SEACAR Coastal Wetlands Analysis: Species Richness

Last compiled on 08 June, 2023

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# Important Notes

These scripts were created by [J.E. Panzik](mailto:jepanzik@usf.edu) ([jepanzik@usf.edu](mailto:jepanzik@usf.edu)) for SEACAR.

All scripts and outputs can be found on the SEACAR GitHub repository:

<https://github.com/FloridaSEACAR/SEACAR_Trend_Analyses>

This markdown file is designed to be compiled by [SEACAR\_CoastalWetlands\_SpeciesRichness\_ReportRender.R](https://github.com/FloridaSEACAR/SEACAR_Trend_Analyses/blob/main/Coastal_Wetlands/SEACAR_CoastalWetlands_SpeciesRichness_ReportRender.R) (<https://github.com/FloridaSEACAR/SEACAR_Trend_Analyses/blob/main/Coastal_Wetlands/SEACAR_CoastalWetlands_SpeciesRichness_ReportRender.R>).

# Libraries and Settings

Loads libraries used in the script. The inclusion of scipen option limits how frequently R defaults to scientific notation. Sets default settings for displaying warning and messages in created document, and sets figure dpi.

library(knitr)  
library(data.table)  
library(dplyr)  
library(lubridate)  
library(ggplot2)  
library(scales)  
library(tidyr)  
library(gridExtra)  
#library(tidyverse)  
library(ggpubr)  
library(scales)  
options(scipen=999)  
knitr::opts\_chunk$set(  
 warning=FALSE,  
 message=FALSE,  
 dpi=200  
 )

# File Import

Imports file that is determined in the SEACAR\_CoastalWetlands\_SpeciesRichness\_ReportRender.R script.

The command fread is used because of its improved speed while handling large data files. Only columns that are used by the script are imported from the file, and are designated in the select input.

The script then gets the name of the parameter as it appears in the data file and units of the parameter.

The latest version of Coastal Wetlands data is available at: <https://usf.box.com/s/jpwsi8kram54xt6zyma5wo9mqferddcn>

The file being used for the analysis is: **All\_CW\_Parameters-2023-Jun-05.txt**

#Import data from coastal wetlands file  
data <- fread(file\_in, sep="|", header=TRUE, stringsAsFactors=FALSE,  
 na.strings=c("NULL","","NA"))  
  
cat(paste("The data file used is:", file\_short, sep="\n"))

## The data file used is:  
## All\_CW\_Parameters-2023-Jun-05.txt

# Data Filtering

The processing and filtering that is done to the data is as follows:

1. Only take data rows that are percent cover
2. Only keep data rows that are Marsh, Marsh succulents, and Mangroves and associate
3. Set parameter names to Species Richness
4. Sets units
5. Removes rows that contains NA values in ManagedAreaName, GenusName, SpeciesName, Month, Year, SpeciesGroup1, and removes invasive species data
6. Sets ResultValue to be numeric values and removes rows where percent cover is 0
7. Removes duplicates (MADup==1)
8. Combines genus and species names
9. Corrects some managed area names to match what is being used with other habitats
10. Creates species richness dataset
    * Grouped based on common ManagedAreaName, ProgramID, ProgramName, ProgramLocationID, and SampleDate
    * SpeciesRichness determined based on the number of unique species (gensp) in each group
11. Merges data with managed area data to determine correct AreaID
12. Writes to file with “\_UsedData” file name to indicate what data was used for species richness.

# Only interested in Percent Cover measurements  
data <- data[data$ParameterName=="Percent Cover - Species Composition"]  
# Make species group name uniform  
data$SpeciesGroup1[data$SpeciesGroup1=="Marsh Succulents"] <- "Marsh succulents"  
# Only keep data rows that are Marsh, Marsh succulents, and Mangroves and assoc.  
data <- data[SpeciesGroup1=="Marsh"|  
 SpeciesGroup1=="Marsh succulents"|  
 SpeciesGroup1=="Mangroves and associate", ]  
setnames(data, "SpeciesGroup1", "SpeciesGroup")  
# Create ParameterName Column  
data$ParameterName <- "Species Richness"  
parameter <- "Species Richness"  
  
# Sets units for species richness  
unit <- "# of species"  
data$ParameterUnits <- unit  
  
# Replace instances where NA values imported as blank character string or as "NA"  
# data <- replace(data, data=="", NA)  
# data <- replace(data, data=="NA", NA)  
  
# Remove rows with missing ManagedAreaName  
data <- data[!is.na(data$ManagedAreaName),]  
data <- data[data$ManagedAreaName!="NA",]  
# Remove rows with missing GenusName  
data <- data[!is.na(data$GenusName),]  
# Remove rows with missing SpeciesName  
data <- data[!is.na(data$SpeciesName),]  
# Remove rows with missing Months  
data <- data[!is.na(data$Month),]  
# Remove rows with missing Years  
data <- data[!is.na(data$Year),]  
# Set ResultValue to be a number value  
data$ResultValue <- as.numeric(data$ResultValue)  
# Remove rows where ResultValue is 0  
data <- data[data$ResultValue!=0,]  
# Remove duplicate rows  
data <- data[data$MADup==1,]  
# Create variable that combines the genus and species name  
data$gensp <- paste(data$GenusName, data$SpeciesName, sep=" ")  
# Corrects Managed Area names to be consistent with official names  
data$ManagedAreaName[data$ManagedAreaName=="Apalachicola Bay"] <-  
 "Apalachicola Bay Aquatic Preserve"  
data$ManagedAreaName[data$ManagedAreaName=="Big Bend Seagrasses"] <-  
 "Big Bend Seagrasses Aquatic Preserve"  
data$ManagedAreaName[data$ManagedAreaName=="Cockroach Bay"] <-  
 "Cockroach Bay Aquatic Preserve"  
data$ManagedAreaName[data$ManagedAreaName=="Guana River Marsh"] <-  
 "Guana River Marsh Aquatic Preserve"  
data$ManagedAreaName[data$ManagedAreaName=="Guana Tolomato Matanzas NERR"] <-  
 "Guana Tolomato Matanzas National Estuarine Research Reserve"  
  
# Create Species Richness values for groups of unique combinations of  
# ManagedAreaName, ProgramID, ProgramName, ProgramLocationID, and SampleDate.  
data <- data %>%  
 group\_by(ManagedAreaName, ProgramID, ProgramName, ProgramLocationID,  
 SampleDate, SpeciesGroup) %>%  
 summarise(ParameterName=parameter,  
 Year=unique(Year), Month=unique(Month),  
 SpeciesRichness=length(unique(gensp)))  
  
# Adds AreaID for each managed area by combining the MA\_All datatable to the  
# data based on ManagedAreaName  
data <- merge.data.frame(MA\_All[,c("AreaID", "ManagedAreaName")],  
 data, by="ManagedAreaName", all=TRUE)  
  
# Writes this data that is used by the rest of the script to a text file  
fwrite(data, paste0(out\_dir,"/CoastalWetlands\_", param\_file, "\_UsedData.txt"),  
 sep="|")  
  
# Makes sure SampleDate is being stored as a Date object  
data$SampleDate <- as.Date(data$SampleDate)  
  
# Creates a variable with the names of all the managed areas that contain  
# species observations  
MA\_Include <- unique(data$ManagedAreaName[!is.na(data$SpeciesRichness)])  
  
# Puts the managed areas in alphabetical order  
MA\_Include <- MA\_Include[order(MA\_Include)]  
  
# Determines the number of managed areas used  
n <- length(MA\_Include)

# Managed Area Statistics

Gets summary statistics for each managed area. Uses piping from dplyr package to feed into subsequent steps. The following steps are performed:

1. Group data that have the same ManagedAreaName, Year, Month, and SpeciesGroup.
   * Second summary statistics do not use the Month grouping and are only for ManagedAreaName, Year, and SpeciesGroup..
   * Third summary statistics do not use Year grouping and are only for ManagedAreaName, Month, and SpeciesGroup.
   * Fourth summary statistics are only grouped based on ManagedAreaName and SpeciesGroup.
     + Determines the years that the minimum and maximum species richness occurred
2. For each group, provide the following information: Parameter Name (ParameterName), Number of Entries (N\_Data), Lowest Value (Min), Largest Value (Max), Median, Mean, Standard Deviation, and a list of all Programs included in these measurements.
3. Sort the data in ascending (A to Z and 0 to 9) order based on ManagedAreaName then Year then Month
4. Write summary stats to a pipe-delimited .txt file in the output directory
   * [Coastal Wetlands Output Files in SEACAR GitHub](https://github.com/FloridaSEACAR/SEACAR_Trend_Analyses/tree/main/Coastal_Wetlands/output) (<https://github.com/FloridaSEACAR/SEACAR_Trend_Analyses/tree/main/Coastal_Wetlands/output>)

# Create summary statistics for each managed area based on Year and Month  
# intervals.  
MA\_YM\_Stats <- data %>%  
 group\_by(AreaID, ManagedAreaName, Year, Month, SpeciesGroup) %>%  
 summarize(ParameterName=parameter,  
 N\_Data=length(na.omit(SpeciesRichness)),  
 Min=min(SpeciesRichness),  
 Max=max(SpeciesRichness),  
 Median=median(SpeciesRichness),  
 Mean=mean(SpeciesRichness),  
 StandardDeviation=sd(SpeciesRichness),  
 Programs=paste(sort(unique(ProgramName), decreasing=FALSE),  
 collapse=', '),  
 ProgramIDs=paste(sort(unique(ProgramID), decreasing=FALSE),  
 collapse=', '))  
# Puts the data in order based on ManagedAreaName, Year, then Month  
MA\_YM\_Stats <- as.data.table(MA\_YM\_Stats[order(MA\_YM\_Stats$ManagedAreaName,  
 MA\_YM\_Stats$Year,  
 MA\_YM\_Stats$Month), ])  
# Writes summary statistics to file  
fwrite(MA\_YM\_Stats, paste0(out\_dir,"/CoastalWetlands\_", param\_file,  
 "\_MA\_MMYY\_Stats.txt"), sep="|")  
# Removes variable storing data to improve computer memory  
rm(MA\_YM\_Stats)  
  
# Create summary statistics for each managed area based on Year intervals  
MA\_Y\_Stats <- data %>%  
 group\_by(AreaID, ManagedAreaName, Year, SpeciesGroup) %>%  
 summarize(ParameterName=parameter,  
 N\_Data=length(na.omit(SpeciesRichness)),  
 Min=min(SpeciesRichness),  
 Max=max(SpeciesRichness),  
 Median=median(SpeciesRichness),  
 Mean=mean(SpeciesRichness),  
 StandardDeviation=sd(SpeciesRichness),  
 Programs=paste(sort(unique(ProgramName), decreasing=FALSE),  
 collapse=', '),  
 ProgramIDs=paste(sort(unique(ProgramID), decreasing=FALSE),  
 collapse=', '))  
# Puts the data in order based on ManagedAreaName then Year  
MA\_Y\_Stats <- as.data.table(MA\_Y\_Stats[order(MA\_Y\_Stats$ManagedAreaName,  
 MA\_Y\_Stats$Year), ])  
# Writes summary statistics to file  
fwrite(MA\_Y\_Stats, paste0(out\_dir,"/CoastalWetlands\_", param\_file,  
 "\_MA\_Yr\_Stats.txt"), sep="|")  
  
# Create summary statistics for each managed area based on Month intervals.  
MA\_M\_Stats <- data %>%  
 group\_by(AreaID, ManagedAreaName, Month, SpeciesGroup) %>%  
 summarize(ParameterName=parameter,  
 N\_Data=length(na.omit(SpeciesRichness)),  
 Min=min(SpeciesRichness),  
 Max=max(SpeciesRichness),  
 Median=median(SpeciesRichness),  
 Mean=mean(SpeciesRichness),  
 StandardDeviation=sd(SpeciesRichness),  
 Programs=paste(sort(unique(ProgramName), decreasing=FALSE),  
 collapse=', '),  
 ProgramIDs=paste(sort(unique(ProgramID), decreasing=FALSE),  
 collapse=', '))  
# Puts the data in order based on ManagedAreaName then Month  
MA\_M\_Stats <- as.data.table(MA\_M\_Stats[order(MA\_M\_Stats$ManagedAreaName,  
 MA\_M\_Stats$Month), ])  
# Writes summary statistics to file  
fwrite(MA\_M\_Stats, paste0(out\_dir,"/CoastalWetlands\_", param\_file,  
 "\_MA\_Mo\_Stats.txt"), sep="|")  
# Removes variable storing data to improve computer memory  
rm(MA\_M\_Stats)  
  
# Create summary overall statistics for each managed area.  
MA\_Ov\_Stats <- data %>%  
 group\_by(AreaID, ManagedAreaName, SpeciesGroup) %>%  
 summarize(ParameterName=parameter,  
 N\_Years=length(unique(na.omit(Year))),  
 EarliestYear=min(Year),  
 LatestYear=max(Year),  
 N\_Data=length(na.omit(SpeciesRichness)),  
 Min=min(SpeciesRichness),  
 Max=max(SpeciesRichness),  
 Median=median(SpeciesRichness),  
 Mean=mean(SpeciesRichness),  
 StandardDeviation=sd(SpeciesRichness),  
 Programs=paste(sort(unique(ProgramName), decreasing=FALSE),  
 collapse=', '),  
 ProgramIDs=paste(sort(unique(ProgramID), decreasing=FALSE),  
 collapse=', '))  
# Puts the data in order based on ManagedAreaName  
MA\_Ov\_Stats <- as.data.table(MA\_Ov\_Stats[order(MA\_Ov\_Stats$ManagedAreaName), ])  
# Creates Year\_MinRichness and Year\_MaxRichness columns  
MA\_Ov\_Stats$Year\_MinRichness <- NA  
MA\_Ov\_Stats$Year\_MaxRichness <- NA  
  
# Loops through each ManagedAreaName.  
# Determines what year the minimum and maximum species richness occurred  
for(m in 1:nrow(MA\_Ov\_Stats)){  
 # Stores ManagedAreaName for this row  
 ma <- MA\_Ov\_Stats$ManagedAreaName[m]  
   
 # Skips to next row if there are no data for this combination  
 if(MA\_Ov\_Stats$N\_Data[m]==0){  
 next  
 }  
 # Gets subset of data from MA\_Y\_Stats (yearly summary stats) with this  
 # ManagedAreaName  
 ds <- MA\_Y\_Stats[MA\_Y\_Stats$ManagedAreaName==ma,]  
 # Gets the minimum and maximum Mean (yearly averages)  
 min <- min(ds$Mean)  
 max <- max(ds$Mean)  
 #Determines what years those minimum and maximum values occured  
 year\_min <- ds$Year[ds$Mean==min]  
 year\_max <- ds$Year[ds$Mean==max]  
 # Stores the occurrence years of the minimum and maximum into the overall  
 # stats for this row  
 MA\_Ov\_Stats$Year\_MinRichness[m] <- year\_min  
 MA\_Ov\_Stats$Year\_MaxRichness[m] <- year\_max  
}  
# Replaces blank ProgramIDs with NA (missing values)  
MA\_Ov\_Stats$ProgramIDs <- replace(MA\_Ov\_Stats$ProgramIDs,  
 MA\_Ov\_Stats$ProgramIDs=="", NA)  
MA\_Ov\_Stats$Programs <- replace(MA\_Ov\_Stats$Programs,  
 MA\_Ov\_Stats$Programs=="", NA)  
# Write overall statistics to file  
fwrite(MA\_Ov\_Stats, paste0(out\_dir,"/CoastalWetlands\_", param\_file,  
 "\_MA\_Overall\_Stats.txt"), sep="|")  
# Removes entries from the overall statistics that do not have data.  
# Based on presence or absence of EarliestYear  
MA\_Ov\_Stats <- MA\_Ov\_Stats[!is.na(MA\_Ov\_Stats$EarliestYear), ]

# Appendix I: Managed Area Species Richness

The plots shown here are the species richness for each managed area with a yearly average.

1. Set common plot theme.
2. Determine the earliest and latest year of the data to create x-axis scale and intervals
3. Determine the upper and lower limit of the plot for better y-axis labels
4. Determines what species groups are present and adjusts legend entries
5. Add the plot line
6. Set the plot type as a point plot with the size of the points
7. Create the title, x-axis, y-axis, and color fill labels
8. Set the y and x limits
9. Apply common plot theme
10. Add table with summary statistics below each figure

* Numerical non-integer values are rounded to 2 decimal places
* StandardDeviation is renamed StDev for space reasons

1. Create file name to save figure
2. Save figure as png file

* [Coastal Wetlands Figures in SEACAR GitHub](https://github.com/FloridaSEACAR/SEACAR_Trend_Analyses/tree/main/Coastal_Wetlands/output/Figures) (<https://github.com/FloridaSEACAR/SEACAR_Trend_Analyses/tree/main/Coastal_Wetlands/output/Figures>)

# Defines standard plot theme: black and white, no major or minor grid lines,  
# Arial font. Title is centered, size 12, and blue (hex coded). Subtitle is  
# centered, size 10, and blue (hex coded). Legend title is size 10 and the  
# legend is left-justified. X-axis title is size 10 and the margins are padded  
# at the top and bottom to give more space for angled axis labels. Y-axis title  
# is size 10 and margins are padded on the right side to give more space for  
# axis labels. Axis labels are size 10 and the x-axis labels are rotated -45  
# degrees with a horizontal justification that aligns them with the tick mark  
plot\_theme <- theme\_bw() +  
 theme(panel.grid.major = element\_blank(),  
 panel.grid.minor = element\_blank(),  
 text=element\_text(family="Arial"),  
 plot.title=element\_text(hjust=0.5, size=12, color="#314963"),  
 plot.subtitle=element\_text(hjust=0.5, size=10, color="#314963"),  
 legend.title=element\_text(size=10),  
 legend.text.align = 0,  
 axis.title.x = element\_text(size=10, margin = margin(t = 5, r = 0,  
 b = 10, l = 0)),  
 axis.title.y = element\_text(size=10, margin = margin(t = 0, r = 10,  
 b = 0, l = 0)),  
 axis.text=element\_text(size=10),  
 axis.text.x=element\_text(angle = -45, hjust = 0))  
  
# Color palette for SEACAR  
color\_palette <- c("#005396", "#0088B1", "#00ADAE", "#65CCB3", "#AEE4C1",  
 "#FDEBA8", "#F8CD6D", "#F5A800", "#F17B00")  
  
# Defines and sets variable with standardized group colors for plots  
group\_colors <- c("Marsh"=color\_palette[1],  
 "Marsh succulents"=color\_palette[2],  
 "Mangroves and associate"=color\_palette[3])  
  
# Defines and sets variable with standardized group shapes for plots  
group\_shapes <- c("Marsh"=21,  
 "Marsh succulents"=22,  
 "Mangroves and associate"=24)  
  
# Loop that cycles through each managed area with data  
if(n==0){  
 # Prints a statement if there are no managed areas with appropriate data  
 print("There are no monitoring locations that qualify.")  
} else {  
 for (i in 1:n) {  
 # Gets data for target managed area  
 plot\_data <- MA\_Y\_Stats[MA\_Y\_Stats$ManagedAreaName==MA\_Include[i]]  
 # Determines most recent year with available data for managed area  
 t\_max <- max(MA\_Ov\_Stats$LatestYear[MA\_Ov\_Stats$ManagedAreaName==  
 MA\_Include[i]])  
 # Determines earliest recent year with available data for managed area  
 t\_min <- min(MA\_Ov\_Stats$EarliestYear[MA\_Ov\_Stats$ManagedAreaName==  
 MA\_Include[i]])  
 # Determines how many years of data are present  
 t <- t\_max-t\_min  
   
 # Creates break intervals for plots based on number of years of data  
 if(t>=30){  
 # Set breaks to every 10 years if more than 30 years of data  
 brk <- -10  
 }else if(t<30 & t>=10){  
 # Set breaks to every 5 years if between 30 and 10 years of data  
 brk <- -5  
 }else if(t<10 & t>=4){  
 # Set breaks to every 2 years if between 10 and 4 years of data  
 brk <- -2  
 }else if(t<4){  
 # Set breaks to every year if less than 4 years of data  
 brk <- -1  
 }  
 # Determine range of data values for the managed area  
 y\_range <- max(plot\_data$Mean) - min(plot\_data$Mean)  
   
 # Determines lower bound of y-axis based on data range. Set based on  
 # relation of data range to minimum value. Designed to set lower boundary  
 # to be 10% of the data range below the minimum value  
 y\_min <- if(min(plot\_data$Mean)-(0.1\*y\_range)<0){  
 # If 10% of the data range below the minimum value is less than 0,  
 # set as 0  
 y\_min <- 0  
 } else {  
 # Otherwise set minimum bound as 10% data range below minimum value  
 y\_min <- min(plot\_data$Mean)-(0.1\*y\_range)  
 }  
   
 # Sets upper bound of y-axis to be 10% of the data range above the  
 # maximum value.  
 y\_max <- max(plot\_data$Mean)+(0.1\*y\_range)  
   
 # Determines what combination of groups are present for managed area  
 # and subsets color and shape scheme to be used by plots.  
 # Used so only group combinations present for managed area appear in  
 # the legend.  
 group\_colors\_plot <- group\_colors[unique(plot\_data$SpeciesGroup)]  
 group\_shapes\_plot <- group\_shapes[unique(plot\_data$SpeciesGroup)]  
   
 # Creates plot object using plot\_data.  
 # Data is plotted as symbols with connected lines.  
 p1 <- ggplot(data=plot\_data, group=as.factor(SpeciesGroup)) +  
 geom\_line(aes(x=Year, y=Mean, color=as.factor(SpeciesGroup)),  
 size=0.75, alpha=1) +  
 geom\_point(aes(x=Year, y=Mean, fill=as.factor(SpeciesGroup),  
 shape=as.factor(SpeciesGroup)), size=2,  
 color="#333333", alpha=1) +  
 labs(title="Coastal Wetlands Species Richness",  
 subtitle=MA\_Include[i],  
 x="Year", y="Richness (# of species)",  
 fill="Species group", color="Species group",  
 shape="Species group") +  
 scale\_x\_continuous(limits=c(t\_min-0.25, t\_max+0.25),  
 breaks=seq(t\_max, t\_min, brk)) +  
 scale\_y\_continuous(limits=c(y\_min, y\_max),  
 breaks=pretty\_breaks(n=5)) +  
 scale\_fill\_manual(values=group\_colors\_plot) +  
 scale\_color\_manual(values=group\_colors\_plot) +  
 scale\_shape\_manual(values=group\_shapes\_plot) +  
 plot\_theme  
 # Sets file name of plot created  
 outname <- paste0("CoastalWetlands\_", param\_file, "\_",  
 gsub(" ", "", MA\_Include[i]), ".png")  
 # Saves plot as a png image  
 png(paste0(out\_dir, "/Figures/", outname),  
 width = 8,  
 height = 4,  
 units = "in",  
 res = 200)  
 print(p1)  
 dev.off()  
   
 # Creates a data table object to be shown underneath plots in report  
 ResultTable <-  
 MA\_Ov\_Stats[MA\_Ov\_Stats$ManagedAreaName==MA\_Include[i],]  
 # Removes location, species group, and parameter information because it is  
 # in plot labels  
 ResultTable <- ResultTable[,-c("AreaID", "ManagedAreaName",  
 "ProgramIDs", "Programs", "ParameterName")]  
 # Renames StandardDeviation to StDev to save horizontal space  
 ResultTable <- ResultTable %>%  
 rename("StDev"="StandardDeviation")  
 # Converts all non-integer values to 2 decimal places for space  
 ResultTable$Min <- round(ResultTable$Min, digits=2)  
 ResultTable$Max <- round(ResultTable$Max, digits=2)  
 ResultTable$Median <- round(ResultTable$Median, digits=2)  
 ResultTable$Mean <- round(ResultTable$Mean, digits=2)  
 ResultTable$StDev <- round(ResultTable$StDev, digits=2)  
 # Stores as plot table object  
 t1 <- ggtexttable(ResultTable, rows = NULL,  
 theme=ttheme(base\_size=7))  
 # Combines plot and table into one figure  
 print(ggarrange(p1, t1, ncol=1, heights=c(0.85, 0.15)))  
   
 # Add extra space at the end to prevent the next figure from being too  
 # close. Does not add space after last plot  
 if(i!=n){  
 cat("\n \n \n \n")   
 }  
 }  
}













 