# draw the figures illustrating maximum likelihood

x<-c(1,3,4,6,8,9,12)

y<-c(5,8,6,10,9,13,12)

windows(14,6)

par(mfrow=c(1,3))

plot(x,y,pch=21,bg="blue",ylim=c(0,15))

abline(0,0.6793,col="red")

plot(x,y,pch=21,bg="blue",ylim=c(0,15))

abline(8,0.6793,col="red")

plot(x,y,pch=21,bg="blue",ylim=c(0,15))

abline(lm(y~x))

abline(lm(y~x),col="blue")

plot(x,y,pch=21,bg="blue",ylim=c(0,15))

abline(4.8273,1.5,col="red")

plot(x,y,pch=21,bg="blue",ylim=c(0,15))

abline(4.8273,0.2,col="red")

plot(x,y,pch=21,bg="blue",ylim=c(0,15))

abline(lm(y~x))

abline(lm(y~x),col="blue")

# randomizing treatments for experimental design

treatments <- c("aloprin","vitex","formixin","panto","allclear")

# use sample to shuffle them for the active insects in dishes 1 to 5

sample(treatments)

# this produces a warning message because the same variable name

# appears in two attached dataframes

first.frame <- read.csv("c:\\temp\\test.pollute.csv")

second.frame <- read.csv("c:\\temp\\ozone.data.csv")

attach(first.frame)

attach(second.frame)

# this is how you should avoid this kind of problem

first.frame <- read.csv("c:\\temp\\test.pollute.csv")

second.frame <- read.csv("c:\\temp\\ozone.data.csv")

attach(first.frame)

# ........

# this is where you work on the information from first.frame.

# Then when you are finished

# ........

detach(first.frame)

attach(second.frame)