SEACAR Coral Analysis: Species Richness

Last compiled on 06 October, 2025

Contents

Important Notes

The purpose of this script is to determine species richness by species of grazers and reef-dependent species, create managed area statistics, generate plots, and create reports in pdf form for Coral data.

These scripts were created by J.E. Panzik (jepanzik@usf.edu) for SEACAR. Updated by T.G. Hill (Tyler.Hill@FloridaDEP.gov).

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 Coral_SpeciesRichness_ReportRender.R (https://github.com/FloridaSEACAR/SEACAR_Trend_Analyses/blob/main/Coral/Coral_SpeciesRichness_ReportRender.R).

Coral Species Richness

Biscayne Bay-Cape Florida to Monroe County Line Aquatic Preserve

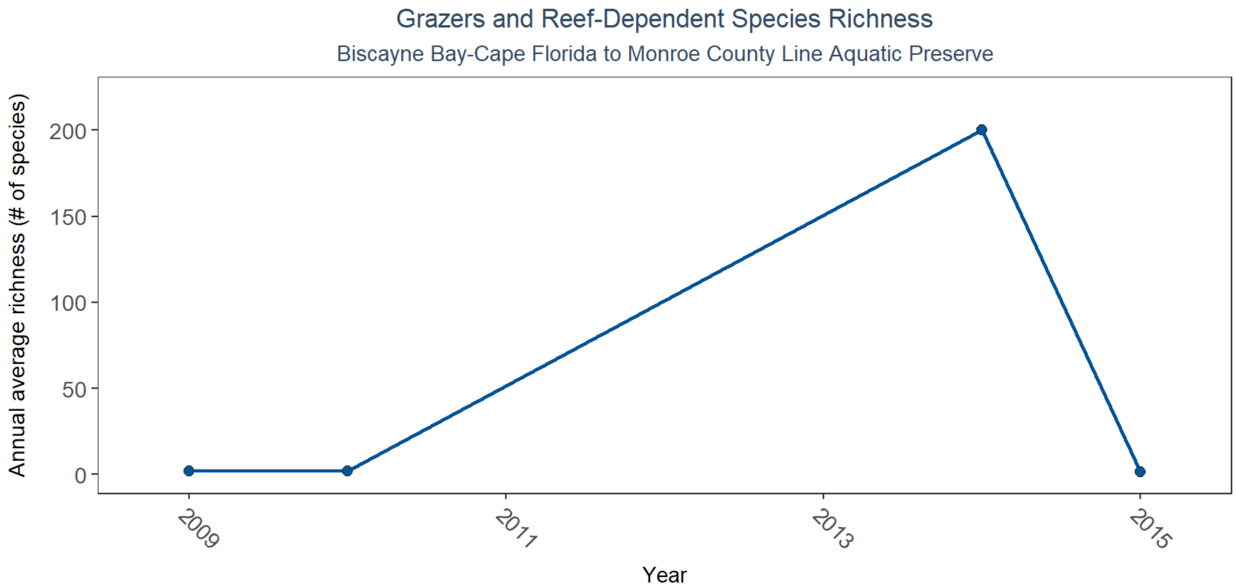
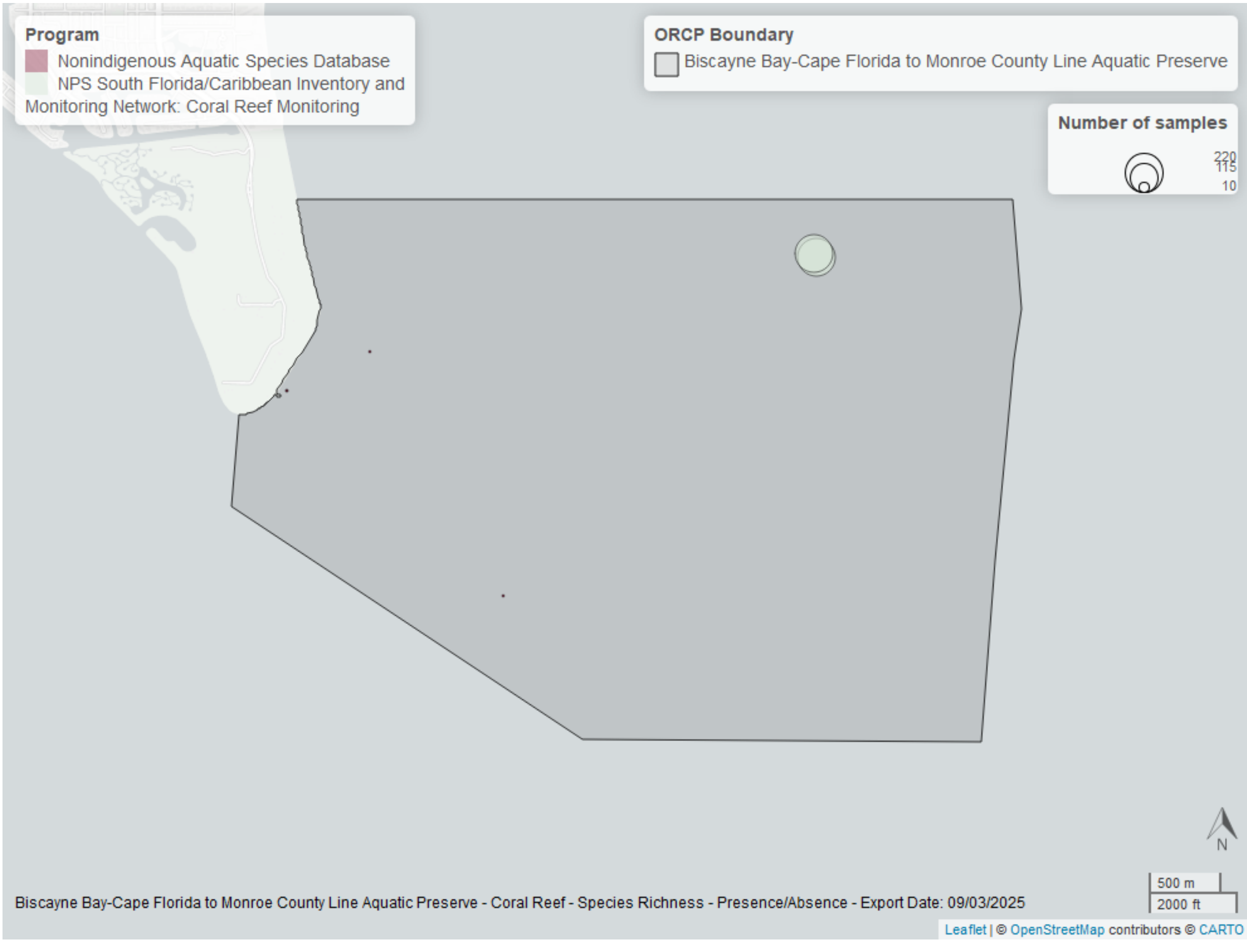


Figure 1: Line graph of annual average species richness of grazers and reef-dependent species over time. If the time series included more than one year of observations, a line connects the data points for visualization.

Table 1: Coral Species Richness - Biscayne Bay-Cape Florida to Monroe County Line Aquatic Preserve

N-Years	EarliestYear	LatestYear	N-Data	Min	Max	Median	Mean	StDev	Year-MinRichness	Year-MaxRichness
4	2009	2015	6	1	200	2	67.83	102.38	2015	2014

The median annual number of taxa was 2 based on 6 observations collected between 2009 and 2015.



Biscayne Bay Aquatic Preserve

Table 2: Coral Species Richness - Biscayne Bay Aquatic Preserve

N-Years	EarliestYear	LatestYear	N-Data	Min	Max	Median	Mean	StDev	Year-MinRichness	Year-MaxRichness
7	2010	2017	23	1	2	2	1.83	0.39	2013	2010

The median annual number of taxa was 2 based on 23 observations collected between 2010 and 2017.

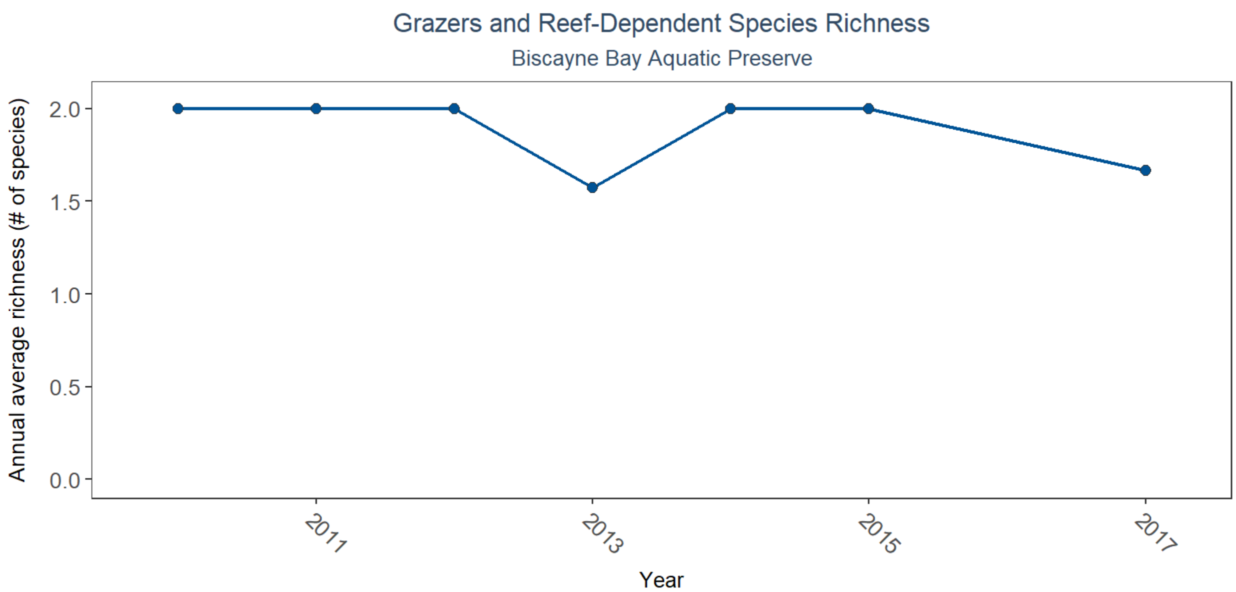
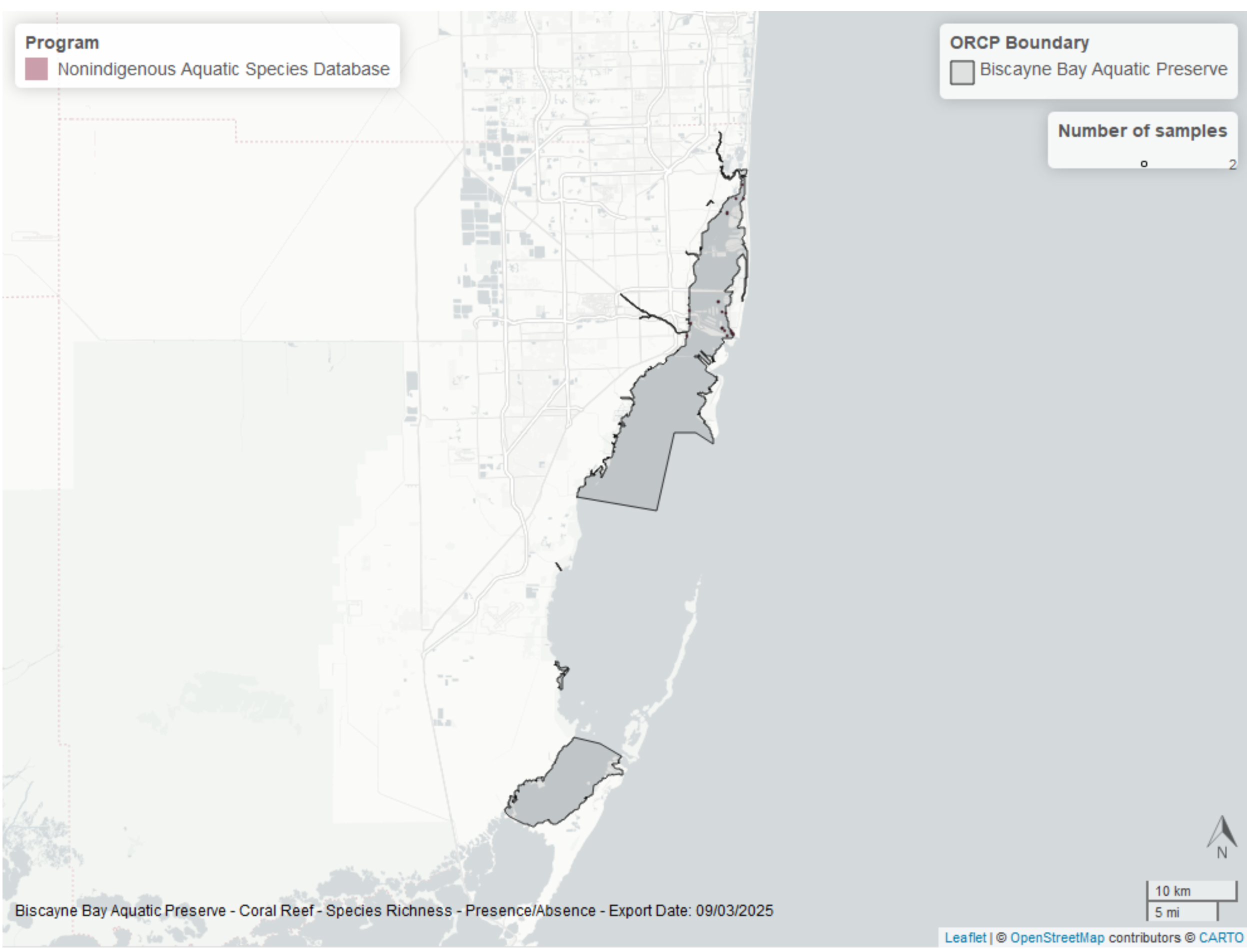


Figure 2: Line graph of annual average species richness of grazers and reef-dependent species over time. If the time series included more than one year of observations, a line connects the data points for visualization.



Coupon Bight Aquatic Preserve

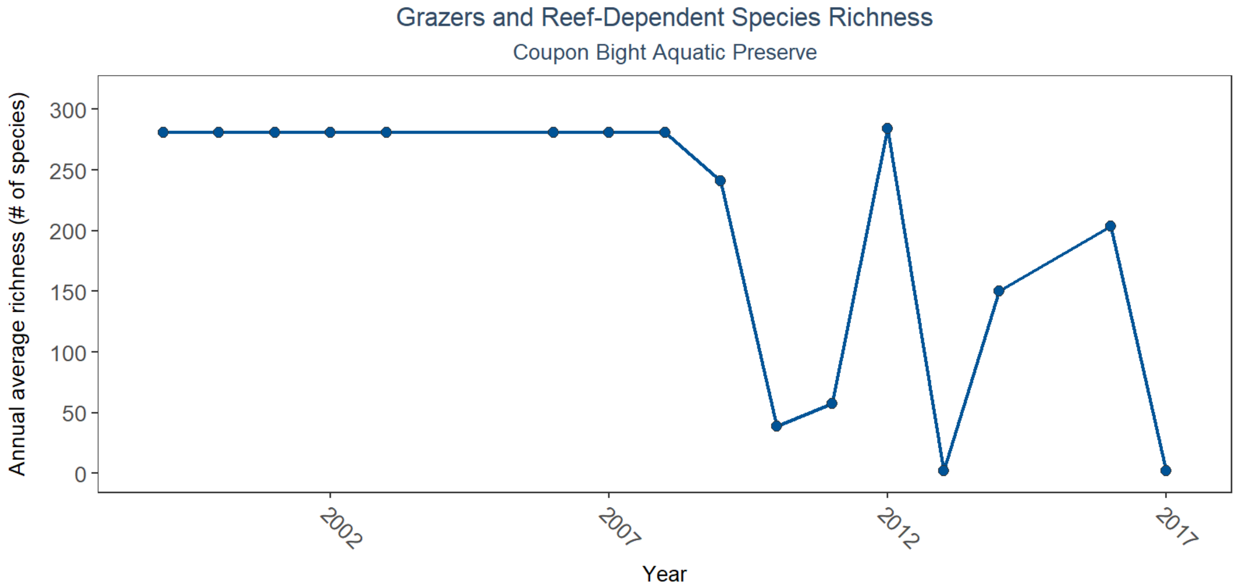
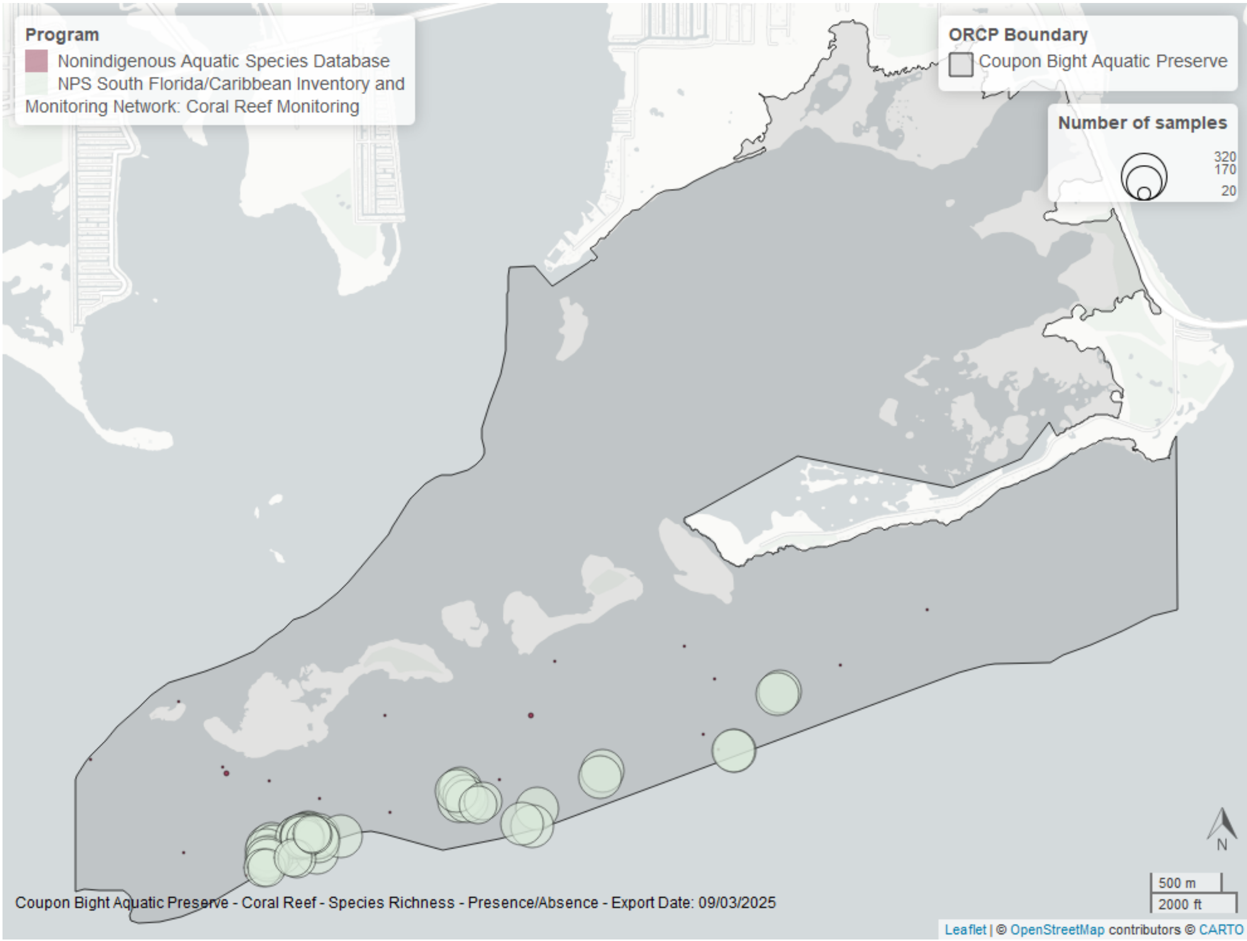


Figure 3: Line graph of annual average species richness of grazers and reef-dependent species over time. If the time series included more than one year of observations, a line connects the data points for visualization.

Table 3: Coral Species Richness - Coupon Bight Aquatic Preserve

N-Years	EarliestYear	LatestYear	N-Data	Min	Max	Median	Mean	StDev	Year-MinRichness	Year-MaxRichness
16	1999	2017	72	2	284	281	182.12	126.81	2013	2012

The median annual number of taxa was 281 based on 72 observations collected between 1999 and 2017.



Florida Keys National Marine Sanctuary

Table 4: Coral Species Richness - Florida Keys National Marine Sanctuary

N-Years	EarliestYear	LatestYear	N-Data	Min	Max	Median	Mean	StDev	Year-MinRichness	Year-MaxRichness
21	1999	2019	11167	1	302	281	220.23	106.46	2019	2001

The median annual number of taxa was 281 based on 11,167 observations collected between 1999 and 2019.

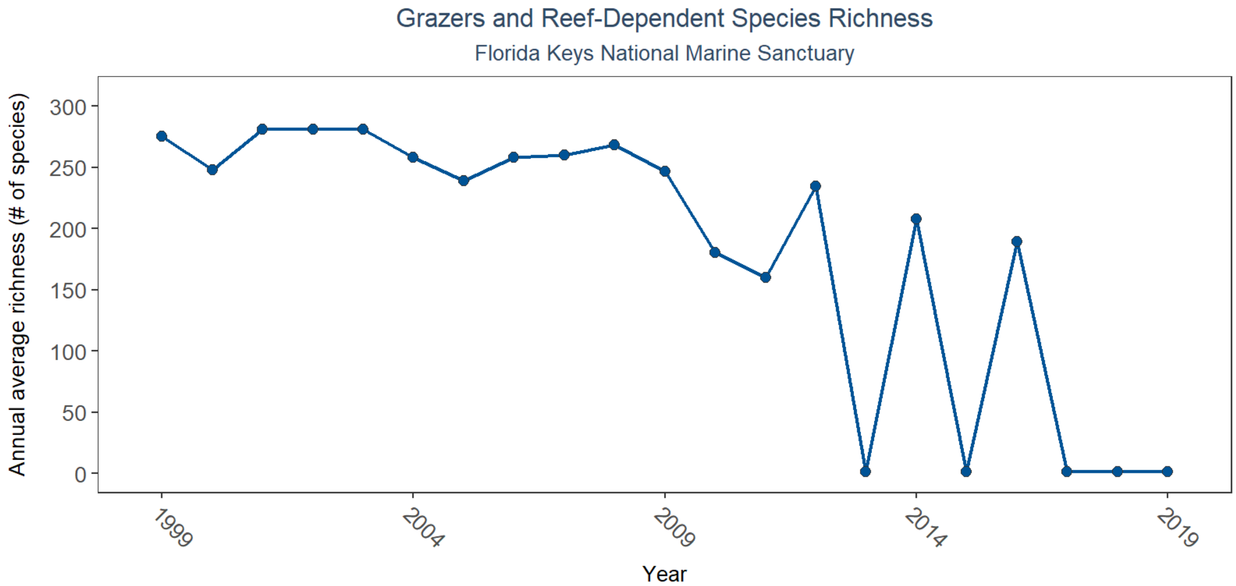
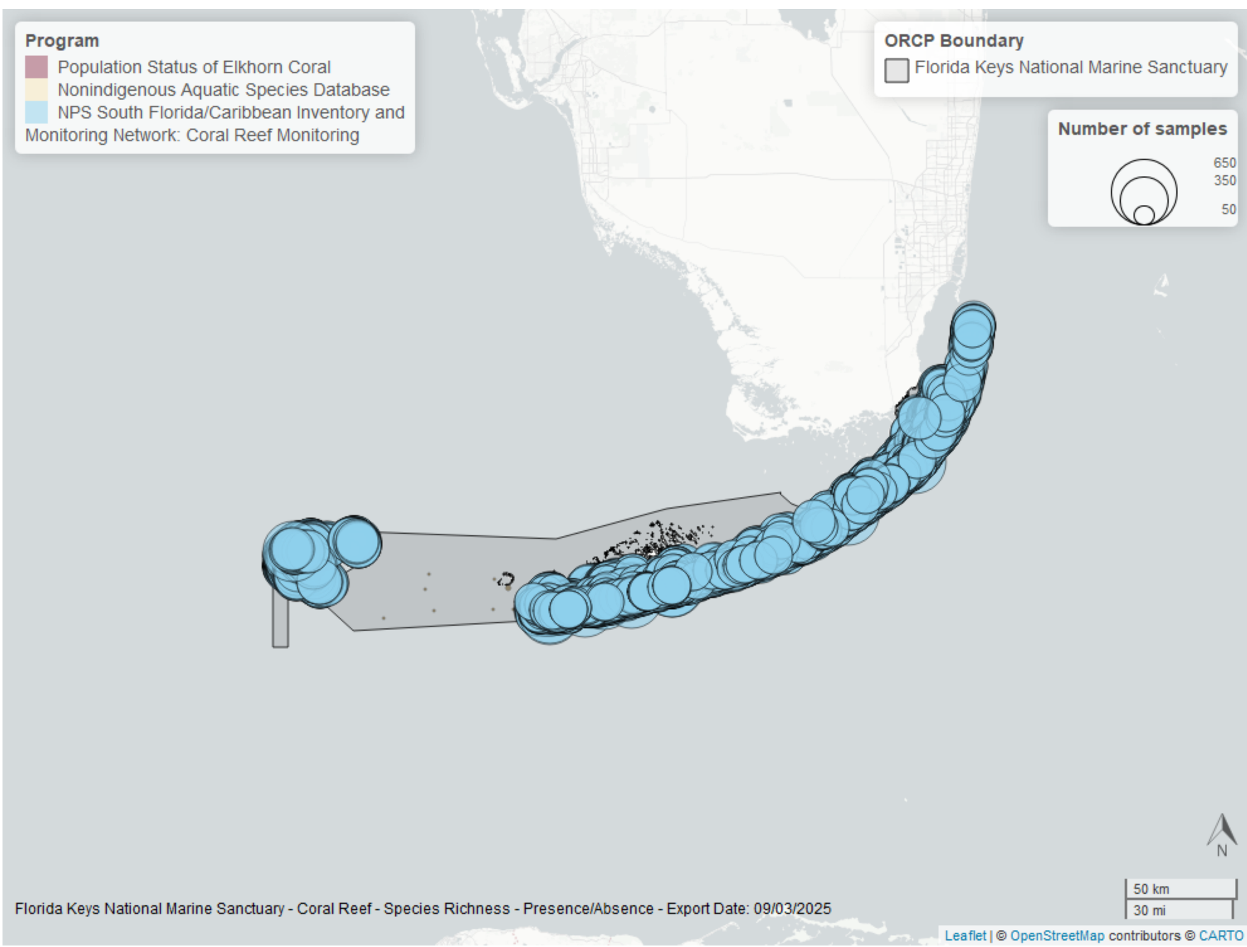


Figure 4: Line graph of annual average species richness of grazers and reef-dependent species over time. If the time series included more than one year of observations, a line connects the data points for visualization.



Jensen Beach to Jupiter Inlet Aquatic Preserve

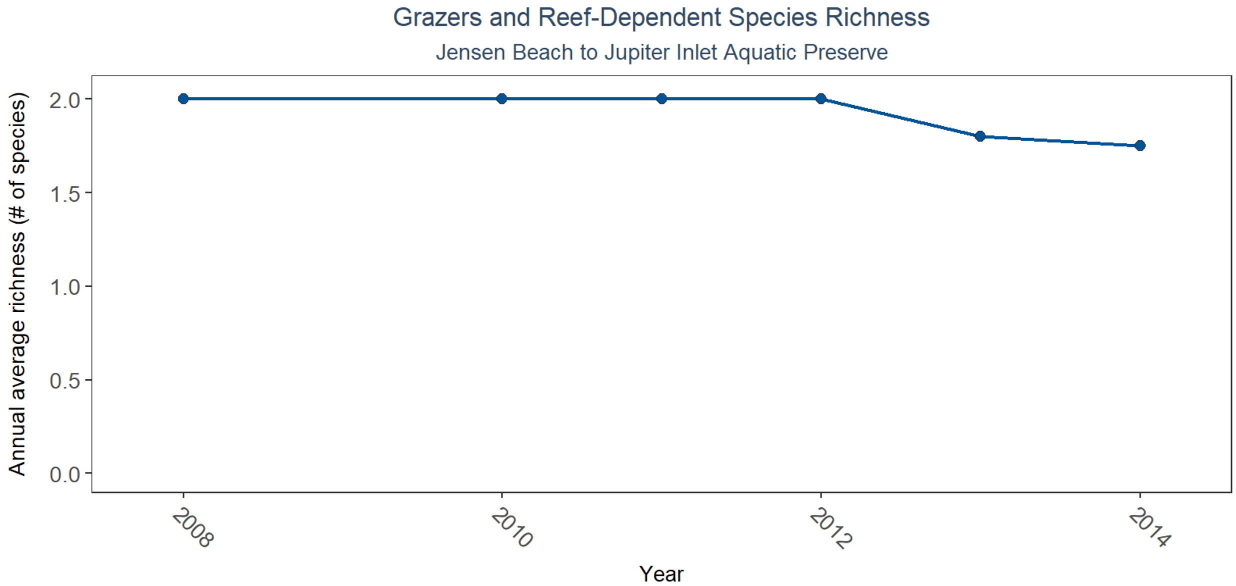
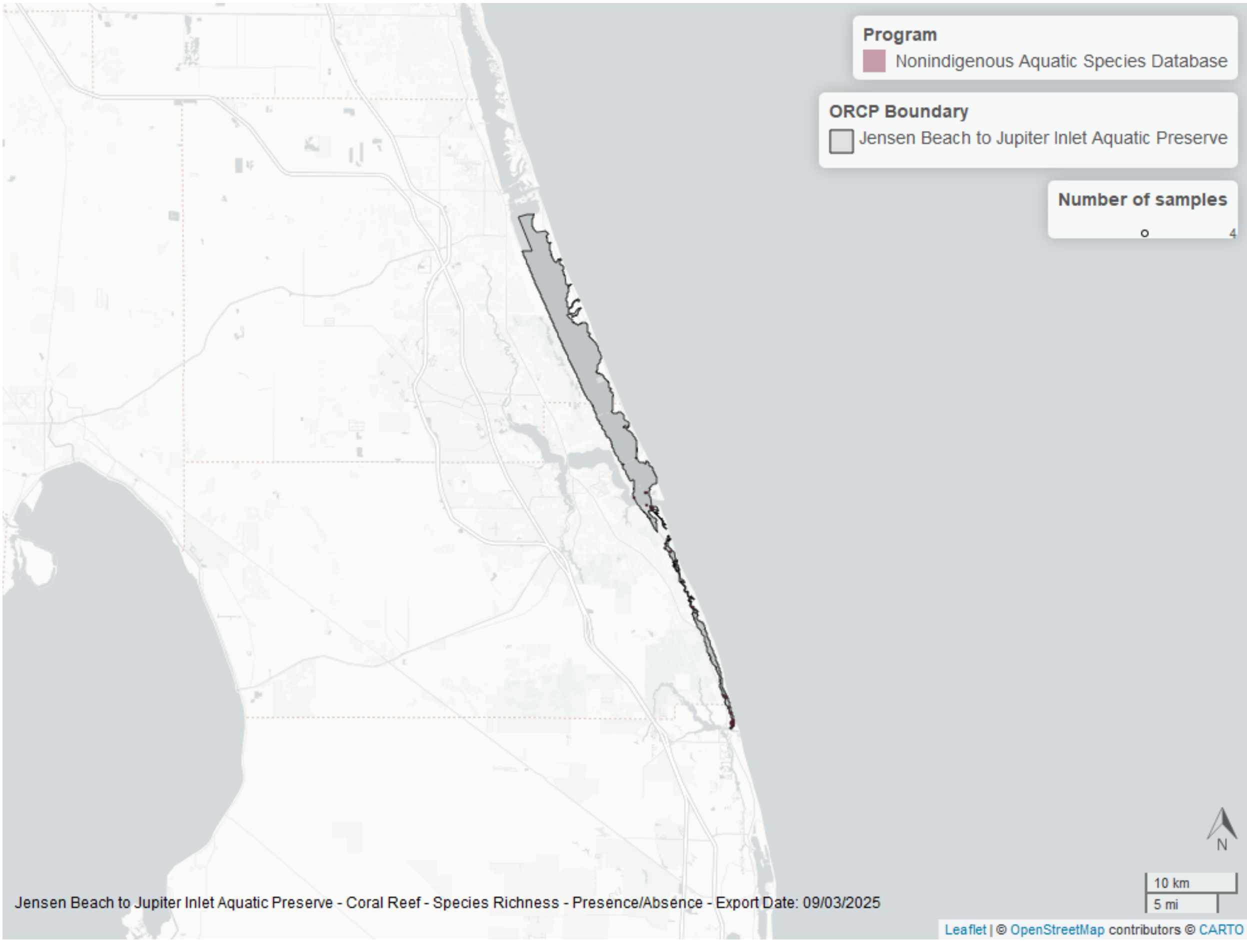


Figure 5: Line graph of annual average species richness of grazers and reef-dependent species over time. If the time series included more than one year of observations, a line connects the data points for visualization.

Table 5: Coral Species Richness - Jensen Beach to Jupiter Inlet Aquatic Preserve

N-Years	EarliestYear	LatestYear	N-Data	Min	Max	Median	Mean	StDev	Year-MinRichness	Year-MaxRichness
6	2008	2014	25	1	2	2	1.92	0.28	2014	2008

The median annual number of taxa was 2 based on 25 observations collected between 2008 and 2014.



Kristin Jacobs Coral Aquatic Preserve

Table 6: Coral Species Richness - Kristin Jacobs Coral Aquatic Preserve

N-Years	EarliestYear	LatestYear	N-Data	Min	Max	Median	Mean	StDev	Year-MinRichness	Year-MaxRichness
26	1985	2020	3686	1	302	294	193.88	123.01	2020	2014

The median annual number of taxa was 294 based on 3,686 observations collected between 1985 and 2020.

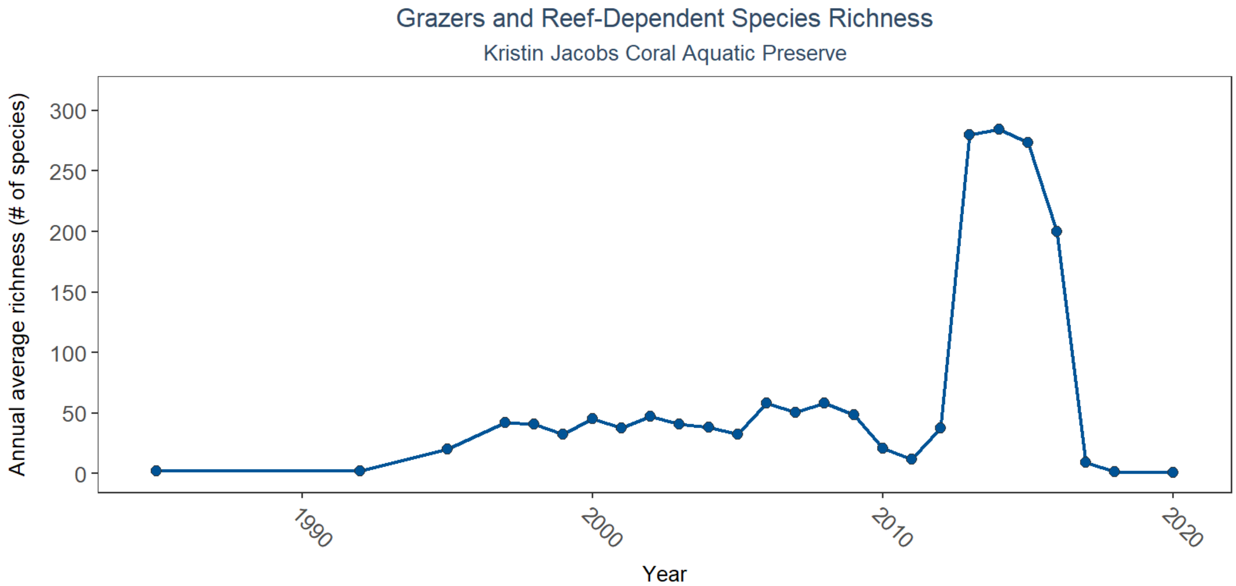
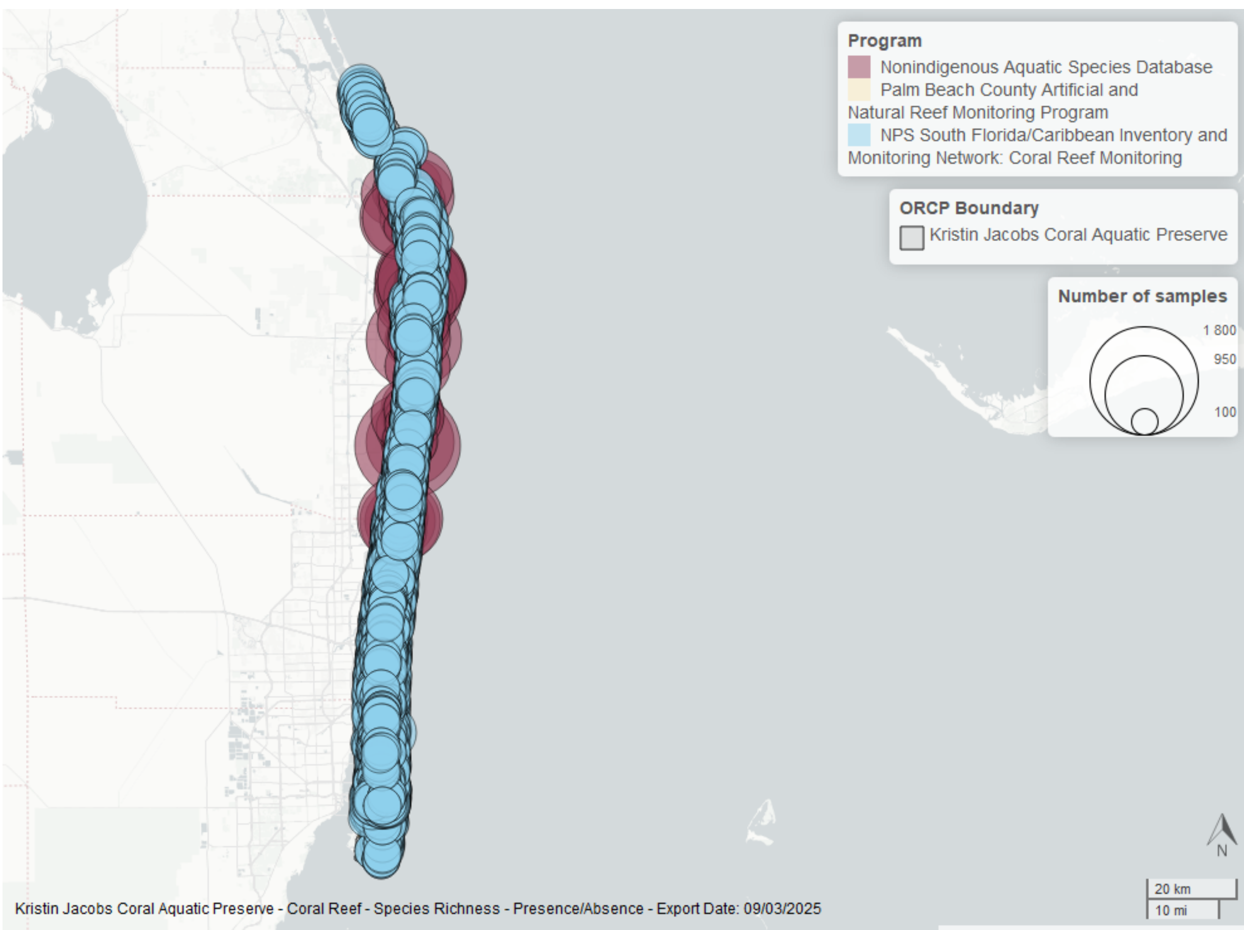


Figure 6: Line graph of annual average species richness of grazers and reef-dependent species over time. If the time series included more than one year of observations, a line connects the data points for visualization.



Lignumvitae Key Aquatic Preserve

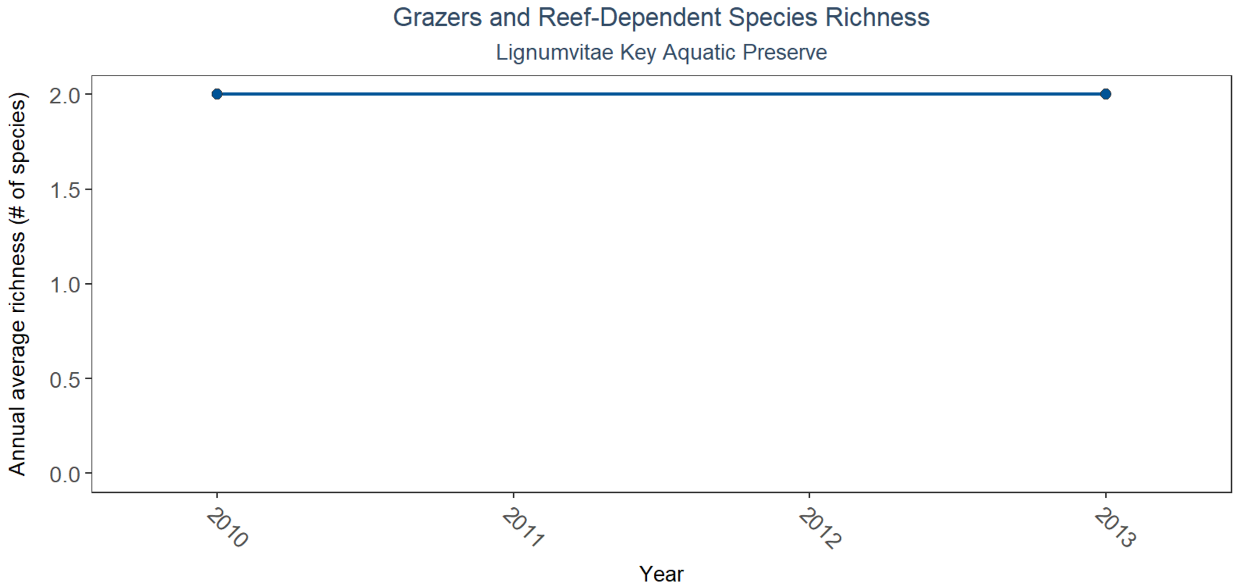
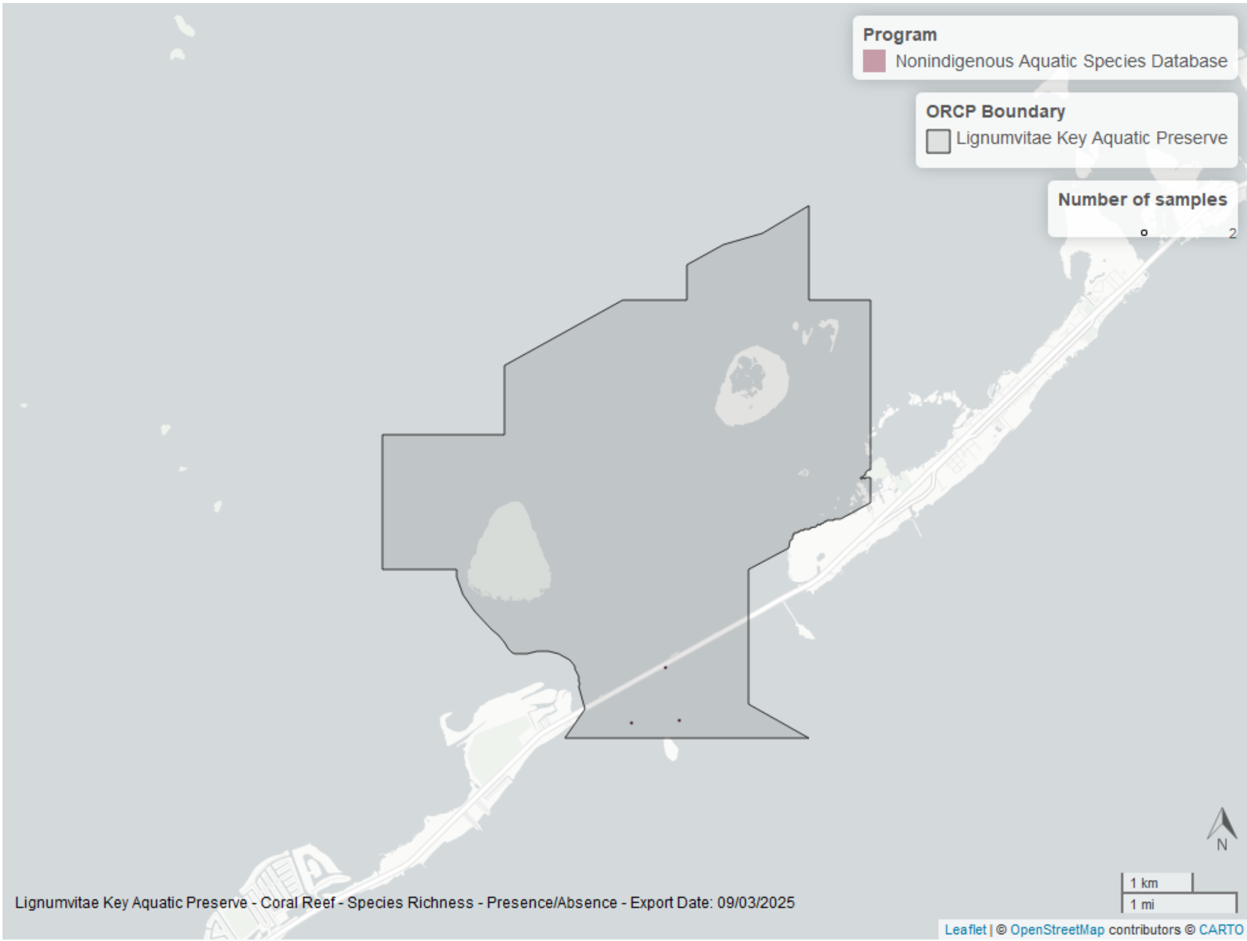


Figure 7: Line graph of annual average species richness of grazers and reef-dependent species over time. If the time series included more than one year of observations, a line connects the data points for visualization.

Table 7: Coral Species Richness - Lignumvitae Key Aquatic Preserve

N-Years	EarliestYear	LatestYear	N-Data	Min	Max	Median	Mean	StDev	Year-MinRichness	Year-MaxRichness
2	2010	2013	3	2	2	2	2	0	2010	2010

The median annual number of taxa was 2 based on 3 observations collected between 2010 and 2013.



Loxahatchee River-Lake Worth Creek Aquatic Preserve

Table 8: Coral Species Richness - Loxahatchee River-Lake Worth Creek Aquatic Preserve

N-Years	EarliestYear	LatestYear	N-Data	Min	Max	Median	Mean	StDev	Year-MinRichness	Year-MaxRichness
4	2010	2017	11	1	2	2	1.73	0.47	2017	2011

The median annual number of taxa was 2 based on 11 observations collected between 2010 and 2017.

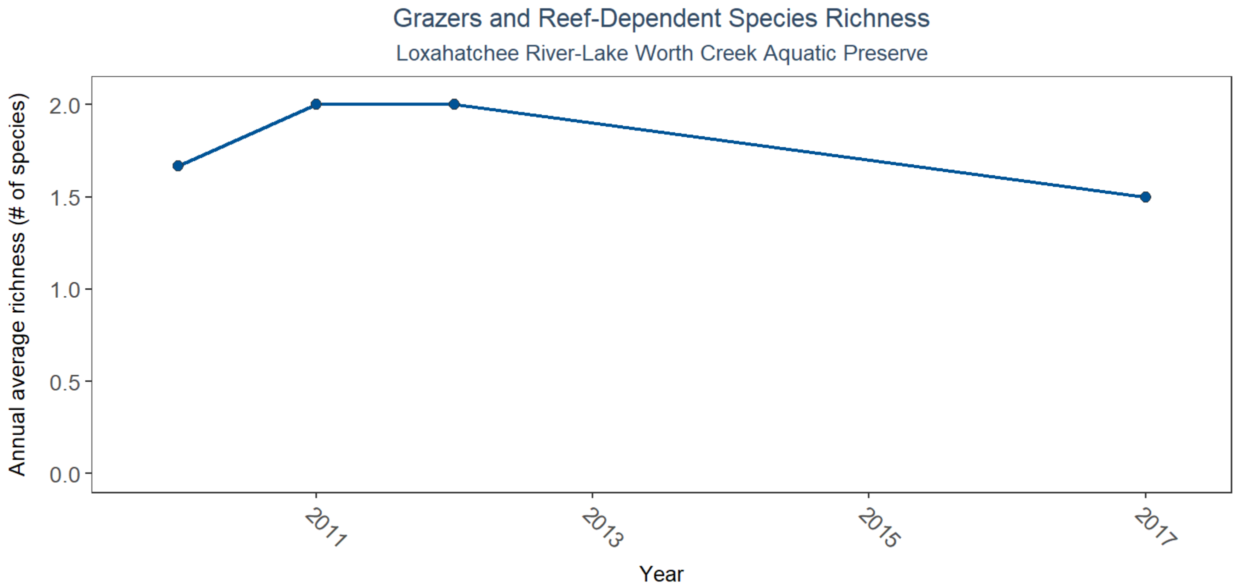
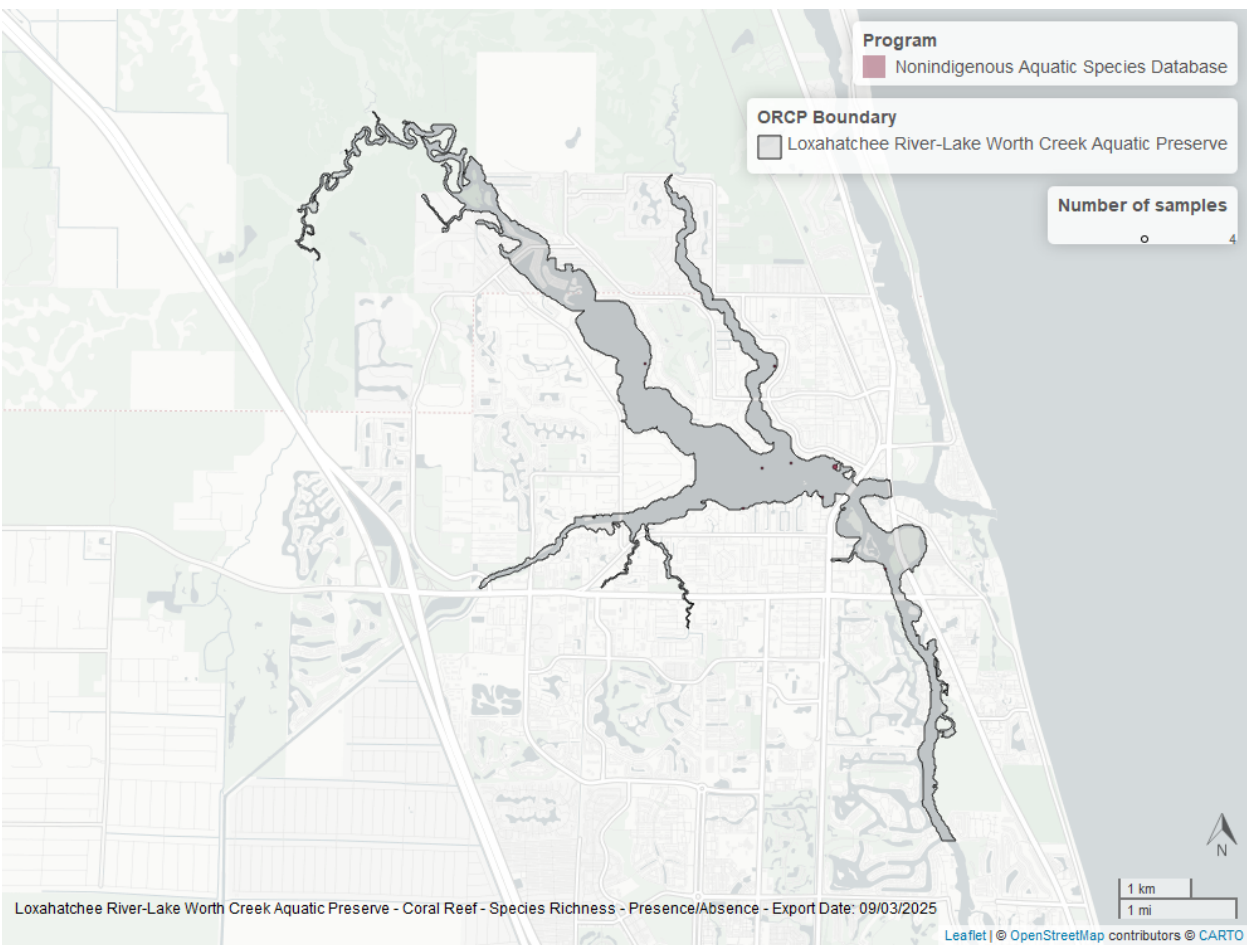


Figure 8: Line graph of annual average species richness of grazers and reef-dependent species over time. If the time series included more than one year of observations, a line connects the data points for visualization.



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(ggpubr)
library(scales)
library(EnvStats)
library(tidyr)
library(kableExtra)
library(glue)
library(grid)
library(stringr)
options(scipen=999)
knitr::opts_chunk$set(
   warning=FALSE,
   message=FALSE,
   echo=FALSE
)
options(knitr.kable.NA = '-')
```

File Import

Imports file that is determined in the Coral_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 Coral data is available at: https://usf.box.com/s/8hyj2ur5arothlifg1isnq2gxisjzbdg

The file being used for the analysis is: **All_CORAL_Parameters-2025-Sep-04.txt**

```
# Gets the files with the file names containing the desired parameter
file_in <- list.files(seacar_data_location, pattern="All_CORAL", full=TRUE)

# Reads in data file using fread
data <- fread(file_in, sep="|", header=TRUE, stringsAsFactors=FALSE,
              na.strings=c("NULL","","NA"))

cat(paste("The data file(s) used:", file_short, sep="\n"))
```

Data Filtering

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

1. Only take data rows that are Presence/Absence measurements for SpeciesGroup1 values "Grazers and reef dependent species" and "Reef fish"
2. Set parameter names to `Species Richness`
3. Sets units

4. Removes rows that contains NA values in `ManagedAreaName`, `GenusName`, `SpeciesName`, `Month`, `Year`, `SpeciesGroup1`, and removes invasive species data
5. Sets ResultValue to be numeric values and removes rows where presence is 0
6. Removes duplicates (`MADup`==1)
7. Combines genus and species names
8. Corrects some managed area names to match what is being used with other habitats
9. Creates species richness data set
    - Grouped based on common `ManagedAreaName`, `ProgramID`, `ProgramName`, `ProgramLocationID`, and `SampleDate`
    - `SpeciesRichness` determined based on the number of unique species (`gensp`) in each group
10. Merges data with managed area data to determine correct `AreaID`
11. Writes to file with "_UsedData" file name to indicate what data was used for species richness.

```
# Only keep data for Presence of grazers and reef-dependent species
data <- data[ParameterName=="Presence/Absence" &
               SpeciesGroup1 %in% c("Grazers and reef dependent species",
                                    "Reef fish"), ]

# Create ParameterName Column
data$ParameterName <- "Species Richness"
parameter <- "Species Richness"
title_param <- "Species Richness - Grazers and Reef-Dependent Species"

# Sets units for species richness
unit <- "# of species"
data$ParameterUnits <- unit

# 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),]
# Remove rows with missing SpeciesGroup1
data <- data[!is.na(data$SpeciesGroup1),]
# Set ResultValue to be a number value
data$ResultValue <- as.numeric(data$ResultValue)
# Remove rows where ResultValue is 0 and missing
data <- data[data$ResultValue!=0,]
data <- data[!is.na(data$ResultValue),]
# Remove duplicate rows
data <- data[data$MADup==1,]
# Create variable that combines the genus and species name
data$gensp <- paste(data$GenusName, data$SpeciesName, sep=" ")

# Create Species Richness values for groups of unique combinations of
# ManagedAreaName, ProgramID, ProgramName, ProgramLocationID, and SampleDate.
data <- data[data$ResultValue==1] %>%
  group_by(AreaID, ManagedAreaName, ProgramID, ProgramName, ProgramLocationID,
```

```
           SampleDate) %>%
  summarise(ParameterName=parameter,
            Year=unique(Year), Month=unique(Month),
            SpeciesRichness=length(unique(gensp)))
setDT(data)

# Writes this data that is used by the rest of the script to a text file
fwrite(data, paste0(out_dir,"/Coral_", 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
coral_sr_MA_Include <- unique(data$ManagedAreaName[!is.na(data$SpeciesRichness)])

# Puts the managed areas in alphabetical order
coral_sr_MA_Include <- coral_sr_MA_Include[order(coral_sr_MA_Include)]

# Determines the number of managed areas used
n <- length(coral_sr_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`, and `Month`.
   - Second summary statistics do not use the `Month` grouping and are only for `ManagedAreaName` and `Year`.
   - Third summary statistics do not use `Year` grouping and are only for `ManagedAreaName` and `Month`
   - Fourth summary statistics are only grouped based on `ManagedAreaName`
     - 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
   - [Coral Species Richness Output Files in SEACAR GitHub](https://github.com/FloridaSEACAR/SEACAR_Trend_Analyses/tree/main/Coral/output/SpeciesRichness) (https://github.com/FloridaSEACAR/SEACAR_Trend_Analyses/tree/main/Coral/output/SpeciesRichness)

```
# Create summary statistics for each managed area based on Year and Month
# intervals.
MA_YM_Stats <- data %>%
  group_by(AreaID, ManagedAreaName, Year, Month) %>%
  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=', '),
            .groups = "keep")
# 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,"/Coral_", 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) %>%
  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=', '),
            .groups = "keep")
# 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,"/Coral_", 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) %>%
  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=', '),
            .groups = "keep")
# 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,"/Coral_", 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) %>%
  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=', '),
            .groups = "keep")
# 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$N_Data[m]==0){
    next
  }
  # Gets subset of data from MA_Y_Stats (yearly summary stats) with this
  # ManagedAreaName
  ds <- MA_Y_Stats[ManagedAreaName==ma,]
  # Gets the minimum and maximum Mean (yearly averages)
  min <- min(ds$Mean)
  max <- max(ds$Mean)
  #Determines what years those minimum and maximum values occured
  year_min <- ds[Mean==min, Year]
  year_max <- ds[Mean==max, Year]
  # Stores the occurrence years of the minimum and maximum into the overall
  # stats for this row
  MA_Ov_Stats$Year_MinRichness[m] <- year_min
```

```r
  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$Programs=="", NA)
# Write overall statistics to file
fwrite(MA_Ov_Stats, paste0(out_dir,"/Coral_", param_file,
                           "_MA_Overall_Stats.txt"), sep="|")
# Removes entries from the overall statistics that do not have data.
# Based on presence or absence of EarliestYear
MA_Ov_Stats <- MA_Ov_Stats[!is.na(MA_Ov_Stats$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. Add the plot line
5. Set the plot type as a point plot with the size of the points
6. Create the title, x-axis, y-axis
7. Set the y and x limits
8. Apply common plot theme
9. 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
10. Create file name to save figure
11. Save figure as png file

- Coral Species Richness Figures in SEACAR GitHub (https://github.com/FloridaSEACAR/SEACAR_Trend_Analyses/tree/main/Coral/output/SpeciesRichness/Figures)

```r
# 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 = element_text(hjust=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")

# 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) {
    ma_i <- coral_sr_MA_Include[i]
    # Gets data for target managed area
    plot_data <- MA_Y_Stats[ManagedAreaName==ma_i, ]
    # Determines most recent year with available data for managed area
    t_max <- max(MA_Ov_Stats[ManagedAreaName==ma_i, LatestYear])
    # Determines earliest recent year with available data for managed area
    t_min <- min(MA_Ov_Stats[ManagedAreaName==ma_i, EarliestYear])
    # 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 & t>=2){
      # Set breaks to every year if between 4 and 2 years of data
      brk <- -1
    }else if(t<2){
      # Set breaks to every year if less than 2 years of data
      brk <- -1
      # Sets t_max to be 1 year greater and t_min to be 1 year lower
      # Forces graph to have at least 3 tick marks
      t_max <- t_max+1
      t_min <- t_min-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,
```

```r
    # 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)

  # Creates plot object using plot_data.
  # Data is plotted as symbols with connected lines.
  p1 <- ggplot(data=plot_data) +
    geom_line(aes(x=Year, y=Mean), color=color_palette[1],
              size=0.75, alpha=1) +
    geom_point(aes(x=Year, y=Mean), fill=color_palette[1],
               shape=21, size=2, color="#333333", alpha=1) +
    labs(title="Grazers and Reef-Dependent Species Richness",
         subtitle=ma_i,
         x="Year", y="Richness (# of species)") +
    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)) +
    plot_theme
  # Sets file name of plot created
  outname <- paste0("Coral_", param_file, "_", gsub(" ", "", ma_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[ManagedAreaName==ma_i,]
  # Removes location, 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")
    }
  }
}
```