

# SEACAR Coral Analysis: Species Richness - Grazers and Reef-Dependent Species

Last compiled on 08 June, 2023

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## Important Notes

These scripts were created by [J.E. Panzik \(jepanzik@usf.edu\)](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](https://github.com/FloridaSEACAR/SEACAR_Trend_Analyses)

This markdown file is designed to be compiled by [SEACAR\\_Coral\\_SpeciesRichness\\_ReportRender.R](https://github.com/FloridaSEACAR/SEACAR_Trend_Analyses/blob/main/Coral/SEACAR_Coral_SpeciesRichness_ReportRender.R) ([https://github.com/FloridaSEACAR/SEACAR\\_Trend\\_Analyses/blob/main/Coral/SEACAR\\_Coral\\_SpeciesRichness\\_ReportRender.R](https://github.com/FloridaSEACAR/SEACAR_Trend_Analyses/blob/main/Coral/SEACAR_Coral_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)
library(formatR)
options(scipen=999)
knitr::opts_chunk$set(
  warning=FALSE,
  message=FALSE,
  dpi=200,
  tidy.opts = list(width.cutoff = 60),
  tidy = TRUE
)
```

## File Import

Imports file that is determined in the SEACAR\_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-2023-Jun-06.txt**

```
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"))
```

```
## The data file(s) used:
## All_CORAL_Parameters-2023-Jun-06.txt
```

## Data Filtering

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

1. Only take data rows that are Presence measurements for grazers and reef-dependent species
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[data$ParameterName == "Presence - Grazers and Reef Dependent Species"]

# 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$SpeciesGroup1), ]
# Remove rows with invasive species
data <- data[data$SpeciesGroup1 != "Invasive", ]
# 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 = " ")
# Corrects Managed Area names to be consistent with
# official names
data$ManagedAreaName[data$ManagedAreaName == "Florida Keys NMS"] <- "Florida Keys National Marine Sanctu"
data$ManagedAreaName[data$ManagedAreaName == "Biscayne Bay-Cape Florida to Monroe County Line"] <- "Bis"
data$ManagedAreaName[data$ManagedAreaName == "Coupon Bight"] <- "Coupon Bight Aquatic Preserve"
data$ManagedAreaName[data$ManagedAreaName == "Coral ECA"] <- "Southeast Florida Coral Reef Ecosystem Co"

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

```

    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, "/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
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`, 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](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 = ", "))
# 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_MMY_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 = ", "))
# 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 = ", "))
# 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 = ", "))
  # 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 occurred
  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, "/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 \(https://github.com/FloridaSEACAR/SEACAR\\_Trend\\_Analyses/tree/main/Coral/output/SpeciesRichness/Figures\)](https://github.com/FloridaSEACAR/SEACAR_Trend_Analyses/tree/main/Coral/output/SpeciesRichness/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")
```

```

# 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)

# 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_Include[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_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()

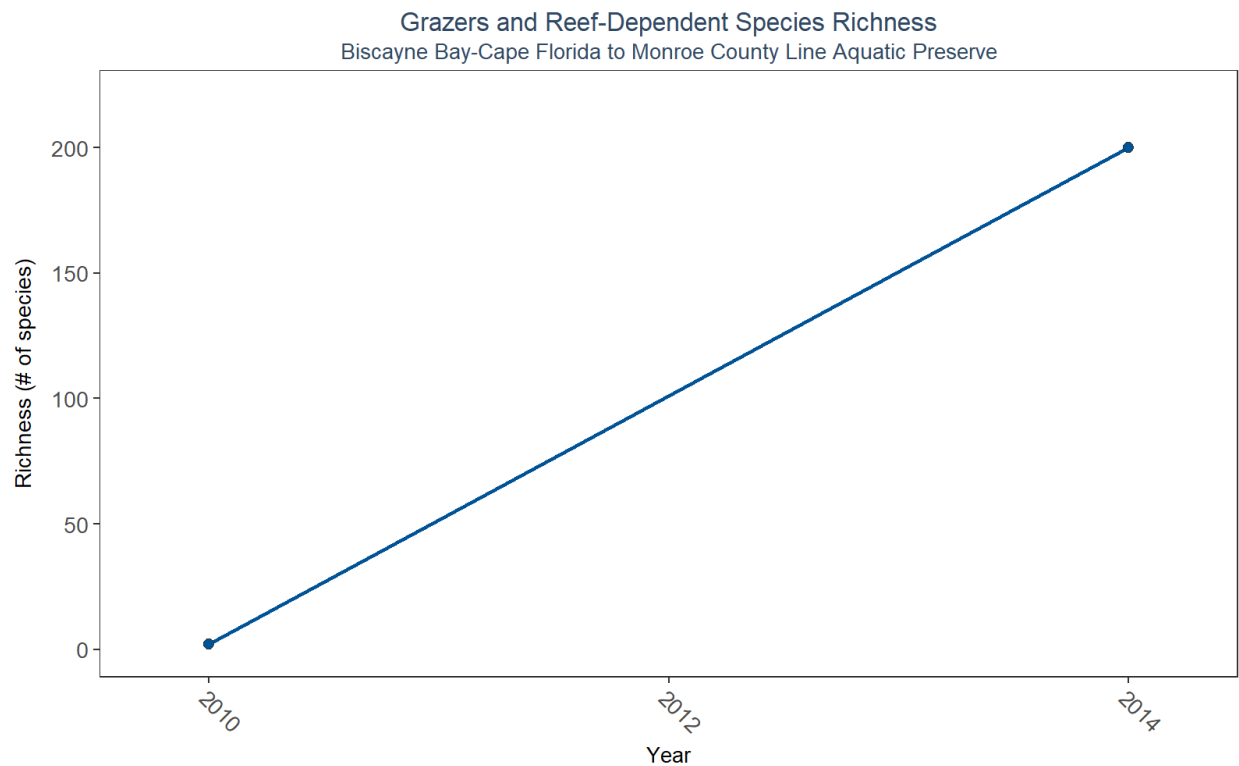
# Creates a data table object to be shown
# underneath plots in report
ResultTable <- MA_Ov_Stats[MA_Ov_Stats$ManagedAreaName ==
  MA_Include[i], ]
# Removes location, and parameter information
# because it is in plot labels
ResultTable <- ResultTable[, -c("AreaID", "ManagedAreaName",
  "ProgramIDs", "Programs", "ParameterName")]
# Renames StandardDeviation to StDev to save
# horizontal space
ResultTable <- ResultTable %>%
  rename(StDev = "StandardDeviation")
# Converts all non-integer values to 2 decimal
# places for space
ResultTable$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)))

```

```

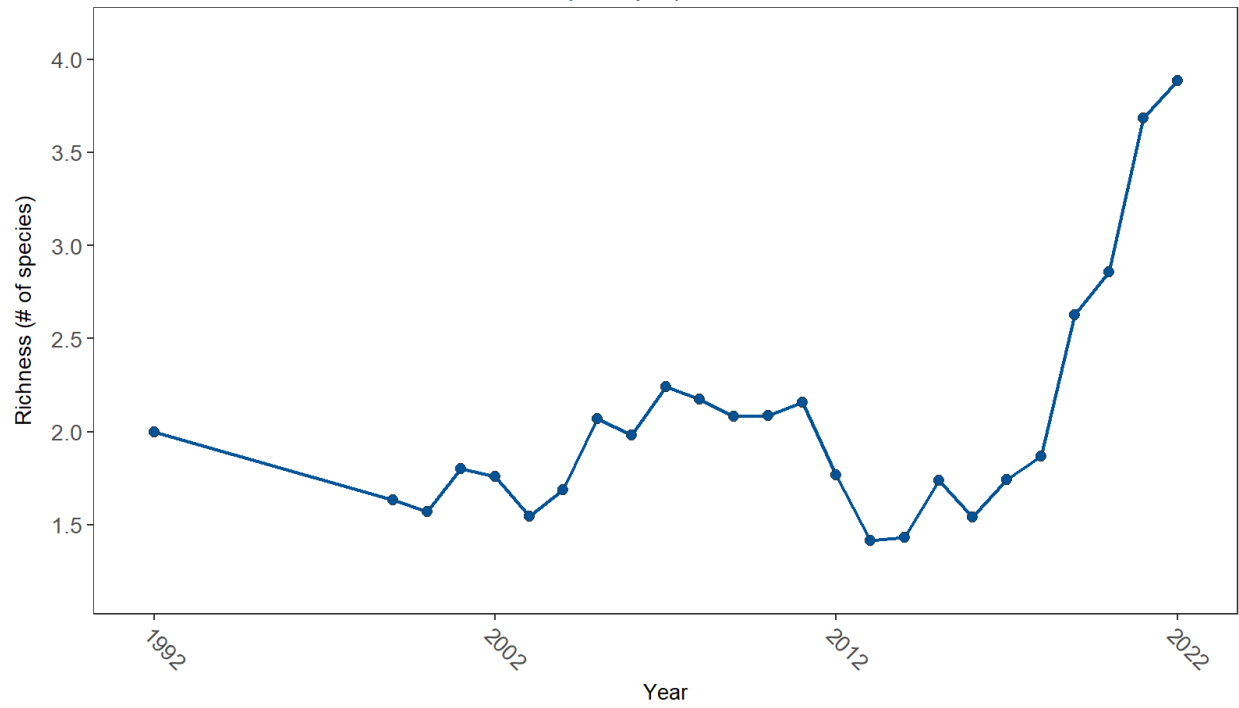
# Add extra space at the end to prevent the next
# figure from being too close. Does not add space
# after last plot
if (i != n) {
  cat("\n \n \n \n")
}
}
}

```

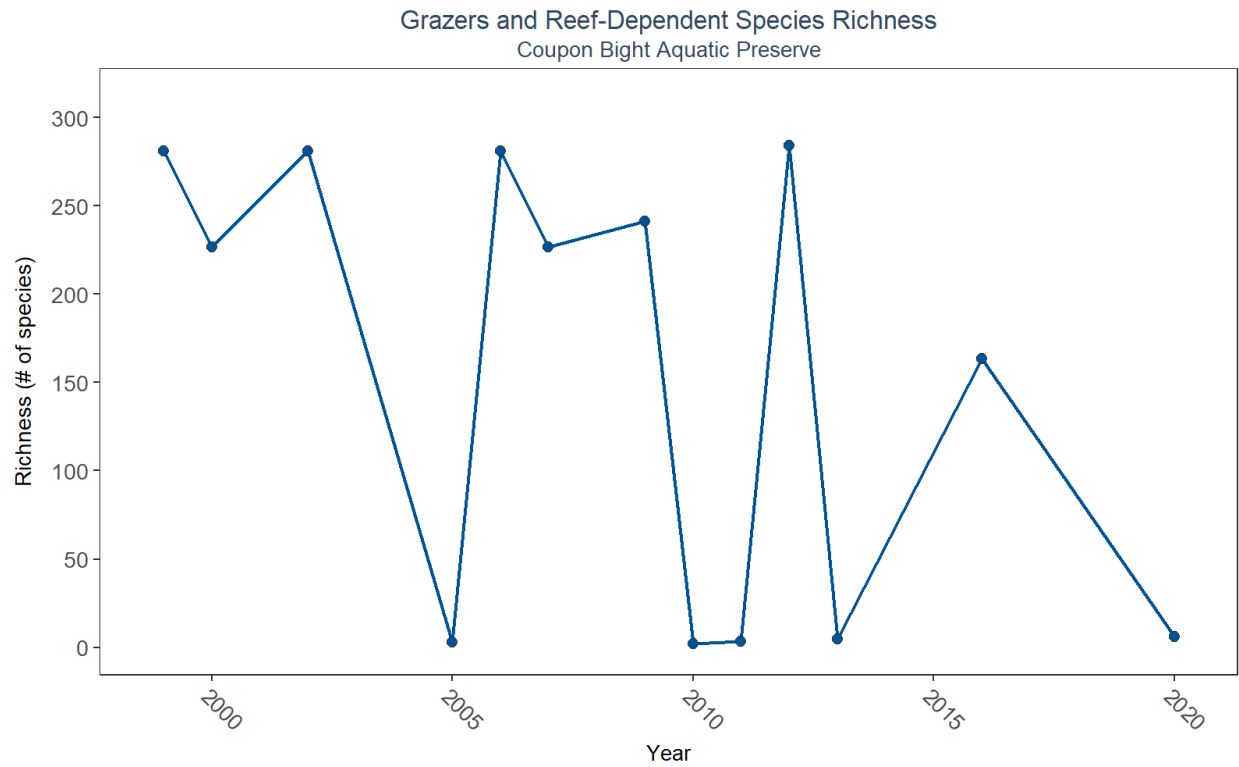


N_Years	EarliestYear	LatestYear	N_Data	Min	Max	Median	Mean	StDev	Year_MinRichness	Year_MaxRichness
2	2010	2014	3	2	200	200	134	114.32	2010	2014

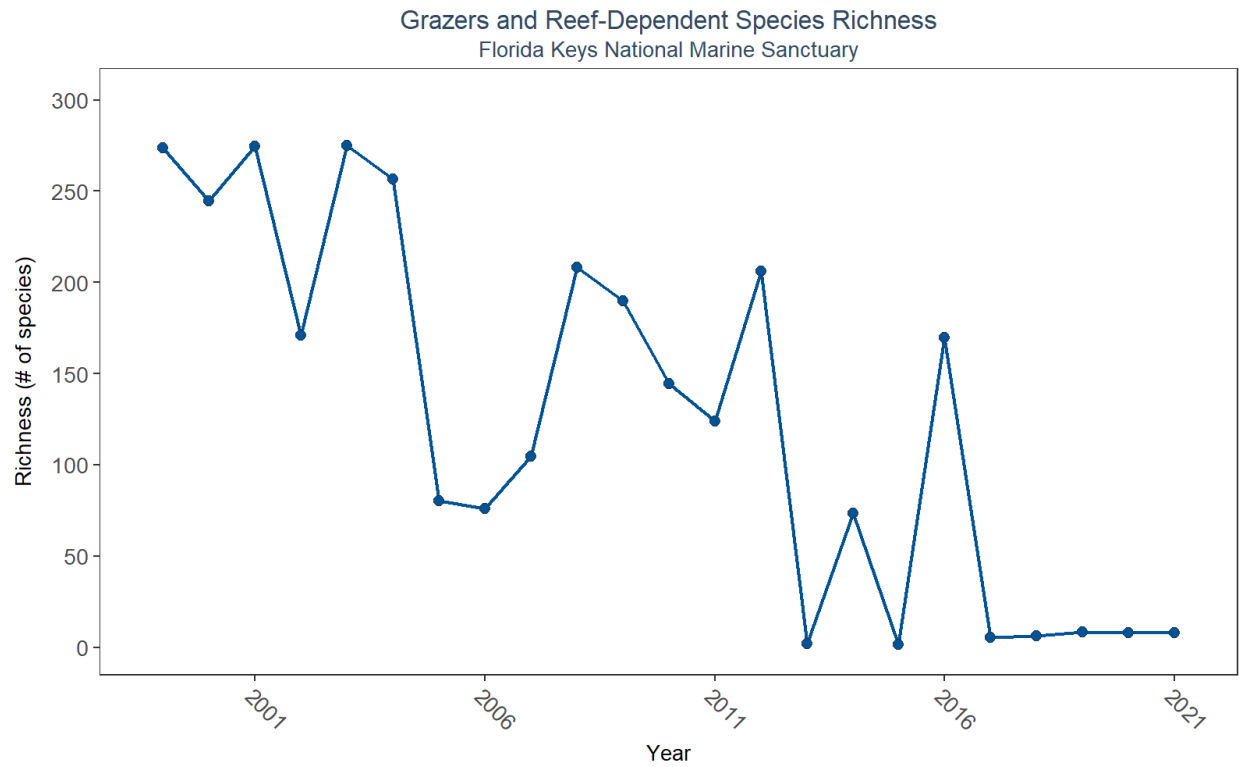
# Grazers and Reef-Dependent Species Richness Biscayne Bay Aquatic Preserve



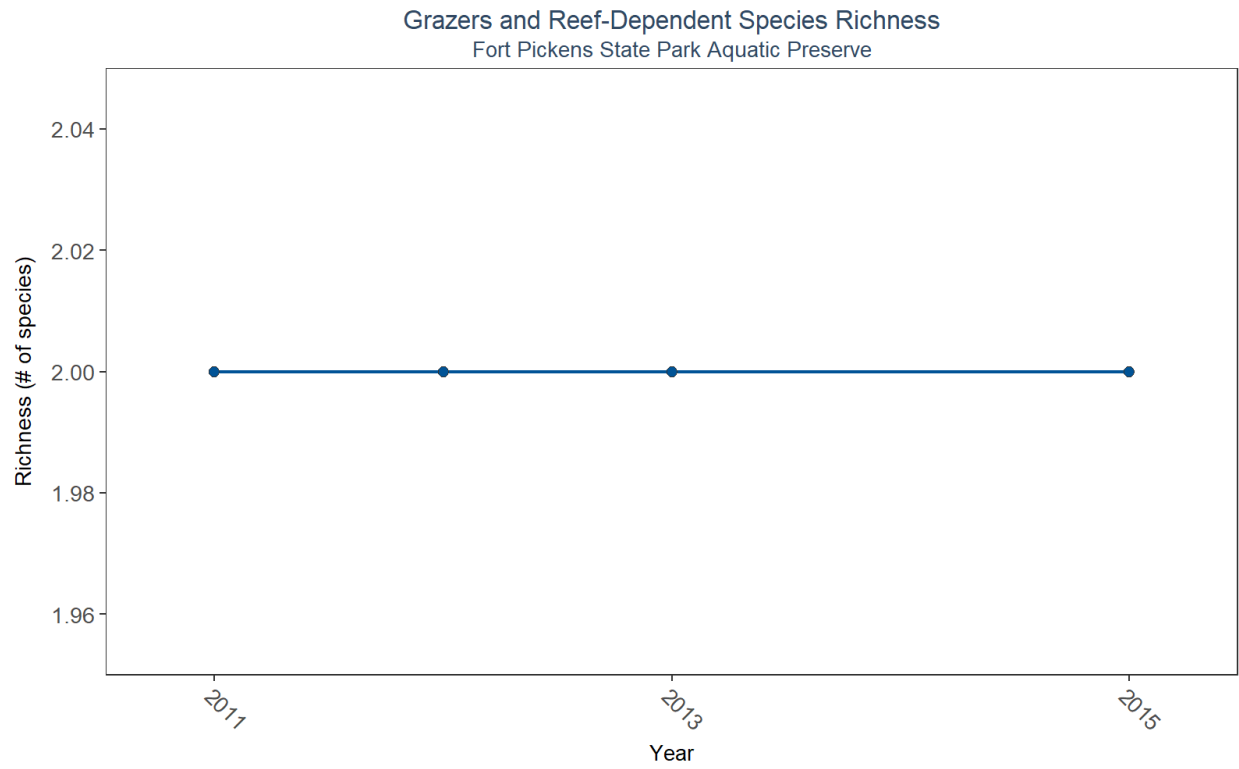
N_Years	EarliestYear	LatestYear	N_Data	Min	Max	Median	Mean	StDev	Year_MinRichness	Year_MaxRichness
25	1992	2022	1963	1	8	2	2.18	1.11	2013	2022



N_Years	EarliestYear	LatestYear	N_Data	Min	Max	Median	Mean	StDev	Year_MinRichness	Year_MaxRichness
13	1999	2020	44	2	284	204	145.41	133.65	2010	2012

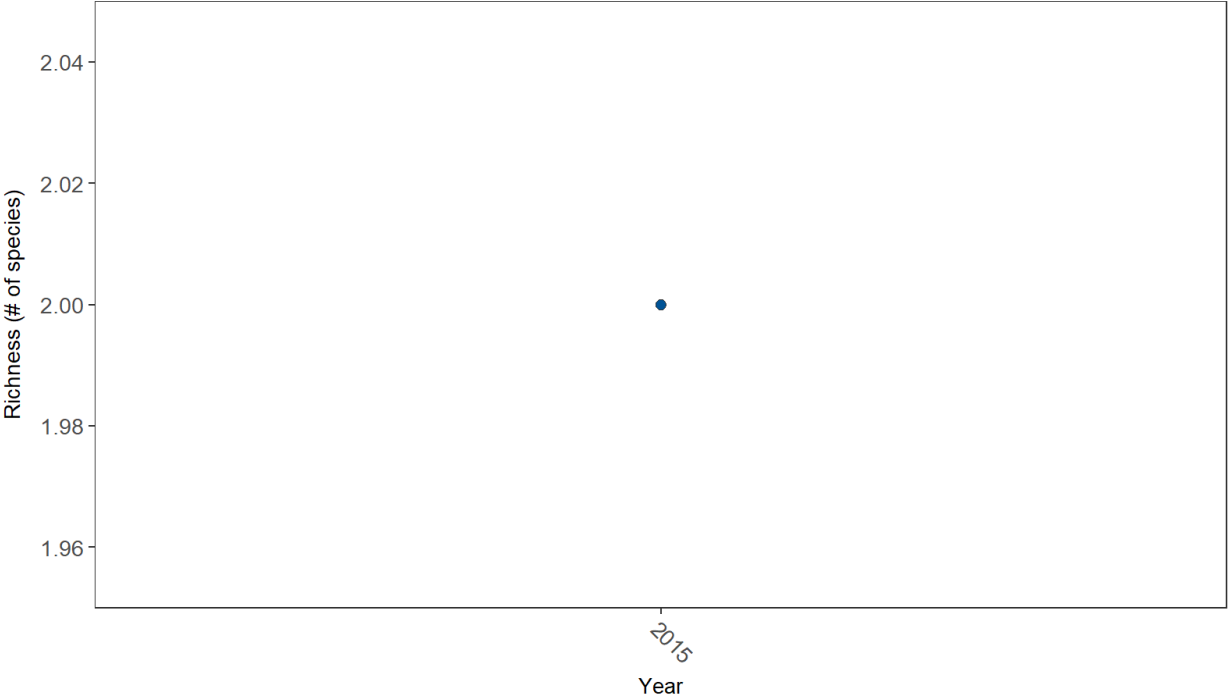


N_Years	EarliestYear	LatestYear	N_Data	Min	Max	Median	Mean	StDev	Year_MinRichness	Year_MaxRichness
23	1999	2021	20738	1	302	7	119.51	133.65	2015	2003



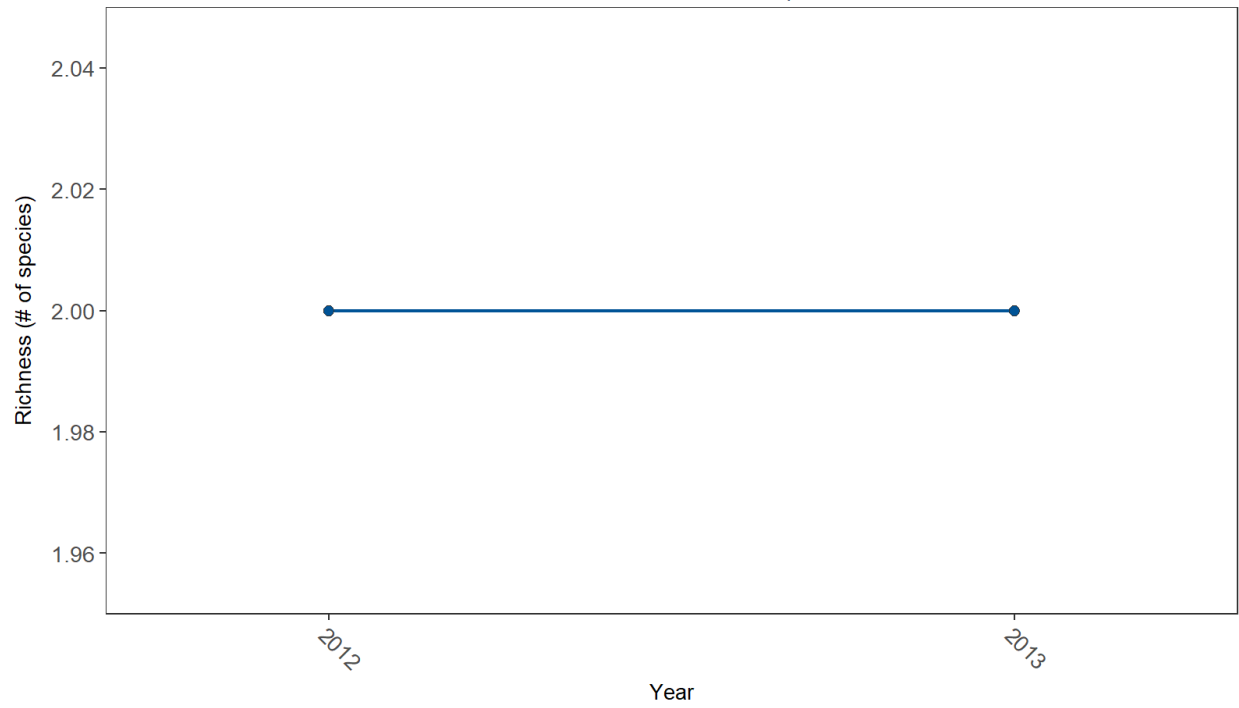
N_Years	EarliestYear	LatestYear	N_Data	Min	Max	Median	Mean	StDev	Year_MinRichness	Year_MaxRichness
4	2011	2015	6	2	2	2	2	0	2011	2011

Grazers and Reef-Dependent Species Richness  
Gasparilla Sound-Charlotte Harbor Aquatic Preserve



N_Years	EarliestYear	LatestYear	N_Data	Min	Max	Median	Mean	StDev	Year_MinRichness	Year_MaxRichness
1	2015	2015	1	2	2	2	2	NA	2015	2015

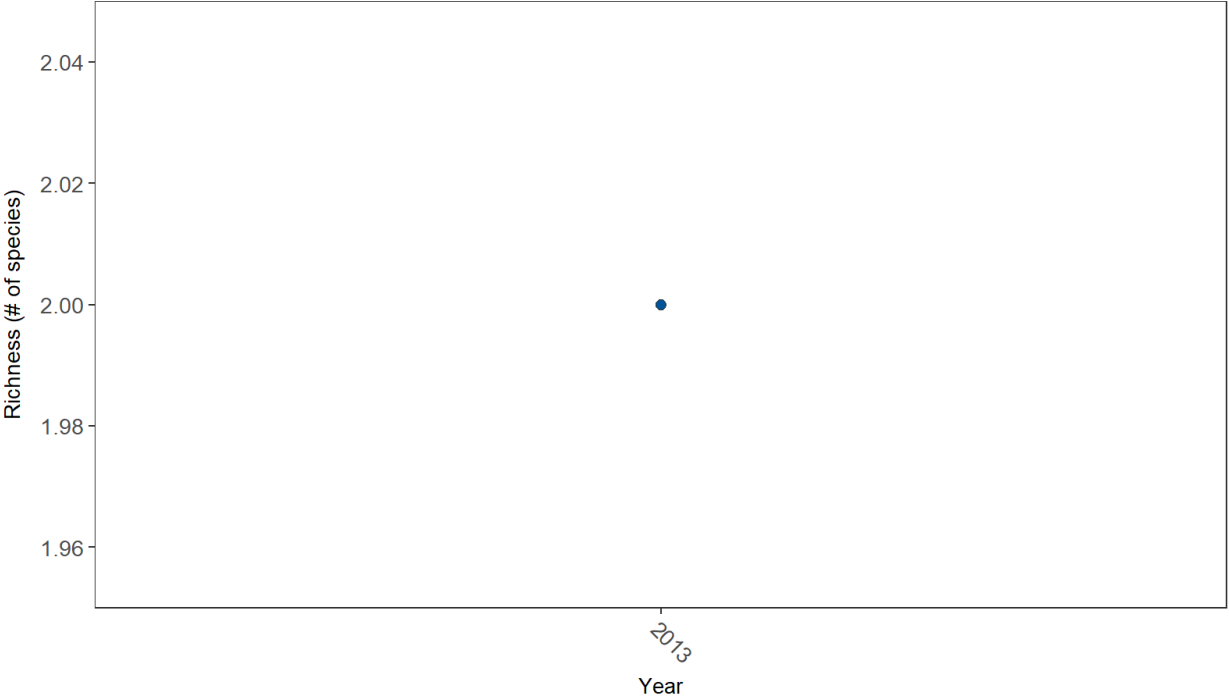
# Grazers and Reef-Dependent Species Richness Indian River-Malabar to Vero Beach Aquatic Preserve



N_Years	EarliestYear	LatestYear	N_Data	Min	Max	Median	Mean	StDev	Year_MinRichness	Year_MaxRichness
2	2012	2013	3	2	2	2	2	0	2012	2012

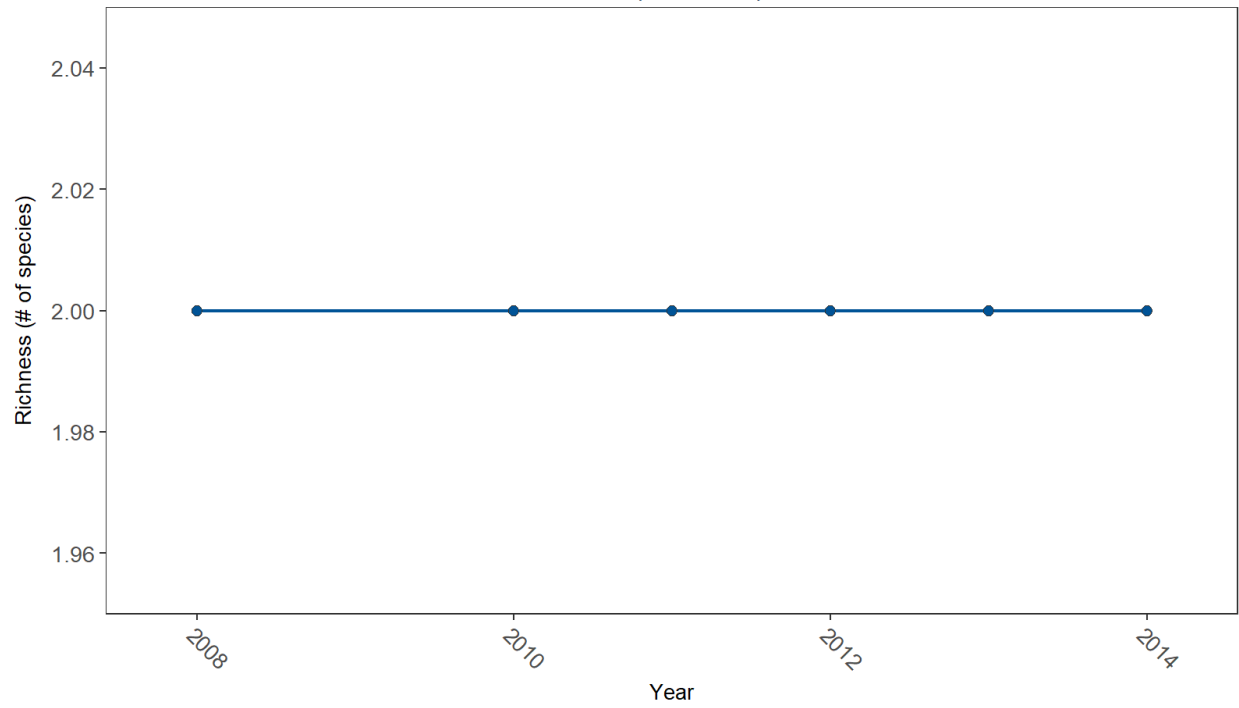


Grazers and Reef-Dependent Species Richness  
Indian River-Vero Beach to Ft. Pierce Aquatic Preserve

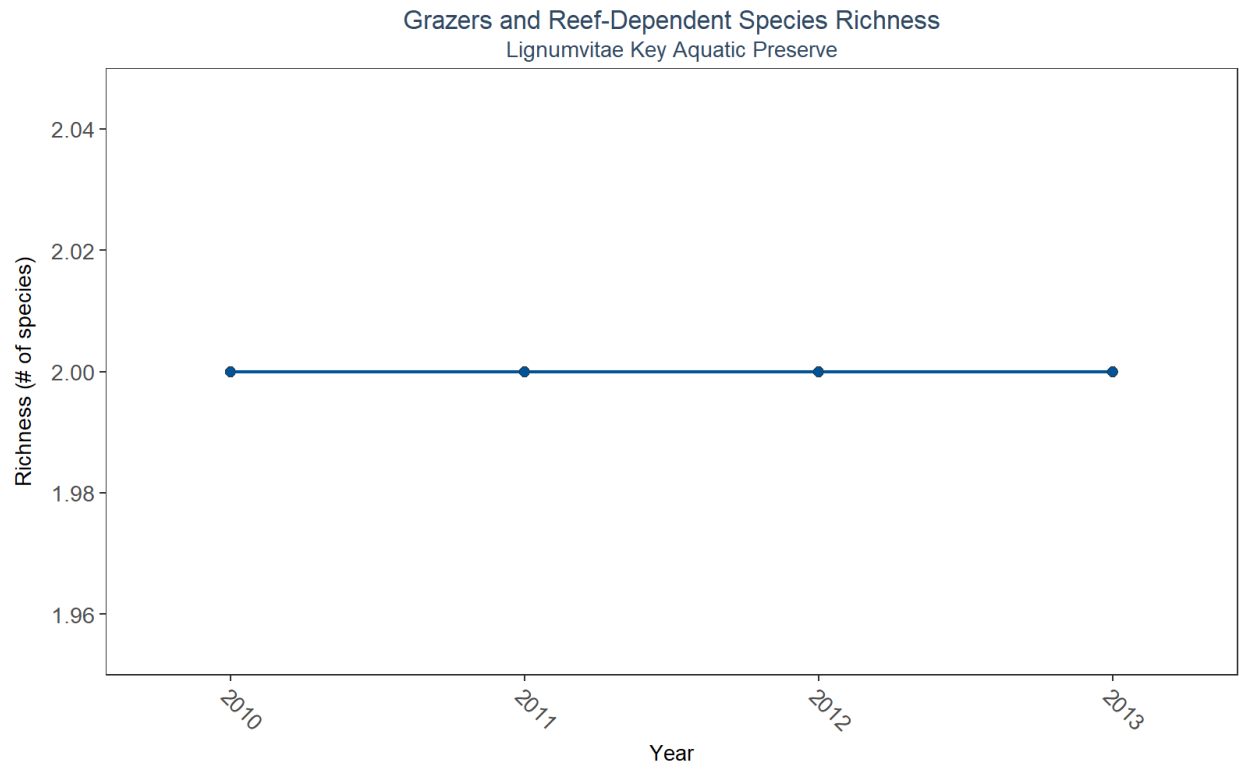


N_Years	EarliestYear	LatestYear	N_Data	Min	Max	Median	Mean	StDev	Year_MinRichness	Year_MaxRichness
1	2013	2013	5	2	2	2	2	0	2013	2013

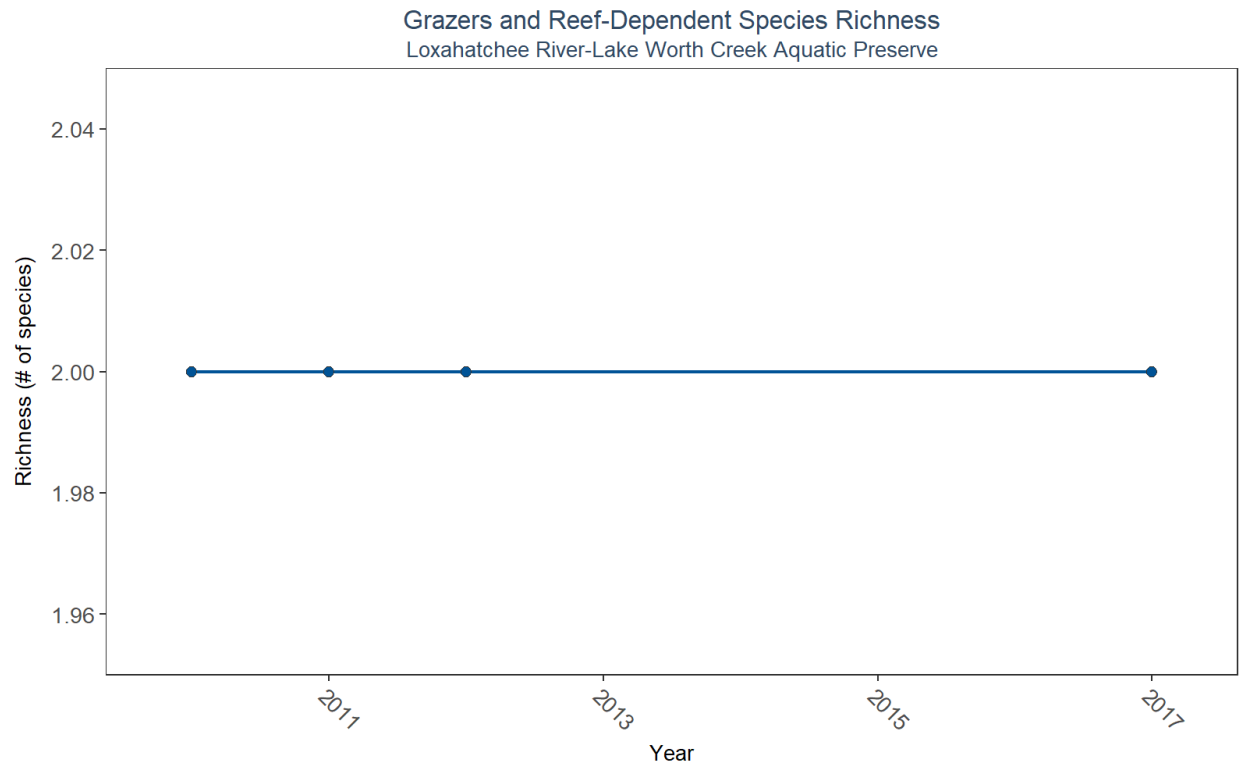
# Grazers and Reef-Dependent Species Richness Jensen Beach to Jupiter Inlet Aquatic Preserve



N_Years	EarliestYear	LatestYear	N_Data	Min	Max	Median	Mean	StDev	Year_MinRichness	Year_MaxRichness
6	2008	2014	24	2	2	2	2	0	2008	2008

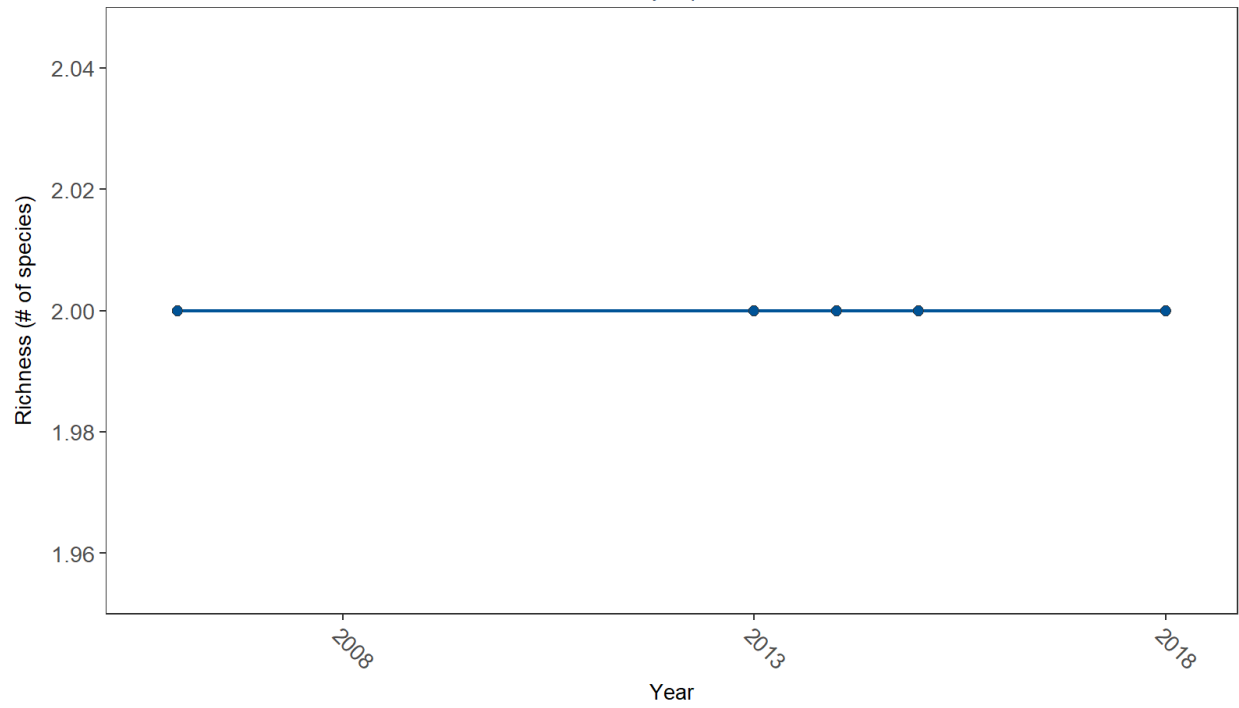


N_Years	EarliestYear	LatestYear	N_Data	Min	Max	Median	Mean	StDev	Year_MinRichness	Year_MaxRichness
4	2010	2013	4	2	2	2	2	0	2010	2010



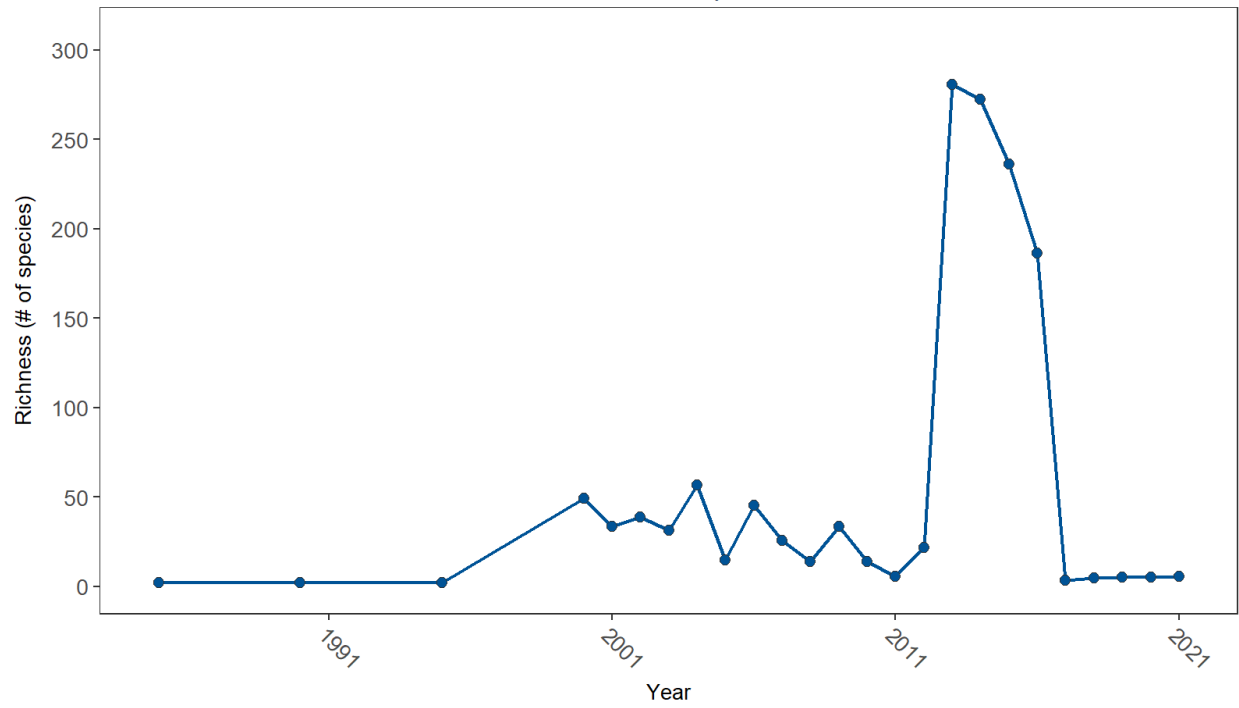
N_Years	EarliestYear	LatestYear	N_Data	Min	Max	Median	Mean	StDev	Year_MinRichness	Year_MaxRichness
4	2010	2017	8	2	2	2	2	0	2010	2010

# Grazers and Reef-Dependent Species Richness Pinellas County Aquatic Preserve



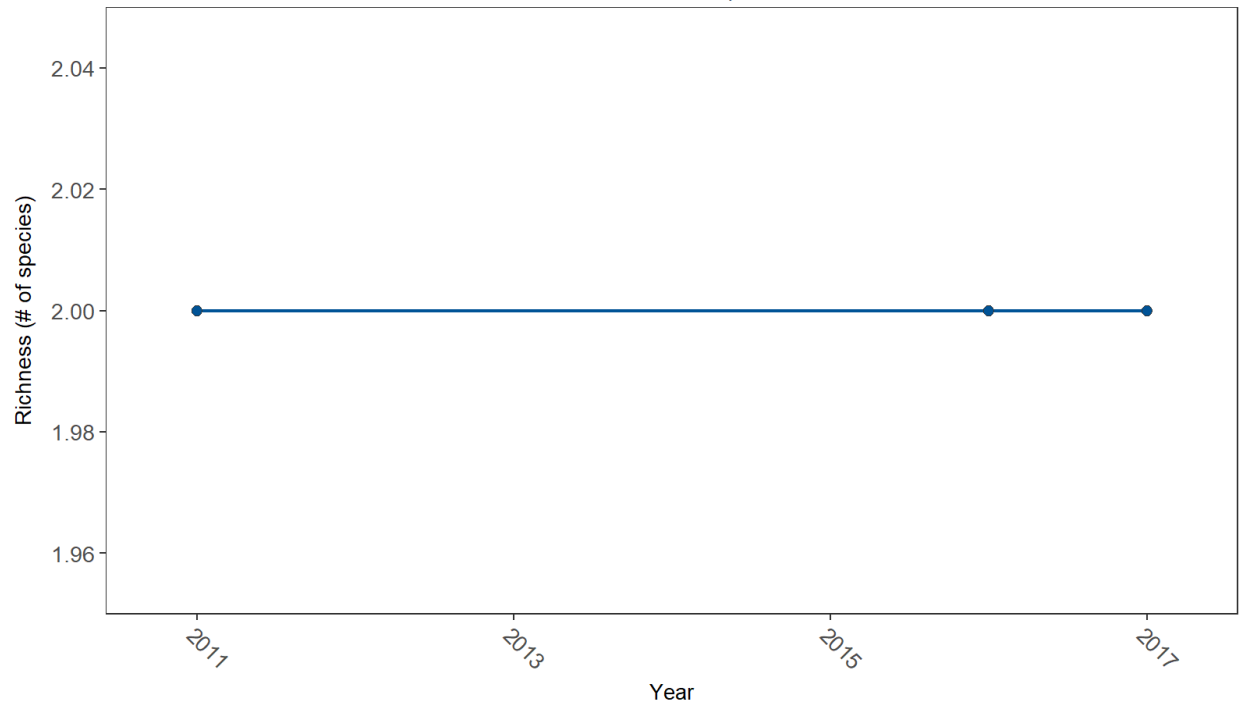
N_Years	EarliestYear	LatestYear	N_Data	Min	Max	Median	Mean	StDev	Year_MinRichness	Year_MaxRichness
5	2006	2018	9	2	2	2	2	0	2006	2006

Grazers and Reef-Dependent Species Richness  
 Southeast Florida Coral Reef Ecosystem Conservation Area

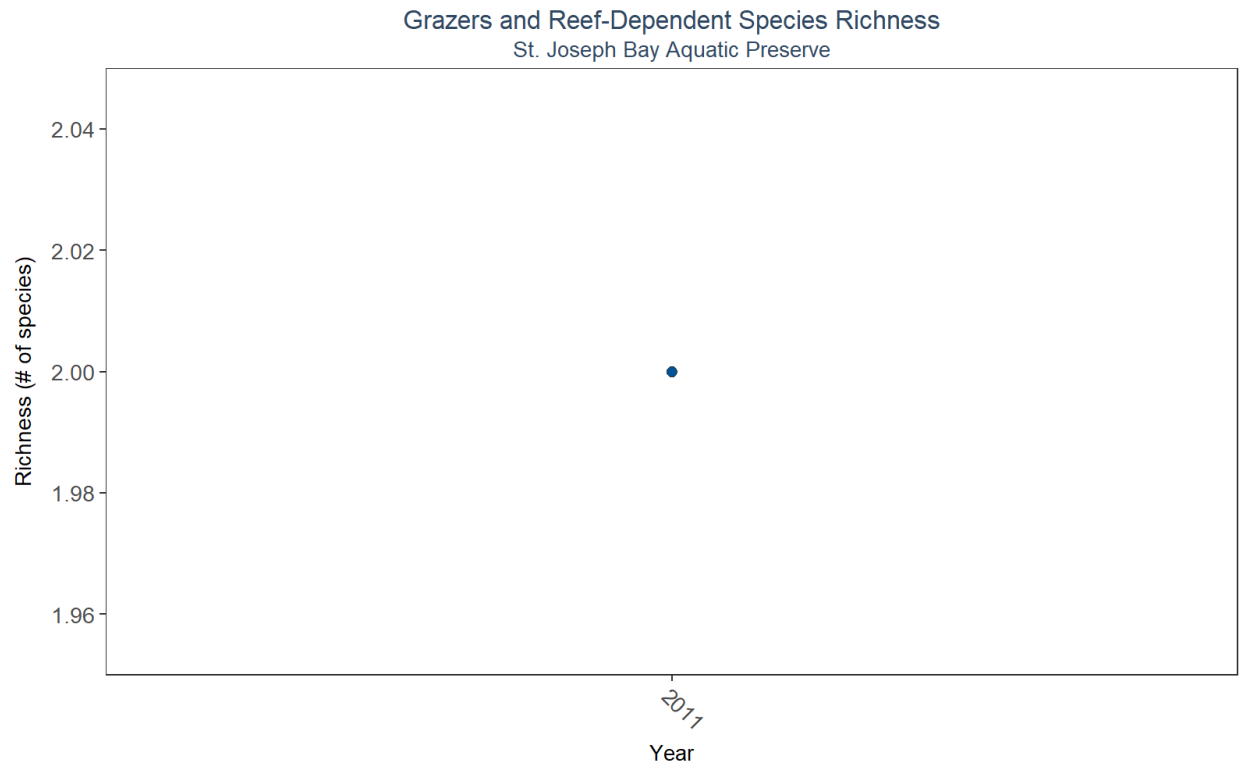


N_Years	EarliestYear	LatestYear	N_Data	Min	Max	Median	Mean	StDev	Year_MinRichness	Year_MaxRichness
25	1985	2021	4030	1	302	202	172.44	134.89	1985	2013

# Grazers and Reef-Dependent Species Richness St. Andrews State Park Aquatic Preserve



N_Years	EarliestYear	LatestYear	N_Data	Min	Max	Median	Mean	StDev	Year_MinRichness	Year_MaxRichness
3	2011	2017	5	2	2	2	2	0	2011	2011



N_Years	EarliestYear	LatestYear	N_Data	Min	Max	Median	Mean	StDev	Year_MinRichness	Year_MaxRichness
1	2011	2011	3	2	2	2	2	0	2011	2011