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# Name: Sriram Selvakumar
#a
dframe = data.frame(person=c("Stan", "Francine", "Steve", "Roger", "Hayley", "Klaus"),
                     sex=factor(c("M","F","M","M","F", "M")),
                     funny = factor(c("High", "Med", "Low", "High","Med","Med")))
)

#b
age = c(41,41,15,1600,21,60)
dframe = cbind(dframe,age)
#c
dframe = dframe[,c(1,4,2,3)]
#d
mydata <- data.frame(person=c("Peter","Lois","Meg","Chris","Stewie"),
                     age=c(42,40,17,14,1),
                     sex=factor(c("M","F","F","M","M")))
newrecord = data.frame(person="Brian",age=7,
                       sex=factor("M",levels=levels(mydata$sex)))

mydata = rbind(mydata,newrecord)
funny = c("High","High","Low","Med","High","Med")
funny = factor(x=funny,levels=c("Low","Med","High"))
mydata = cbind(mydata,funny)
mydata$age.mon = mydata$age*12

mydata2 = mydata[-c(5)]
#e
mydataframe = rbind(dframe,mydata2)
#f
mydataframe[mydataframe$sex=="F" & (mydataframe$funny == "Med" | mydataframe$funny
== "High"), c("person","age")]
#g
mydataframe[substr(mydataframe$person,1,1) == "S", c("person","age","sex","funny")]

#Soybeans Exercise
stemLengths = c(20.2, 22.9, 23.3, 20.0, 19.4, 22.0, 22.1, 22.0, 21.9, 21.5, 20.9)
#making histogram of stem lengths
hist(stemLengths)

t.test(stemLengths,mu =23,alternative = "two.sided",conf.level = 0.98)
qqnorm(stemLengths,datax = TRUE, col = 2)
qqline(stemLengths,datax = TRUE)

# from the qqplot here it is confirmed that this distribution is not normal
# distributed because they are not aligned with the qqline properly

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