

ALY6000: Executive Summary Report 3

Dataset Instructions

Complete the following instructions to create the dataset and output required for the Executive Summary Report in Module 3. Use the R in Action textbook and web searches when needed to write the appropriate R script. The output you create by following these steps must be incorporated into the Appendix of your report. Be sure to save your R script file with the following naming convention:

LastName_M3_Project3

Append your completed R-Script to the Executive Summary

Instructions

To complete this assignment you must create an R script file that includes the code required to complete the following steps:

1. Print your name at the top of the script and load these libraries: FSA, FSAdata, magrittr, dplyr, tidyr plyr and tidyverse
2. Import the inchBio.csv and name the table <bio>
3. Display the head, tail and structure of <bio>
4. Create an object, <counts>, that counts and lists all the species records
5. Display just the 8 levels (names) of the species
6. Create a <tmp> object that displays the different species and the number of record of each species in the dataset. Include this information in your report.-
7. Create a subset, <tmp2>, of just the species variable and display the first five records
8. Create a table, <w>, of the species variable. Display the class of w
9. Convert <w> to a data frame named <t> and display the results
10. Extract and display the frequency values from the <t> data frame
11. Create a table named <cSpec> from the bio species attribute (variable) and confirm that you created a table which displays the number of species in the dataset <bio>
12. Create a table named <cSpecPct> that displays the species and percentage of records for each species. Confirm you created a table class.

13. Convert the table, <cSpecPct>, to a data frame named <u> and confirm that <u> is a data frame
14. Create a barplot of <cSpec> with the following: titled Fish Count with the following specifications:
 - Title: Fish Count
 - Y axis is labeled "COUNTS"
 - Color the bars Light Green
 - Rotate Y axis to be horizontal
 - Set the X axis font magnification to 60% of nominal
15. Create a barplot of <cSpecPct>, with the following specifications:
 - Y axis limits of 0 to 4
 - Y axis label color of Light Blue
 - Title of "Fish Relative Frequency"
16. Rearrange the <u> cSpec Pct data frame in descending order of relative frequency. Save the rearranged data frame as the object <d>
17. Rename the <d> columns Var 1 to Species, and Freq to RelFreq
18. Add new variables to <d> and call them cumfreq, counts, and cumcounts
19. Create a parameter variable <def_par> to store parameter variables
20. Create a barplot, <pc>, with the following specifications:
 - d\$counts of width 1, spacing of .15
 - no boarder
 - Axes: F
 - Yaxis limit 0,3.05*max
 - d\$counts na.rm is true
 - y label is Cumulative Counts
 - scale x axis to 70%
 - names.arg: d\$Species
 - Title of the barplot is "Species Pareto"

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21. Add a cumulative counts line to the <pc> plot with the following:

- Spec line type is b
- Scale plotting text at 70%
- Data values are solid circles with color cyan4

22. Place a grey box around the pareto plot (hint:

<https://www.statmethods.net/advgraphs/parameters.html>)

23. Add a left side axis with the following specifications

- Horizontal values at tick marks at cumcounts on side 2
- Tickmark color of grey62
- Color of axis is grey62
- Axis scaled to 80% of normal

(hint: <https://www.statmethods.net/advgraphs/axes.html>)

24. Add axis details on right side of box with the specifications:

- Spec: Side 4
- Tickmarks at cumcounts with labels from 0 to cumfreq with %,
- Axis color of cyan5 and label color of cyan4
- Axis font scaled to 80% of nominal

25. Display the finished Species Pareto Plot (without the star watermarks). Have your last name on the plot

26. Commit your code in your github/gitlab repo