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Coding_Assignment2_DataVis.R
Source on Save
Run
Source

1 ##Coding assignment part1
2
3 data("mtcars")
4 str(mtcars)
5
6
7 ### Plotting using base R ###
8 plot(mtcars$wt, mtcars$mpg,
9       xlab = "car weight",
10      ylab = "miles per gallon",
11      font.lab=6,
12      pch = 23)
13
14
15 ### ggplot ###
16
17 library(ggplot2) #loading ggplot
18 ggplot() #provide input in brackets
19
20 ggplot(mtcars, aes(x = wt, y = mpg)) + # + sign adds layers
21   geom_point() + #adds points
22   geom_smooth(method = lm, se = FALSE) # adds straight line, fitting linear model
23
24 #change in order of layers (minor but matters sometimes)
25 #aes means aesthetic, it is interesting but caution where you apply.
26 #If you apply aes in main frame (i.e in x,y bracket at start it will apply to everything).
27 #Instead apply aes specifically in the layer where necessary. (This decision will vary as per requirement)
28
29 ggplot(mtcars, aes(x = wt, y = mpg))+
30   geom_smooth(method = lm, se = FALSE, color = "grey")+
31   geom_point(aes(size = wt), color = "blue") + #can add color or other stuff inside bracket for points
32   xlab("weight") +
33   ylab("miles per gallon")
34
35 ggplot(mtcars, aes(x = wt, y = mpg))+
36   geom_smooth(method = lm, se = FALSE, color = "grey") +
37   geom_point(aes(size = wt, color = wt)) + #can color as per quantity of the variable as interest
38   xlab("weight") +
39   ylab("miles per gallon") +
40   scale_color_gradient(low = "green", high = "red")+ #gradient based coloring for high low quantity
41   scale_x_log10() #adding log based scale
42   scale_y_continuous(labels = scales::percent)
43
44
45 ## setting working directory for further part of assignment
46 #setwd("C:/Users/panka/OneDrive - Auburn University/PLPA_class")
47
48 #Categorical
49
50 #loading file from the set working directory
51 bull.richness <- read.csv("Bull_richness.csv")
52
53
54 bull.richness.soy.no.till <- bull.richness[bull.richness$Crop == "Soy" &
55   bull.richness$Treatment == "No-till",]
56
57 ## Position use case, categorical variable
58
59 ggplot(bull.richness.soy.no.till, aes(x = GrowthStage, y = richness, color = Fungicide)) +
60   geom_boxplot() +
61   xlab("") +
62   ylab("fungal richness") +
63   geom_point(position = position_jitterdodge) # Positiona help prevent overlapping, Also dodge, it will dodge the points, but jitter will overlay but not be in the way of plot.
64
65 ## Bar chart ##
66

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## Bar chart ##

## Box plot

##INTERESTING, if you move geom_point to second line/layer, the points on bar will get hidden, but if you keep it at end then point will be on the bar!
ggplot(bull.richness.soy.no.till, aes(x = GrowthStage, y = richness, color = Fungicide)) +
  stat_summary(fun=mean, geom = "bar") +
  stat_summary(fun.data = mean_se, geom = "errorbar", position = "dodge") +
  xlab("") +
  ylab("fungal richness") +
  geom_point(position = position_jitterdodge(dodge.width = 0.9))

## Line plots

ggplot(bull.richness.soy.no.till, aes(x = GrowthStage, y = richness, group = Fungicide, color = Fungicide)) + #need to add group function to connect the lines, can play around by removing and adding any function,variable.
  #geom_point(position = position_jitterdodge(dodge.width = 0.9)) +
  stat_summary(fun=mean, geom = "line") + #Change the type of graph bar/line here in geom
  stat_summary(fun.data = mean_se, geom = "errorbar") +
  xlab("") +
  ylab("fungal richness")

#For large structured data - Faceting

## Faceting

##Example1
ggplot(bull.richness, aes(x = GrowthStage, y = richness, group = Fungicide, color = Fungicide)) +
  stat_summary(fun=mean, geom = "line") +
  stat_summary(fun.data = mean_se, geom = "errorbar") +
  xlab("") +
  ylab("fungal richness") +
  facet_wrap(~Treatment) #FACETING as per treatment

##Example2
ggplot(bull.richness, aes(x = GrowthStage, y = richness, group = Fungicide, color = Fungicide)) +
  stat_summary(fun=mean, geom = "line") +
  stat_summary(fun.data = mean_se, geom = "errorbar") +
  xlab("") +
  ylab("fungal richness") +
  facet_wrap(~Treatment*Crop)

##Example3 - scales
ggplot(bull.richness, aes(x = GrowthStage, y = richness, group = Fungicide, color = Fungicide)) +
  stat_summary(fun=mean, geom = "line") +
  stat_summary(fun.data = mean_se, geom = "errorbar") +
  xlab("") +
  ylab("fungal richness") +
  #facet_wrap(~Treatment*Crop, scales = "free") #playing around scales
  facet_wrap(~Treatment*Crop, scales = "free_y")

##Example4 changing order of facet wrap
ggplot(bull.richness, aes(x = GrowthStage, y = richness, group = Fungicide, color = Fungicide)) +
  stat_summary(fun=mean, geom = "line") +
  stat_summary(fun.data = mean_se, geom = "errorbar") +
  xlab("") +
  ylab("fungal richness") +
  facet_wrap(Crop ~ Treatment, scales = "free") #Changing order of crop and treatment

#####

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