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#Annotated R code for Epidemiology Assignment 1
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#First, make sure that your data are saved as two columns with headers, and is a .txt file
#Second, know the pathway where your file is saved
#My personal file is one word called AlfalfaData1.txt
#My column headers are Lesion_True and Lesion_Guess (note: no spaces in the header name)
#Note: you can rename anything before an "<->" to your preference, just be consistent through the code
#Note: you can adjust other parameters in the plot, so play around and explore R!
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getwd() #Check where R is looking for files
setwd("C:/Users/Basima/Desktop/Epidemiology") #Set R to the directory where your data is saved
getwd() #Verify R is now looking in the correct location

alfalfal = read.table("AlfalfaData1.txt", #Name and read your data file into R
                    header=TRUE)

alfalfal #Check that your data has loaded correctly
head(alfalfal) #Review the column names of your file

#install.packages("epiR") #Install this R package for CCC analysis
library(epiR) #This opens the package for this session

truesev <- as.numeric(alfalfal$Lesion_True) #This makes a numeric vector from my Lesion_True column
truesev #Verify that a vector was made
class(truesev) #Verify that the vector is numeric
estsev <- as.numeric(alfalfal$Lesion_Guess) #Repeat for your second column of data
estsev
class(estsev)

try.ccc <- epi.ccc(truesev, #Concordance Correlation Coefficient
                 estsev, #This calls the CCC program, and loads the first vector
                 ci = "z-transform", #loads the second vector
                 conf.level=0.95) #ignore this for now
#This lets you define a confidence level for the CI

SLRalfalfal <- lm (estsev ~ truesev) #Name and apply a simple linear regression model to vectors
par(pty = "s") #Parameter sets plot to square shape
plot(truesev, estsev, #Makes scatterplot of both vectors (x,y)
     xlim = c(0,100), #Defines x-axis range
     ylim = c(0,100), #Defines y-axis range
     xlab = "True Severity (w)", #Legend title for X-axis
     ylab = "Estimated Severity (u)", #Legend title for y-axis
     pch = 16, #Shape of the scatterplot points
     main = "AlfalfaPro First Estimations") #Plot title
abline (a = 0, b = 1, lty =2) #Adds the perfect concordance line (interept=0, slope=1)
abline (SLRalfalfal, lty = 1) #Adds the regression line

lab <- paste("CCC = ", #TAdds the CCC value to the plot
            round(try.ccc$rho.c[,1], digits = 2)) #Rounds the values, sets decimal to two places
lab #Check that the label looks okay
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lab2 <- paste("Cb = ",
              round(try.ccc$C.b, digits = 2))
lab2
#Adds the bias (Cb) value to the plot
#Rounds the values, sets decimal to two places
#Check that the label looks okay

lab3 <- paste("r = ",
              (round(cor(alfalfal$Lesion_True,
                        alfalfal$Lesion_Guess),
                    digits = 2)))
lab3
#Adds the Pearson's Correlation (r) to the plot
#Rounds the values, sets decimal to two places
#Check that the label looks okay

legend(x = "bottomright",
       legend = c("Concordance Line",
                  "SLR Line"),
       lty = c(2,1),
       lwd = c(1,1),
       bty = "n")
#The legend for the two lines

text(x = 20, y = 90,
     paste(lab, "\n", lab2, "\n", lab3))
#List correlation values on plot

summary(alfalfal)
sd(estsev)
sd(truesev)
cor(alfalfal$Lesion_True,alfalfal$Lesion_Guess)
summary(SLRalfalfal)
try.ccc
#Simple summary of your data
#Standard deviation of estimations
#Standard deviation of true values
#Correlation
#Detailed SLR summary
#CCC summary
```