Exam #1

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2023-03-09

knitr::opts\_chunk$set(include = TRUE)  
library(knitr)  
library(ggplot2)  
library(markdown)

######Question #4: #  
#Layering:   
ggplot(mycotoxin, aes(x = Treatment, y = DON, fill = Cultivar)) +  
 geom\_boxplot() +  
 geom\_point(position=position\_jitterdodge(dodge.width=0.9), shape=21, color = "black")

####Question #4:   
#Scales:   
ggplot(mycotoxin, aes(x= Treatment, y= DON, fill= Cultivar)) +   
 stat\_summary(Fun = mean, geom = "bar", position = "dodge", color = "black") +  
 stat\_summary(fun.data = mean\_se, geom = "errorbar", position = "dodge") +  
 geom\_point(position = position\_jitterdodge(dodge.width = 1), shape = 21, color = "black") +  
 scale\_color\_manual(values=c("#56B4E9", "#CC79A7")) +  
 scale\_fill\_manual(values=c("#56B4E9", "#CC79A7"))

#Question #4:   
#Themes:   
ggplot(mycotoxin, aes(x = Treatment, y = DON, fill = Cultivar)) +   
 geom\_boxplot() +  
 theme\_dark()

#Question #4:   
#Facets:   
ggplot(mycotoxin, aes(x= Treatment, y= DON, fill= Cultivar)) +  
 stat\_summary(Fun = mean, geom = "bar", position = "dodge", color = "black") +  
 facet\_wrap(~Treatment\*Cultivar,scales = "free")

######Question #5:   
library(datasets); data("ToothGrowth"); str(ToothGrowth)  
data1 <- subset(ToothGrowth, supp == "VC")  
data2 <- subset(ToothGrowth, supp == "VC" & dose == "0.5")  
data3 <- subset(ToothGrowth, select = c(len), supp == "VC" & dose == "0.5")