      : 0      Min.      : -0.636    Length:312
## 1st Qu.: 78.75    1st Qu.: 2309270    1st Qu.: 1.201    Class :character
## Median :156.50    Median : 3746310    Median : 5.730    Mode  :character
## Mean      :156.50    Mean      : 4430731    Mean      : 10.345
## 3rd Qu.:234.25    3rd Qu.: 5729620    3rd Qu.: 13.752
## Max.      :312.00    Max.      :52717198    Max.      :133.268
##      length      width      height      weight_final
## Length:312      Length:312      Length:312      Min.      : 2.484
## Class :character    Class :character    Class :character    1st Qu.: 3.801
## Mode  :character    Mode  :character    Mode  :character    Median : 4.417
##                                     Mean      : 4.656
##                                     3rd Qu.: 5.003
##                                     Max.      :20.625
## weight_change      condition_factor      avg_thickness      economic_index
## Length:312      Length:312      Min.      :0.3550    Length:312
## Class :character    Class :character    1st Qu.:0.6800    Class :character
## Mode  :character    Mode  :character    Median :0.7975    Mode  :character
##                                     Mean      :0.7835
##                                     3rd Qu.:0.8762
##                                     Max.      :1.2600

```

summary(pah)

```

##      latitude      longitude      LabSampleID      SampleID
## Min.      :47.05    Min.      :-123.5    Length:390      Length:390
## 1st Qu.:47.34    1st Qu.: -122.7    Class :character    Class :character
## Median :47.62    Median : -122.6    Mode  :character    Mode  :character
## Mean      :47.74    Mean      :-122.6
## 3rd Qu.:48.05    3rd Qu.: -122.4
## Max.      :48.99    Max.      :-122.2
##      SiteName      Analyte      Units      PctSolids
## Length:390      Length:390      Length:390      Min.      : 7.726
## Class :character    Class :character    Class :character    1st Qu.:15.149
## Mode  :character    Mode  :character    Mode  :character    Median :15.855
##                                     Mean      :16.037
##                                     3rd Qu.:16.953
##                                     Max.      :21.245
##      DryValue      Comments
## Min.      : 11.61    Length:390
## 1st Qu.: 119.14    Class :character
## Median : 201.58    Mode  :character
## Mean      : 659.37
## 3rd Qu.: 409.00
## Max.      :15313.22

```

```
summary(indv)
```

```
##      Latitude      Longitude      LabSampleID      SampleID
## Min.      :47.05    Min.      :-123.5    Length:2886    Length:2886
## 1st Qu.:47.34    1st Qu.: -122.7    Class :character    Class :character
## Median :47.62    Median :-122.6    Mode  :character    Mode  :character
## Mean   :47.74    Mean   :-122.6
## 3rd Qu.:48.05    3rd Qu.: -122.4
## Max.   :48.99    Max.   :-122.2
##      SiteName      Analyte      Units      PctSolids
## Length:2886      Length:2886      Length:2886      Min.      : 7.726
## Class :character    Class :character    Class :character    1st Qu.:15.149
## Mode  :character    Mode  :character    Mode  :character    Median :15.855
##                                     Mean   :16.037
##                                     3rd Qu.:16.953
##                                     Max.   :21.245
##      DryValue      Qualifier      LabMethodConcat      Comments
## Min.      : -12.502    Length:2886      Length:2886      Length:2886
## 1st Qu.:  -3.491    Class :character    Class :character    Class :character
## Median :   4.481    Mode  :character    Mode  :character    Mode  :character
## Mean   :   16.329
## 3rd Qu.:   13.843
## Max.   :  1776.333
```

```
# Data contains 0's and must be adjusted in this order to preserve all usable data.
```

```
#sod
```

```
#replace any SOD values at or below 0 with half of the lower detection limit of .005 (.005*.5). Lower d
```

```
data$SOD[data$SOD <= 0] <- 0.0025
```

```
#p450
```

```
#remove any p450 values that are 0 - those are true 0's not non-detectable. I am replacing with na so I
```

```
data$p450[data$p450 <= 0] <- NA
```

Explore

These are basic statistical tests to explore the current data post cleaning.

```
#Mean, median, sd, and variance
```

```
#stats p450
```

```
mean_p450 <- mean(data$p450, na.rm = TRUE)
```

```
median_p450 <- median(data$p450, na.rm = TRUE)
```

```
sd_p450 <- sd(data$p450, na.rm = TRUE)
```

```
var_p450 <- var(data$p450, na.rm = TRUE) #just to see, using sd
```

```
#make it a list
```

```
stats_p450 <- list(mean = mean_p450, median = median_p450, sd = sd_p450, variance = var_p450)
```

```
# Print the results
```

```
print(stats_p450)
```

```
## $mean
```

```
## [1] 4547329
```

```
##
## $median
## [1] 3873418
##
## $sd
## [1] 4027626
##
## $variance
## [1] 1.622177e+13
#Mean, median, sd, and variance

#stats sod
mean_SOD <- mean(data$SOD, na.rm = TRUE)
median_SOD <- median(data$SOD, na.rm = TRUE)
sd_SOD <- sd(data$SOD, na.rm = TRUE)
var_SOD <- var(data$SOD, na.rm = TRUE) #just to see, using sd

stats_sod <- list(mean = mean_SOD, median = median_SOD, sd = sd_SOD, variance = var_SOD)

print(stats_sod)
```

```
## $mean
## [1] 10.34759
##
## $median
## [1] 5.73
##
## $sd
## [1] 15.66503
##
## $variance
## [1] 245.3932
```

```
#Quartiles

#p450
quartiles_p450 <- quantile(data$p450, probs = c(0.25, 0.5, 0.75), na.rm = TRUE)
print(quartiles_p450)
```

```
##      25%      50%      75%
## 2413951 3873418 5787570
```

```
#Quartiles

#SOD
quartiles_SOD <- quantile(data$SOD, probs = c(0.25, 0.5, 0.75), na.rm = TRUE)
print(quartiles_SOD)
```

```
##      25%      50%      75%
##  1.2010  5.7300 13.7525
```

#Reduction of dataset to the average of biomarker values by site. Individual value analyses were performed

```
library(dplyr)
```

#simplifying the dataframe for joining with next steps

```

averaged_data <- data %>%
  group_by(site_number, latitude, longitude, site_name) %>%
  summarise(
    avg_p450 = mean(p450, na.rm = TRUE),
    avg_SOD = mean(SOD, na.rm = TRUE)
  ) %>%
  ungroup() # Remove grouping for the new dataframe

# View the new dataframe with averaged values
averaged_data

```

```

## # A tibble: 74 x 6
##   site_number latitude longitude site_name      avg_p450 avg_SOD
##   <int>      <dbl>    <dbl> <chr>      <dbl>    <dbl>
## 1         1      48.1    -123. Port Angeles Yacht Club 5751355    7.39
## 2         2      48.0    -123. Jamestown      3263515   24.5
## 3         3      48.2    -123. Penn Cove Reference 2427656.  23.9
## 4         7      48.3    -123. North Camano    12290521   0.752
## 5         8      48.0    -123. Chimacum Creek delta 2641574.   2.19
## 6         9      48.0    -123. S of Skunk Island  3556923.  11.3
## 7        10      48.0    -123. Oak Bay County Park 2335145   19.8
## 8        11      48.0    -123. Maristone Island  4772561.   5.68
## 9        12      48.1    -123. Discovery Bay    4029898.   8.74
## 10       13      47.5    -122. Arroyo Beach     4480860.   8.83
## # i 64 more rows

```

Outliers

```

# Outliers

# Detect outliers and plot them. Averaging the values reduced the SOD outliers from approximately 9% to
library(ggplot2)
detect_outliers_mad <- function(averaged_data, accuracy = 0.99) {
  # Calculate z-score equivalent for the given accuracy
  z_threshold <- qnorm(accuracy + (1 - accuracy) / 2)

  # Initialize a list to store outlier indices for each numeric column
  outliers_list <- list()

  # Initialize a vector to keep track of rows with outliers
  rows_with_outliers <- rep(FALSE, nrow(averaged_data))

  # Loop through each column in the dataframe
  for (col_name in names(averaged_data)) {
    # Check if the column is numeric
    if (is.numeric(averaged_data[[col_name]])) {
      # Calculate MAD and median for the column
      mad_value <- median(abs(averaged_data[[col_name]] - median(averaged_data[[col_name]])))
      median_value <- median(averaged_data[[col_name]])

      # Calculate the deviation scores (using a modified z-score formula)
      deviation_scores <- 0.6745 * (averaged_data[[col_name]] - median_value) / mad_value
    }
  }
}

```

```

    # Identify indices of outliers
    outlier_indices <- which(abs(deviation_scores) > z_threshold)

    # Store the indices in the list
    outliers_list[[col_name]] <- outlier_indices

    # Update rows with outliers
    rows_with_outliers[outlier_indices] <- TRUE
  }
}

# Return the list of outliers and rows with outliers
list(outliers_list = outliers_list, rows_with_outliers = rows_with_outliers)
}

outliers_info <- detect_outliers_mad(averaged_data)

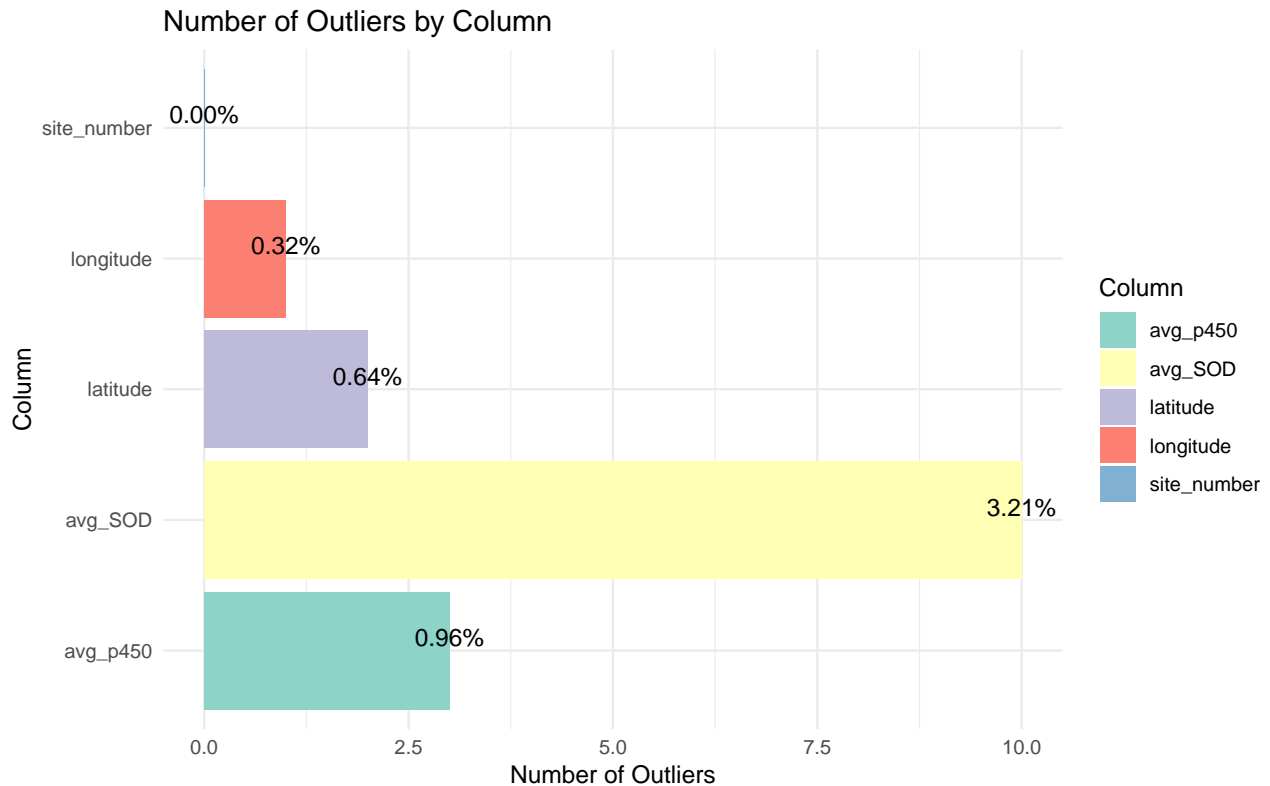
# Convert the list of outliers to a named vector of counts
num_outliers_each_col <- sapply(outliers_info$outliers_list, length)
num_rows_with_outliers <- sum(outliers_info$rows_with_outliers)

# Check if there are any outliers
if (all(num_outliers_each_col == 0)) {
  print("There are no outliers in any columns.")
} else {
  # Create a data frame for plotting
  outliers_data_df <- data.frame(
    Column = names(num_outliers_each_col),
    Outliers = as.integer(num_outliers_each_col),
    OutlierPercentage = (as.integer(num_outliers_each_col) / nrow(data)) * 100
  )

  # Plot the number of outliers for all columns
  outlier_plot <- ggplot(outliers_data_df, aes(x = Column, y = Outliers, fill = Column)) +
    geom_bar(stat = "identity") +
    geom_text(aes(label = sprintf("%.2f%%", OutlierPercentage)), position = position_dodge(width = 0.9)) +
    coord_flip() +
    labs(title = "Number of Outliers by Column", x = "Column", y = "Number of Outliers") +
    scale_fill_brewer(palette = "Set3") +
    theme_minimal()

  print(outlier_plot)
}

```



```
#ggsave(plot= outlier_plot, filename="/Users/cmantegna/Documents/WDFWmussels/output/outliersavg.png", w
```

Histograms

```
#p450 Histogram

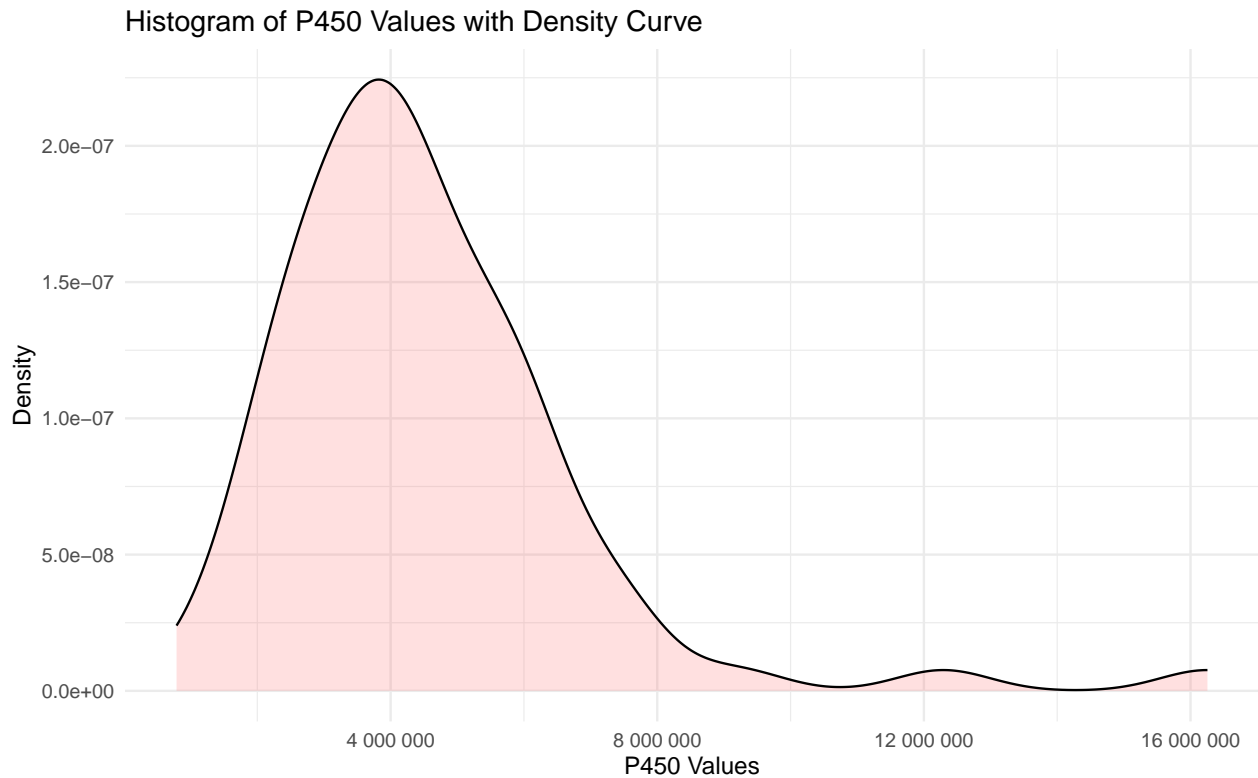
#basic histogram + basic density plot
#hist(averaged_data$p450)
#plot(density(averaged_data$p450), main="Density Plot", xlab="p450 Value")

#ggplot histogram with density curve
library(scales) # Make sure this package is loaded for label_number()

phist<- ggplot(averaged_data, aes(x = avg_p450)) +
  geom_histogram(aes(y = after_stat(density)), binwidth = diff(range(data$avg_p450))/30, colour = "black") +
  geom_density(alpha = .2, fill = "#FF6666") +
  labs(x = "P450 Values", y = "Density", title = "Histogram of P450 Values with Density Curve") +
  theme_minimal() +
  scale_x_continuous(labels = label_number()) # This line adjusts the x-axis labels

print(phist)
```

Interpretation - data appears not to be normally distributed, but could be transformed via log transformation to get closer if necessary. As a result, any tests for normality will be run in pairs (normal distribution and Poisson distribution).



```
#ggsave(plot=phist, filename="/Users/cmantegna/Documents/WDFWmussels/output/p450aughistogram.png", width=1000, height=500)
```

```
# SOD histogram
```

```
#basic histogram + basic density plot
```

```
#hist(averaged_data$SOD)
```

```
#plot(density(averaged_data$SOD), main="Density Plot", xlab="SOD Value")
```

```
#ggplot histogram with density curve
```

```
library(scales) # Make sure this package is loaded for label_number()
```

```
shist <- ggplot(averaged_data, aes(x = avg_SOD)) +
```

```
  geom_histogram(aes(y = after_stat(density)), binwidth = diff(range(data$avg_SOD))/30, colour = "black") +
```

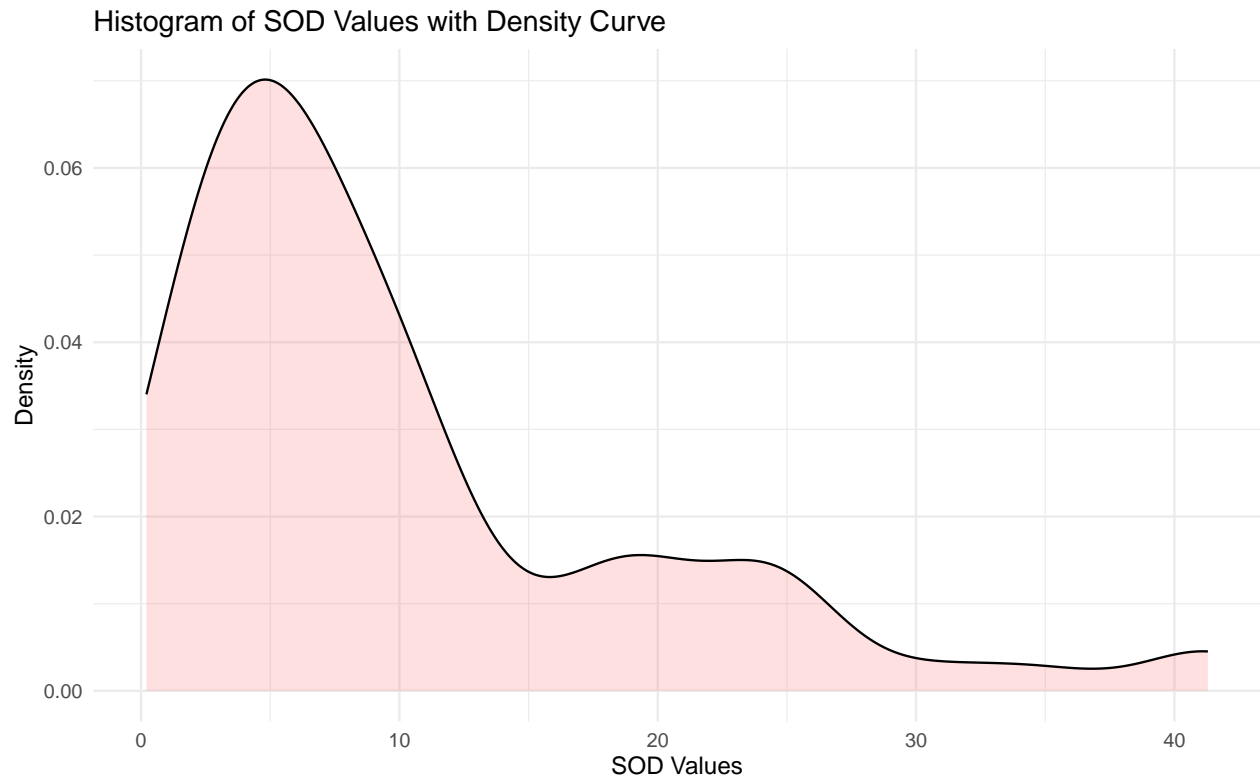
```
  geom_density(alpha = .2, fill = "#FF6666") +
```

```
  labs(x = "SOD Values", y = "Density", title = "Histogram of SOD Values with Density Curve") +
```

```
  theme_minimal() +
```

```
  scale_x_continuous(labels = label_number()) # This line adjusts the x-axis labels
```

```
print(shist)
```



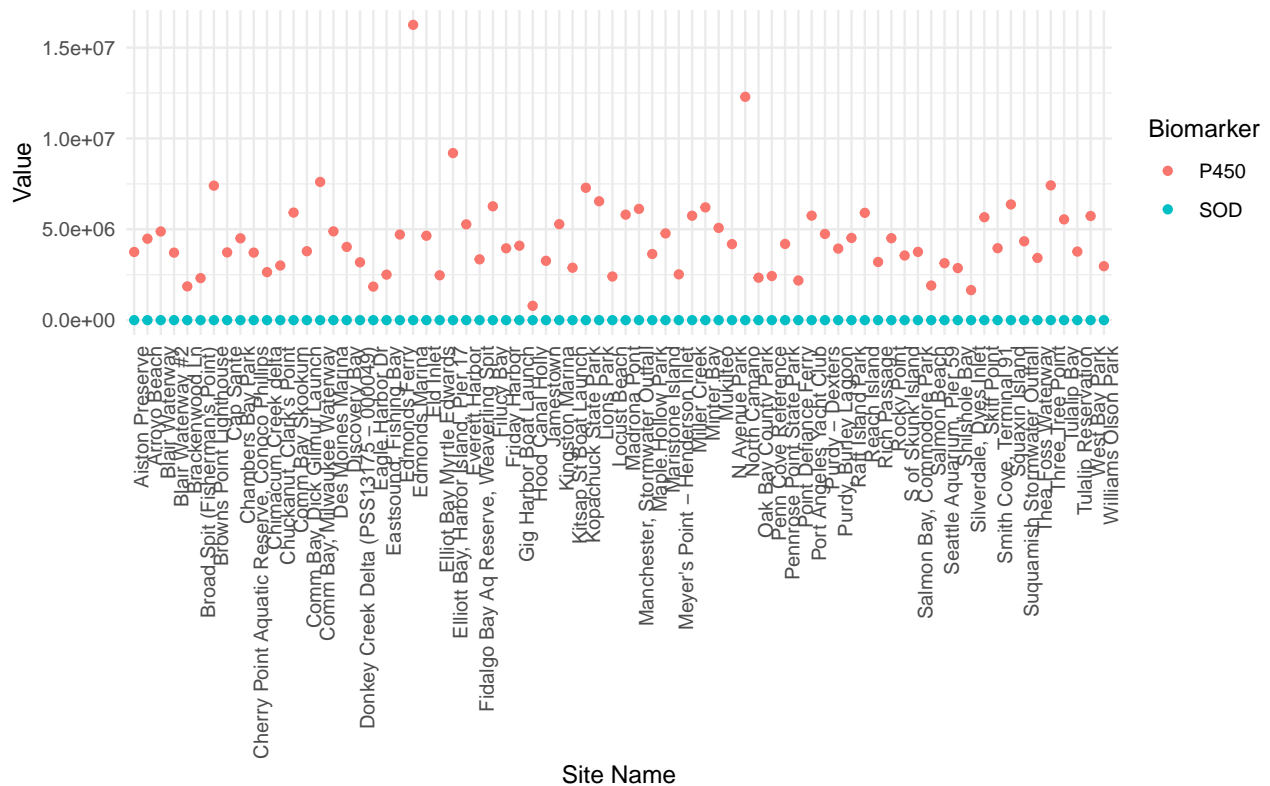
```
#ggsave(plot=shist, filename="/Users/cmantegna/Documents/WDFWmussels/output/SODaughistogram.png", width
```

Boxplots

```
# Plotting both biomarkers in a box plot
all<-plot<- ggplot(averaged_data) +
  geom_point(aes(x = site_name, y = avg_SOD, color = "SOD")) +
  geom_point(aes(x = site_name, y = avg_p450, color = "P450")) +
  labs(x = "Site Name", y = "Value", color = "Biomarker") +
  theme_minimal() +
  theme(axis.text.x = element_text(angle = 90, hjust = 1))

print(all)
```

Interpretation - two clear outliers exist (~2.7% of the 3.21% outliers) with a third outlier less obvious.



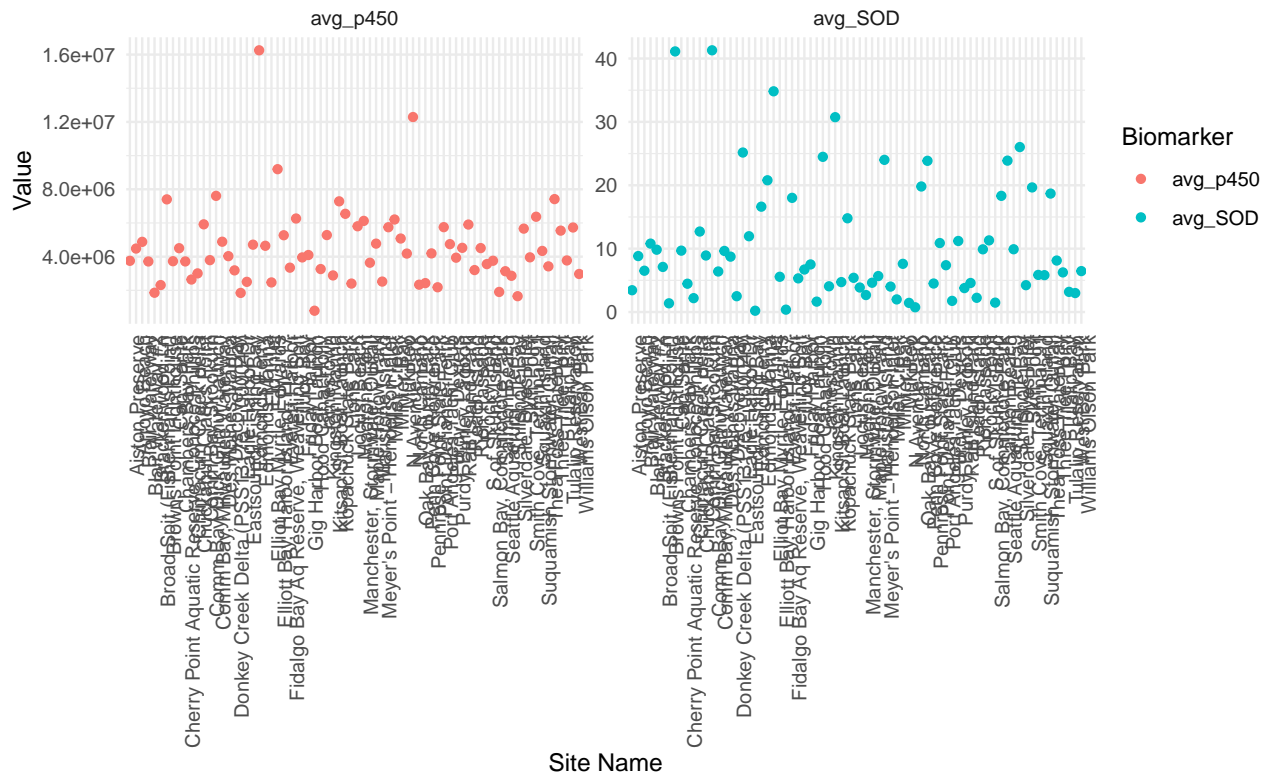
```
#ggsave(plot=all, filename="/Users/cmantegna/Documents/WDFWmussels/output/allavgBoxPlot.png", width=15,
# Individual boxplots for comparison since the scale for each biomarker is very different.

library(tidyr)

# Reshape
long_data <- pivot_longer(averaged_data, cols = c(avg_SOD, avg_p450), names_to = "Biomarker", values_to = "Value")

# Faceted plot with separate scales.
plotf<- ggplot(long_data, aes(x = site_name, y = Value)) +
  geom_point(aes(color = Biomarker)) +
  facet_wrap(~ Biomarker, scales = "free_y") +
  labs(x = "Site Name", y = "Value", color = "Biomarker") +
  theme_minimal() +
  theme(axis.text.x = element_text(angle = 90, hjust = 1))

print(plotf)
```



```
#ggsave(plot=plotf, filename="/Users/cmantegna/Documents/WDFWmussels/output/allavgBoxPlotFacetPanels.png")
```

```
# Plotting p450 values ranked from smallest to largest
```

```
#order the sites by value
```

```
data_ordered <- averaged_data[order(averaged_data$avg_p450),]
```

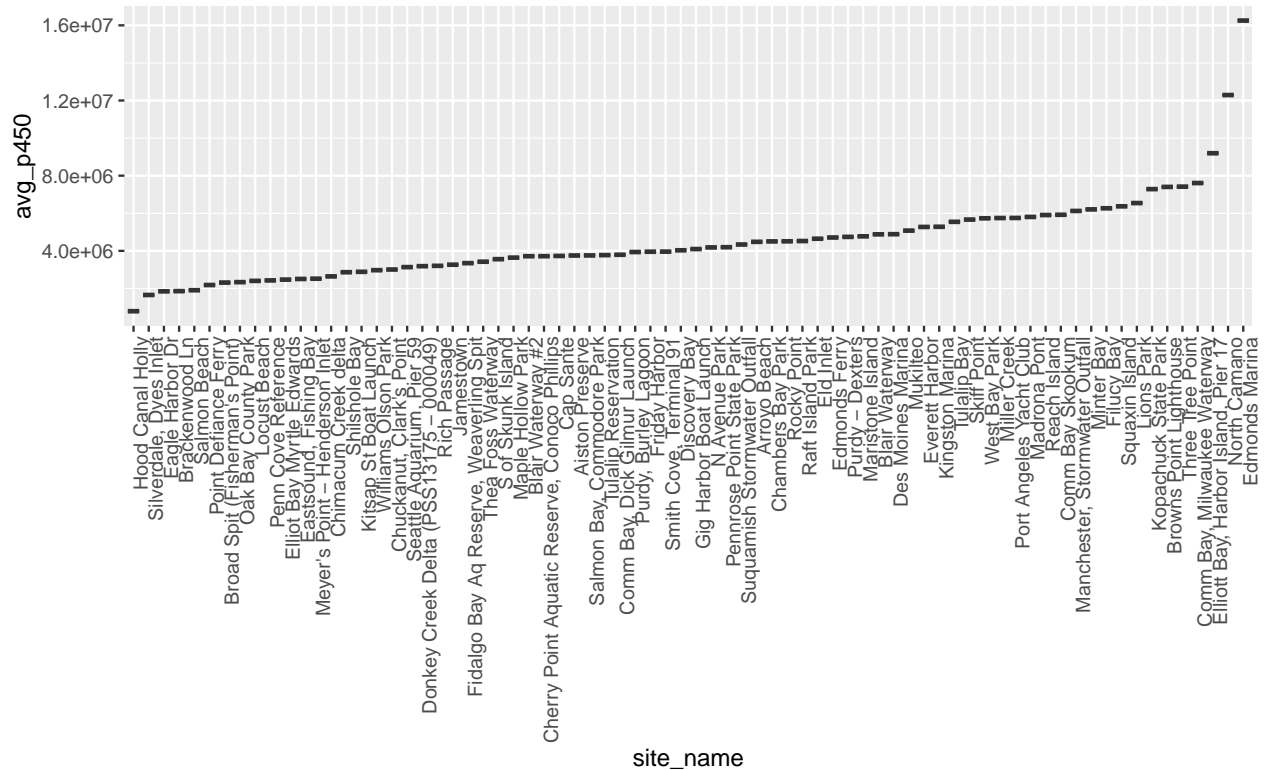
```
#create a factor with the ordered site names
```

```
data_ordered$site_name <- factor(data_ordered$site_name, levels = unique(data_ordered$site_name))
```

```
#plot with ordered site names
```

```
rankp<- ggplot(data_ordered, aes(x = site_name, y = avg_p450)) +  
  geom_boxplot() +  
  theme(axis.text.x = element_text(angle = 90, hjust = 1)) # Rotate x labels if needed
```

```
print(rankp)
```



```
#ggsave(plot=rankp, filename="/Users/cmantegna/Documents/WDFWmussels/output/avgp450ranked.png", width=1000, height=1000)
```

```
# Plotting SOD values ranked from smallest largest
```

```
#order the sites by value
```

```
data_ordered <- averaged_data[order(averaged_data$avg_SOD),]
```

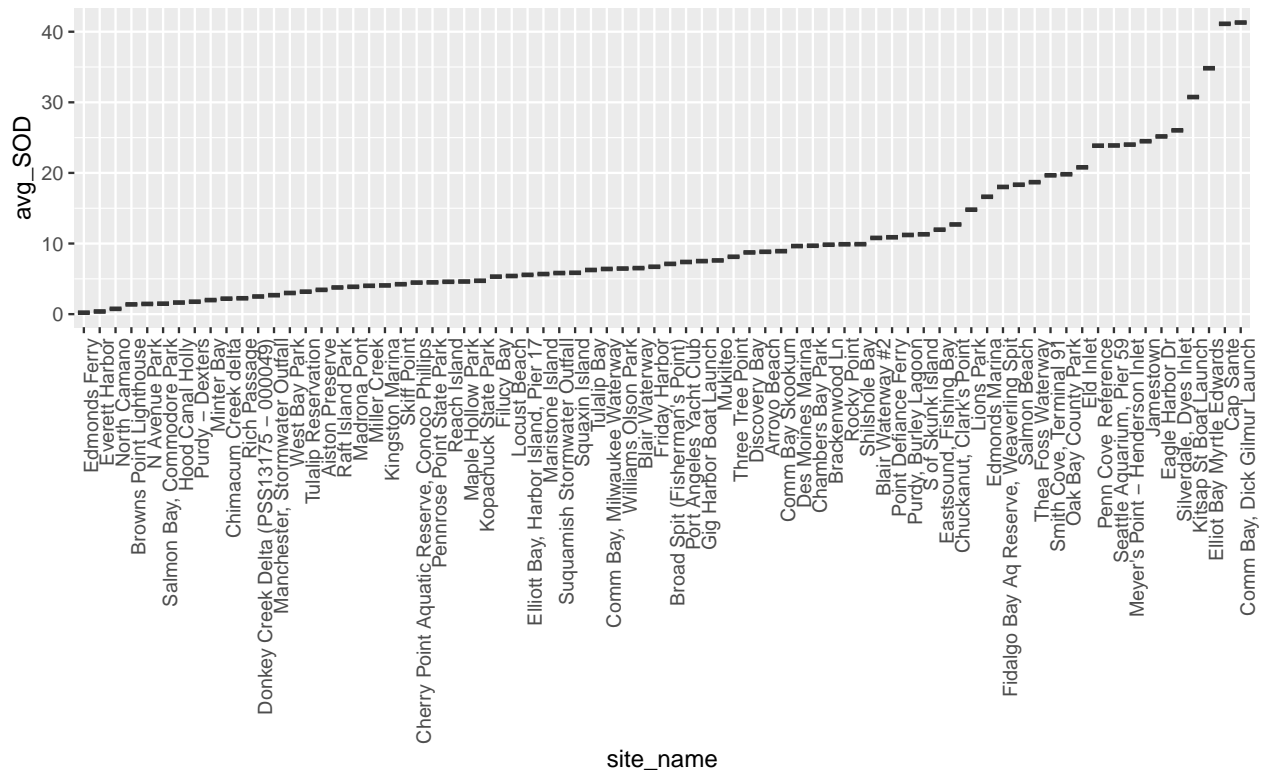
```
#create a factor with the ordered site names
```

```
data_ordered$site_name <- factor(data_ordered$site_name, levels = unique(data_ordered$site_name))
```

```
#plot with ordered site names
```

```
ranks<- ggplot(data_ordered, aes(x = site_name, y = avg_SOD)) +  
  geom_boxplot() +  
  theme(axis.text.x = element_text(angle = 90, hjust = 1)) # Rotate x labels if needed
```

```
print(ranks)
```



```
#ggsave(plot=ranks, filename="/Users/cmantegna/Documents/WDFWmussels/output/avgSODranked.png", width=15
```

Statistics

These are more descriptive statistics to test for normality and correlation.

```
library(tidyr)
library(tidyverse)
library(ggplot2)
library(vegan)
```

Shapiro- Wilkes

```
#Test for data normality
shapiro.test(averaged_data$avg_p450)
```

Interpretation - both biomarkers are close to a normal distribution ($W=1$) but are not normally distributed based on both W and the p -value.

```
##
## Shapiro-Wilk normality test
##
## data: averaged_data$avg_p450
## W = 0.82368, p-value = 5.781e-08
```

```
#Test for data normality
shapiro.test(averaged_data$avg_SOD)
```

```
##
## Shapiro-Wilk normality test
##
## data: averaged_data$avg_SOD
## W = 0.82966, p-value = 8.711e-08
```

Correlation, Pearson Correlation

```
# Correlation, Pearson Correlation

#add condition_factor back to the dataframe

#individual correlation test between the biomarkers

cor.test(averaged_data$avg_p450, averaged_data$avg_SOD)
```

Interpretation - the biomarkers show a statistically significant *weak* negative correlation. Where one biomarker increases, the other decreases.

```
##
## Pearson's product-moment correlation
##
## data: averaged_data$avg_p450 and averaged_data$avg_SOD
## t = -2.4138, df = 72, p-value = 0.01833
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.47256554 -0.04812135
## sample estimates:
## cor
## -0.2736115
```

Pearson Correlation Plot

```
library(corrplot)

cor.mtest <- function(mat, conf.level = 0.95){
  mat <- as.matrix(mat)
  n <- ncol(mat)
  p.mat <- matrix(NA, n, n)
  diag(p.mat) <- 0

  for(i in 1:(n-1)){
    for(j in (i+1):n){
      tmp <- cor.test(mat[,i], mat[,j], conf.level = conf.level)
      p.mat[i,j] <- tmp$p.value
      p.mat[j,i] <- tmp$p.value
    }
  }
  list(p = p.mat, conf.level = conf.level)
}

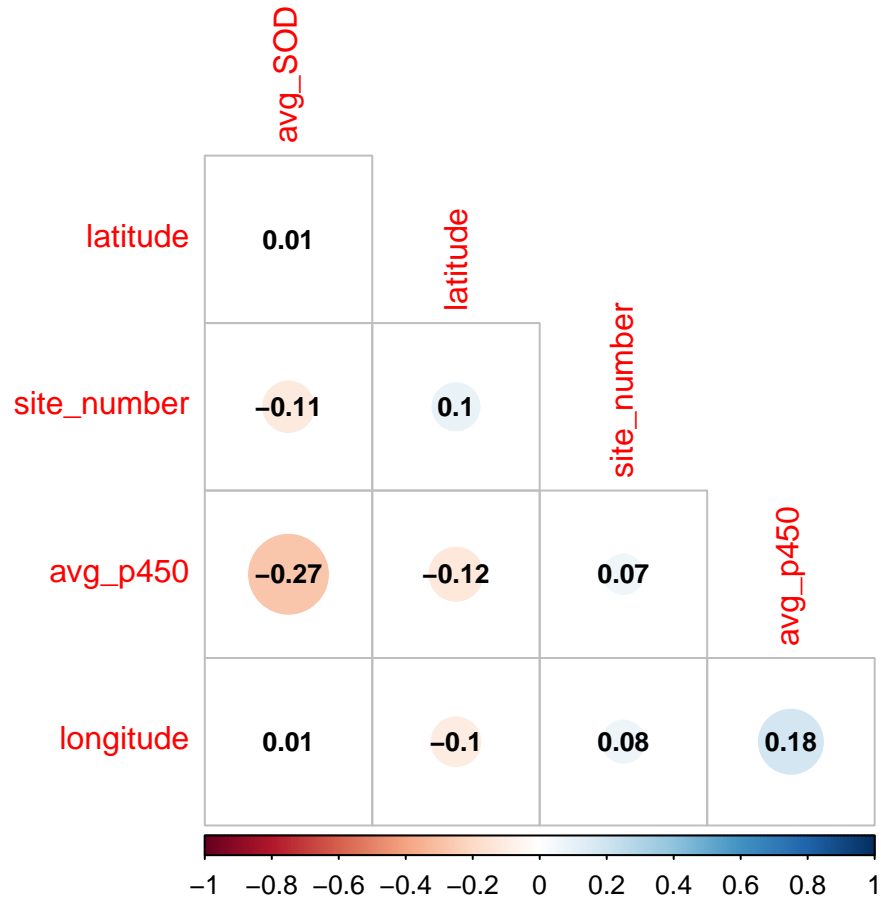
# Assuming 'mdata' and 'data' are defined and 'data' is used to subset 'mdata'
```

```

df2 <- averaged_data[sapply(averaged_data, is.numeric)] # Ensure 'mdata' is used here
df2 <- na.omit(df2)
M <- cor(df2)
testRes <- cor.mtest(df2, conf.level = 0.95)

# Visualization with corrplot
corrplot::corrplot(M,
  method = "circle", type = "lower", insig = "blank",
  addCoef.col = "black", number.cex = 0.8, order = "AOE", diag = FALSE
)

```



```

print(cor)

## function (x, y = NULL, use = "everything", method = c("pearson",
##   "kendall", "spearman"))
## {
##   na.method <- pmatch(use, c("all.obs", "complete.obs", "pairwise.complete.obs",
##     "everything", "na.or.complete"))
##   if (is.na(na.method))
##     stop("invalid 'use' argument")
##   method <- match.arg(method)
##   if (is.data.frame(y))
##     y <- as.matrix(y)
##   if (is.data.frame(x))
##     x <- as.matrix(x)

```



```

##   if (!is.matrix(x) && is.null(y))
##       stop("supply both 'x' and 'y' or a matrix-like 'x'")
##   if (!(is.numeric(x) || is.logical(x)))
##       stop("'x' must be numeric")
##   stopifnot(is.atomic(x))
##   if (!is.null(y)) {
##       if (!(is.numeric(y) || is.logical(y)))
##           stop("'y' must be numeric")
##       stopifnot(is.atomic(y))
##   }
##   Rank <- function(u) {
##       if (length(u) == 0L)
##           u
##       else if (is.matrix(u)) {
##           if (nrow(u) > 1L)
##               apply(u, 2L, rank, na.last = "keep")
##           else row(u)
##       }
##       else rank(u, na.last = "keep")
##   }
##   if (method == "pearson")
##       .Call(C_cor, x, y, na.method, FALSE)
##   else if (na.method %in% c(2L, 5L)) {
##       if (is.null(y)) {
##           .Call(C_cor, Rank(na.omit(x)), NULL, na.method, method ==
##               "kendall")
##       }
##       else {
##           nas <- attr(na.omit(cbind(x, y)), "na.action")
##           dropNA <- function(x, nas) {
##               if (length(nas)) {
##                   if (is.matrix(x))
##                       x[-nas, , drop = FALSE]
##                   else x[-nas]
##               }
##               else x
##           }
##           .Call(C_cor, Rank(dropNA(x, nas)), Rank(dropNA(y,
##               nas)), na.method, method == "kendall")
##       }
##   }
##   else if (na.method != 3L) {
##       x <- Rank(x)
##       if (!is.null(y))
##           y <- Rank(y)
##       .Call(C_cor, x, y, na.method, method == "kendall")
##   }
##   else {
##       if (is.null(y)) {
##           ncy <- ncol(x)
##           if (ncy == 0)
##               stop("'x' is empty")
##           r <- matrix(0, nrow = ncy, ncol = ncy)
##           for (i in seq_len(ncy)) {

```

```

##           for (j in seq_len(i)) {
##             x2 <- x[, i]
##             y2 <- x[, j]
##             ok <- complete.cases(x2, y2)
##             x2 <- rank(x2[ok])
##             y2 <- rank(y2[ok])
##             r[i, j] <- if (any(ok))
##               .Call(C_cor, x2, y2, 1L, method == "kendall")
##             else NA
##           }
##         }
##       r <- r + t(r) - diag(diag(r))
##       rownames(r) <- colnames(x)
##       colnames(r) <- colnames(x)
##     }
##   }
##   else {
##     if (length(x) == 0L || length(y) == 0L)
##       stop("both 'x' and 'y' must be non-empty")
##     matrix_result <- is.matrix(x) || is.matrix(y)
##     if (!is.matrix(x))
##       x <- matrix(x, ncol = 1L)
##     if (!is.matrix(y))
##       y <- matrix(y, ncol = 1L)
##     ncx <- ncol(x)
##     ncy <- ncol(y)
##     r <- matrix(0, nrow = ncx, ncol = ncy)
##     for (i in seq_len(ncx)) {
##       for (j in seq_len(ncy)) {
##         x2 <- x[, i]
##         y2 <- y[, j]
##         ok <- complete.cases(x2, y2)
##         x2 <- rank(x2[ok])
##         y2 <- rank(y2[ok])
##         r[i, j] <- if (any(ok))
##           .Call(C_cor, x2, y2, 1L, method == "kendall")
##         else NA
##       }
##     }
##     rownames(r) <- colnames(x)
##     colnames(r) <- colnames(y)
##     if (matrix_result)
##       r
##     else drop(r)
##   }
## }
## }
## <bytecode: 0x136d61eb0>
## <environment: namespace:stats>

```

```
#ggsave(plot=cor, filename="/Users/cmantegna/Documents/WDFWmussels/output/avgpearson.png", width=15, height=15)
```

PCA Plot

```

# PCA Plot with biomarkers
#install.packages("FactoMineR")
#install.packages("factoextra")
library('FactoMineR')
library("factoextra")

# Remove NAs from the dataset
df_clean <- na.omit(averaged_data)

# Selecting the relevant variables for PCA
pca_data <- df_clean[, c("avg_SOD", "avg_p450")]

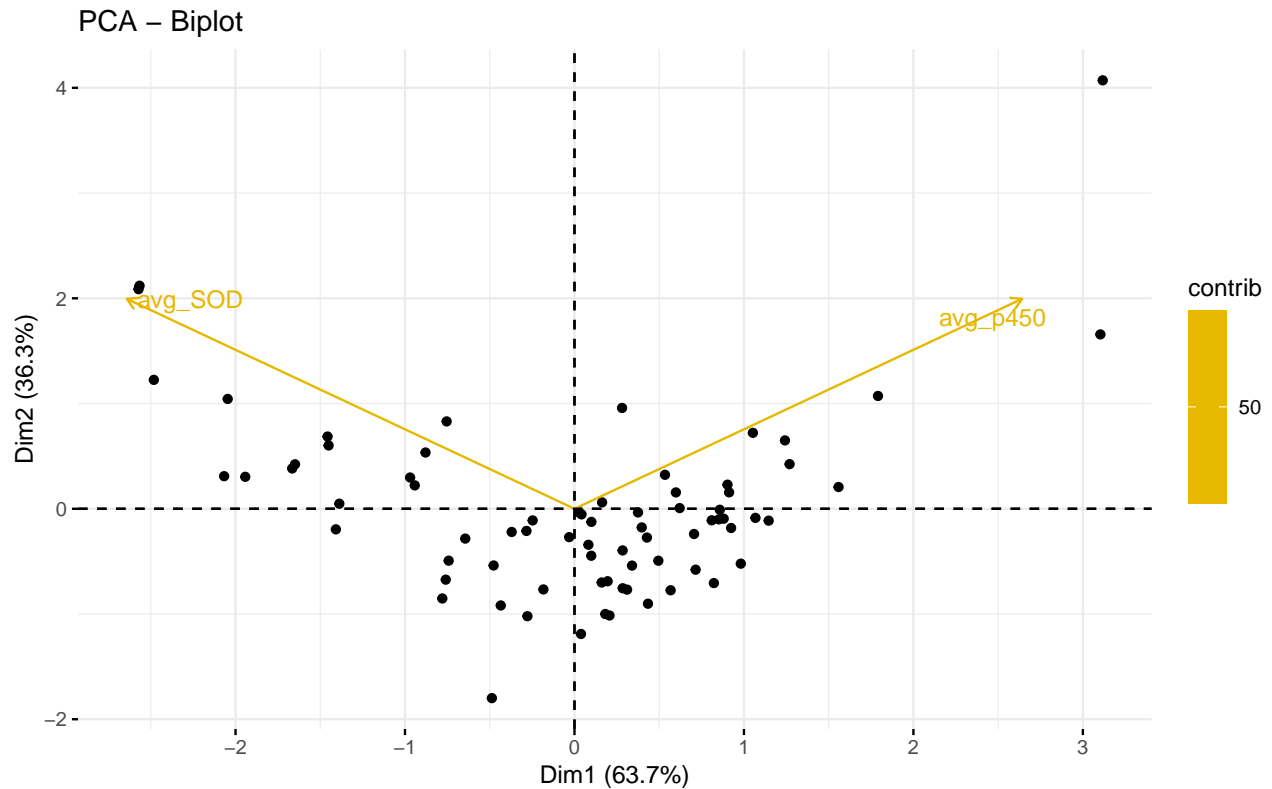
# Performing PCA
pca_res <- PCA(pca_data, scale.unit = TRUE, graph = FALSE)

# Plotting the PCA
pcaplot<- fviz_pca_biplot(pca_res, label = "var", col.var = "contrib",
                          gradient.cols = c("#00AFBB", "#E7B800", "#FC4E07"),
                          repel = TRUE) # Avoid text overlapping (slow if many points)

print(pcaplot)

```

Interpretation - This plot has to be interpreted in space, each axis represents a different variance and the attached percentage to each axis is the total variance captured by that axis; the x-axis is the max variation in the data and should have the higher percentage. The y-axis is the second most variation. The points are observations, more distance mean more difference. The plot is not particularly helpful.



```
#ggsave(plot=pcaplot, filename="/Users/cmantegna/Documents/WDFWmussels/output/pca.png", width=15, height=10)
```

K-means cluster/ relationship test

```
#fixing data for kmeans
```

```
sum(is.na(averaged_data$avg_p450)) # Checks for NA values in p450
```

Interpretation- there are three clusters that vary in size and that is an indicator of a significant number of outliers, see above for the code for the plot of the outliers. There are significant outliers for SOD, this may be rendering this test unhelpful. “The means of each cluster give you an idea of the centroid values around which the data points in each cluster are aggregated.”

```
## [1] 0
```

```
sum(is.nan(averaged_data$avg_p450)) # Checks for NaN values in p450
```

```
## [1] 0
```

```
sum(is.infinite(averaged_data$avg_p450)) # Checks for Inf values in p450
```

```
## [1] 0
```

```
sum(is.na(averaged_data$avg_SOD))
```

```
## [1] 0
```

```
sum(is.nan(averaged_data$avg_SOD))
```

```
## [1] 0
```

```

sum(is.infinite(averaged_data$avg_SOD))

## [1] 0

#sum(is.na(mdata$condition_factor))
#sum(is.nan(mdata$condition_factor))
#sum(is.infinite(mdata$condition_factor))

averaged_data$avg_p450 <- as.numeric(averaged_data$avg_p450)
averaged_data$avg_SOD <- as.numeric(averaged_data$avg_SOD)
#mdata$condition_factor <- as.numeric(mdata$condition_factor)

# Remove rows with NA or NaN values in specified columns
clean_data <- averaged_data[complete.cases(averaged_data[, c("avg_p450", "avg_SOD")]), ]

# Ensure all data is numeric for the Inf check to make sense
clean_data <- transform(clean_data,
                        avg_p450 = as.numeric(avg_p450),
                        avg_SOD = as.numeric(avg_SOD))

# Now check for and handle Inf values
clean_data <- clean_data[!is.infinite(clean_data$avg_p450) & !is.infinite(clean_data$avg_SOD), ]

kmeans_result <- kmeans(clean_data[, c("avg_p450", "avg_SOD")], centers = 3)

print(kmeans_result)

## K-means clustering with 3 clusters of sizes 2, 41, 31
##
## Cluster means:
##   avg_p450   avg_SOD
## 1 14272130   8.688250
## 2  3103566  13.610124
## 3  5766556   6.062117
##
## Clustering vector:
##  1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26
##  3  2  2  1  2  2  2  3  2  3  3  2  2  2  2  2  3  3  3  2  3  2  2  3  3  2
## 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52
##  2  2  2  3  2  2  3  3  3  3  2  3  2  2  2  3  2  2  2  3  2  2  3  3  3  3
## 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74
##  3  3  2  3  2  2  2  2  2  3  3  3  1  3  2  2  3  3  2  2  2  2
##
## Within cluster sum of squares by cluster:
## [1] 7.853548e+12 2.798817e+13 3.779290e+13
## (between_SS / total_SS =  81.3 %)
##
## Available components:
##
## [1] "cluster"      "centers"      "totss"        "withinss"     "tot.withinss"
## [6] "betweenss"    "size"         "iter"         "ifault"

```

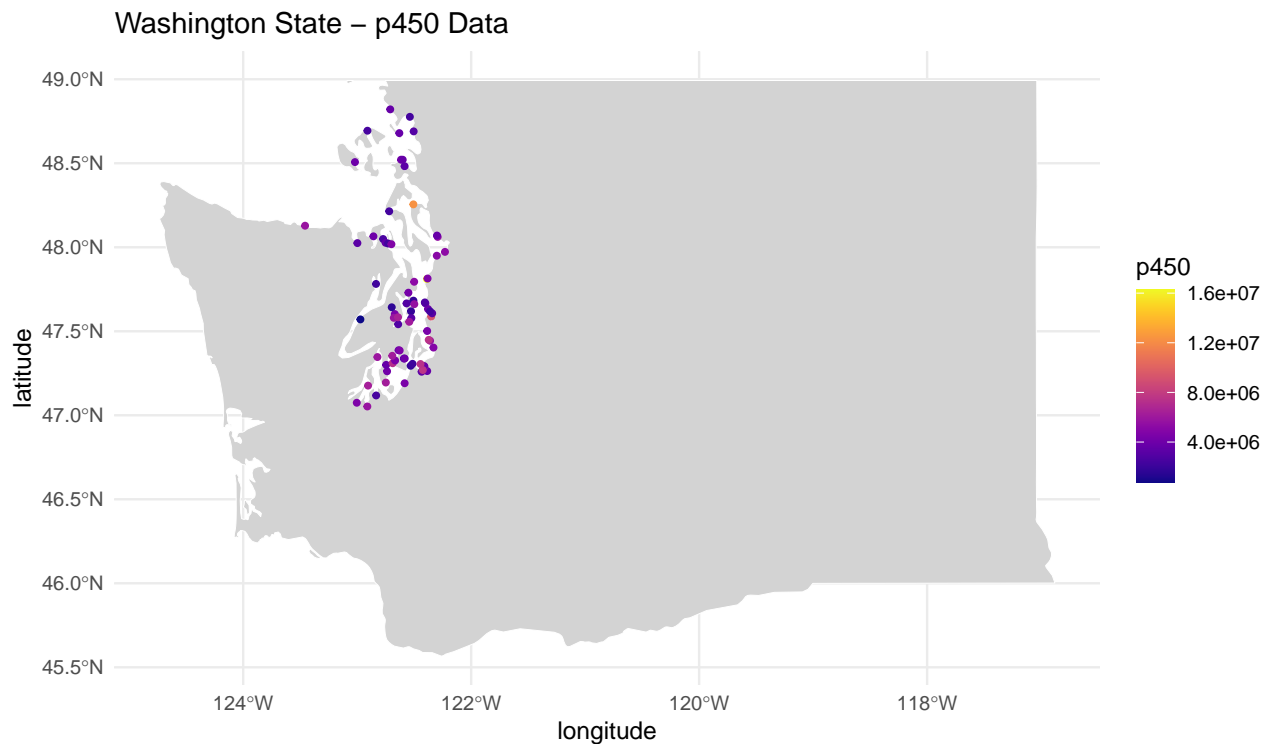
Mapping

```
library(tidyr)
#library(tidyverse)
library(ggplot2)
library(vegan)
library(sf)
library(viridis)
library(rnaturalearth)
library(rnaturalearthdata)
```

```
world <- ne_states(country = "united states of america", returnclass = "sf")
washington_map <- world[world$name == "Washington", ]
```

```
# p450 map
pmap<- ggplot() +
  geom_sf(data = washington_map, fill = "lightgrey", color = "white") +
  geom_point(data = averaged_data, aes(x = longitude, y = latitude, color = avg_p450), size = 1) +
  scale_color_viridis(option = "C", name = "p450") +
  theme_minimal() +
  labs(title = "Washington State - p450 Data")

print(pmap)
```



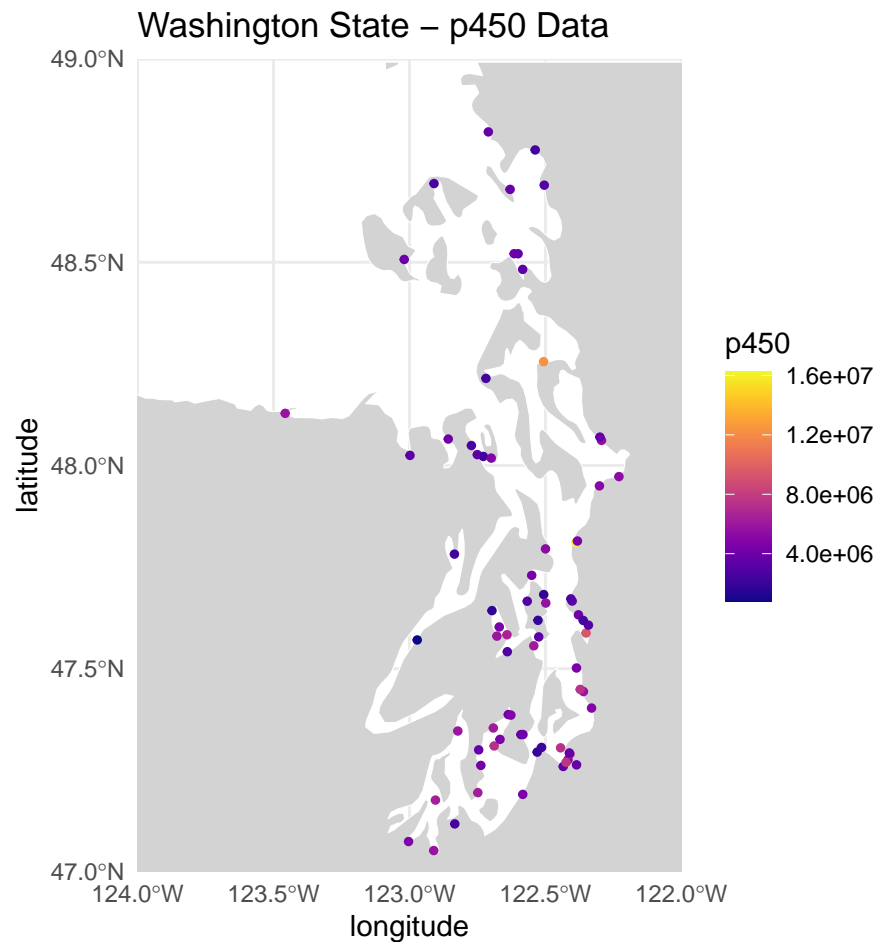
```
#ggsave(plot=pmap, filename="/Users/cmantegna/Documents/WDFWmussels/output/avgp450map.png", width=15, h
```

```
#zoom into puget sound region
xlim <- c(-124, -122) # longitude bounds
ylim <- c(47, 49) # latitude bounds

pmap<- ggplot() +
```

```
geom_sf(data = washington_map, fill = "lightgrey", color = "white") +
geom_point(data = averaged_data, aes(x = longitude, y = latitude, color = avg_p450), size = 1) +
scale_color_viridis(option = "C", name = "p450") +
coord_sf(xlim = xlim, ylim = ylim, expand = FALSE)+
theme_minimal() +
labs(title = "Washington State - p450 Data")
```

```
print(pmap)
```

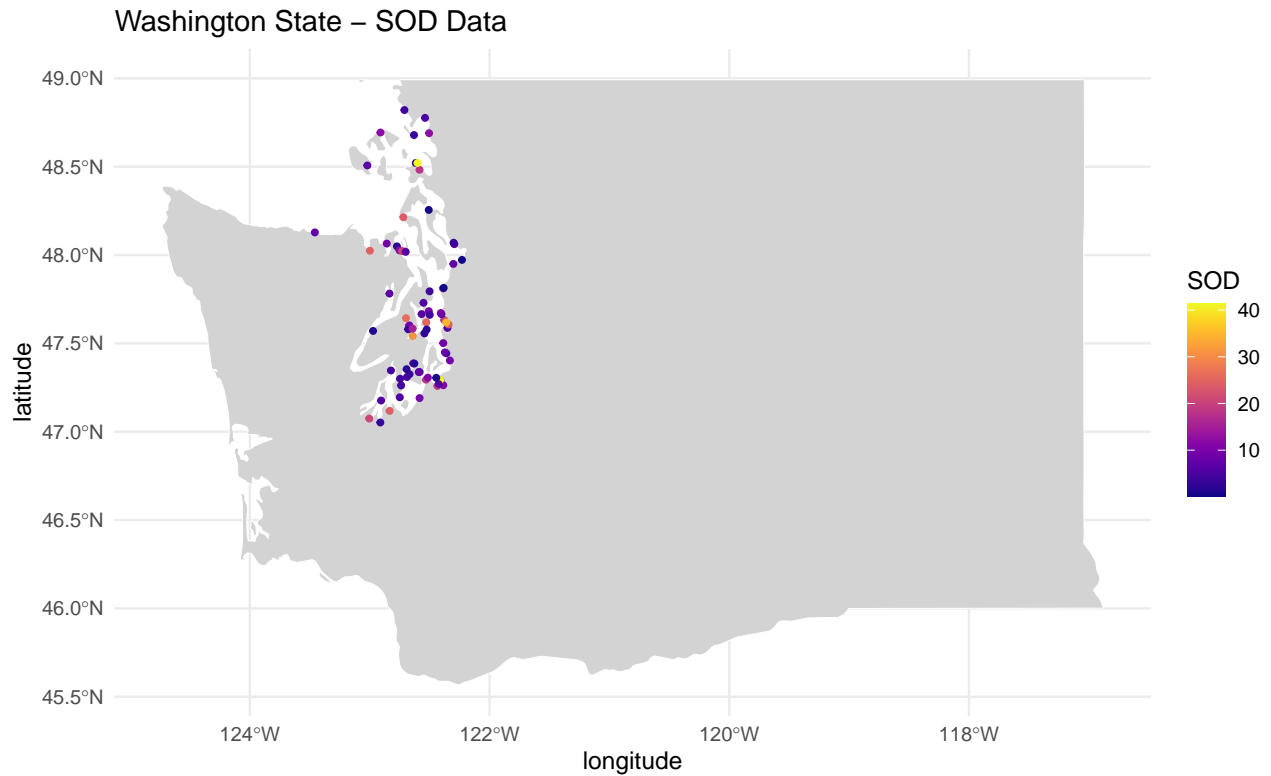


```
#ggsave(plot=pmap, filename="/Users/cmantegna/Documents/WDFWmussels/output/avgp450psmap.png", width=15,
```

```
#SOD map
```

```
smap<- ggplot() +
geom_sf(data = washington_map, fill = "lightgrey", color = "white") +
geom_point(data = averaged_data, aes(x = longitude, y = latitude, color = avg_SOD), size = 1) +
scale_color_viridis(option = "C", name = "SOD") +
theme_minimal() +
labs(title = "Washington State - SOD Data")
```

```
print(smap)
```



```
#ggsave(plot=smap, filename="/Users/cmantegna/Documents/WDFWmussels/output/avgsodmap.png", width=15, height=10)
```

```
#zoom into puget sound region & note the legend, lighter colors are higher values
```

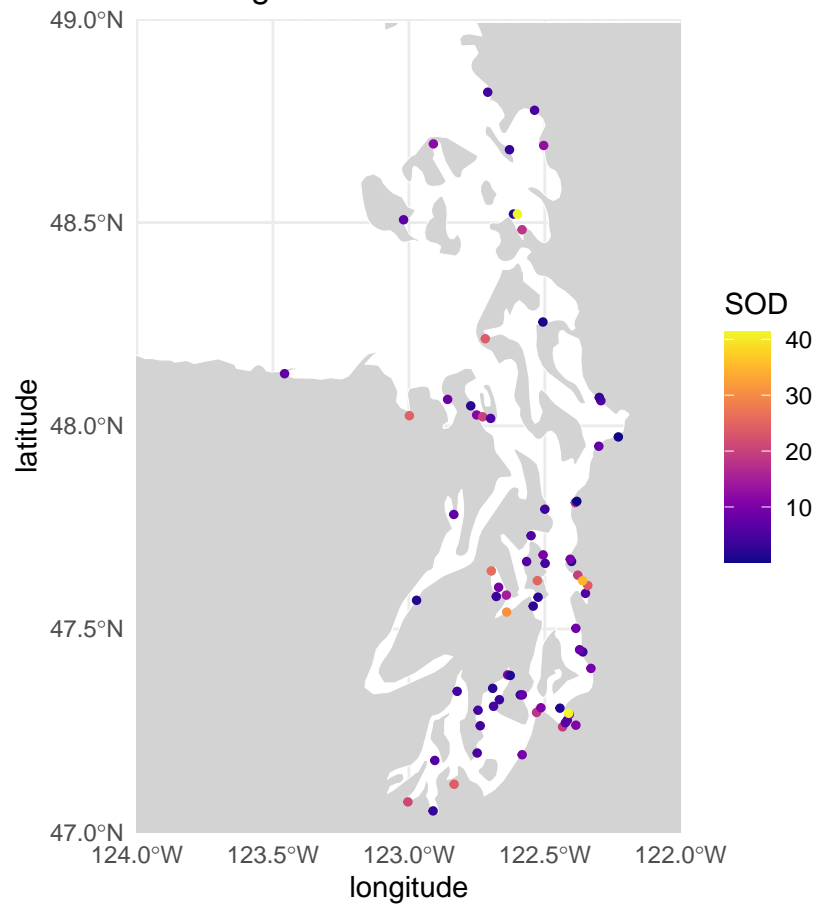
```
xlim <- c(-124, -122) # longitude bounds
```

```
ylim <- c(47, 49) # latitude bounds
```

```
pmap<- ggplot() +
  geom_sf(data = washington_map, fill = "lightgrey", color = "white") +
  geom_point(data = averaged_data, aes(x = longitude, y = latitude, color = avg_SOD), size = 1) +
  scale_color_viridis(option = "C", name = "SOD") +
  coord_sf(xlim = xlim, ylim = ylim, expand = FALSE)+
  theme_minimal() +
  labs(title = "Washington State - SOD Data")

print(pmap)
```


Washington State – SOD Data

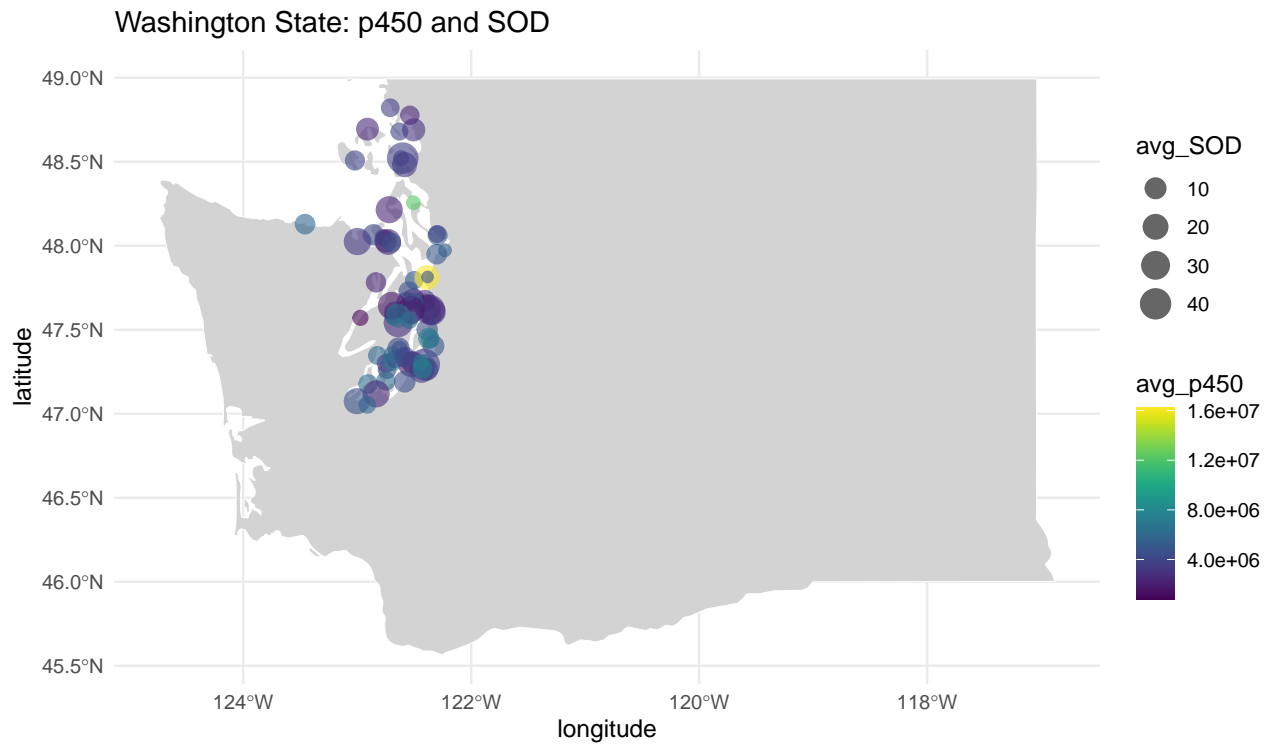


```
#ggsave(plot=pmap, filename="/Users/cmantegna/Documents/WDFWmussels/output/avgSODpsmap.png", width=15,
```

```
#mapping both
```

```
# Assuming washington_map is your sf object for Washington State
```

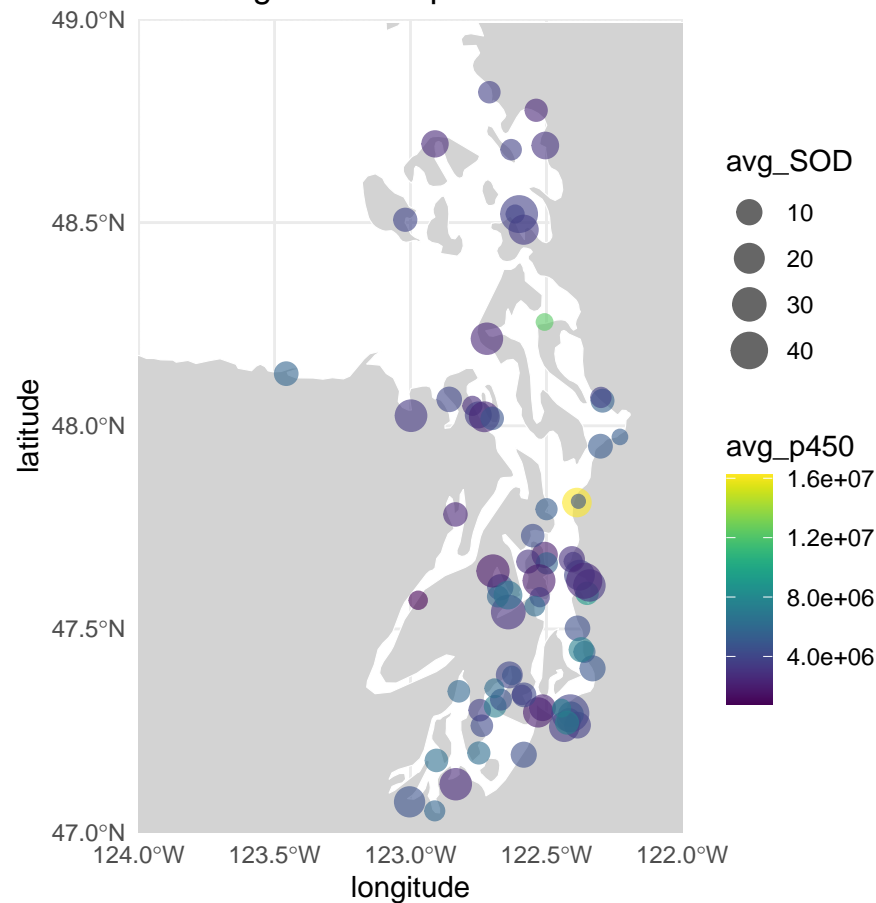
```
ggplot(data = washington_map) +
  geom_sf(fill = "lightgrey", color = "white") +
  geom_point(data = averaged_data, aes(x = longitude, y = latitude, color = avg_p450, size = avg_SOD),
    scale_color_viridis(name = "avg_p450", option = "D") +
    scale_size_continuous(name = "avg_SOD", range = c(2, 6)) +
    theme_minimal() +
    labs(title = "Washington State: p450 and SOD")
```



```
#still not a helpful visualization
xlim <- c(-124, -122) # longitude bounds
ylim <- c(47, 49) # latitude bounds

# Assuming washington_map is your sf object for Washington State
ggplot(data = washington_map) +
  geom_sf(fill = "lightgrey", color = "white") +
  geom_point(data = averaged_data, aes(x = longitude, y = latitude, color = avg_p450, size = avg_SOD),
    scale_color_viridis(name = "avg_p450", option = "D") +
    scale_size_continuous(name = "avg_SOD", range = c(2, 6)) +
    coord_sf(xlim = xlim, ylim = ylim, expand = FALSE)+
    theme_minimal() +
    labs(title = "Washington State: p450 and SOD")
```

Washington State: p450 and SOD



Spatial Analysis

Note this workflow is used to determine if there are spatial data patterns that wouldn't stand out in the exploratory or relational statistics.

```
# Data prep for geospatial analysis

#install.packages("spatstat")
library(spatstat)

# Create the kind of data frame that works in spatstat package
sites_pp <- ppp(x = averaged_data$longitude, y = averaged_data$latitude,
               window = owin(xrange = range(averaged_data$longitude),
                             yrange = range(averaged_data$latitude)))

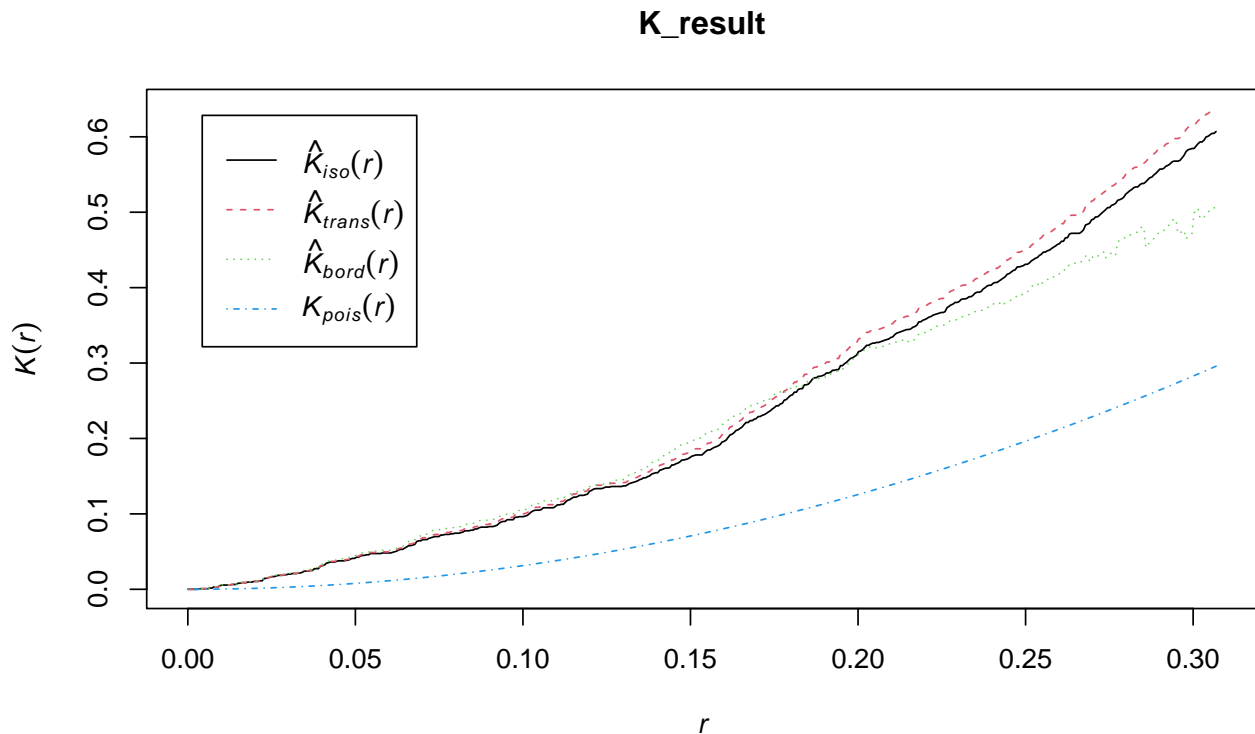
#Add biomarker layer to the geographical data
sites_pp$marks <- data.frame(p450 = averaged_data$avg_p450,
                             SOD = averaged_data$avg_SOD)
```

K test, 1 of 2.

```
# average values result's mirror the results returned in the full biomarker run. see 04-spatial for int
```

```
K_result <- Kest(sites_pp)
print(plot(K_result))
```

Interpretation- the clustering of the black, red, and green lines (isotropic, and two transformations) lie significantly above the blue line, the Poisson distribution line. This means that the biomarker data is more clustered than random. The proximity of the black, red and green lines show agreement across the isotropic and transformation analyses. This result is in agreement with the Shapiro- Wilkes tests for normality.



```
##      lty col  key      label
## iso      1  1   iso  italic(hat(K)[iso](r))
## trans    2  2 trans italic(hat(K)[trans](r))
## border   3  3 border italic(hat(K)[bord](r))
## theo     4  4  theo      italic(K[pois](r))
##                                     meaning
## iso      isotropic-corrected estimate of K(r)
## trans    translation-corrected estimate of K(r)
## border    border-corrected estimate of K(r)
## theo      theoretical Poisson K(r)
```

Point Process Model (PPM) model, 2 of 2

```
# Fit a point process model
#ppm_model <- ppm(sites_pp ~ p450)
#summary(ppm_model)

#option 2
sites_pp$marks <- as.factor(cut(sites_pp$marks$p450, breaks = quantile(sites_pp$marks$p450, probs = 0:3,
```

```
# Now run the ppm model
ppm_model <- ppm(sites_pp ~ marks, covariates = NULL)
print(summary(ppm_model))
```

Interpretation - this model measures the independence and intensity of the occurrence of something in space or time based on whatever marks you determine. In this case the occurrences are the data point locations, the intensity is the value of the marks and the marks are the biomarkers. This model is confusing to me and will be removed as I do not understand it well enough to interpret the results.

```
## Point process model
## Fitted to data: sites_pp
## Fitting method: maximum likelihood (Berman-Turner approximation)
## Model was fitted using glm()
## Algorithm converged
## Call:
## ppm.formula(Q = sites_pp ~ marks, covariates = NULL)
## Edge correction: "border"
## [border correction distance r = 0 ]
## -----
## Quadrature scheme (Berman-Turner) = data + dummy + weights
##
## Data pattern:
## Marked planar point pattern: 74 points
## Average intensity 34.1 points per square unit
## Multitype:
##
## frequency proportion intensity
## [7.88e+05,3.58e+06] 25 0.338 11.5
## (3.58e+06,4.84e+06] 24 0.324 11.1
## (4.84e+06,1.63e+07] 25 0.338 11.5
##
## Window: rectangle = [-123.45715, -122.22977] x [47.05236, 48.8208] units
## (1.227 x 1.768 units)
## Window area = 2.17055 square units
##
## Dummy quadrature points:
## 32 x 32 grid of dummy points, plus 4 corner points
## dummy spacing: 0.03835562 x 0.05526369 units
##
## Original dummy parameters: =
## Marked planar point pattern: 3232 points
## Average intensity 1490 points per square unit
## Multitype:
##
## frequency proportion intensity
## [7.88e+05,3.58e+06] 1080 0.333 496
## (3.58e+06,4.84e+06] 1080 0.334 497
## (4.84e+06,1.63e+07] 1080 0.333 496
##
## Window: rectangle = [-123.45715, -122.22977] x [47.05236, 48.8208] units
## (1.227 x 1.768 units)
## Window area = 2.17055 square units
## Quadrature weights:
## (counting weights based on 32 x 32 array of rectangular tiles)
## All weights:
```

```
## range: [0.00053, 0.00212]    total: 6.51
## Weights on data points:
## range: [0.00053, 0.00106]    total: 0.0684
## Weights on dummy points:
## range: [0.00053, 0.00212]    total: 6.44
## -----
## FITTED :
##
## Stationary multitype Poisson process
## Possible marks:
## [7.88e+05,3.58e+06] (3.58e+06,4.84e+06] (4.84e+06,1.63e+07]
## ---- Intensity: ----
##
## Log intensity: ~marks
##
## Intensities:
## beta_[7.88e+05,3.58e+06] beta_(3.58e+06,4.84e+06] beta_(4.84e+06,1.63e+07]
##                11.51784                11.05713                11.51784
##
##                Estimate      S.E.    CI95.lo    CI95.hi Ztest
## (Intercept)          2.443897e+00 0.2000000  2.0519045  2.8358901   ***
## marks(3.58e+06,4.84e+06] -4.082199e-02 0.2857738 -0.6009284  0.5192844
## marks(4.84e+06,1.63e+07] -9.960261e-14 0.2828427 -0.5543615  0.5543615
##                Zval
## (Intercept)          1.221949e+01
## marks(3.58e+06,4.84e+06] -1.428472e-01
## marks(4.84e+06,1.63e+07] -3.521484e-13
##
## ----- gory details -----
##
## Fitted regular parameters (theta):
##                (Intercept) marks(3.58e+06,4.84e+06] marks(4.84e+06,1.63e+07]
##                2.443897e+00          -4.082199e-02          -9.960261e-14
##
## Fitted exp(theta):
##                (Intercept) marks(3.58e+06,4.84e+06] marks(4.84e+06,1.63e+07]
##                11.51784                0.96000                1.00000
```

Spatial Autocorrelation Analysis, Global

Note: there are global and local tests that assess the likelihood of the biomarker values to be randomly ‘assigned’. My hypothesis is that the biomarkers values are not random.

```
#load packages & prep dataframe for "sf" package

#install.packages(spdep)
#install.packages("/Users/cmantegna/Downloads/spdep_1.2-8.tar.gz", repos = NULL, type = "source")
library(sf)
library(sp)
library(spdep)

sf_data <- st_as_sf(averaged_data, coords = c("longitude", "latitude"), crs = 4326)
```

```
# Take a look at your sf object
print(sf_data)
```

```
## Simple feature collection with 74 features and 4 fields
## Geometry type: POINT
## Dimension: XY
## Bounding box: xmin: -123.4572 ymin: 47.05236 xmax: -122.2298 ymax: 48.8208
## Geodetic CRS: WGS 84
## # A tibble: 74 x 5
##   site_number site_name          avg_p450 avg_SOD          geometry
## *   <int> <chr>          <dbl> <dbl>          <POINT [°]>
## 1         1 Port Angeles Yacht Cl~  5.75e6  7.39  (-123.4571 48.12823)
## 2         2 Jamestown          3.26e6 24.5   (-122.9981 48.02479)
## 3         3 Penn Cove Reference  2.43e6 23.9   (-122.719 48.21423)
## 4         7 North Camano        1.23e7  0.752  (-122.507 48.25536)
## 5         8 Chimacum Creek delta  2.64e6  2.19  (-122.7724 48.04906)
## 6         9 S of Skunk Island    3.56e6 11.3   (-122.7508 48.02667)
## 7        10 Oak Bay County Park  2.34e6 19.8   (-122.7287 48.02218)
## 8        11 Maristone Island     4.77e6  5.68  (-122.6995 48.01813)
## 9        12 Discovery Bay       4.03e6  8.74  (-122.8575 48.06496)
## 10       13 Arroyo Beach        4.48e6  8.83  (-122.3859 47.50161)
## # i 64 more rows
```

```
# Create a spatial weights matrix to assess nearest neighbors and distance-based neighbors to define sp
# You can extract the matrix of coordinates using st_coordinates
coords <- st_coordinates(sf_data)
```

```
# Now use the knearneigh function from the spdep package directly on the coordinates
neighbors <- knn2nb(knearneigh(coords, k = 4))
```

```
# Then convert the neighbors into spatial weights with nb2listw
weights <- nb2listw(neighbors, style = "W")
```

Moran's I and Geary's C determine if the distribution of the biomarker values across the entire Puget Sound region are random or not- random.

Interpretation - Moran's I statistic's, used for normally distributed data, ranges from 0 - 1. A value close to 0 mean randomness and a value close to 1 means less randomness. A statistic of .04 means points that are close to each other are more likely to have similar *p450* values than you would expect by chance but this is not statistically significant. The *SOD* values are random and not statistically significant.

Geary's C statistic, used for non- normal data, ranges from 0-2. A value close to 0 is a positive spatial correlation, a value close to 1 is an indication of randomness, and a value close to 2 is an indication of dispersion (negative correlation). A statistic of .8 with a p-value below .05 shows a statistically significant weak indication of negative autocorrelation of *p450* values. The *SOD* values are just above 1 and are not statistically significant. Since Geary's C is influenced by "local" and "global" neighbors, this should not be used.

```
## Run Moran's I and Geary's C for p450
```

```
moran_result <- moran.test(sf_data$avg_p450, weights)
print(moran_result)
```

```
##
## Moran I test under randomisation
##
```

```
## data: sf_data$avg_p450
## weights: weights
##
## Moran I statistic standard deviate = 0.75836, p-value = 0.2241
## alternative hypothesis: greater
## sample estimates:
## Moran I statistic      Expectation      Variance
##      0.038455120      -0.013698630      0.004729608

geary_result <- geary.test(sf_data$avg_p450, weights)
print(geary_result)
```

```
##
## Geary C test under randomisation
##
## data: sf_data$avg_p450
## weights: weights
##
## Geary C statistic standard deviate = 1.9348, p-value = 0.02651
## alternative hypothesis: Expectation greater than statistic
## sample estimates:
## Geary C statistic      Expectation      Variance
##      0.7858923      1.0000000      0.0122455

## Run Moran's I and Geary's C for SOD
moran_result <- moran.test(sf_data$avg_SOD, weights)
print(moran_result)
```

```
##
## Moran I test under randomisation
##
## data: sf_data$avg_SOD
## weights: weights
##
## Moran I statistic standard deviate = -0.66613, p-value = 0.7473
## alternative hypothesis: greater
## sample estimates:
## Moran I statistic      Expectation      Variance
##      -0.061916602      -0.013698630      0.005239556

geary_result <- geary.test(sf_data$avg_SOD, weights)
print(geary_result)
```

```
##
## Geary C test under randomisation
##
## data: sf_data$avg_SOD
## weights: weights
##
## Geary C statistic standard deviate = -1.9389, p-value = 0.9737
## alternative hypothesis: Expectation greater than statistic
## sample estimates:
## Geary C statistic      Expectation      Variance
##      1.172658406      1.000000000      0.007929774
```


Spatial Regression Analysis

Note: Each of the models analyzes if the observations (biomarker values) are not independent of each other but rather influenced by their location and the spatial arrangement.

```
#library(spdep)
#install.packages("sphet")
library(sphet)

# Spatial Lag Model. Is the value of one point influencing the value of a neighboring point?
# Interpretation - No. No statistically significant result.

library(spatialreg)
#accounts for spatial dependence in the dependent variable
slm_model <- lagsarlm(avg_p450 ~ avg_SOD, data = sf_data, listw = weights)
print(summary(slm_model))

##
## Call:lagsarlm(formula = avg_p450 ~ avg_SOD, data = sf_data, listw = weights)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4271767 -1218409  -442173   835360 12194381
##
## Type: lag
## Coefficients: (numerical Hessian approximate standard errors)
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  4675566      834605  5.6021 2.117e-08
## avg_SOD      -68781       27521 -2.4992  0.01245
##
## Rho: 0.12696, LR test value: 0.50819, p-value: 0.47592
## Approximate (numerical Hessian) standard error: 0.17385
##      z-value: 0.73029, p-value: 0.46521
## Wald statistic: 0.53333, p-value: 0.46521
##
## Log likelihood: -1186.116 for lag model
## ML residual variance (sigma squared): 4.8805e+12, (sigma: 2209200)
## Number of observations: 74
## Number of parameters estimated: 4
## AIC: 2380.2, (AIC for lm: 2378.7)

# Spatial Error Model. This accounts for the spatial autocorrelation in the error term. Could statistic
# No. There is a trend of a mild negative correlation in the data set but it is not statistically signi.
sem_model <- errorsarlm(avg_p450 ~ avg_SOD, data = sf_data, listw = weights)
print(summary(sem_model))

##
## Call:errorsarlm(formula = avg_p450 ~ avg_SOD, data = sf_data, listw = weights)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4259627 -1212073  -416963   792277 12298927
##
## Type: error
## Coefficients: (asymptotic standard errors)
```

```
##           Estimate Std. Error z value Pr(>|z|)
## (Intercept)  5269555      413117 12.7556 < 2e-16
## avg_SOD      -70421       26944 -2.6136 0.00896
##
## Lambda: 0.17124, LR test value: 0.87442, p-value: 0.34974
## Approximate (numerical Hessian) standard error: 0.17817
##      z-value: 0.96115, p-value: 0.33648
## Wald statistic: 0.9238, p-value: 0.33648
##
## Log likelihood: -1185.933 for error model
## ML residual variance (sigma squared): 4.8437e+12, (sigma: 2200800)
## Number of observations: 74
## Number of parameters estimated: 4
## AIC: 2379.9, (AIC for lm: 2378.7)

# Spatial Durbin Model. An all-in-one model that combines both SLM and SEM. No expected result change.

#install.packages("spatialreg")
library(spatialreg)

#combines SLM and SEM
sdm_model <- spatialreg::lagsarlm(avg_p450 ~ avg_SOD, data = sf_data, listw = weights, type="mixed")
print(summary(sdm_model))

##
## Call:spatialreg::lagsarlm(formula = avg_p450 ~ avg_SOD, data = sf_data,
##      listw = weights, type = "mixed")
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4207088 -1182408  -366986   848985 12511496
##
## Type: mixed
## Coefficients: (numerical Hessian approximate standard errors)
##           Estimate Std. Error z value Pr(>|z|)
## (Intercept)  3960266    1112014  3.5613 0.000369
## avg_SOD      -66343      27412 -2.4202 0.015512
## lag.avg_SOD   46095      48212  0.9561 0.339020
##
## Rho: 0.16963, LR test value: 0.86994, p-value: 0.35097
## Approximate (numerical Hessian) standard error: 0.17709
##      z-value: 0.95791, p-value: 0.33811
## Wald statistic: 0.91759, p-value: 0.33811
##
## Log likelihood: -1185.666 for mixed model
## ML residual variance (sigma squared): 4.8095e+12, (sigma: 2193100)
## Number of observations: 74
## Number of parameters estimated: 5
## AIC: 2381.3, (AIC for lm: 2380.2)
```

Spatial Autocorrelation Analysis, Local

Local Indicator of Spatial Association (LISA)

```
# Prep data

#install.packages("spdep")
#install.packages("sf") # for spatial data handling
#install.packages("tmap") # for visualization
library(spdep)
library(sf)
library(tmap)

lisa_values <- localmoran(sf_data$avg_p450, weights)

# Add LISA values and p-values to your spatial data

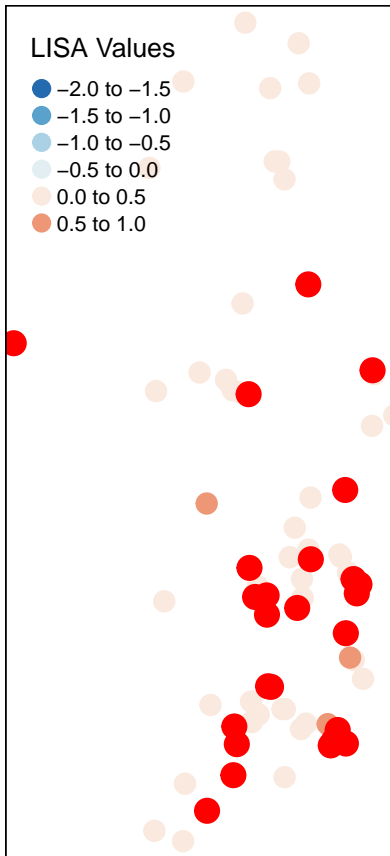
sf_data$lisa <- lisa_values[,1] # Local Moran's I values
sf_data$p.value <- lisa_values[,4] # p-values for significance

# Use tmap for plotting
library(tmap)

# Define breaks for significance levels, e.g., 0.05 for 95% confidence
sig_breaks <- c(0, 0.05, 1) # Change according to your significance level

# Create a map
tm_shape(sf_data) +
  tm_dots(col = "lisa", size = 0.5, palette = "-RdBu", title = "LISA Values") +
  tm_layout(legend.position = c("left", "top")) +
  tm_shape(sf_data[sf_data$p.value <= 0.05, ]) + # Add a layer for significant points only
  tm_dots(col = "red", size = 0.7, title = "Significant Clusters") +
  tm_layout(main.title = "LISA Cluster Map", main.title.position = "center")
```

LISA Cluster Map



Plot the LISA data over the map from the base Washington State map found in file: 03-map.rmd

```
library(sf)
library(viridis)
library(rnaturalearth)
library(rnaturalearthdata)
library(ggplot2)
```

```
world <- ne_states(country = "united states of america", returnclass = "sf")
washington_map <- world[world$name == "Washington", ]
```

```
pmap <- ggplot() +
  geom_sf(data = washington_map, fill = "lightgrey", color = "white") +
  theme_minimal() +
  labs(title = "Washington State Map")
```

Ensure CRS compatibility

```
sf_data <- st_transform(sf_data, st_crs(washington_map))
```

Prepare the base map

```
pmap <- ggplot() +
  geom_sf(data = washington_map, fill = "lightgrey", color = "white") +
  theme_minimal() +
```

```

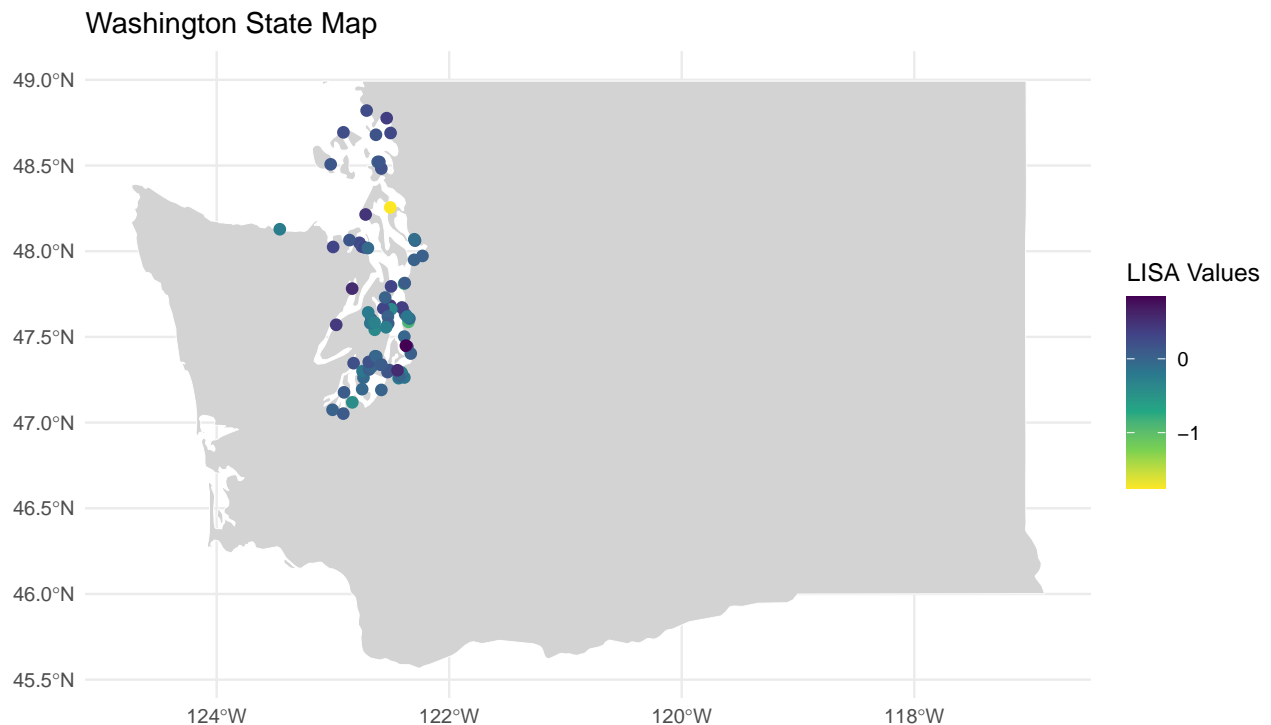
labs(title = "Washington State Map")

# Add the LISA points layer to the map
complete_map <- pmap +
  geom_sf(data = sf_data, aes(color = lisa), size = 2) +
  scale_color_viridis_c(option = "D", direction = -1, name = "LISA Values")

# Display the combined map
print(complete_map)

```

Interpretation - LISA uses the global application of the Moran's I statistic. This is used to determine any point clustering or significant outliers. There are no sites that are clustered significantly.



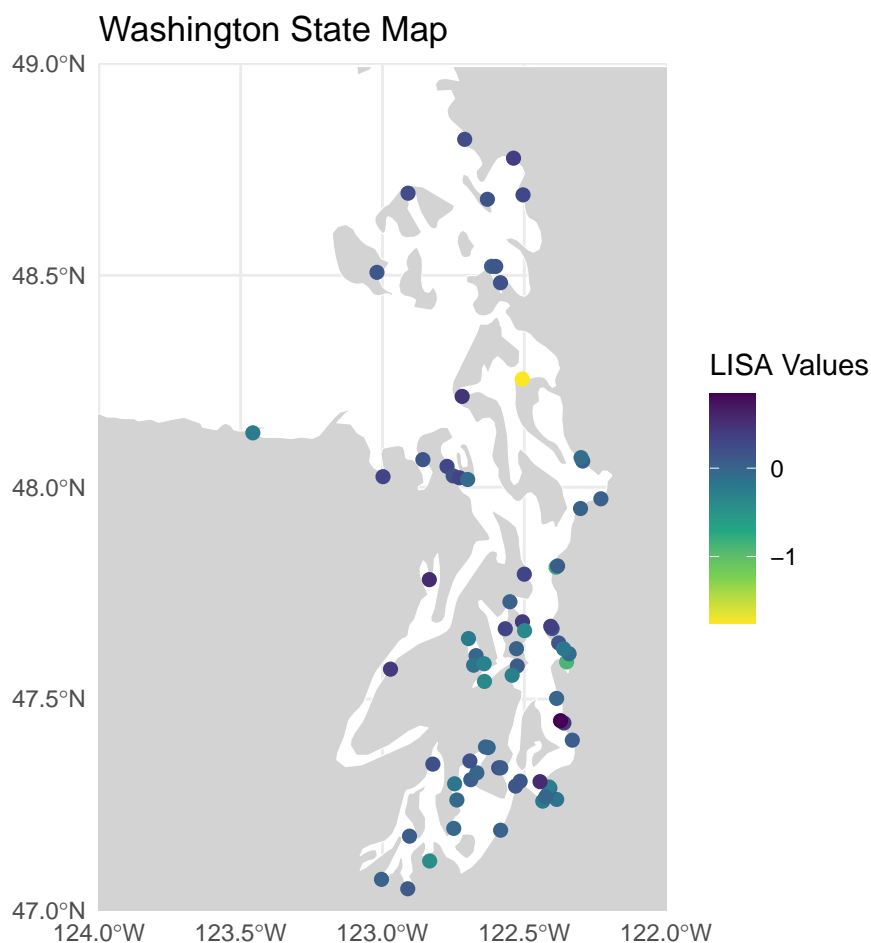
```

#zoom in on the puget sound region
# Assuming you know the bounding box coordinates you want to zoom in on
# For example: xmin, xmax, ymin, ymax
xlim <- c(-124, -122) # longitude bounds
ylim <- c(47, 49) # latitude bounds

complete_map <- pmap +
  geom_sf(data = sf_data, aes(color = lisa), size = 2) +
  scale_color_viridis_c(option = "D", direction = -1, name = "LISA Values") +
  coord_sf(xlim = xlim, ylim = ylim, expand = FALSE)

print(complete_map)

```



Analytes

Have to merge and reshape for a data frame that lets me compare biomarker and analytes in the models

```
library(reshape2)
#merge data frames and reshape for input.
colnames(pah)[colnames(pah) == "SiteName"] <- "site_name"
merged_df <- merge(averaged_data, pah, by = c("site_name"), all.x = TRUE)
```

#reshape to get the analytes into their own columns with the DryValue as their values

```
reshaped_df <- dcast(merged_df, site_name + site_number + latitude.x + longitude.x + avg_p450 + avg_SOD
```

```
print(reshaped_df)
```

```
##              site_name site_number latitude.x
## 1      Aiston Preserve           77  48.67938
## 2      Arroyo Beach             13  47.50161
## 3      Blair Waterway           41  47.27568
## 4      Blair Waterway #2         42  47.26324
## 5      Brackenwood Ln           23  47.68234
## 6      Broad Spit (Fisherman's Point) 30  47.78184
## 7      Browns Point Lighthouse     54  47.30515
```

## 8	Cap Sante	64	48.52097
## 9	Chambers Bay Park	56	47.19057
## 10	Cherry Point Aquatic Reserve, Conoco Phillips	75	48.82080
## 11	Chimacum Creek delta	8	48.04906
## 12	Chuckanut, Clark's Point	74	48.68975
## 13	Comm Bay Skookum	45	47.29000
## 14	Comm Bay, Dick Gilmur Launch	48	47.29255
## 15	Comm Bay, Milwaukee Waterway	49	47.26940
## 16	Des Moines Marina	21	47.40301
## 17	Discovery Bay	12	48.06496
## 18	Donkey Creek Delta (PSS13175 - 000049)	44	47.33775
## 19	Eagle Harbor Dr	31	47.61889
## 20	Eastsound, Fishing Bay	60	48.69368
## 21	Edmonds Ferry	69	47.81407
## 22	Edmonds Marina	68	47.81110
## 23	Eld Inlet	72	47.07460
## 24	Elliot Bay Myrtle Edwards	19	47.61862
## 25	Elliott Bay, Harbor Island, Pier 17	14	47.58766
## 26	Everett Harbor	66	47.97260
## 27	Fidalgo Bay Aq Reserve, Weaverling Spit	63	48.48245
## 28	Filucy Bay	59	47.19483
## 29	Friday Harbor	61	48.50694
## 30	Gig Harbor Boat Launch	58	47.33785
## 31	Hood Canal Holly	29	47.57060
## 32	Jamestown	2	48.02479
## 33	Kingston Marina	36	47.79469
## 34	Kitsap St Boat Launch	25	47.54167
## 35	Kopachuck State Park	52	47.30973
## 36	Lions Park	37	47.58335
## 37	Locust Beach	76	48.77637
## 38	Madrona Pont	28	47.57996
## 39	Manchester, Stormwater Outfall	33	47.55622
## 40	Maple Hollow Park	51	47.30008
## 41	Maristone Island	11	48.01813
## 42	Meyer's Point - Henderson Inlet	71	47.11795
## 43	Miller Creek	20	47.44360
## 44	Minter Bay	55	47.35397
## 45	Mukilteo	65	47.94968
## 46	N Avenue Park	62	48.52108
## 47	North Camano	7	48.25536
## 48	Oak Bay County Park	10	48.02218
## 49	Penn Cove Reference	3	48.21423
## 50	Pennrose Point State Park	50	47.26190
## 51	Point Defiance Ferry	43	47.30620
## 52	Port Angeles Yacht Club	1	48.12823
## 53	Purdy - Dexters	57	47.38566
## 54	Purdy, Burley Lagoon	47	47.38698
## 55	Raft Island Park	53	47.32598
## 56	Reach Island	39	47.34654
## 57	Rich Passage	32	47.57812
## 58	Rocky Point	27	47.60255
## 59	S of Skunk Island	9	48.02667
## 60	Salmon Bay, Commodore Park	16	47.66630
## 61	Salmon Beach	40	47.29464

## 62		Seattle Aquarium, Pier 59	17	47.60700		
## 63		Shilshole Bay	18	47.67168		
## 64		Silverdale, Dyes Inlet	35	47.64279		
## 65		Skiff Point	24	47.66142		
## 66		Smith Cove, Terminal 91	15	47.63237		
## 67		Squaxin Island	38	47.17650		
## 68		Suquamish Stormwater Outfall	34	47.72961		
## 69		Thea Foss Waterway	46	47.25919		
## 70		Three Tree Point	22	47.44896		
## 71		Tulalip Bay	67	48.06170		
## 72		Tulalip Reservation	70	48.06979		
## 73		West Bay Park	73	47.05236		
## 74		Williams Olson Park	26	47.66586		
##	longitude.x	avg_p450	avg_SOD	SumPAHs	SumPAHs16	SumPAHs42_DMNcorrected
## 1	-122.6301	3752618	3.440125	97.40305	31.65599	97.40305
## 2	-122.3859	4480860	8.832583	408.22636	168.09321	408.22636
## 3	-122.4173	4879642	6.517750	715.09344	247.53234	715.09344
## 4	-122.3857	3714918	10.796000	1038.61553	299.36565	1038.61553
## 5	-122.5064	1857012	9.835125	389.36704	176.98502	389.36704
## 6	-122.8347	2311731	7.116250	NA	NA	NA
## 7	-122.4444	7401612	1.378875	438.80107	175.52043	438.80107
## 8	-122.6007	3728576	41.120250	375.61898	63.66423	375.61898
## 9	-122.5835	4502338	9.687875	182.85775	70.78365	182.85775
## 10	-122.7101	3716209	4.467750	325.98083	126.77032	325.98083
## 11	-122.7724	2641574	2.193375	168.45933	68.63158	168.45933
## 12	-122.5043	3006724	12.702500	206.57357	80.33416	206.57357
## 13	-122.4100	5919817	8.918500	857.31981	342.92792	857.31981
## 14	-122.4122	3792068	41.297750	781.27358	332.04127	781.27358
## 15	-122.4243	7608742	6.397700	599.01078	195.18329	599.01078
## 16	-122.3306	4886368	9.639750	14700.69093	9800.46062	15313.21971
## 17	-122.8575	4029898	8.739125	235.35381	117.67691	235.35381
## 18	-122.5901	3185175	2.500625	NA	NA	NA
## 19	-122.5275	1846201	25.167500	1031.19294	577.46805	1031.19294
## 20	-122.9099	2504169	11.961125	512.49588	292.06755	518.00659
## 21	-122.3825	4710937	0.206375	532.00981	268.92804	526.16355
## 22	-122.3880	16253739	16.624750	702.84765	374.85208	702.84765
## 23	-123.0035	4644881	20.791000	171.59812	64.34930	171.59812
## 24	-122.3611	2469548	34.825200	12078.42170	8052.28113	12078.42170
## 25	-122.3507	9194072	5.563250	3195.16749	1882.86656	3195.16749
## 26	-122.2298	5271456	0.375875	372.81540	173.09287	372.81540
## 27	-122.5839	3345616	18.015000	699.56200	165.35102	699.56200
## 28	-122.7487	6265040	5.313125	148.27311	65.24017	148.27311
## 29	-123.0194	3954243	6.709600	532.69368	338.41716	532.69368
## 30	-122.5828	4097010	7.509375	418.64682	233.94969	418.64682
## 31	-122.9717	788472	1.640417	116.10138	24.58618	88.78341
## 32	-122.9981	3263515	24.487333	119.31910	31.15554	119.31910
## 33	-122.4999	5281103	4.064000	273.01097	123.50496	273.01097
## 34	-122.6403	2885042	30.745000	758.67818	303.47127	758.67818
## 35	-122.6887	7285132	4.726000	141.69495	59.37693	141.69495
## 36	-122.6415	6543254	14.793250	289.59279	118.46978	289.59279
## 37	-122.5379	2401828	5.401500	147.20503	46.08157	147.20503
## 38	-122.6786	5804701	3.871500	259.13965	108.47706	259.13965
## 39	-122.5428	6122830	2.682375	369.42136	171.02841	369.42136
## 40	-122.7457	3639570	4.621500	176.66667	71.97531	176.66667

## 41	-122.6995	4772561	5.678750	134.05496	41.62759	134.05496
## 42	-122.8336	2519276	24.012500	200.73694	66.16884	200.73694
## 43	-122.3603	5747266	4.015375	292.31683	114.38485	285.96212
## 44	-122.6917	6206749	1.991375	164.47704	78.94898	164.47704
## 45	-122.3016	5076323	7.606500	440.19763	207.15183	440.19763
## 46	-122.6153	4183302	1.443625	2333.52357	976.82382	2333.52357
## 47	-122.5070	12290521	0.751750	165.04623	63.47932	165.04623
## 48	-122.7287	2335145	19.807750	141.06998	47.45081	141.06998
## 49	-122.7190	2427656	23.860000	160.93092	64.37237	160.93092
## 50	-122.7376	4193870	4.499500	NA	NA	NA
## 51	-122.5145	2181857	10.884250	694.82398	335.83159	694.82398
## 52	-123.4571	5751355	7.385500	1983.40206	1081.85567	1983.40206
## 53	-122.6273	4743078	1.760875	149.15677	68.84159	149.15677
## 54	-122.6367	3937679	11.214000	215.42133	86.16853	215.42133
## 55	-122.6672	4523052	3.778125	147.74866	70.35651	147.74866
## 56	-122.8224	5905498	4.583750	192.65779	81.73361	192.65779
## 57	-122.5248	3203053	2.245000	338.95875	142.71947	338.95875
## 58	-122.6699	4508401	9.895500	310.52017	133.94988	310.52017
## 59	-122.7508	3556923	11.307000	294.28413	144.13917	294.28413
## 60	-122.4018	3756618	1.481750	1041.76471	409.26471	1041.76471
## 61	-122.5305	1904019	18.330875	428.65764	214.32882	428.65764
## 62	-122.3420	3135234	23.887625	3304.96063	1879.29134	3304.96063
## 63	-122.4067	2862824	9.906750	2029.62742	1052.39940	1954.45604
## 64	-122.6967	1652091	26.031000	363.26584	137.08145	370.11991
## 65	-122.4988	5664099	4.236250	449.87987	213.10099	449.87987
## 66	-122.3787	3958924	19.661250	7153.27706	4161.90665	7153.27706
## 67	-122.9046	6368736	5.858750	174.78708	71.20955	174.78708
## 68	-122.5506	4338556	5.819250	NA	NA	NA
## 69	-122.4347	3423038	18.690800	1103.39463	454.33897	1103.39463
## 70	-122.3723	7417010	8.125125	312.23111	129.60537	312.23111
## 71	-122.2939	5544824	6.253833	356.89176	181.69035	356.89176
## 72	-122.2998	3773556	3.182125	253.49047	123.79767	253.49047
## 73	-122.9109	5731487	2.996125	391.41916	161.96655	384.67055
## 74	-122.5670	2970859	6.457625	301.25306	150.62653	301.25306
##	SumPAHsHMW	SumPAHsLMW	NA			
## 1	19.48061	79.13998	NA			
## 2	186.10320	216.11984	NA			
## 3	280.53666	456.55966	NA			
## 4	403.22721	610.95031	NA			
## 5	176.98502	212.38202	NA			
## 6	NA	NA	NA			
## 7	181.37111	257.42996	NA			
## 8	120.96204	254.65693	NA			
## 9	76.68228	106.17547	NA			
## 10	150.91705	169.02709	NA			
## 11	56.77703	112.30622	NA			
## 12	74.59601	131.97756	NA			
## 13	369.30699	461.63374	NA			
## 14	338.55189	442.72170	NA			
## 15	215.37466	390.36658	NA			
## 16	8575.40304	6125.28789	NA			
## 17	98.84860	136.50521	NA			
## 18	NA	NA	NA			
## 19	653.08886	364.35484	NA			

## 20	270.02471	242.47117	NA
## 21	268.92804	257.23551	NA
## 22	374.85208	304.56731	NA
## 23	75.07418	96.52394	NA
## 24	9394.32799	3220.91245	NA
## 25	2054.03624	1141.13125	NA
## 26	166.43545	206.37995	NA
## 27	254.38618	438.81616	NA
## 28	59.30925	88.96387	NA
## 29	319.61621	206.81049	NA
## 30	246.26283	172.38398	NA
## 31	11.61014	109.27189	NA
## 32	15.24633	106.06143	NA
## 33	123.50496	149.50601	NA
## 34	354.04982	419.80193	NA
## 35	53.97903	87.71592	NA
## 36	131.63309	157.95970	NA
## 37	27.52094	121.60416	NA
## 38	120.53007	138.60958	NA
## 39	171.02841	198.39295	NA
## 40	64.77778	111.23457	NA
## 41	23.98878	112.88839	NA
## 42	52.78638	148.69403	NA
## 43	120.73956	171.57727	NA
## 44	65.79082	98.68622	NA
## 45	194.20484	245.99279	NA
## 46	1085.35980	1248.16377	NA
## 47	54.59221	107.91484	NA
## 48	33.98504	102.59635	NA
## 49	46.81627	109.72563	NA
## 50	NA	NA	NA
## 51	335.83159	370.57279	NA
## 52	1202.06186	781.34021	NA
## 53	57.36799	91.78878	NA
## 54	86.16853	129.25280	NA
## 55	61.91373	91.46346	NA
## 56	81.73361	110.92418	NA
## 57	142.71947	190.29263	NA
## 58	133.94988	176.57029	NA
## 59	132.12757	162.15656	NA
## 60	535.76471	476.23529	NA
## 61	226.23598	202.42166	NA
## 62	2203.30709	1101.65354	NA
## 63	1277.91356	714.12817	NA
## 64	150.78959	212.47624	NA
## 65	213.10099	236.77888	NA
## 66	4682.14498	2145.98312	NA
## 67	77.68315	97.10393	NA
## 68	NA	NA	NA
## 69	545.20676	584.15010	NA
## 70	141.38767	176.73459	NA
## 71	168.71247	188.17929	NA
## 72	117.90254	135.58792	NA
## 73	202.45819	182.21237	NA

```
## 74 156.65159 144.60147 NA
```

Linear Regression - only here to show that the non- normal data passed through this model is unsuccessful.

```
# Linear Regression- p450 as response
lm_model <- lm(avg_p450 ~ avg_SOD + SumPAHs + SumPAHs16 + SumPAHs42_DMNcorrected + SumPAHsHmw + SumPAHsLMW, data = reshaped_df)
print(summary(lm_model))

##
## Call:
## lm(formula = avg_p450 ~ avg_SOD + SumPAHs + SumPAHs16 + SumPAHs42_DMNcorrected +
##     SumPAHsHmw + SumPAHsLMW, data = reshaped_df)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4234121 -1358333  -398182   761952 12118565
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    5420352.5   579886.3    9.347 1.63e-13 ***
## avg_SOD         -73508.2    32849.9   -2.238  0.0288 *
## SumPAHs         -5306.1    28666.3   -0.185  0.8537
## SumPAHs16       -1482.1     8273.8   -0.179  0.8584
## SumPAHs42_DMNcorrected  7481.0    30613.3    0.244  0.8077
## SumPAHsHmw       -674.5     6797.7   -0.099  0.9213
## SumPAHsLMW      -2572.0     6519.6   -0.395  0.6945
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2366000 on 63 degrees of freedom
## (4 observations deleted due to missingness)
## Multiple R-squared:  0.08903, Adjusted R-squared:  0.002275
## F-statistic: 1.026 on 6 and 63 DF, p-value: 0.4167
```

Generalized Linear Model - used for non- normal data.

```
# GLM - p450 as response
glm_model <- glm(avg_p450 ~ avg_SOD + SumPAHs + SumPAHs16 + SumPAHs42_DMNcorrected + SumPAHsHmw + SumPAHsLMW, data = reshaped_df, family = poisson())
print(summary(glm_model))
```

Interpretation - All categories of PAH's show a statistically significant relationship to the p450 biomarker result.

```
##
## Call:
## glm(formula = avg_p450 ~ avg_SOD + SumPAHs + SumPAHs16 + SumPAHs42_DMNcorrected +
##     SumPAHsHmw + SumPAHsLMW, family = poisson(), data = reshaped_df)
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    1.553e+01  1.140e-04 136245.3  <2e-16 ***
## avg_SOD        -1.811e-02  7.311e-06 -2476.4  <2e-16 ***
## SumPAHs        -1.048e-03  5.764e-06  -181.7  <2e-16 ***
```

```
## SumPAHs16          -3.171e-04  1.656e-06  -191.5  <2e-16 ***
## SumPAHs42_DMNcorrected  1.646e-03  6.132e-06   268.5  <2e-16 ***
## SumPAHsHWMW        -2.747e-04  1.411e-06  -194.7  <2e-16 ***
## SumPAHsLMW         -6.914e-04  1.302e-06  -531.0  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
## Null deviance: 71801382  on 69  degrees of freedom
## Residual deviance: 63582448  on 63  degrees of freedom
## (4 observations deleted due to missingness)
## AIC: Inf
##
## Number of Fisher Scoring iterations: 5
```

```
# LR- p450 as response
```

```
#### Replicating with individual analytes to see if anything really sticks out.
```

```
#merge and reshape just like above
```

```
colnames(indv)[colnames(indv) == "SiteName"] <- "site_name"
```

```
merged_df2 <- merge(averaged_data, indv, by = c("site_name"), all.x = TRUE)
```

```
#reshape to get the analytes into their own columns with the DryValue as their values
```

```
reshaped2_df <- dcast(merged_df2, site_name + site_number + latitude + longitude + avg_p450 + avg_SOD ~
```

```
print(reshaped2_df)
```

```
##           site_name site_number latitude longitude
## 1           Aiston Preserve          77 48.67938 -122.6301
## 2           Arroyo Beach           13 47.50161 -122.3859
## 3           Blair Waterway          41 47.27568 -122.4173
## 4           Blair Waterway #2         42 47.26324 -122.3857
## 5           Brackenwood Ln           23 47.68234 -122.5064
## 6           Broad Spit (Fisherman's Point) 30 47.78184 -122.8347
## 7           Browns Point Lighthouse      54 47.30515 -122.4444
## 8           Cap Sante                64 48.52097 -122.6007
## 9           Chambers Bay Park          56 47.19057 -122.5835
## 10          Cherry Point Aquatic Reserve, Conoco Phillips 75 48.82080 -122.7101
## 11           Chimacum Creek delta          8 48.04906 -122.7724
## 12           Chuckanut, Clark's Point      74 48.68975 -122.5043
## 13           Comm Bay Skookum           45 47.29000 -122.4100
## 14           Comm Bay, Dick Gilmur Launch 48 47.29255 -122.4122
## 15           Comm Bay, Milwaukee Waterway 49 47.26940 -122.4243
## 16           Des Moines Marina          21 47.40301 -122.3306
## 17           Discovery Bay            12 48.06496 -122.8575
## 18           Donkey Creek Delta (PSS13175 - 000049) 44 47.33775 -122.5901
## 19           Eagle Harbor Dr           31 47.61889 -122.5275
## 20           Eastsound, Fishing Bay       60 48.69368 -122.9099
## 21           Edmonds Ferry            69 47.81407 -122.3825
## 22           Edmonds Marina           68 47.81110 -122.3880
## 23           Eld Inlet                72 47.07460 -123.0035
## 24           Elliot Bay Myrtle Edwards    19 47.61862 -122.3611
## 25           Elliott Bay, Harbor Island, Pier 17 14 47.58766 -122.3507
```

## 26	Everett Harbor	66	47.97260	-122.2298		
## 27	Fidalgo Bay Aq Reserve, Weaverling Spit	63	48.48245	-122.5839		
## 28	Filucy Bay	59	47.19483	-122.7487		
## 29	Friday Harbor	61	48.50694	-123.0194		
## 30	Gig Harbor Boat Launch	58	47.33785	-122.5828		
## 31	Hood Canal Holly	29	47.57060	-122.9717		
## 32	Jamestown	2	48.02479	-122.9981		
## 33	Kingston Marina	36	47.79469	-122.4999		
## 34	Kitsap St Boat Launch	25	47.54167	-122.6403		
## 35	Kopachuck State Park	52	47.30973	-122.6887		
## 36	Lions Park	37	47.58335	-122.6415		
## 37	Locust Beach	76	48.77637	-122.5379		
## 38	Madrona Pont	28	47.57996	-122.6786		
## 39	Manchester, Stormwater Outfall	33	47.55622	-122.5428		
## 40	Maple Hollow Park	51	47.30008	-122.7457		
## 41	Maristone Island	11	48.01813	-122.6995		
## 42	Meyer's Point - Henderson Inlet	71	47.11795	-122.8336		
## 43	Miller Creek	20	47.44360	-122.3603		
## 44	Minter Bay	55	47.35397	-122.6917		
## 45	Mukilteo	65	47.94968	-122.3016		
## 46	N Avenue Park	62	48.52108	-122.6153		
## 47	North Camano	7	48.25536	-122.5070		
## 48	Oak Bay County Park	10	48.02218	-122.7287		
## 49	Penn Cove Reference	3	48.21423	-122.7190		
## 50	Pennrose Point State Park	50	47.26190	-122.7376		
## 51	Point Defiance Ferry	43	47.30620	-122.5145		
## 52	Port Angeles Yacht Club	1	48.12823	-123.4571		
## 53	Purdy - Dexters	57	47.38566	-122.6273		
## 54	Purdy, Burley Lagoon	47	47.38698	-122.6367		
## 55	Raft Island Park	53	47.32598	-122.6672		
## 56	Reach Island	39	47.34654	-122.8224		
## 57	Rich Passage	32	47.57812	-122.5248		
## 58	Rocky Point	27	47.60255	-122.6699		
## 59	S of Skunk Island	9	48.02667	-122.7508		
## 60	Salmon Bay, Commodore Park	16	47.66630	-122.4018		
## 61	Salmon Beach	40	47.29464	-122.5305		
## 62	Seattle Aquarium, Pier 59	17	47.60700	-122.3420		
## 63	Shilshole Bay	18	47.67168	-122.4067		
## 64	Silverdale, Dyes Inlet	35	47.64279	-122.6967		
## 65	Skiff Point	24	47.66142	-122.4988		
## 66	Smith Cove, Terminal 91	15	47.63237	-122.3787		
## 67	Squaxin Island	38	47.17650	-122.9046		
## 68	Suquamish Stormwater Outfall	34	47.72961	-122.5506		
## 69	Thea Foss Waterway	46	47.25919	-122.4347		
## 70	Three Tree Point	22	47.44896	-122.3723		
## 71	Tulalip Bay	67	48.06170	-122.2939		
## 72	Tulalip Reservation	70	48.06979	-122.2998		
## 73	West Bay Park	73	47.05236	-122.9109		
## 74	Williams Olson Park	26	47.66586	-122.5670		
##	avg_p450	avg_SOD	acenaphthene	acenaphthylene	anthracene	benz[a]anthracene
## 1	3752618	3.440125	-3.165599	-3.165599	-3.165599	-3.104722
## 2	4480860	8.832583	-3.902164	-3.902164	-3.902164	13.207324
## 3	4879642	6.517750	5.500719	-2.915381	6.050791	17.052228
## 4	3714918	10.796000	7.942354	-4.948698	5.315268	17.717559

## 5	1857012	9.835125	-3.598695	-3.598695	-3.598695	12.978901
## 6	2311731	7.116250	NA	NA	NA	NA
## 7	7401612	1.378875	4.212490	-3.334888	5.031586	12.286430
## 8	3728576	41.120250	-4.774818	-4.711153	-4.774818	4.902146
## 9	4502338	9.687875	-2.713373	-2.713373	-2.713373	5.426746
## 10	3716209	4.467750	-3.682376	-3.622009	-3.622009	9.055023
## 11	2641574	2.193375	-3.868325	-3.868325	-3.868325	3.493971
## 12	3006724	12.702500	-3.155985	-3.098603	-3.155985	6.311970
## 13	5919817	8.918500	7.913721	-5.671500	7.913721	31.654885
## 14	3792068	41.297750	8.463797	-4.752748	9.765920	20.182901
## 15	7608742	6.397700	6.124717	-4.307493	4.913235	12.787871
## 16	4886368	9.639750	257.262091	5.083989	287.888531	673.781667
## 17	4029898	8.739125	-1.976972	-1.929901	2.541821	9.414152
## 18	3185175	2.500625	NA	NA	NA	NA
## 19	1846201	25.167500	6.393396	-4.331010	6.874620	33.685636
## 20	2504169	11.961125	-3.747282	-3.747282	4.573888	20.389621
## 21	4710937	0.206375	-4.267771	-4.267771	6.430888	23.385047
## 22	16253739	16.624750	4.275657	-3.397097	9.957008	33.385263
## 23	4644881	20.791000	-2.252225	-2.252225	-2.252225	2.466723
## 24	2469548	34.825200	54.352898	-5.099778	80.522811	597.210851
## 25	9194072	5.563250	24.534322	-3.594563	51.350906	165.464031
## 26	5271456	0.375875	-5.126212	-5.126212	-5.126212	11.983352
## 27	3345616	18.015000	-6.168865	-6.105268	-6.168865	7.631585
## 28	6265040	5.313125	-3.439936	-3.380627	-3.439936	3.677173
## 29	3954243	6.709600	3.509511	-2.882813	6.204315	19.427652
## 30	4097010	7.509375	-3.878640	-3.878640	-3.878640	12.928799
## 31	788472	1.640417	-3.824516	-3.824516	-3.824516	-3.961106
## 32	3263515	24.487333	-4.640187	-4.573899	-4.640187	-4.905341
## 33	5281103	4.064000	-3.445138	-3.445138	-3.445138	8.450339
## 34	2885042	30.745000	4.046284	-2.680663	5.563640	18.714062
## 35	7285132	4.726000	-3.238742	-3.171268	-3.171268	3.171268
## 36	6543254	14.793250	-4.541341	-4.541341	-4.541341	7.897985
## 37	2401828	5.401500	-4.352149	-4.352149	-4.352149	-4.416151
## 38	5804701	3.871500	-3.615902	-3.555637	-3.555637	4.760938
## 39	6122830	2.682375	-3.967859	-3.967859	4.788795	12.998159
## 40	3639570	4.621500	-3.337037	-3.271605	-3.271605	4.318519
## 41	4772561	5.678750	-4.797757	-4.797757	-4.797757	-5.150533
## 42	2519276	24.012500	-5.724720	-5.724720	-5.724720	-5.724720
## 43	5747266	4.015375	-3.622187	-3.622187	-3.622187	9.532071
## 44	6206749	1.991375	-3.750077	-3.684286	-3.684286	4.079031
## 45	5076323	7.606500	-4.401976	-4.337241	7.768194	14.889038
## 46	4183302	1.443625	8.682878	-3.310347	17.908437	70.548387
## 47	12290521	0.751750	-3.554842	-3.491363	-3.491363	-3.047007
## 48	2335145	19.807750	-4.232099	-4.167977	-4.232099	-4.488590
## 49	2427656	23.860000	-3.291769	-3.291769	-3.291769	-3.291769
## 50	4193870	4.499500	NA	NA	NA	NA
## 51	2181857	10.884250	5.326984	-3.358316	11.580400	21.423739
## 52	5751355	7.385500	10.818557	-3.005155	32.455670	78.134021
## 53	4743078	1.760875	-3.384711	-3.327343	-3.327343	3.384711
## 54	3937679	11.214000	-4.123780	-4.062231	-4.062231	4.554623
## 55	4523052	3.778125	-3.728895	-3.728895	-3.728895	3.799251
## 56	5905498	4.583750	-3.035820	-2.977439	-3.035820	4.261824
## 57	3203053	2.245000	-3.627453	-3.627453	-3.627453	10.703960
## 58	4508401	9.895500	-2.983429	-2.922543	-2.922543	6.088631

## 59	3556923	11.307000	-3.543421	-3.543421	-3.543421	7.206958
## 60	3756618	1.481750	-5.655294	-5.655294	5.729706	29.764706
## 61	1904019	18.330875	-5.179613	-5.120077	-5.120077	17.860735
## 62	3135234	23.887625	14.904724	-4.341811	57.674803	162.007874
## 63	2862824	9.906750	12.027422	-5.261997	11.275708	105.239940
## 64	1652091	26.031000	-3.564118	-3.564118	-3.564118	6.031584
## 65	5664099	4.236250	-5.682693	-5.682693	-5.682693	17.166469
## 66	3958924	19.661250	71.532771	3.511609	84.538729	273.125124
## 67	6368736	5.858750	-2.589438	-2.589438	-2.589438	3.689949
## 68	4338556	5.819250	NA	NA	NA	NA
## 69	3423038	18.690800	12.981113	-5.062634	11.683002	29.856561
## 70	7417010	8.125125	-4.123807	-4.123807	-4.123807	10.604076
## 71	5544824	6.253833	-4.477369	-4.412480	-4.477369	11.031200
## 72	3773556	3.182125	-3.713930	-3.654979	-3.654979	6.484640
## 73	5731487	2.996125	6.073746	-4.656538	-4.656538	9.448049
## 74	2970859	6.457625	-3.494535	-3.494535	-3.494535	7.832579
##	benzo[a]pyrene	benzo[b]fluoranthene	benzo[e]pyrene	benzo[ghi]perylene		
## 1	-3.104722	-3.104722	-3.104722	-3.104722		
## 2	-3.001664	11.406325	8.404660	-2.941631		
## 3	2.915381	9.901294	12.101581	2.915381		
## 4	-5.009793	17.106609	26.270863	6.720453		
## 5	-2.713770	9.439201	6.489451	-2.713770		
## 6	NA	NA	NA	NA		
## 7	-3.217875	7.605885	7.605885	-3.159368		
## 8	-4.838482	-4.838482	-4.838482	-4.774818		
## 9	-2.536414	5.308773	2.890332	-2.536414		
## 10	-3.501276	5.312280	4.768979	-3.440909		
## 11	-3.119617	3.182010	-3.057225	-3.057225		
## 12	-2.467406	4.533142	-2.467406	-2.410025		
## 13	-5.671500	17.146396	17.805873	-5.605553		
## 14	-4.622535	11.068042	18.229717	-4.557429		
## 15	-4.509407	7.403504	8.749596	-4.442102		
## 16	165.382773	483.897743	349.141410	34.914141		
## 17	-1.553335	7.060614	2.588892	-1.506264		
## 18	NA	NA	NA	NA		
## 19	15.124163	61.871576	43.310103	11.686853		
## 20	-2.755354	16.532125	11.021417	-2.700247		
## 21	4.326234	16.369533	11.107897	-4.150846		
## 22	8.199889	22.256842	14.642659	3.338526		
## 23	-1.769606	4.289953	2.895718	-1.769606		
## 24	174.466091	442.875462	456.295931	48.313687		
## 25	46.215815	148.347062	108.407468	18.828666		
## 26	-5.192786	6.524270	5.592231	-5.126212		
## 27	-6.359655	7.631585	8.903516	-6.359655		
## 28	-3.380627	3.855101	-3.380627	-3.380627		
## 29	3.196162	15.040763	9.400477	-2.318784		
## 30	4.494297	16.007084	12.313142	5.233085		
## 31	-4.029401	-3.961106	-3.961106	-3.961106		
## 32	-4.971629	-4.971629	-4.905341	-4.905341		
## 33	-3.185128	7.800313	5.070204	-3.185128		
## 34	6.069425	25.795058	18.714062	6.069425		
## 35	-3.036320	3.373689	-3.036320	-3.036320		
## 36	-4.541341	9.214316	6.581654	-4.475525		
## 37	-4.480153	-4.480153	-4.416151	-4.416151		

## 38	-3.676167	9.642406	7.834455	-3.615902
## 39	-3.625802	10.261704	7.525250	-3.557391
## 40	-3.206173	4.907407	-3.140741	-3.140741
## 41	-5.221088	-5.221088	-5.150533	-5.150533
## 42	-5.724720	-5.724720	-5.724720	-5.650373
## 43	-3.431545	7.625656	4.194111	-3.367998
## 44	-3.618495	4.079031	-3.618495	-3.552704
## 45	-4.401976	9.062892	6.473495	-4.337241
## 46	17.365757	81.401985	59.694789	12.481638
## 47	-3.047007	-3.047007	-3.047007	-3.047007
## 48	-4.488590	-4.488590	-4.488590	-4.424468
## 49	-3.291769	-3.291769	-3.291769	-3.218618
## 50	NA	NA	NA	NA
## 51	5.790200	17.370599	13.317460	3.705728
## 52	15.626804	66.113402	52.289691	7.212371
## 53	-3.269975	3.958391	-3.269975	-3.212607
## 54	-4.369976	5.724053	-4.308427	-4.308427
## 55	-3.588182	4.221390	-3.588182	-3.588182
## 56	-2.335246	6.421926	3.386107	-2.276865
## 57	-3.686920	9.514631	5.233047	-3.627453
## 58	-2.191907	10.350672	7.915220	3.348747
## 59	-2.702609	7.807538	4.984813	-2.642551
## 60	9.673529	29.764706	38.694118	11.905882
## 61	4.107969	17.860735	8.930368	-3.750754
## 62	62.859055	142.566929	116.645669	23.329134
## 63	26.309985	75.171386	75.171386	15.034277
## 64	-3.289955	8.224887	8.910294	3.495577
## 65	-4.853967	14.206733	8.287261	-4.794772
## 66	104.047666	240.610228	273.125124	36.416683
## 67	-2.006815	4.207837	3.042590	-1.942079
## 68	NA	NA	NA	NA
## 69	8.437724	25.313171	27.260338	7.788668
## 70	-4.241630	8.247614	5.478772	-4.182719
## 71	-4.477369	6.488941	5.191153	-4.412480
## 72	-3.654979	5.541419	4.244492	-3.596028
## 73	-4.791510	10.122909	7.423467	-4.724024
## 74	-2.711278	10.242604	7.832579	-2.651027
##	benzo[k]fluoranthene	C1-benzanthracenes/chrysenes	C1-dibenzothiophenes	
## 1	-3.104722		-2.252446	-3.104722
## 2	13.207324		9.605326	-3.842130
## 3	10.451366		12.651653	3.905510
## 4	16.495658		28.103714	-4.887603
## 5	11.799001		7.079401	-3.539700
## 6	NA		NA	NA
## 7	9.946158		9.946158	-3.276381
## 8	-4.902146		7.639708	-4.711153
## 9	5.131814		3.893101	-2.713373
## 10	5.795215		5.855581	-3.622009
## 11	3.993110		-2.495694	-3.868325
## 12	5.393865		3.557656	-3.098603
## 13	19.124826		21.762734	-5.605553
## 14	13.021226		16.276533	-4.752748
## 15	7.403504		14.807008	-4.307493
## 16	343.016122		202.134500	85.754030

## 17	7.060614	3.200812	-1.929901
## 18	NA	NA	NA
## 19	75.620816	28.185940	-4.331010
## 20	21.491763	9.919275	-3.692175
## 21	14.615654	9.354019	-4.209308
## 22	23.428255	14.056953	-3.397097
## 23	5.147944	2.949343	-2.252225
## 24	543.528977	328.801480	43.616523
## 25	148.347062	85.584843	10.270181
## 26	9.986127	6.657418	-5.126212
## 27	6.995620	13.991240	-6.105268
## 28	5.041286	3.439936	-3.380627
## 29	17.547557	7.520381	-2.882813
## 30	23.394969	9.850513	-3.878640
## 31	-4.029401	-2.868387	-3.824516
## 32	-4.971629	-3.446996	-4.573899
## 33	9.100366	5.590225	-3.380136
## 34	27.818200	15.173564	2.781820
## 35	4.858112	3.103794	-3.171268
## 36	9.872481	7.239820	-4.475525
## 37	-4.480153	-3.200109	-4.352149
## 38	10.245056	6.629154	-3.555637
## 39	11.629932	8.209363	-3.899448
## 40	6.085185	3.795062	-3.271605
## 41	-5.221088	-3.598317	-4.727201
## 42	-5.799067	-3.940392	-5.650373
## 43	8.261128	6.990185	-3.558640
## 44	6.579082	3.618495	-3.684286
## 45	12.299640	8.415543	-4.337241
## 46	75.975186	40.700993	7.054839
## 47	3.935718	-2.475693	-3.491363
## 48	-4.488590	-3.077890	-4.167977
## 49	4.023273	-2.340813	-3.218618
## 50	NA	NA	NA
## 51	19.107659	14.475500	3.474120
## 52	72.123711	45.678351	5.349175
## 53	6.310479	3.614183	-3.327343
## 54	6.154895	4.800818	-4.062231
## 55	5.909947	-2.673547	-3.728895
## 56	7.589549	3.561250	-2.977439
## 57	10.109296	7.730638	-3.567987
## 58	11.568399	6.027744	-2.922543
## 59	9.008698	4.564407	-3.543421
## 60	39.438235	29.020588	-5.655294
## 61	22.028240	10.121083	-5.120077
## 62	155.527559	103.685039	10.368504
## 63	97.722802	60.888823	5.412340
## 64	9.595701	8.224887	-3.564118
## 65	15.390627	9.471155	-5.623498
## 66	292.634062	214.598312	22.110129
## 67	5.308348	3.172062	-2.589438
## 68	NA	NA	NA
## 69	27.260338	29.856561	-5.062634
## 70	8.836730	7.658499	-4.064896

## 71	8.435624		5.840047	-4.412480
## 72	7.663665		4.185540	-3.654979
## 73	12.147491		11.472631	-4.656538
## 74	11.447616		5.543056	-3.494535
##	C1-fluoranthenes/pyrenes	C1-fluorenes	C1-naphthalenes	
## 1	-3.104722	-3.104722	-3.104722	
## 2	15.008322	3.902164	-6.003329	
## 3	22.002875	5.115668	-3.630474	
## 4	28.714665	6.109503	-4.887603	
## 5	15.338702	-3.539700	-5.309551	
## 6	NA	NA	NA	
## 7	15.796839	-3.276381	3.568915	
## 8	10.186277	-4.711153	-4.838482	
## 9	6.488501	-2.713373	2.949319	
## 10	10.262359	-3.622009	-3.501276	
## 11	5.864880	-3.868325	-4.554641	
## 12	6.885786	-3.098603	-3.844564	
## 13	32.314362	6.001239	-5.539605	
## 14	29.297759	5.403809	6.510613	
## 15	19.518329	4.644016	5.451671	
## 16	673.781667	104.129894	61.252879	
## 17	8.472737	-1.929901	-2.118184	
## 18	NA	NA	NA	
## 19	39.185332	-4.331010	4.468503	
## 20	19.287479	-3.692175	-7.714992	
## 21	22.800421	-4.209308	-4.033921	
## 22	31.042438	4.158515	-3.279956	
## 23	5.308817	-2.252225	-2.573972	
## 24	738.125771	35.564242	20.801726	
## 25	159.758375	13.123009	6.276222	
## 26	13.980578	-5.126212	-4.926489	
## 27	18.442998	-6.105268	-6.168865	
## 28	5.634378	-3.380627	-3.321318	
## 29	23.814541	-2.882813	-2.945483	
## 30	16.622741	-3.878640	-3.755508	
## 31	-3.824516	-3.824516	-3.756221	
## 32	-4.573899	-4.573899	-4.573899	
## 33	11.050444	-3.380136	3.380136	
## 34	27.312415	5.057855	-3.388763	
## 35	5.262955	-3.171268	-3.103794	
## 36	10.530647	-4.475525	-4.475525	
## 37	-4.352149	-4.352149	-4.416151	
## 38	8.437105	-3.555637	-3.555637	
## 39	14.366386	-3.899448	4.104682	
## 40	5.954321	-3.271605	3.598765	
## 41	-4.727201	-4.727201	-4.727201	
## 42	6.616884	-5.650373	-6.170802	
## 43	9.532071	-3.558640	3.685734	
## 44	5.921173	-3.684286	-3.618495	
## 45	18.125785	4.401976	-4.143037	
## 46	86.828784	14.652357	-5.318263	
## 47	4.760949	-3.491363	-3.618321	
## 48	4.937449	-4.167977	-4.167977	
## 49	5.925184	-3.218618	-3.291769	

## 50	NA	NA	NA
## 51	25.476879	5.095376	4.226846
## 52	90.154639	6.611340	-4.928454
## 53	5.105751	-3.327343	-3.269975
## 54	6.770385	-4.062231	-4.185329
## 55	5.276738	-3.728895	-3.588182
## 56	6.421926	-2.977439	-3.327725
## 57	12.487954	-3.567987	4.400517
## 58	3.957610	-2.922543	-4.140269
## 59	11.411017	-3.543421	-5.525335
## 60	32.741176	-5.655294	-5.432059
## 61	16.670019	-5.120077	-12.502515
## 62	174.968504	13.608661	4.536220
## 63	90.205663	7.517139	6.464739
## 64	10.281109	-3.564118	4.043903
## 65	18.350363	-5.623498	-8.879208
## 66	390.178749	29.913704	16.907746
## 67	5.437820	-2.589438	-3.431006
## 68	NA	NA	NA
## 69	41.539563	7.139612	-4.932823
## 70	11.782306	-4.064896	-4.241630
## 71	14.275671	-4.412480	-4.282701
## 72	9.432203	-3.654979	-4.185540
## 73	14.172073	-4.656538	-4.589052
## 74	11.447616	-3.494535	-4.639297
##	C1-phenanthrenes/anthracenes	C2-benzanthracenes/chrysenes	
## 1	8.522767		-2.252446
## 2	25.814314		6.603662
## 3	45.105894		11.001437
## 4	45.210323		29.325615
## 5	27.137703		3.775680
## 6	NA		NA
## 7	27.498200		7.605885
## 8	18.462628		12.096204
## 9	12.387138		2.890332
## 10	19.921050		7.847687
## 11	13.102392		-2.495694
## 12	14.345387		-2.008354
## 13	47.482328		14.508489
## 14	42.970047		12.370165
## 15	34.325337		13.460916
## 16	918.793183		73.503455
## 17	17.416182		-1.223840
## 18	NA		NA
## 19	40.560256		17.186549
## 20	29.757825		5.180066
## 21	30.400561		5.203173
## 22	38.070914		7.028476
## 23	12.333615		2.359474
## 24	624.051788		114.073983
## 25	154.052718		39.369028
## 26	25.298188		5.192786
## 27	33.706169		19.078964
## 28	11.861849		-2.490988

## 29	32.588319	3.070822		
## 30	22.779312	6.772228		
## 31	6.488018	-2.868387		
## 32	9.280375	-3.446996		
## 33	16.900679	-2.145086		
## 34	39.957051	11.127280		
## 35	11.470543	-2.226635		
## 36	19.086797	5.594406		
## 37	12.800437	-3.200109		
## 38	16.874210	5.905973		
## 39	23.259863	4.788795		
## 40	13.086420	-2.355556		
## 41	10.583287	-3.598317		
## 42	15.612873	-3.940392		
## 43	19.064141	4.575394		
## 44	12.500255	-2.697423		
## 45	30.425425	4.855121		
## 46	130.243176	32.018114		
## 47	14.600243	-2.475693		
## 48	10.900862	-3.077890		
## 49	13.898580	-2.340813		
## 50	NA	NA		
## 51	44.005519	9.843340		
## 52	102.175258	27.647423		
## 53	11.473598	-2.409456		
## 54	14.771749	-3.015899		
## 55	11.257041	-2.673547		
## 56	15.179098	-1.868197		
## 57	22.597250	4.341051		
## 58	20.701345	5.236222		
## 59	20.419715	-2.162088		
## 60	37.205882	26.044118		
## 61	26.195745	5.001006		
## 62	162.007874	60.266929		
## 63	75.171386	38.337407		
## 64	20.562217	6.511369		
## 65	31.373201	4.913162		
## 66	325.148957	97.544687		
## 67	12.947191	2.395230		
## 68	NA	NA		
## 69	53.222565	27.260338		
## 70	21.208151	5.537684		
## 71	26.604659	-2.855134		
## 72	18.864407	-2.593856		
## 73	20.245819	7.423467		
## 74	19.280196	3.253533		
##	C2-dibenzothiophenes	C2-fluoranthenes/pyrenes	C2-fluorenes	C2-naphthalenes
## 1	-3.104722	-3.104722	-3.104722	7.305229
## 2	-3.842130	9.004993	4.742630	10.205659
## 3	9.351222	14.851941	9.901294	17.437278
## 4	13.440907	23.827062	17.717559	18.328509
## 5	-3.539700	8.259301	4.719600	10.029151
## 6	NA	NA	NA	NA
## 7	4.622038	8.776021	5.850681	12.286430

## 8	5.793445	10.822920	-4.711153	8.912993
## 9	-2.713373	3.657155	-2.713373	5.839651
## 10	-3.622009	8.451355	-3.622009	9.055023
## 11	-3.868325	-3.868325	-3.868325	8.111005
## 12	-3.098603	4.188853	-3.098603	8.607232
## 13	7.913721	17.146396	9.232675	18.465350
## 14	7.812736	16.276533	9.765920	20.833962
## 15	6.730458	11.441779	8.076550	20.864420
## 16	91.879318	202.134500	98.004606	179.470935
## 17	-1.929901	3.906873	2.024043	5.648491
## 18	NA	NA	NA	NA
## 19	8.249544	21.998783	8.249544	11.686853
## 20	-3.692175	9.368204	-3.692175	9.368204
## 21	-4.209308	8.769393	4.793935	11.107897
## 22	3.689950	12.299834	5.857064	11.128421
## 23	-2.252225	3.700085	2.466723	6.971174
## 24	59.721085	275.119605	53.681874	39.590382
## 25	16.546403	79.879187	18.828666	18.600439
## 26	-5.126212	5.325934	-5.126212	8.654643
## 27	13.355275	21.622825	8.267551	13.355275
## 28	-3.380627	-3.380627	-3.380627	6.524017
## 29	-2.882813	8.147080	3.196162	9.400477
## 30	-3.878640	7.387885	4.063337	-3.878640
## 31	-3.824516	-3.824516	-3.824516	14.341935
## 32	-4.573899	-4.573899	-4.573899	8.617491
## 33	-3.380136	5.460219	3.510141	9.100366
## 34	5.563640	16.690920	12.138851	10.621495
## 35	-3.171268	-3.171268	-3.171268	6.072641
## 36	-4.475525	5.857672	-4.475525	9.214316
## 37	-4.352149	-4.352149	-4.352149	10.240350
## 38	-3.555637	5.544383	-3.555637	7.834455
## 39	-3.899448	6.841136	4.241504	10.261704
## 40	-3.271605	-3.271605	-3.271605	7.197531
## 41	-4.727201	-4.727201	-4.727201	9.877734
## 42	-5.650373	-5.650373	-5.650373	11.895522
## 43	-3.558640	5.465054	3.812828	8.896599
## 44	-3.684286	-3.684286	-3.684286	6.447500
## 45	-4.337241	7.120844	4.725651	11.004941
## 46	14.109677	46.670471	46.127792	16.280397
## 47	-3.491363	-3.491363	-3.491363	7.617518
## 48	-4.167977	-4.167977	-4.167977	8.335953
## 49	-3.218618	-3.218618	-3.218618	8.778050
## 50	NA	NA	NA	NA
## 51	4.747964	13.896480	7.527260	14.475500
## 52	10.818557	46.880412	9.015464	11.960515
## 53	-3.327343	-3.327343	-3.327343	6.310479
## 54	-4.062231	-4.062231	-4.062231	7.385874
## 55	-3.728895	-3.728895	-3.728895	6.683868
## 56	-2.977439	3.794775	-2.977439	8.173361
## 57	-3.567987	6.541309	3.686920	11.298625
## 58	-2.922543	-2.922543	4.505587	7.306357
## 59	-3.543421	5.225045	3.663537	9.609278
## 60	8.185294	26.044118	9.673529	14.138235
## 61	-5.120077	9.525725	-5.120077	11.311799

## 62	17.496850	97.204724	22.033071	15.811969
## 63	11.275708	46.606259	13.530849	19.544560
## 64	-3.564118	6.854072	4.866391	9.595701
## 65	-5.623498	8.287261	5.919472	11.246997
## 66	33.815492	188.586395	42.269364	35.116087
## 67	-2.589438	3.366270	-2.589438	7.120955
## 68	NA	NA	NA	NA
## 69	9.086779	29.856561	12.332058	20.769781
## 70	-4.064896	5.537684	-4.064896	8.836730
## 71	-4.412480	5.061374	-4.412480	10.382306
## 72	-3.654979	4.303443	-3.654979	8.253178
## 73	-4.656538	7.423467	-4.656538	8.773188
## 74	-3.494535	5.723808	3.615037	7.230073
##	C2-phenanthrenes/anthracenes C3-benzanthracenes/chrysenes			
## 1	9.740305		-2.252446	
## 2	40.222304		3.181764	
## 3	66.008625		5.500719	
## 4	103.861553		15.884708	
## 5	38.346754		-2.182815	
## 6	NA		NA	
## 7	35.104086		4.212490	
## 8	37.561898		9.549635	
## 9	17.695911		-1.887564	
## 10	25.354064		6.640350	
## 11	22.461244		-2.495694	
## 12	20.657357		-2.008354	
## 13	65.947678		7.254245	
## 14	53.387028		6.445507	
## 15	46.440162		6.730458	
## 16	673.781667		28.788853	
## 17	24.006089		-1.223840	
## 18	NA		NA	
## 19	48.122337		8.249544	
## 20	38.023888		-2.204283	
## 21	39.169953		-2.689280	
## 22	42.170859		-2.049972	
## 23	18.232300		1.823230	
## 24	570.369914		32.880148	
## 25	176.875343		15.975837	
## 26	31.955606		-3.328709	
## 27	63.596545		13.991240	
## 28	15.420404		-2.490988	
## 29	35.095113		-1.942765	
## 30	27.704569		-2.770457	
## 31	4.575760		-2.868387	
## 32	14.583446		-3.446996	
## 33	21.450862		-2.145086	
## 34	70.809964		6.575211	
## 35	16.193708		-2.226635	
## 36	27.642948		-3.290827	
## 37	17.280590		-3.200109	
## 38	24.106014		-2.591397	
## 39	29.416886		-2.462809	
## 40	17.666667		-2.355556	

## 41	13.405496	-3.598317		
## 42	19.330224	-3.940392		
## 43	27.325269	-2.541885		
## 44	15.789796	-2.697423		
## 45	33.662172	-2.783603		
## 46	227.925558	20.079156		
## 47	20.948175	-2.475693		
## 48	14.106998	-3.077890		
## 49	10.972563	-2.340813		
## 50	NA	NA		
## 51	50.374738	5.095376		
## 52	114.195876	14.424742		
## 53	16.063037	-2.409456		
## 54	19.080175	-3.015899		
## 55	15.478431	-2.673547		
## 56	23.352459	-1.868197		
## 57	25.570572	-2.557057		
## 58	34.096333	3.409633		
## 59	27.026094	-2.162088		
## 60	69.947059	14.138235		
## 61	37.507544	-3.036325		
## 62	181.448819	25.273228		
## 63	97.722802	17.289419		
## 64	30.843326	3.975362		
## 65	43.804092	-3.906851		
## 66	325.148957	35.116087		
## 67	21.362865	-1.618399		
## 68	NA	NA		
## 69	84.377237	15.577336		
## 70	30.044881	-3.004488		
## 71	31.795812	-2.855134		
## 72	21.222458	-2.593856		
## 73	26.994425	-3.374303		
## 74	28.920293	-2.169022		
##	C3-dibenzothiophenes	C3-fluoranthenes/pyrenes	C3-fluorenes	C3-naphthalenes
## 1	-3.104722	-3.104722	-3.104722	9.131536
## 2	-3.842130	6.003329	5.883262	13.807656
## 3	10.451366	13.751797	17.602300	34.104456
## 4	18.939460	26.881814	40.933671	34.824168
## 5	-3.539700	4.424625	10.619101	14.158801
## 6	NA	NA	NA	NA
## 7	5.558147	7.020817	10.531226	16.381907
## 8	14.006131	15.279416	8.276350	12.732847
## 9	-2.713373	2.831346	3.893101	7.668228
## 10	-3.622009	14.488037	-3.622009	14.488037
## 11	-3.868325	-3.868325	-3.868325	11.230622
## 12	-3.098603	-3.098603	3.155985	10.902494
## 13	9.892152	13.849012	12.530059	32.314362
## 14	11.068042	12.370165	16.276533	29.297759
## 15	8.749596	10.768733	16.153100	28.940970
## 16	67.378167	104.129894	110.255182	336.890834
## 17	-1.929901	2.071114	2.400609	7.531322
## 18	NA	NA	NA	NA
## 19	10.999391	18.561473	14.436701	17.186549

## 20	4.022817	6.612850	5.124959	12.123558
## 21	-4.209308	6.430888	5.437023	19.877290
## 22	3.865662	8.785596	5.857064	17.571191
## 23	-2.252225	2.788469	2.788469	9.652394
## 24	51.668804	161.045623	80.522811	80.522811
## 25	19.399231	57.056562	31.381109	37.086766
## 26	-5.126212	-5.126212	-5.126212	16.643545
## 27	29.254411	25.438618	17.171067	21.622825
## 28	-3.380627	-3.380627	-3.380627	7.710202
## 29	-2.882813	4.637569	3.760191	11.907271
## 30	-3.878640	6.095005	7.387885	13.544456
## 31	-3.824516	-3.824516	-3.824516	8.878341
## 32	-4.573899	-4.573899	-4.573899	9.280375
## 33	-3.380136	-3.380136	4.095164	11.050444
## 34	6.575211	16.185135	23.771916	22.760346
## 35	-3.171268	-3.171268	-3.171268	7.422116
## 36	-4.475525	5.265323	-4.475525	13.163309
## 37	-4.352149	-4.352149	-4.352149	12.160416
## 38	-3.555637	5.122528	-3.555637	11.450357
## 39	-3.899448	4.720384	5.130852	13.682272
## 40	-3.271605	-3.271605	-3.271605	8.506173
## 41	-4.727201	-4.727201	-4.727201	10.583287
## 42	-5.650373	-5.650373	-5.650373	12.638993
## 43	-3.558640	4.130564	4.829582	11.438485
## 44	-3.684286	-3.684286	-3.684286	7.894898
## 45	-4.337241	-4.337241	4.596181	18.125785
## 46	22.792556	36.902233	81.401985	86.828784
## 47	-3.491363	-3.491363	-3.491363	9.521898
## 48	-4.167977	-4.167977	-4.167977	8.977181
## 49	-3.218618	-3.218618	-3.218618	10.241059
## 50	NA	NA	NA	NA
## 51	7.527260	10.422360	14.475500	20.265699
## 52	16.828866	40.269072	19.834021	21.036082
## 53	-3.327343	-3.327343	-3.327343	6.884159
## 54	-4.062231	-4.062231	4.123780	9.847832
## 55	-3.728895	-3.728895	-3.728895	7.739216
## 56	-2.977439	-2.977439	-2.977439	9.924795
## 57	-3.567987	4.519450	5.411447	13.677283
## 58	3.287861	-2.922543	6.088631	12.177262
## 59	-3.543421	-3.543421	3.603479	12.612177
## 60	12.650000	25.300000	15.626471	25.300000
## 61	-5.120077	5.953578	-5.120077	16.074662
## 62	21.385039	71.283465	24.625197	39.529921
## 63	13.530849	36.082265	28.565127	26.309985
## 64	5.414717	6.648450	7.539480	13.708145
## 65	-5.623498	-5.623498	7.103366	15.982574
## 66	38.367577	123.556604	65.029791	78.035750
## 67	-2.589438	-2.589438	-2.589438	9.710393
## 68	NA	NA	NA	NA
## 69	14.928280	27.909394	16.875447	31.154672
## 70	-4.064896	4.712922	5.773330	11.782306
## 71	-4.412480	-4.412480	-4.412480	17.520141
## 72	-3.654979	-3.654979	-3.654979	11.200742
## 73	-4.656538	6.748606	-4.656538	12.147491

## 74	-3.494535	4.097042	4.277793	12.050122
##	C3-phenanthrenes/anthracenes	C4-benzanthracenes/chrysenes		
## 1	5.600675		-2.252446	
## 2	34.819308		-2.401332	
## 3	71.509344		-1.815237	
## 4	128.299566		-3.543512	
## 5	30.087453		-2.182815	
## 6	NA		NA	
## 7	29.253405		-2.340272	
## 8	50.931387		-3.501533	
## 9	11.797274		-1.887564	
## 10	19.921050		-2.233572	
## 11	12.478469		-2.495694	
## 12	13.197756		-2.008354	
## 13	65.947678		-3.627122	
## 14	52.735967		-3.190200	
## 15	49.805391		-3.096011	
## 16	361.391985		7.350345	
## 17	16.474767		-1.223840	
## 18	NA		NA	
## 19	48.122337		-2.681102	
## 20	30.308896		-2.204283	
## 21	26.308178		-2.689280	
## 22	35.142382		-2.049972	
## 23	10.724883		-1.447859	
## 24	342.221948		8.723305	
## 25	148.347062		4.336299	
## 26	25.963930		-3.328709	
## 27	76.315854		6.995620	
## 28	9.489479		-2.490988	
## 29	22.561144		-1.942765	
## 30	22.779312		-2.770457	
## 31	-3.824516		-2.868387	
## 32	6.363686		-3.446996	
## 33	16.250653		-2.145086	
## 34	75.867818		-1.618513	
## 35	8.771592		-2.226635	
## 36	25.668452		-3.290827	
## 37	8.960306		-3.200109	
## 38	21.695413		-2.591397	
## 39	22.575750		-2.462809	
## 40	9.814815		-2.355556	
## 41	7.761077		-3.598317	
## 42	10.408582		-3.940392	
## 43	20.335084		-2.541885	
## 44	8.552806		-2.697423	
## 45	26.541328		-2.783603	
## 46	195.364764		7.597519	
## 47	11.426277		-2.475693	
## 48	9.618408		-3.077890	
## 49	8.778050		-2.340813	
## 50	NA		NA	
## 51	38.215319		-2.084472	
## 52	120.206186		5.409278	

## 53	9.178878	-2.409456
## 54	11.694301	-3.015899
## 55	7.739216	-2.673547
## 56	12.260041	-1.868197
## 57	19.623927	-2.557057
## 58	29.834291	-1.765703
## 59	18.617976	-2.162088
## 60	104.176471	-3.497353
## 61	29.172534	-3.036325
## 62	155.527559	5.637874
## 63	105.239940	11.275708
## 64	31.528733	-2.193303
## 65	32.557096	-3.906851
## 66	260.119166	14.306554
## 67	12.299831	-1.618399
## 68	NA	NA
## 69	103.848907	-3.115467
## 70	25.921074	-3.004488
## 71	21.413506	-2.855134
## 72	14.737818	-2.593856
## 73	23.620122	-3.374303
## 74	20.485208	-2.169022
##	C4-dibenzothiophenes	C4-fluoranthenes/pyrenes
## 1	-3.104722	-3.104722
## 2	-3.842130	-3.842130
## 3	11.551509	5.005654
## 4	15.884708	8.553304
## 5	-3.539700	-3.539700
## 6	NA	NA
## 7	4.270997	-3.276381
## 8	14.006131	5.602453
## 9	-2.713373	-2.713373
## 10	-3.622009	4.286044
## 11	-3.868325	-3.868325
## 12	-3.098603	-3.098603
## 13	6.001239	-5.605553
## 14	7.812736	5.338703
## 15	8.749596	-4.307493
## 16	34.301612	50.227361
## 17	-1.929901	-1.929901
## 18	NA	NA
## 19	6.874620	8.937005
## 20	4.684102	-3.692175
## 21	-4.209308	-4.209308
## 22	-3.397097	3.807091
## 23	-2.252225	-2.252225
## 24	30.867078	73.812577
## 25	16.546403	26.816584
## 26	-5.126212	-5.126212
## 27	21.622825	8.267551
## 28	-3.380627	-3.380627
## 29	-2.882813	-2.882813
## 30	-3.878640	-3.878640
## 31	-3.824516	-3.824516

## 32	-4.573899	-4.573899	7.291723
## 33	-3.380136	-3.380136	5.070204
## 34	5.563640	7.080996	21.242989
## 35	-3.171268	-3.171268	-3.171268
## 36	-4.475525	-4.475525	5.660223
## 37	-4.352149	-4.352149	5.440186
## 38	-3.555637	-3.555637	4.881468
## 39	-3.899448	-3.899448	6.635902
## 40	-3.271605	-3.271605	3.402469
## 41	-4.727201	-4.727201	7.055524
## 42	-5.650373	-5.650373	7.434701
## 43	-3.558640	-3.558640	3.939923
## 44	-3.684286	-3.684286	-3.684286
## 45	-4.337241	-4.337241	10.357591
## 46	23.335236	16.280397	97.682382
## 47	-3.491363	-3.491363	5.840097
## 48	-4.167977	-4.167977	5.322186
## 49	-3.218618	-3.218618	-3.218618
## 50	NA	NA	NA
## 51	4.747964	4.111042	13.317460
## 52	16.227835	21.036082	13.823711
## 53	-3.327343	-3.327343	-3.327343
## 54	-4.062231	-4.062231	6.770385
## 55	-3.728895	-3.728895	-3.658538
## 56	-2.977439	-2.977439	6.421926
## 57	-3.567987	-3.567987	7.730638
## 58	3.044315	-2.922543	7.915220
## 59	-3.543421	-3.543421	8.408118
## 60	6.771471	9.673529	19.347059
## 61	-5.120077	-5.120077	10.121083
## 62	13.608661	31.753543	27.865354
## 63	15.034277	16.537705	21.799702
## 64	5.414717	-3.564118	6.648450
## 65	-5.623498	-5.623498	9.471155
## 66	35.766385	53.974727	59.827408
## 67	-2.589438	-2.589438	4.466781
## 68	NA	NA	NA
## 69	9.735835	11.033946	22.716948
## 70	-4.064896	-4.064896	6.480268
## 71	-4.412480	-4.412480	9.084518
## 72	-3.654979	-3.654979	5.777225
## 73	-4.656538	-4.656538	5.398885
## 74	-3.494535	-3.494535	7.832579
##	C4-phenanthrenes/anthracenes	chrysene dibenz[a,h]anthracene	
## 1	6.026814	4.139630	-3.104722
## 2	30.616977	23.412983	-3.001664
## 3	55.007187	24.753234	-2.200287
## 4	85.533044	39.711770	-4.948698
## 5	23.008052	21.828152	-2.713770
## 6	NA	NA	NA
## 7	28.083268	21.647519	-3.159368
## 8	36.925255	10.822920	-4.838482
## 9	14.156729	10.617547	-2.536414
## 10	19.317382	13.884368	-3.501276

## 11	12.478469	8.111005	-3.119617
## 12	24.100249	12.050125	-2.467406
## 13	46.822851	44.844421	-5.671500
## 14	39.063679	33.855189	-4.622535
## 15	41.728841	23.556604	-4.442102
## 16	140.881621	735.034546	18.375864
## 17	13.179813	11.296983	-1.506264
## 18	NA	NA	NA
## 19	27.498478	59.121729	-3.987279
## 20	21.491763	35.268534	-2.755354
## 21	32.154439	28.646682	-4.150846
## 22	24.599668	42.170859	-3.221385
## 23	10.724883	7.507418	-1.769606
## 24	154.335388	671.023428	16.775586
## 25	91.290500	171.169687	7.987919
## 26	21.303737	19.306512	-5.126212
## 27	54.693029	21.622825	-6.359655
## 28	9.489479	11.268757	-3.380627
## 29	13.787366	23.814541	-2.381454
## 30	16.007084	31.398511	-3.755508
## 31	4.644055	5.873364	-3.961106
## 32	5.435648	6.098532	-4.905341
## 33	11.700470	16.250653	-3.185128
## 34	50.072760	30.852913	-1.972563
## 35	8.771592	10.121068	-3.036320
## 36	18.428632	18.428632	-4.541341
## 37	17.920612	5.568190	-4.416151
## 38	15.066259	15.066259	-3.615902
## 39	15.050500	22.575750	-3.625802
## 40	12.432099	12.432099	-3.140741
## 41	5.926640	6.843859	-5.150533
## 42	8.921642	10.408582	-5.724720
## 43	19.064141	18.428670	-3.367998
## 44	9.868622	13.816071	-3.618495
## 45	21.362532	22.657231	-4.337241
## 46	97.682382	70.548387	4.992655
## 47	16.504623	8.887105	-3.047007
## 48	6.412272	8.977181	-4.488590
## 49	13.167076	9.509555	-3.291769
## 50	NA	NA	NA
## 51	26.055899	30.109039	-3.010904
## 52	96.164948	102.175258	2.884948
## 53	9.752558	12.047278	-3.269975
## 54	12.309791	15.387238	-4.308427
## 55	6.543155	11.257041	-3.588182
## 56	16.346721	12.260041	-2.276865
## 57	13.677283	19.623927	-3.686920
## 58	20.092482	15.221577	-2.191907
## 59	14.413917	15.014497	-2.642551
## 60	74.411765	45.391176	-5.506471
## 61	19.051451	26.791103	-3.750754
## 62	90.724409	162.007874	9.072441
## 63	75.171386	135.308495	-5.412340
## 64	21.933032	17.135181	-3.289955

## 65		24.269835	28.413465		-4.853967
## 66		136.562562	383.675770		14.956852
## 67		12.299831	10.357753		-1.942079
## 68		NA	NA		NA
## 69		71.396123	48.030119		-4.867917
## 70		20.029920	20.619036		-4.182719
## 71		-4.412480	18.817929		-4.477369
## 72		11.790254	12.379767		-3.596028
## 73		31.718449	16.871515		-4.724024
## 74		12.652628	17.472677		-2.711278
##	dibenzothiophene	indeno[1,2,3-cd]pyrene	phenanthrene	NA	
## 1	-3.104722		-3.104722	12.17538	NA
## 2	-3.842130		-3.001664	30.61698	NA
## 3	-2.915381		-2.200287	37.95496	NA
## 4	-4.887603		-5.009793	39.10082	NA
## 5	-3.539700		-2.713770	37.16685	NA
## 6	NA		NA	NA	NA
## 7	-3.276381		-3.217875	32.17875	NA
## 8	-4.647489		-4.902146	19.09927	NA
## 9	-2.654387		-2.536414	15.33646	NA
## 10	-3.561642		-3.501276	33.20175	NA
## 11	-3.805933		-3.119617	18.71770	NA
## 12	-3.098603		-2.467406	22.37880	NA
## 13	-5.539605		-5.671500	57.37448	NA
## 14	-4.687642		-4.622535	59.89764	NA
## 15	-4.240189		-4.509407	39.03666	NA
## 16	140.881621		39.201842	1776.33349	NA
## 17	-1.929901		-1.553335	33.89095	NA
## 18	NA		NA	NA	NA
## 19	-4.262264		13.061777	57.74680	NA
## 20	-3.692175		-2.755354	60.61779	NA
## 21	-4.209308		-4.209308	43.26234	NA
## 22	-3.338526		-3.221385	64.42770	NA
## 23	-2.198601		-1.769606	12.86986	NA
## 24	36.906289		42.274476	657.60296	NA
## 25	11.411312		18.828666	199.69797	NA
## 26	-5.059638		-5.192786	41.94173	NA
## 27	-6.041672		-6.359655	36.88600	NA
## 28	-3.380627		-3.380627	17.19968	NA
## 29	-2.820143		-2.381454	52.64267	NA
## 30	-3.817074		4.124902	32.62983	NA
## 31	-3.756221		-4.029401	12.97604	NA
## 32	-4.507611		-4.971629	15.90921	NA
## 33	-3.380136		-3.185128	25.35102	NA
## 34	-2.630084		4.754383	37.93391	NA
## 35	-3.171268		-3.036320	14.16949	NA
## 36	-4.475525		-4.541341	22.37762	NA
## 37	-4.288147		-4.480153	18.56063	NA
## 38	-3.495372		-3.676167	19.28481	NA
## 39	-3.899448		-3.625802	32.15334	NA
## 40	-3.271605		-3.206173	17.01235	NA
## 41	-4.727201		-5.221088	17.63881	NA
## 42	-5.576026		-5.724720	19.33022	NA
## 43	-3.558640		-3.431545	27.96074	NA

```
## 44      -3.618495      -3.618495      18.42143 NA
## 45      -4.272506      -4.401976      42.72506 NA
## 46       5.969479      14.652357     113.96278 NA
## 47      -3.427883      -3.047007      19.04380 NA
## 48      -4.103854      -4.488590      17.95436 NA
## 49      -3.218618      -3.291769      24.13964 NA
## 50              NA              NA              NA NA
## 51      -3.300414      -3.068806      63.69220 NA
## 52       5.830000       7.813402     144.24742 NA
## 53      -3.269975      -3.269975      16.06304 NA
## 54      -4.000682      -4.369976      18.46469 NA
## 55      -3.658538      -3.588182      15.47843 NA
## 56      -2.977439      -2.335246      15.17910 NA
## 57      -3.567987      -3.686920      33.30121 NA
## 58      -2.861656       2.618111      21.91907 NA
## 59      -3.483363      -2.702609      30.62957 NA
## 60      -5.580882       8.185294      38.69412 NA
## 61      -5.060542      -3.750754      35.72147 NA
## 62       9.720472      22.681102     187.92913 NA
## 63       6.013711      11.275708     105.23994 NA
## 64      -3.495577      -3.289955      26.04548 NA
## 65      -5.564304      -4.853967      44.39604 NA
## 66      22.110129      31.864598     390.17875 NA
## 67      -2.524702      -2.006815      13.59455 NA
## 68              NA              NA              NA NA
## 69      -4.997729      -4.932823      61.01123 NA
## 70      -4.064896      -4.241630      28.86665 NA
## 71      -4.347591      -4.477369      40.88033 NA
## 72      -3.596028      -3.654979      27.70710 NA
## 73      -4.589052      -4.791510      27.66929 NA
## 74      -3.434285      -2.711278      25.90776 NA
```

```
#get the column names so I don't have to individually type each one
```

```
all_columns <- names(reshaped2_df)
```

```
# Remove the columns you don't want to include in the model
```

```
excluded_columns <- c('avg_p450', 'latitude', 'longitude', 'avg_SOD', 'site_name', 'site_number', 'NA')
```

```
independent_columns <- all_columns[!all_columns %in% excluded_columns]
```

```
# Enclose each column name in backticks to handle special characters
```

```
independent_columns <- sapply(independent_columns, function(x) paste0("`", x, "`"))
```

```
# Create a string representing the formula
```

```
formula_str <- paste("avg_p450 ~", paste(independent_columns, collapse = " + "))
```

```
# Convert the string to a formula object
```

```
formula <- as.formula(formula_str)
```

```
# Now you can use this formula in your model
```

```
#lm_model <- lm(formula, data = reshaped_df)
```

```
#summary(lm_model)
```

```
indvlm_model <- lm(formula, data = reshaped2_df)
```

```
print(summary(indvlm_model))
```

```
##
## Call:
## lm(formula = formula, data = reshaped2_df)
##
## Residuals:
```

	Min	1Q	Median	3Q	Max
	-3998260	-925684	-46998	893887	6773539

```
##
## Coefficients:
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	8253120	2893118	2.853	0.00754 **
acenaphthene	103342	182869	0.565	0.57593
acenaphthylene	1822594	1027471	1.774	0.08560 .
anthracene	44812	148264	0.302	0.76442
`benz[a]anthracene`	152252	108074	1.409	0.16854
`benzo[a]pyrene`	-121907	266145	-0.458	0.65001
`benzo[b]fluoranthene`	-40744	206181	-0.198	0.84460
`benzo[e]pyrene`	-212536	209781	-1.013	0.31860
`benzo[ghi]perylene`	-161066	412598	-0.390	0.69885
`benzo[k]fluoranthene`	38340	212082	0.181	0.85768
`C1-benzanthracenes/chrysenes`	-139353	230364	-0.605	0.54949
`C1-dibenzothiophenes`	-358848	479115	-0.749	0.45934
`C1-fluoranthenes/pyrenes`	-130668	185601	-0.704	0.48651
`C1-fluorenes`	-81602	226397	-0.360	0.72089
`C1-naphthalenes`	201789	149565	1.349	0.18675
`C1-phenanthrenes/anthracenes`	78012	233322	0.334	0.74030
`C2-benzanthracenes/chrysenes`	300661	226475	1.328	0.19371
`C2-dibenzothiophenes`	195132	455744	0.428	0.67140
`C2-fluoranthenes/pyrenes`	-23132	238330	-0.097	0.92328
`C2-fluorenes`	-9409	216261	-0.044	0.96557
`C2-naphthalenes`	-217272	226659	-0.959	0.34495
`C2-phenanthrenes/anthracenes`	7161	217795	0.033	0.97398
`C3-benzanthracenes/chrysenes`	-346058	300052	-1.153	0.25732
`C3-dibenzothiophenes`	562430	601522	0.935	0.35679
`C3-fluoranthenes/pyrenes`	-159452	168664	-0.945	0.35155
`C3-fluorenes`	-209370	174778	-1.198	0.23975
`C3-naphthalenes`	76862	177662	0.433	0.66819
`C3-phenanthrenes/anthracenes`	83530	151012	0.553	0.58402
`C4-benzanthracenes/chrysenes`	69312	424837	0.163	0.87143
`C4-dibenzothiophenes`	-694340	512308	-1.355	0.18481
`C4-fluoranthenes/pyrenes`	148775	216692	0.687	0.49730
`C4-naphthalenes`	109153	167164	0.653	0.51844
`C4-phenanthrenes/anthracenes`	2694	70794	0.038	0.96988
chrysene	241653	155819	1.551	0.13077
`dibenz[a,h]anthracene`	414524	876871	0.473	0.63961
dibenzothiophene	-195285	630474	-0.310	0.75876
`indeno[1,2,3-cd]pyrene`	-35786	415577	-0.086	0.93191
phenanthrene	-103317	98558	-1.048	0.30236

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2383000 on 32 degrees of freedom
```

```
## (4 observations deleted due to missingness)
## Multiple R-squared: 0.5308, Adjusted R-squared: -0.01167
## F-statistic: 0.9785 on 37 and 32 DF, p-value: 0.5285

# GLM- p450 as response
indvglm_model<- glm(formula, data = reshaped2_df, family = poisson())
print(summary(indvglm_model))

##
## Call:
## glm(formula = formula, family = poisson(), data = reshaped2_df)
##
## Coefficients:
##
##             Estimate Std. Error  z value Pr(>|z|)
## (Intercept)    1.600e+01  5.888e-04 27175.889 < 2e-16 ***
## acenaphthene    2.481e-02  3.538e-05   701.326 < 2e-16 ***
## acenaphthylene  3.656e-01  2.102e-04 1739.497 < 2e-16 ***
## anthracene      1.233e-02  2.874e-05   428.867 < 2e-16 ***
## `benz[a]anthracene` 3.089e-02  2.274e-05 1358.295 < 2e-16 ***
## `benzo[a]pyrene`   -4.739e-03  5.589e-05  -84.792 < 2e-16 ***
## `benzo[b]fluoranthene` -1.615e-02  4.240e-05 -380.945 < 2e-16 ***
## `benzo[e]pyrene`   -3.192e-02  4.153e-05 -768.562 < 2e-16 ***
## `benzo[ghi]perylene` -6.793e-02  8.911e-05 -762.254 < 2e-16 ***
## `benzo[k]fluoranthene` 1.211e-02  4.504e-05  269.006 < 2e-16 ***
## `C1-benzanthracenes/chrysenes` -1.913e-02  4.366e-05 -438.086 < 2e-16 ***
## `C1-dibenzothiophenes` -9.704e-02  1.057e-04 -917.955 < 2e-16 ***
## `C1-fluoranthenes/pyrenes` -3.781e-02  4.000e-05 -945.323 < 2e-16 ***
## `C1-fluorenes`     -2.006e-02  4.436e-05 -452.288 < 2e-16 ***
## `C1-naphthalenes`   3.969e-02  2.883e-05 1376.795 < 2e-16 ***
## `C1-phenanthrenes/anthracenes` 2.623e-02  4.712e-05  556.590 < 2e-16 ***
## `C2-benzanthracenes/chrysenes` 5.556e-02  4.394e-05 1264.525 < 2e-16 ***
## `C2-dibenzothiophenes` 5.796e-02  9.751e-05  594.422 < 2e-16 ***
## `C2-fluoranthenes/pyrenes` -3.606e-03  4.630e-05  -77.876 < 2e-16 ***
## `C2-fluorenes`     -3.688e-04  4.281e-05   -8.616 < 2e-16 ***
## `C2-naphthalenes`  -5.017e-02  4.767e-05 -1052.447 < 2e-16 ***
## `C2-phenanthrenes/anthracenes` 6.099e-03  4.318e-05  141.254 < 2e-16 ***
## `C3-benzanthracenes/chrysenes` -6.968e-02  6.057e-05 -1150.397 < 2e-16 ***
## `C3-dibenzothiophenes` 6.209e-02  1.233e-04  503.586 < 2e-16 ***
## `C3-fluoranthenes/pyrenes` -3.720e-02  3.300e-05 -1127.241 < 2e-16 ***
## `C3-fluorenes`     -3.880e-02  3.323e-05 -1167.788 < 2e-16 ***
## `C3-naphthalenes`   1.292e-02  3.620e-05  356.898 < 2e-16 ***
## `C3-phenanthrenes/anthracenes` 2.101e-02  3.114e-05  674.450 < 2e-16 ***
## `C4-benzanthracenes/chrysenes` 7.781e-03  9.168e-05   84.869 < 2e-16 ***
## `C4-dibenzothiophenes` -9.891e-02  1.006e-04 -983.087 < 2e-16 ***
## `C4-fluoranthenes/pyrenes` 2.872e-02  4.420e-05  649.876 < 2e-16 ***
## `C4-naphthalenes`   6.489e-03  3.153e-05  205.792 < 2e-16 ***
## `C4-phenanthrenes/anthracenes` 9.562e-04  1.409e-05   67.867 < 2e-16 ***
## chrysene          3.736e-02  2.932e-05 1274.052 < 2e-16 ***
## `dibenz[a,h]anthracene` 3.968e-02  1.731e-04  229.260 < 2e-16 ***
## dibenzothiophene  5.975e-03  1.316e-04   45.395 < 2e-16 ***
## `indeno[1,2,3-cd]pyrene` -4.502e-04  8.860e-05  -5.081 3.76e-07 ***
## phenanthrene      -2.266e-02  1.931e-05 -1173.937 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```



```
## (Dispersion parameter for poisson family taken to be 1)
##
## Null deviance: 71801382 on 69 degrees of freedom
## Residual deviance: 30482761 on 32 degrees of freedom
## (4 observations deleted due to missingness)
## AIC: Inf
##
## Number of Fisher Scoring iterations: 5
```

PCA of biomarkers and analyte data

```
#pca for pah and biomarkers, using reshaped_df
#install.packages("FactoMineR")
#install.packages("factoextra")
library('FactoMineR')
library('factoextra')

# Specify the columns you want to use for PCA
pca_columns <- c("avg_SOD", "avg_p450", "SumPAHs", "SumPAHs16", "SumPAHs42_DMNcorrected", "SumPAHsHMW",

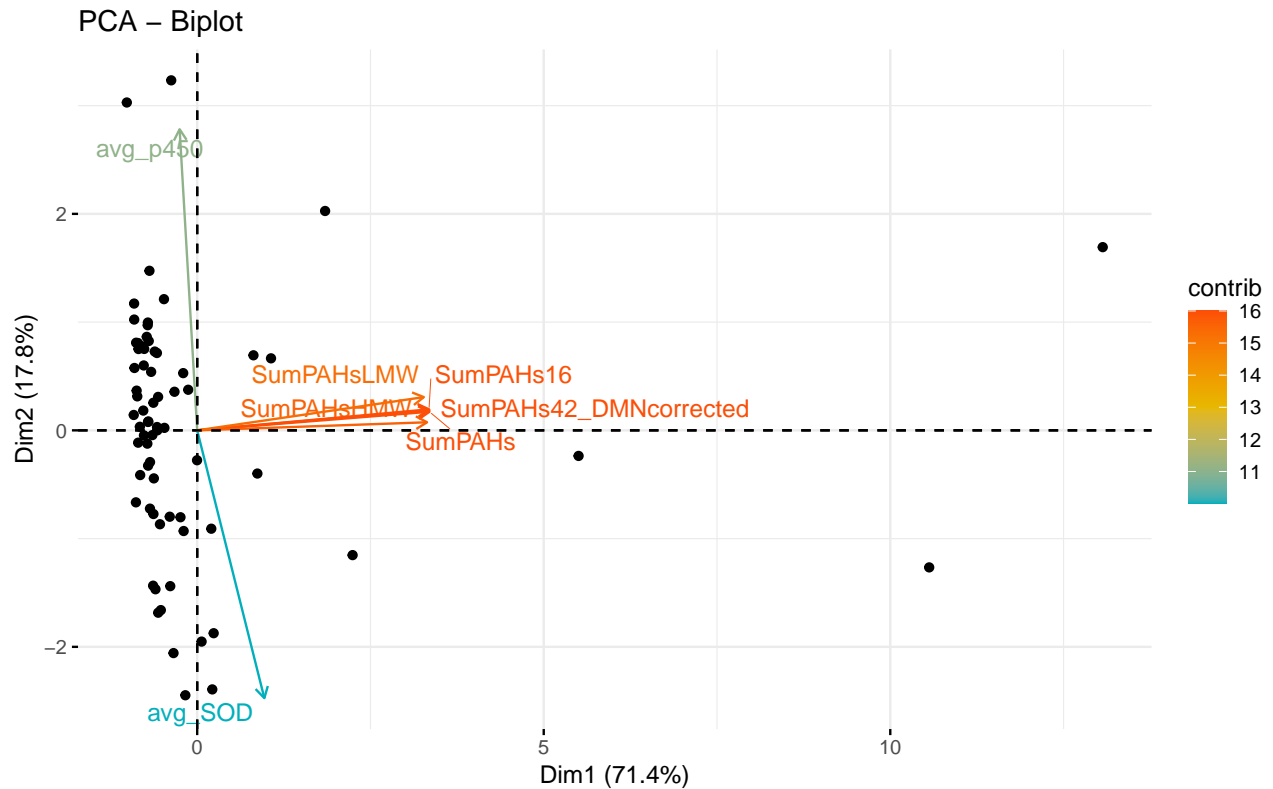
# Remove rows with NAs in the specified columns only
df_clean <- reshaped_df[complete.cases(reshaped_df[, pca_columns]), ]

# Selecting the relevant variables for PCA
pca_data <- df_clean[, pca_columns]

# Performing PCA
pca_res <- PCA(pca_data, scale.unit = TRUE, graph = FALSE)

# Plotting the PCA
analytepcaplot<- fviz_pca_biplot(pca_res, label = "var", col.var = "contrib",
                                gradient.cols = c("#00AFBB", "#E7B800", "#FC4E07"),
                                repel = TRUE) # Avoid text overlapping (slow if many points)

print(analytepcaplot)
```



```
ggsave(plot=analytepcaplot, filename="/Users/cmantegna/Documents/WDFWmussels/output/analytepca.png", width=1000, height=1000)
```

Clustering based on k-means results. Needs to be revisited to verify it is the best option for this purpose

#different pca option

```
library(FactoMineR)
```

```
library(factoextra)
```

Assuming pca_data is prepared for PCA

```
pca_result <- PCA(pca_data, graph = FALSE)
```

If you need to perform clustering (e.g., k-means)

```
set.seed(123) # for reproducibility
```

```
clusters <- kmeans(pca_data, centers = 3) # change centers according to your data
```

Add the cluster assignments to your PCA data

```
pca_data$cluster <- as.factor(clusters$cluster)
```

Now plot the PCA with fviz_pca_ind

```
fviz_pca_ind(pca_result,
  col.ind = pca_data$cluster, # color by cluster
  palette = c("#00AFBB", "#E7B800", "#FC4E07"), # customize colors
  addEllipses = TRUE, # add confidence ellipses around clusters
  ellipse.level = 0.95, # 95% confidence ellipse
  legend.title = "Cluster")
```

