Reef data analysis

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library(tidyverse)

## -- Attaching packages --------------------------------------- tidyverse 1.3.1 --

## v ggplot2 3.3.3 v purrr 0.3.4  
## v tibble 3.1.1 v dplyr 1.0.6  
## v tidyr 1.1.3 v stringr 1.4.0  
## v readr 1.4.0 v forcats 0.5.1

## -- Conflicts ------------------------------------------ tidyverse\_conflicts() --  
## x dplyr::filter() masks stats::filter()  
## x dplyr::lag() masks stats::lag()

library(StereoMorph)  
library(ggplot2)  
library(here)

## here() starts at C:/Users/ericc/Desktop/General-Repository

library(ggthemes)  
library(paletteer)

library(ggstatsplot)

## You can cite this package as:  
## Patil, I. (2021). Visualizations with statistical details: The 'ggstatsplot' approach.  
## PsyArxiv. doi:10.31234/osf.io/p7mku

reef\_fish <- readr::read\_csv("my\_data/105\_coral\_reef\_dataset.csv")

##   
## -- Column specification --------------------------------------------------------  
## cols(  
## Species = col\_character(),  
## Family = col\_character(),  
## Prey = col\_character(),  
## Body\_length = col\_double(),  
## Head\_length = col\_double(),  
## Upper\_jaw\_length = col\_double(),  
## Body\_depth = col\_double(),  
## Caudal\_peduncle\_depth = col\_double(),  
## Jaws\_to\_eye\_distance = col\_double(),  
## Fineness\_ratio = col\_double()  
## )

glimpse(reef\_fish)

## Rows: 81  
## Columns: 10  
## $ Species <chr> "Abudefduf\_sordidus", "Acanthurus\_achilles", "Ac~  
## $ Family <chr> "Pomacentridae", "Acanthuridae", "Acanthuridae",~  
## $ Prey <chr> "benthic", "benthic", "benthic", "benthic", "pla~  
## $ Body\_length <dbl> 0.7224, 0.7030, 0.7217, 0.7148, 0.7586, 0.6963, ~  
## $ Head\_length <dbl> 0.2283, 0.1804, 0.1562, 0.1569, 0.1627, 0.1873, ~  
## $ Upper\_jaw\_length <dbl> 0.0455, 0.0277, 0.0328, 0.0356, 0.0276, 0.0343, ~  
## $ Body\_depth <dbl> 0.4162, 0.3783, 0.3689, 0.3757, 0.2865, 0.3592, ~  
## $ Caudal\_peduncle\_depth <dbl> 0.1444, 0.0791, 0.0966, 0.0881, 0.1328, 0.0945, ~  
## $ Jaws\_to\_eye\_distance <dbl> 0.0906, 0.1398, 0.1704, 0.1742, 0.1003, 0.0901, ~  
## $ Fineness\_ratio <dbl> 1.7359, 1.8584, 1.9565, 1.9027, 2.6482, 1.9385, ~

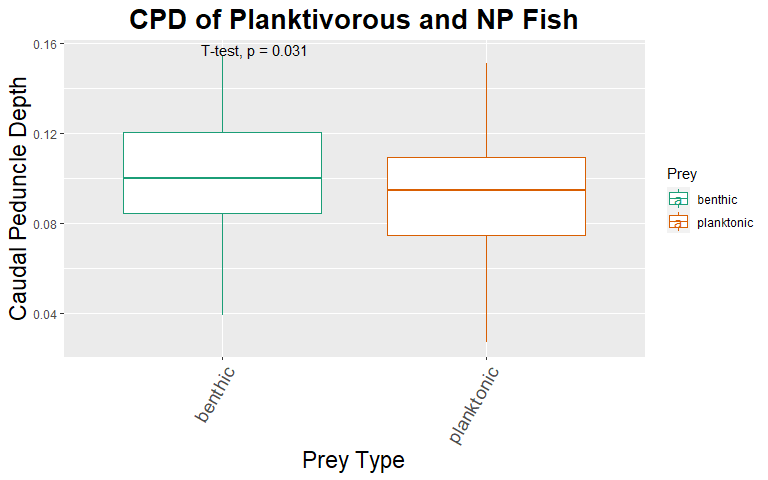
reef\_fish%>%  
 group\_by(Prey)%>%  
 summarise(mean\_body\_length=mean(Body\_length),  
 mean\_body\_depth=mean(Body\_depth),  
 mean\_fineness=mean(Fineness\_ratio),  
 mean\_cd\_depth=mean(Caudal\_peduncle\_depth),  
 mean\_jaw\_distance=mean(Jaws\_to\_eye\_distance))

## # A tibble: 2 x 6  
## Prey mean\_body\_length mean\_body\_depth mean\_fineness mean\_cd\_depth  
## <chr> <dbl> <dbl> <dbl> <dbl>  
## 1 benthic 0.747 0.345 2.22 0.104   
## 2 planktonic 0.762 0.270 3.06 0.0900  
## # ... with 1 more variable: mean\_jaw\_distance <dbl>

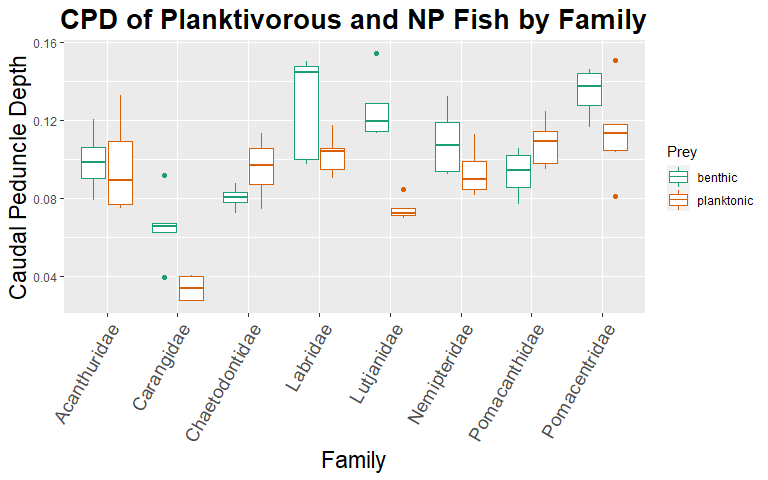
#install.packages("ggExtra")  
#install.packages("ColorPalette")  
library(ggExtra)  
library(ColorPalette)

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

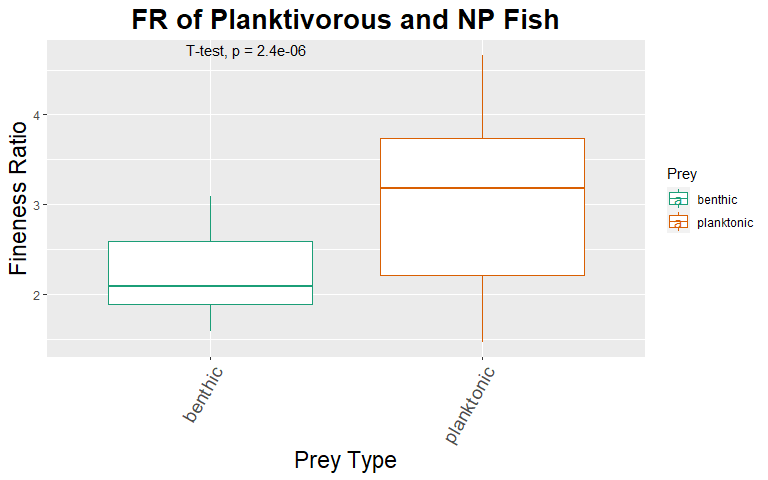
reef\_fish%>%  
 ggplot(aes(x=Prey,y=Caudal\_peduncle\_depth,color=Prey))+  
 geom\_boxplot()+  
 scale\_color\_brewer(palette = "Dark2")+  
 theme(legend.position = "right",  
 axis.text.x = element\_text(angle = 60, hjust=1,size = 14),axis.title = element\_text(size = 17),plot.title = element\_text(size = 20,face = "bold",hjust = .5))+  
 labs(title = "CPD of Planktivorous and NP Fish",x="Prey Type",y="Caudal Peduncle Depth")+  
 stat\_compare\_means(method = "t.test")



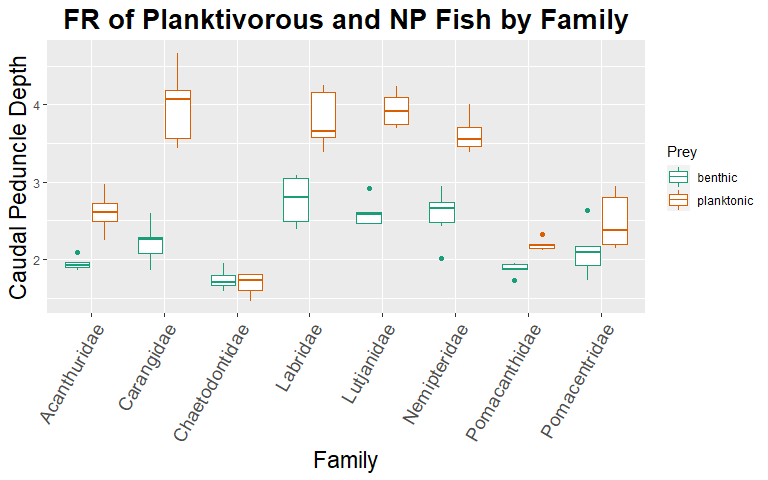
reef\_fish%>%  
 ggplot(aes(x=Family,y=Caudal\_peduncle\_depth,color=Prey))+  
 geom\_boxplot()+  
 scale\_color\_brewer(palette = "Dark2")+  
 theme(legend.position = "right",  
 axis.text.x = element\_text(angle = 60, hjust=1,size = 14),axis.title = element\_text(size = 17),plot.title = element\_text(size = 20,face = "bold",hjust = .5))+  
 labs(title = "CPD of Planktivorous and NP Fish by Family",x="Family",y="Caudal Peduncle Depth")



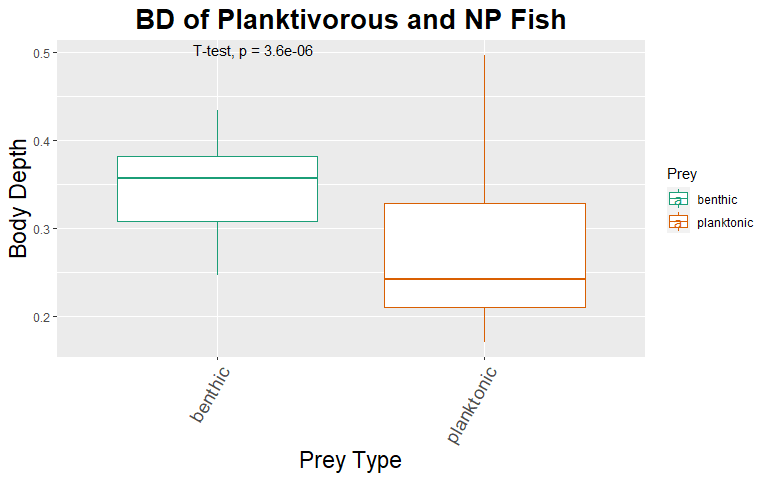
reef\_fish%>%  
 ggplot(aes(x=Prey,y=Fineness\_ratio,color=Prey))+  
 geom\_boxplot()+  
 scale\_color\_brewer(palette = "Dark2")+  
 theme(legend.position = "right",  
 axis.text.x = element\_text(angle = 60, hjust=1,size = 14),axis.title = element\_text(size = 17),plot.title = element\_text(size = 20,face = "bold",hjust = .5))+  
 labs(title = "FR of Planktivorous and NP Fish",x="Prey Type",y="Fineness Ratio")+stat\_compare\_means(method = "t.test")



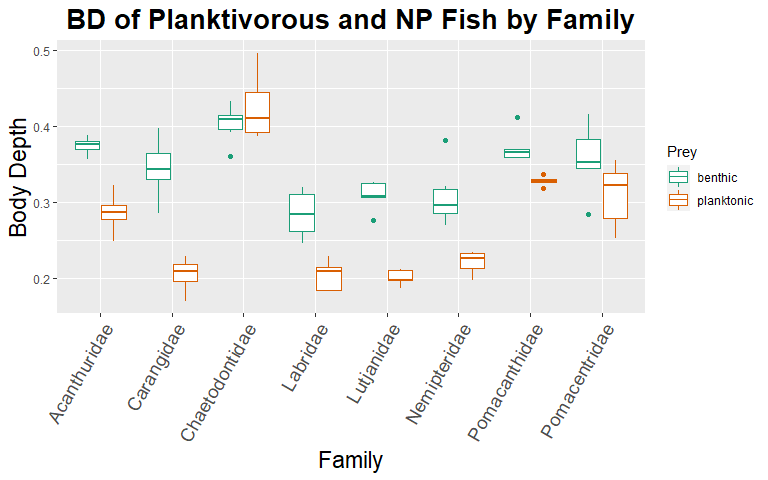
reef\_fish%>%  
 ggplot(aes(x=Family,y=Fineness\_ratio,color=Prey))+  
 geom\_boxplot()+  
 scale\_color\_brewer(palette = "Dark2")+  
 theme(legend.position = "right",  
 axis.text.x = element\_text(angle = 60, hjust=1,size = 14),axis.title = element\_text(size = 17),plot.title = element\_text(size = 20,face = "bold",hjust = .5))+  
 labs(title = "FR of Planktivorous and NP Fish by Family",x="Family",y="Caudal Peduncle Depth")+  
 theme(axis.text.x = element\_text(angle = 60, hjust=1))



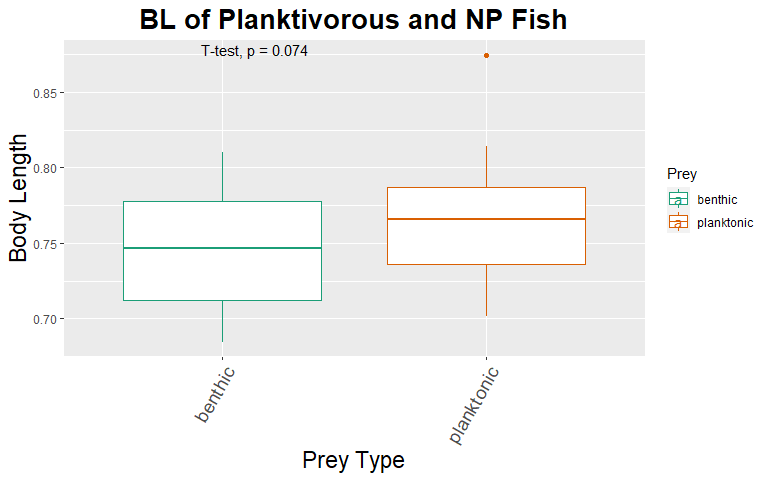
reef\_fish%>%  
 ggplot(aes(x=Prey,y=Body\_depth,color=Prey))+  
 geom\_boxplot()+  
 scale\_color\_brewer(palette = "Dark2")+  
 theme(legend.position = "right",  
 axis.text.x = element\_text(angle = 60, hjust=1,size = 14),axis.title = element\_text(size = 17),plot.title = element\_text(size = 20,face = "bold",hjust = .5))+  
 labs(title = "BD of Planktivorous and NP Fish",x="Prey Type",y="Body Depth")+stat\_compare\_means(method = "t.test")



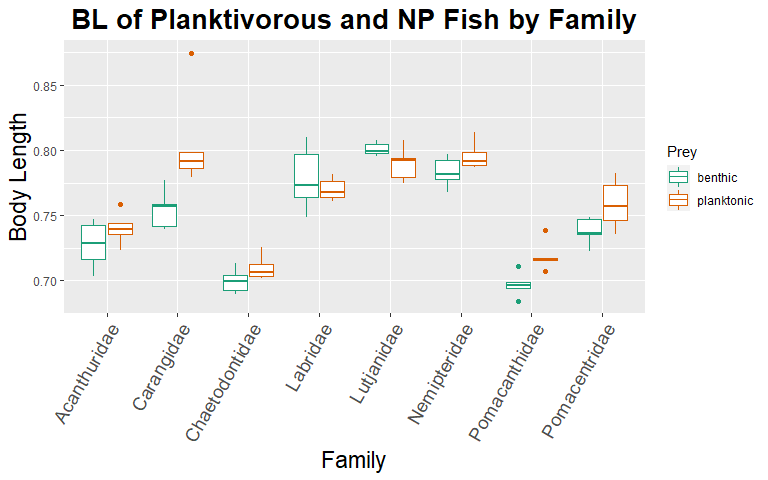
reef\_fish%>%  
 ggplot(aes(x=Family,y=Body\_depth,color=Prey))+  
 geom\_boxplot()+  
 scale\_color\_brewer(palette = "Dark2")+  
 theme(legend.position = "right",  
 axis.text.x = element\_text(angle = 60, hjust=1,size = 14),axis.title = element\_text(size = 17),plot.title = element\_text(size = 20,face = "bold",hjust = .5))+  
 labs(title = "BD of Planktivorous and NP Fish by Family",x="Family",y="Body Depth")



P<-reef\_fish%>%  
 ggplot(aes(x=Prey,y=Body\_length,color=Prey))+  
 geom\_boxplot()+  
 scale\_color\_brewer(palette = "Dark2")+  
 theme(legend.position = "right",  
 axis.text.x = element\_text(angle = 60, hjust=1,size = 14),axis.title = element\_text(size = 17),plot.title = element\_text(size = 20,face = "bold",hjust = .5))+  
 labs(title = "BL of Planktivorous and NP Fish",x="Prey Type",y="Body Length")  
P+stat\_compare\_means(method = "t.test")

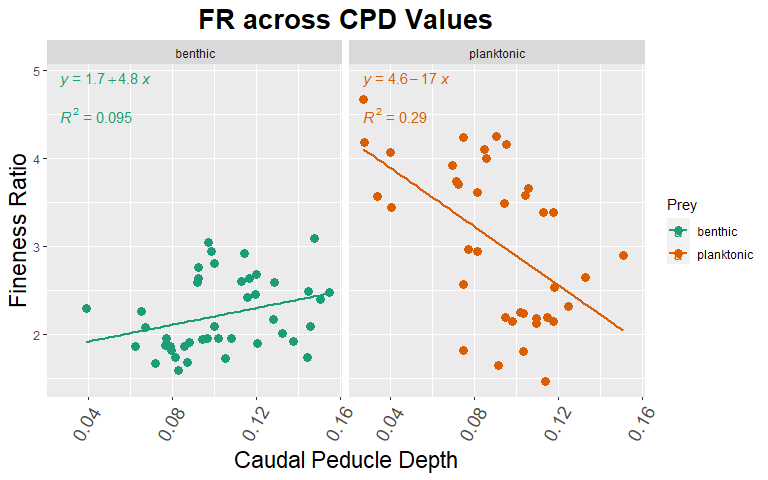


reef\_fish%>%  
 ggplot(aes(x=Family,y=Body\_length,color=Prey))+  
 geom\_boxplot()+  
 scale\_color\_brewer(palette = "Dark2")+  
 theme(legend.position = "right",  
 axis.text.x = element\_text(angle = 60, hjust=1,size = 14),axis.title = element\_text(size = 17),plot.title = element\_text(size = 20,face = "bold",hjust = .5))+  
 labs(title = "BL of Planktivorous and NP Fish by Family",x="Family",y="Body Length")



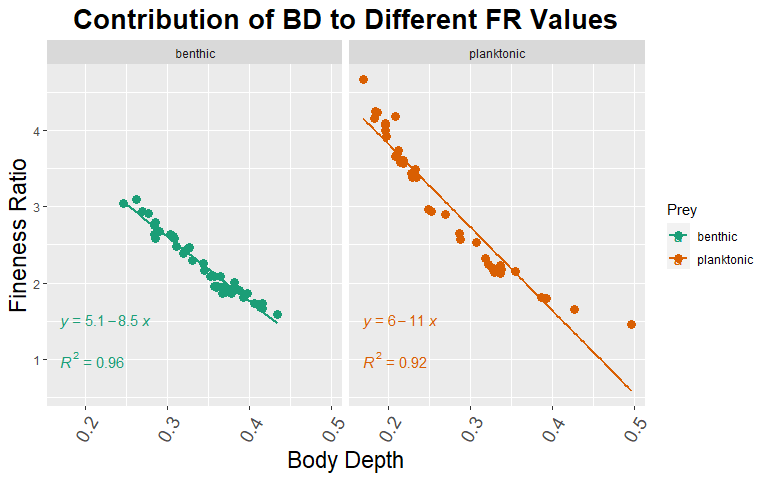
reef\_fish%>%  
 ggplot(aes(x=Caudal\_peduncle\_depth,y=Fineness\_ratio,color=Prey))+  
 geom\_point(size=2.7)+  
 scale\_x\_continuous()+  
 scale\_y\_continuous()+  
 geom\_smooth(method = lm,se=F)+  
 stat\_regline\_equation(label.y=4.9,aes(label = ..eq.label..)) +  
 stat\_regline\_equation(label.y=4.5,aes(label = ..rr.label..))+  
 facet\_wrap(~Prey)+  
 scale\_color\_brewer(palette = "Dark2")+  
 theme(legend.position = "right",  
 axis.text.x = element\_text(angle = 60, hjust=1,size = 14),axis.title = element\_text(size = 17),plot.title = element\_text(size = 20,face = "bold",hjust = .5))+  
 labs(title = "FR across CPD Values",x="Caudal Peducle Depth",y="Fineness Ratio")

## `geom\_smooth()` using formula 'y ~ x'



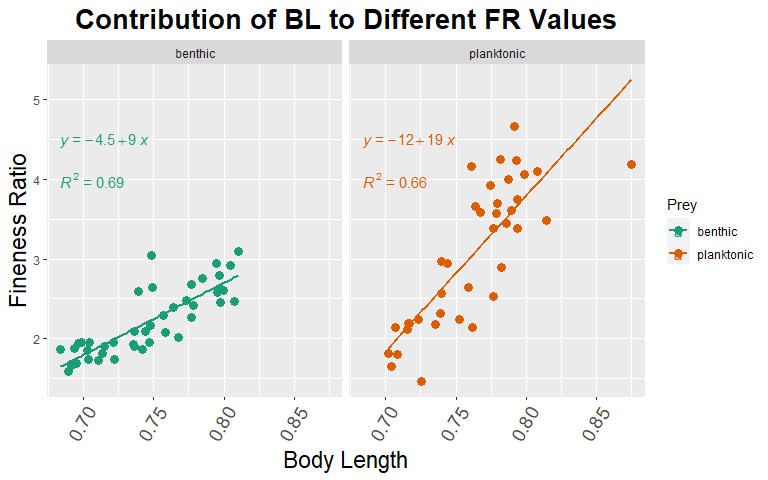
reef\_fish%>%  
 ggplot(aes(x=Body\_depth,y=Fineness\_ratio,color=Prey))+  
 geom\_point(size=2.7)+  
 scale\_x\_continuous()+  
 scale\_y\_continuous()+  
 geom\_smooth(method = lm,se=F)+  
 stat\_regline\_equation(label.y=1.5,aes(label = ..eq.label..)) +  
 stat\_regline\_equation(label.y=1,aes(label = ..rr.label..))+  
 facet\_wrap(~Prey)+  
 scale\_color\_brewer(palette = "Dark2")+  
 theme(legend.position = "right",  
 axis.text.x = element\_text(angle = 60, hjust=1,size = 14),axis.title = element\_text(size = 17),plot.title = element\_text(size = 20,face = "bold",hjust = .5))+  
 labs(title = "Contribution of BD to Different FR Values",x="Body Depth",y="Fineness Ratio")

## `geom\_smooth()` using formula 'y ~ x'



reef\_fish%>%  
 ggplot(aes(x=Body\_length,y=Fineness\_ratio,color=Prey))+  
 geom\_point(size=2.7)+  
 scale\_x\_continuous()+  
 scale\_y\_continuous()+  
 geom\_smooth(method = lm,se=F)+  
 stat\_regline\_equation(label.y=4.5,aes(label = ..eq.label..)) +  
 stat\_regline\_equation(label.y=4,aes(label = ..rr.label..))+  
 facet\_wrap(~Prey)+  
 scale\_color\_brewer(palette = "Dark2")+  
 theme(legend.position = "right",  
 axis.text.x = element\_text(angle = 60, hjust=1,size = 14),axis.title = element\_text(size = 17),plot.title = element\_text(size = 20,face = "bold",hjust = .5))+  
 labs(title = "Contribution of BL to Different FR Values",x="Body Length",y="Fineness Ratio")

## `geom\_smooth()` using formula 'y ~ x'



citation()

##   
## To cite R in publications use:  
##   
## R Core Team (2021). R: A language and environment for statistical  
## computing. R Foundation for Statistical Computing, Vienna, Austria.  
## URL https://www.R-project.org/.  
##   
## A BibTeX entry for LaTeX users is  
##   
## @Manual{,  
## title = {R: A Language and Environment for Statistical Computing},  
## author = {{R Core Team}},  
## organization = {R Foundation for Statistical Computing},  
## address = {Vienna, Austria},  
## year = {2021},  
## url = {https://www.R-project.org/},  
## }  
##   
## We have invested a lot of time and effort in creating R, please cite it  
## when using it for data analysis. See also 'citation("pkgname")' for  
## citing R packages.