homework6

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```
#Question 1
setwd("C:/Users/ashle/OneDrive - Vanderbilt/BIOS 6301-Fall 2023/football23")
#creating path
path <- "C:/Users/ashle/OneDrive - Vanderbilt/BIOS 6301-Fall 2023/football23"
#creating function
ffvalues <- function(path=path, file='outfile.csv', nTeams=12, cap=200, posReq=c(qb=1, rb=2, wr=3, te=1
                      points=c(fg=4, xpt=1, pass_yds=1/25, pass_tds=4, pass_ints=-2,
                                rush_yds=1/10, rush_tds=6, fumbles=-2, rec_yds=1/20, rec_tds=6)) {
  #loading data and creating new columns
 proj_k23 <- read.csv(paste0(path, "/proj_k23.csv"))</pre>
  proj_k23$pos <- "k"</pre>
  proj_qb23 <- read.csv(paste0(path, "/proj_qb23.csv"))</pre>
  proj_qb23$pos <- "qb"</pre>
  proj_rb23 <- read.csv(paste0(path, "/proj_rb23.csv"))</pre>
  proj_rb23$pos <- "rb"</pre>
  proj_te23 <- read.csv(paste0(path, "/proj_te23.csv"))</pre>
  proj_te23$pos <- "te"</pre>
  proj_wr23 <- read.csv(paste0(path, "/proj_wr23.csv"))</pre>
  proj wr23$pos <- "wr"</pre>
# Defining all expected column names
all_columns <- c("PlayerName", "Team", "fg", "fga", "xpt", "fpts", "pos", "pass_att", "pass_cmp", "pass
#Adding missing columns with default values
add_missing_columns <- function(df, all_columns) {</pre>
  missing_columns <- setdiff(all_columns, colnames(df))</pre>
  for (col in missing_columns) {
    df[[col]] <- ifelse(col %in% c("fg", "fga", "xpt", "fpts", "pass_att", "pass_cmp", "pass_yds", "pas</pre>
  }
  return(df)
# Adding missing columns to each data frame
proj_k23 <- add_missing_columns(proj_k23, all_columns)</pre>
proj_qb23 <- add_missing_columns(proj_qb23, all_columns)</pre>
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proj_rb23 <- add_missing_columns(proj_rb23, all_columns)</pre>
proj_te23 <- add_missing_columns(proj_te23, all_columns)</pre>
proj_wr23 <- add_missing_columns(proj_wr23, all_columns)</pre>
#Combining data frames
df <- rbind(proj_k23, proj_qb23, proj_rb23, proj_te23, proj_wr23)</pre>
 #Calculating dollar values
  calculate_value <- function(df, pos, points) {</pre>
    player_points <- rowSums(df[, names(points)] * points)</pre>
    total_points <- sum(player_points)</pre>
    if (total_points != 0) {
      df$points <- player_points</pre>
      df$value <- pos * player_points</pre>
    } else {
      df$points <- 0
      df$value <- 0</pre>
    }
    return(df)
  #Calculating value for each player in the combined data frame
  df <- calculate_value(df, posReq["k"], points)</pre>
  df <- calculate_value(df, posReq["qb"], points)</pre>
  df <- calculate_value(df, posReq["rb"], points)</pre>
  df <- calculate_value(df, posReq["te"], points)</pre>
  df <- calculate_value(df, posReq["wr"], points)</pre>
  #Ordering by value
  df <- df[order(-df$value), ]</pre>
  #Writing to CSV file
  write.csv(df, file = file, row.names = FALSE)
  return(df)
}
#1. Calling the ffvalues function
x1 <- ffvalues('.')</pre>
# Counting the number of players worth more than $20
players_over_20 <- sum(x1$value > 20)
# Identifying the 15th most valuable running back (rb)
rb_players <- subset(x1, pos == 'rb')</pre>
rb_players <- rb_players[order(-rb_players$value), ]</pre>
fifteenth_rb <- rb_players[15, "PlayerName"]</pre>
print(players_over_20)
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print(fifteenth_rb)
## [1] "AJ Dillon"
#2. calling the ffvalues function a second time
x2 <- ffvalues(getwd(), '16team.csv', nTeams=16, cap=150)</pre>
#Summing the number of players over 20
num_players_over_20 <- sum(x2$value > 20)
#Summing the top 40 wrs
num_wr_top_40 \leftarrow sum(x2\$pos == 'wr')
print(num_players_over_20)
## [1] 490
print(num_wr_top_40)
## [1] 256
#3. Calling and updating the ffvalues function
x3 <- ffvalues('.', 'qbheavy.csv', posReq=c(qb=2, rb=2, wr=3, te=1, k=0),
            points=c(fg=0, xpt=0, pass_yds=1/25, pass_tds=6, pass_ints=-2,
                    rush_yds=1/10, rush_tds=6, fumbles=-2, rec_yds=1/20, rec_tds=6))
#Summing the number of players over 20
num_players_over_20 <- sum(x3$value > 20)
#Summing top 30 qbs
num_qb_top_30 <- sum(x3$pos == 'qb') # Assuming 'pos' is the column that specifies the position
print(num_players_over_20)
## [1] 405
print(num_qb_top_30)
## [1] 86
#Question 2
#Loading haart from github
url_to_raw_csv_file <- "https://raw.githubusercontent.com/couthcommander/Bios6301/main/datasets/haart.c
#Reading the lines of haart into R
lines <- readLines(url_to_raw_csv_file)</pre>
## Warning in readLines(url_to_raw_csv_file): incomplete final line found on
## 'https://raw.githubusercontent.com/couthcommander/Bios6301/main/datasets/haart.csv'
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#Removing the incomplete final line if present
if (length(lines) > 0 && nchar(lines[length(lines)]) == 0) {
 lines <- lines[-length(lines)]</pre>
}
#Creating a text connection and reading the data using read.csv
haart_data <- read.csv(text = lines, header = TRUE)</pre>
#Checking the first few rows of the dataset
head(haart_data)
##
     male age aids cd4baseline logvl weight hemoglobin
                                                           init.reg init.date
## 1
       1 25
                0
                           NA
                                         NA
                                                     NA 3TC, AZT, EFV
                                                                       7/1/03
                                  NΑ
## 2
       1 49
                                  NA 58.0608
                 0
                           143
                                                     11 3TC, AZT, EFV 11/23/04
## 3
       1 42
               1
                                  NA 48.0816
                           102
                                                     1 3TC, AZT, EFV
                                                                      4/30/03
## 4
       0 33 0
                           107
                                  NA 46.0000
                                                    NA 3TC, AZT, NVP
                                                                      3/25/06
## 5
      1 27
                0
                            52
                                  4
                                                     NA 3TC, D4T, EFV
                                                                       9/1/04
                                          NA
       0 34
## 6
                0
                           157
                                  NA 54.8856
                                                    NA 3TC, AZT, NVP
                                                                      12/2/03
    last.visit death date.death
## 1
       2/26/07
                  0
                            <NA>
## 2
       2/22/08
                   0
                            <NA>
      11/21/05
## 3
                   1
                        1/11/06
## 4
        5/5/06
                         5/7/06
                   1
## 5
      11/13/07
                   0
                            <NA>
       2/28/08
                            <NA>
## 6
                   0
#1.Converting 'init.date' into a usable date format
haart_data$init.date <- as.Date(haart_data$init.date, format = "%m/%d/%y")
class(haart data$init.date)
## [1] "Date"
# Using the table command to display the counts of the year from 'init.date'
year_counts <- table(format(haart_data$init.date, "%Y"))</pre>
# Printing the counts of the year from 'init.date'
print(year_counts)
## 1998 2000 2001 2002 2003 2004 2005 2006 2007
        5 17 60 270 292 207 104
# Converting 'death.date' to date format, considering NA values
haart_data$date.death <- as.Date(haart_data$date.death, format = "%m/%d/%y", na.rm = TRUE)
# Creating an indicator variable 'death_within_1_year' (1 for death within 1 year, 0 otherwise)
haart_data$death_within_1_year <- ifelse(is.na(haart_data$date.death), NA, as.integer(difftime(haart_da
#Counting the number of observations that died within the first year
deaths_within_1_year <- sum(haart_data$death_within_1_year, na.rm = TRUE)
# Printing the number of observations that died within the first year
print(deaths_within_1_year)
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## [1] 92
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```
#Converting last.visit to usable format
haart_data$last.visit <- as.Date(haart_data$last.visit, format = "%m/%d/%y")
#3. Calculating the follow-up time in days
haart_data$followup_time <- pmin(difftime(pmax(haart_data$last.visit, haart_data$date.death, na.rm = TR
# Printing the quantile for the follow-up time
print(quantile(haart_data$followup_time))
## Time differences in days
                50% 75% 100%
     0%
          25%
     0.0 329.5 365.0 365.0 365.0
##
#4. Creating an indicator variable for loss to follow-up
haart_data$loss_to_followup <- ifelse(is.na(haart_data$date.death) & difftime(haart_data$last.visit, ha
# Counting the number of records that are lost to follow-up
lost_to_followup_count <- sum(haart_data$loss_to_followup)</pre>
# Printing the number of records that are lost to follow-up
print(lost_to_followup_count)
## [1] 710
# 5. Converting 'init.reg' to a factor to create indicator variables for each unique drug
haart_data$init.reg <- as.factor(haart_data$init.reg)</pre>
# Using model.matrix to create indicator variables for each unique drug
regimen_indicator <- model.matrix(~ 0 + init.reg, data = haart_data)</pre>
# Appending the indicator variables to the database as new columns
haart_data <- cbind(haart_data, regimen_indicator)</pre>
# Identifying which drug regimen appears over 100 times
regimen_counts <- colSums(regimen_indicator)</pre>
drugs_over_100_times <- names(regimen_counts[regimen_counts > 100])
# Printing the drug regimen found over 100 times
print(drugs_over_100_times)
## [1] "init.reg3TC,AZT,EFV" "init.reg3TC,AZT,NVP"
# 6. Reading the additional dataset 'haart2.csv'
haart2_data <- read.csv("haart2.csv")</pre>
# Selecting only the relevant columns from each dataset
relevant_haart_data <- haart_data[, 1:12]</pre>
relevant_haart2_data <- haart2_data</pre>
# Appending the relevant data from haart2 to large_data
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```
complete_data <- rbind(relevant_haart_data, relevant_haart2_data)</pre>
# Showing the first five records of the complete dataset
head(complete_data, 5)
     male age aids cd4baseline logvl weight hemoglobin
                                                            init.reg init.date
## 1
        1 25
                 0
                            NA
                                  NA
                                          NA
                                                      NA 3TC, AZT, EFV 2003-07-01
## 2
        1 49
                                  NA 58.0608
                                                      11 3TC, AZT, EFV 2004-11-23
                 0
                           143
## 3
        1 42
                           102
                                  NA 48.0816
                                                     1 3TC, AZT, EFV 2003-04-30
                 1
       0 33
                                  NA 46.0000
                                                     NA 3TC, AZT, NVP 2006-03-25
## 4
                           107
                 0
## 5
        1 27
                 0
                            52
                                   4
                                          NA
                                                     NA 3TC,D4T,EFV 2004-09-01
   last.visit death date.death
## 1 2007-02-26
                    0
                            <NA>
## 2 2008-02-22
                    0
                            <NA>
## 3 2005-11-21
                    1 2006-01-11
## 4 2006-05-05
                    1 2006-05-07
## 5 2007-11-13
                            <NA>
# Showing the last five records of the complete dataset
tail(complete_data, 5)
```

```
age aids cd4baseline
                                           logvl weight hemoglobin
##
        male
                                                                        init.reg
                                              NA 46.2672
                                                                  8 3TC,D4T,NVP
## 1000
           0 40.00000
                         1
                                    131
## 1100
           0 27.00000
                                    232
                                                                  NA 3TC, AZT, NVP
                         0
                                              NA
                                                      NA
## 2100
           1 38.72142
                         0
                                    170
                                              NA 84.0000
                                                                  NA 3TC, AZT, NVP
## 3100
           1 23.00000
                        NA
                                    154 3.995635 65.5000
                                                                  14 3TC, DDI, EFV
## 4100
           0 31.00000
                                    236
                                              NA 45.8136
                                                                  NA 3TC, D4T, NVP
                         0
         init.date last.visit death date.death
## 1000 2003-07-03 2008-02-29
                                   0
                                           <NA>
## 1100 0012-01-03 0001-05-04
                                   0
                                           <NA>
## 2100
              <NA>
                         <NA>
                                   0
                                           <NA>
## 3100
              <NA>
                         <NA>
                                   0
                                           <NA>
## 4100 0012-03-03 0010-11-07
                                   0
                                           <NA>
```