Chad Huntebrinker’s Homework 5

Chad Huntebrinker

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Write a function to calculate BMI using the following formula:

BMI = Weight in KG / Height in Meters^2

The function should receive the two arguments weight and height and return the BMI.

#Write a function to calculate BMI using the following formula:  
  
#BMI = Weight in KG / Height in Meters^2  
  
#The function should receive the two arguments weight and height and return the BMI.  
  
calc\_bmi <- function(weight, height) {  
 return(weight / (height ^ 2))  
}  
  
calc\_bmi(150, 2)

## [1] 37.5

Body surface area (BSA) is an important parameter used in healthcare, particularly in determining medication dosages and assessing burn injury severity. The formula to calculate BSA is as follows

BSA(m^2) = sqrt((Height(cm) \* Weight (Kg)) / 3600)

A Medical data scientist created the following function to calculate BSA. Modify this function to calculate BSA in a single step.

#Body surface area (BSA) is an important parameter used in healthcare, particularly in determining  
#medication dosages and assessing burn injury severity. The formula to calculate BSA is as follows  
  
#BSA(m^2) = sqrt((Height(cm) \* Weight (Kg)) / 3600)  
  
#A Medical data scientist created the following function to calculate BSA.  
#Modify this function to calculate BSA in a single step.  
  
calculate\_BSA <- function(height\_cm, weight\_kg) {  
 bsa <- sqrt((height\_cm \* weight\_kg) / 3600)  
 return(bsa)  
}  
  
calculate\_BSA(300, 50)

## [1] 2.041241

Question 3:

You are provided with cell\_viability.csv file that contains the results from the cell viability assay that recorded the percent of cell viabilities with three drugs treatments.

1. Read the table into cell.via dataframe
2. Write a function calculate\_mean\_viability () to calculate mean viability for each drug treatment. When you call the function calculate\_mean\_viability (cell.via), it should print the mean viability of each drug treatment.
3. Write a Function calculate\_sd\_viability () to calculate standard deviation of viability for each drug treatment. When you call the function calculate\_sd\_viability(cell.via), it should print the standard deviation of each drug treatment.
4. Write a function plot\_dose\_response\_curves () to plot dosage-response curves for each drug where the x-axis should have dosage and y axis contains the percent viability. When you call the function plot\_dose\_response\_curves(cell.via), it should print dose response curve of each drug. You need to use for loop within the function to plot the dose response curve of three drugs. Generate all the three curves into a single figure by mentioning the following function before the plot function.

par(mfrow = c(3, 1))

This function will help to generate all the three plots one below the other.

#Question 3:  
  
#Part a  
cell.via <- read.csv("cell\_viability.csv")  
  
#Part b  
print("Part B")

## [1] "Part B"

calculate\_mean\_viability <- function(cell.via) {  
 print(mean(cell.via$drug1))  
 print(mean(cell.via$drug2))  
 print(mean(cell.via$drug3))  
}  
calculate\_mean\_viability(cell.via)

## [1] 115.6771  
## [1] 103.0057  
## [1] 78.67

#Part c  
print("Part C")

## [1] "Part C"

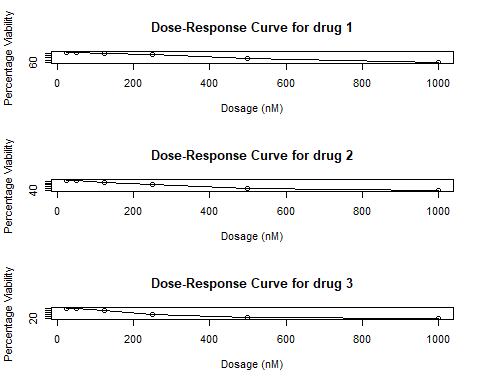
calculate\_sd\_viability <- function(cell.via) {  
 print(sd(cell.via$drug1))  
 print(sd(cell.via$drug2))  
 print(sd(cell.via$drug3))  
}  
calculate\_sd\_viability(cell.via)

## [1] 36.25026  
## [1] 44.96262  
## [1] 39.9095

#Part d  
print("Part D")

## [1] "Part D"

plot\_dose\_response\_curves <- function(cell.via) {  
 par(mfrow = c(3, 1))  
   
 #No need to include the first row, it's just the control row  
 plot(cell.via$drug1[2:7] ~ cell.via$Dosage\_mg[2:7], xlab = "Dosage (nM)", ylab = "Percentage Viability",  
 main = "Dose-Response Curve for drug 1")  
 lines(cell.via$Dosage\_mg[2:7], cell.via$drug1[2:7])  
   
 plot(cell.via$drug2[2:7] ~ cell.via$Dosage\_mg[2:7], xlab = "Dosage (nM)", ylab = "Percentage Viability",  
 main = "Dose-Response Curve for drug 2")  
 lines(cell.via$Dosage\_mg[2:7], cell.via$drug2[2:7])  
   
 plot(cell.via$drug3[2:7] ~ cell.via$Dosage\_mg[2:7], xlab = "Dosage (nM)", ylab = "Percentage Viability",  
 main = "Dose-Response Curve for drug 3")  
 lines(cell.via$Dosage\_mg[2:7], cell.via$drug3[2:7])  
}  
  
plot\_dose\_response\_curves(cell.via)



Question 4:

You are provided with a patient data information Patient\_data.csv Read this table into Pt.data dataframe. Use for loop and if else to perform the following investigations.

1. Write a for loop to print the cancer types of first 10 patients in the dataframe
2. Which patients (Patient\_IDs) are older than 50 and have smoking status as TRUE?
3. What is the marker associated with patients who have age less than or equal to 30?
4. Which patients are Hispanic and have received Stem Cell Transplantation?
5. Which patients are older than 60 and have cancer type “Prostate”?
6. Create a new column “age\_group” based on age categories: “Young” (age <= 30), “Middle-aged” (30 < age <= 60), “Elderly” (age > 60). Use a for loop with if else control statements

#Question 4:  
Pt.data <- read.csv("Patient\_data.csv")  
  
#Part a  
print("Part A")

## [1] "Part A"

for(i in 1:10){  
 print(Pt.data$cancer\_type[i])  
}

## [1] "Colon"  
## [1] "Prostate"  
## [1] "Prostate"  
## [1] "Colon"  
## [1] "Colon"  
## [1] "Colon"  
## [1] "Prostate"  
## [1] "Prostate"  
## [1] "Breast"  
## [1] "Lung"

#Part b  
print("Part B")

## [1] "Part B"

for(i in 1:nrow(Pt.data)){  
 if(Pt.data$age[i] > 50 && Pt.data$smoking[i]) {  
 print(Pt.data$Patient\_id[i])  
 }  
}

## [1] "Patient2"  
## [1] "Patient9"  
## [1] "Patient11"  
## [1] "Patient15"  
## [1] "Patient17"  
## [1] "Patient23"  
## [1] "Patient25"  
## [1] "Patient32"  
## [1] "Patient34"  
## [1] "Patient38"  
## [1] "Patient39"  
## [1] "Patient42"  
## [1] "Patient44"  
## [1] "Patient46"  
## [1] "Patient47"  
## [1] "Patient48"  
## [1] "Patient50"

#Part c  
print("Part C")

## [1] "Part C"

for(i in 1:nrow(Pt.data)){  
 if(Pt.data$age[i] <= 30) {  
 print(Pt.data$marker[i])  
 }  
}

## [1] "AQP3"  
## [1] "MSH5"  
## [1] "HIST2H4A"  
## [1] "MSH5"  
## [1] "AQP3"

#Part d  
print("Part D")

## [1] "Part D"

for(i in 1:nrow(Pt.data)){  
 if(Pt.data$ethnicity[i] == "Hispanic" && Pt.data$therapy[i] == "Stem Cell Transplantation") {  
 print(Pt.data$Patient\_id[i])  
 }  
}

## [1] "Patient28"

#Part e  
print("Part E")

## [1] "Part E"

for(i in 1:nrow(Pt.data)){  
 if(Pt.data$age[i] > 60 && Pt.data$cancer\_type[i] == "Prostate") {  
 print(Pt.data$Patient\_id[i])  
 }  
}

## [1] "Patient3"  
## [1] "Patient7"  
## [1] "Patient19"  
## [1] "Patient23"  
## [1] "Patient32"  
## [1] "Patient44"

#Part f  
print("Part F")

## [1] "Part F"

for(i in 1:nrow(Pt.data)){  
 Pt.data$age\_group[i] <- ifelse(Pt.data$age[i] <= 30, "Young",  
 ifelse(Pt.data$age[i] <= 60, "Middle-aged", "Elderly"))  
}