

# 01 - Intro to R

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1. Calculate the following numerical results to three decimal places:

- a)  $(7 - 8) + 5^3 - 5 / 6 + \sqrt{62}$
- b)  $\ln 3 + \sqrt{2}\sin(\pi) - e^3$

```
#a  
round( (7 - 8) + 5^3 - 5 / 6 + sqrt(62),3 )
```

```
## [1] 131.041
```

```
#b  
round( log(3) + sqrt(2)*sin(pi) - exp(3),3 )
```

```
## [1] -18.987
```

3. Create a vector named Treatment with the entries “Treatment One” appearing 20 times, “Treatment Two” appearing 18 times, and “Treatment Three” appearing 22 times.

```
Treatment <- rep(c("Treatment One", "Treatment Two", "Treatment Three"), c(20, 18, 22))  
xtabs(~Treatment)
```

```
## Treatment  
##   Treatment One Treatment Three   Treatment Two  
##             20             22             18
```

5. Vectors, sequences, and logical operators

```
#b Create the vectors u = (1,2,5,4) and v = (2,2,1,1) using the c() and scan() fctns.
```

```
u = c(1,2,5,4)
```

```
v = c(2,2,1,1)
```

```
#c find which component of u is equal to 5
```

```
which(u == 5)
```

```
## [1] 3
```

```
#i calculate the scalar product (dot product) of q = (3,0,1,6) and r = (1,0,2,4)
```

```
q = c(3,0,1,6)
```

```
r = c(1,0,2,4)
```

```
q %*% r
```

```
##      [,1]
```

```
## [1,]    29
```

```
#j Define the matrix X whose rows are the vectors u and v
```

```
X = matrix(rbind(u,v),2,4)
```

```
#or X = rbind(u,v)
```

```
#k Define the matrix Y whose columns are the vectors u and v
```

```
Y = cbind(u,v)
```

```
#l Find the matrix product X by Y and name is W
```

```
(W = X %*% Y)
```

```
##      u  v
```

```
## [1,] 46 15
## [2,] 15 10
#m Compute the inverse matrix of W and the transpose of that inverse
solve(W)
```

```
##           [,1]      [,2]
## u  0.04255319 -0.06382979
## v -0.06382979  0.19574468
```

```
t( solve(W))
```

```
##           u      v
## [1,]  0.04255319 -0.06382979
## [2,] -0.06382979  0.19574468
```

7. The data frame wheatUSA2004 from the PASWR package has the USA wheat harvested crop surfaces in 2004 by states. It has 2 variables, STATE for state and ACRES for 1000s of acres.

a) Attach the data frame wheatUSA2004 and use the fctn row.names() to define the states as the row names.

```
library(PASWR2)
```

```
## Warning: package 'PASWR2' was built under R version 3.4.2
```

```
## Loading required package: lattice
```

```
## Loading required package: ggplot2
```

```
STATES = WHEATUSA2004$states
row.names(WHEATUSA2004) = STATES
head(WHEATUSA2004)
```

```
##      states acres
## AR      AR    620
## CA      CA    320
## CO      CO   1700
## DE      DE     47
## GA      GA    190
## ID      ID    700
```

b) Define a new var called ha for the surface area given in hectors where 1 acre = 0.40468564224 hectares.

```
WHEATUSA2004$ha <- WHEATUSA2004$acres * 0.40468564224
head(WHEATUSA2004)
```

```
##      states acres      ha
## AR      AR    620 250.90510
## CA      CA    320 129.49941
## CO      CO   1700 687.96559
## DE      DE     47  19.02023
## GA      GA    190  76.89027
## ID      ID    700 283.27995
```

c) Sort the file according to the harvested surface area in acres.

```
sort_wheatUSA2004 <- WHEATUSA2004[order(WHEATUSA2004$acres), ]
head(sort_wheatUSA2004)
```

```
##      states acres      ha
## DE      DE     47 19.02023
```

```
## NY      NY      100 40.46856
## MS      MS      135 54.63256
## PA      PA      135 54.63256
## MD      MD      145 58.67942
## SC      SC      180 72.84342
```

d) Which states fall in the top 10% of states for harvested surface area?

```
top10 <- quantile(WHEATUSA2004$acres, prob = 0.9)
result <- WHEATUSA2004[WHEATUSA2004$acres > top10, ]
row.names(result)
```

```
## [1] "KS" "OK" "TX"
```

e) Save the contents of wheatUSA2004 in a new file called wheatUSA.txt. Then, remove wheatUSA2004 from your workspace and check that the contents of wheatUSA2004 can be recovered from wheatUSA.txt.

```
dump("WHEATUSA2004", "WHEATUSA.txt")
rm(WHEATUSA2004)
source("WHEATUSA.txt")
head(WHEATUSA2004)
```

```
##      states acres      ha
## AR      AR      620 250.90510
## CA      CA      320 129.49941
## CO      CO     1700 687.96559
## DE      DE       47  19.02023
## GA      GA      190  76.89027
## ID      ID      700 283.27995
```

f) Use the command write.table() to store the contents of wheatUSA2004 in a file with the name wheatUSA.dat

```
write.table(WHEATUSA2004, "WHEATUSA.dat")
```

g) Find the total harvested surface area in acres for the bottom 10% of states.

```
bottom10 <- quantile(WHEATUSA2004$acres, prob = 0.1)
result <- WHEATUSA2004[WHEATUSA2004$acres < bottom10, ]
result
```

```
##      states acres      ha
## DE      DE       47  19.02023
## NY      NY      100 40.46856
```

```
total_HA <- sum(result[, "acres"])
total_HA
```

```
## [1] 147
```

9. Use the data frame EPIURALf to answer the following questions:

a) How many patients have been treated with the Hamstring Stretch?

```
head(EPIURALF)
```

```
##      doctor kg  cm      ease      treatment oc complications
## 1      B 116 172 Difficult Traditional Sitting 0          None
## 2      C  86 176      Easy  Hamstring Stretch 0          None
## 3      B  72 157 Difficult Traditional Sitting 0          None
## 4      B  63 169      Easy  Hamstring Stretch 2          None
```

```
## 5      B 114 163 Impossible Traditional Sitting 0      None
## 6      B 121 163 Difficult   Hamstring Stretch 3      None
```

```
xtabs(~treatment, data = EPIDURALF)
```

```
## treatment
##   Hamstring Stretch Traditional Sitting
##                171                171
```

```
xtabs(~treatment, data = EPIDURALF)[1]
```

```
## Hamstring Stretch
##                171
```

- b) What proportion of the patients treated with Hamstring Stretch were classified as each of easy, difficult, and impossible?

```
Treatment1 <- xtabs(~treatment + ease, data = EPIDURALF)
Treatment1
```

```
##                ease
## treatment      Difficult Easy Impossible
##   Hamstring Stretch      63  100         8
##   Traditional Sitting      51  107        13
```

```
prop.table(Treatment1[, ]) * 100
```

```
## Difficult      Easy Impossible
## 36.842105 58.479532  4.678363
```

- c) What proportion of the patients classified as easy to palpitate were assigned to the Traditional Sitting position?

```
Treatment1
```

```
##                ease
## treatment      Difficult Easy Impossible
##   Hamstring Stretch      63  100         8
##   Traditional Sitting      51  107        13
```

```
prop.table(Treatment1[, "Easy"])[2] * 100
```

```
## Traditional Sitting
##                51.69082
```

- d) What is the mean weight for each cell in a contingency table created with the var's Ease and Treatment?

```
head(EPIDURALF)
```

```
## doctor kg cm ease treatment oc complications
## 1      B 116 172 Difficult Traditional Sitting 0      None
## 2      C 86 176 Easy Hamstring Stretch 0      None
## 3      B 72 157 Difficult Traditional Sitting 0      None
## 4      B 63 169 Easy Hamstring Stretch 2      None
## 5      B 114 163 Impossible Traditional Sitting 0      None
## 6      B 121 163 Difficult Hamstring Stretch 3      None
```

```
tapply(EPIDURALF$kg, list(EPIDURALF$ease, EPIDURALF$treatment), mean)
```

```
##                Hamstring Stretch Traditional Sitting
## Difficult      92.66667      94.27451
## Easy          78.67000      79.40187
```

```
## Impossible          127.87500          113.61538
```

- e) What proportion of the patients have a body mass index ( $BMI = kg/(cm/100)^2$ ) less than 25 and are classified as Easy to palpitate?

```
EPIDURALF$BMI <- EPIDURALF$kg/(EPIDURALF$cm/100)^2
EPIDURALF[1:5, 3:8]
```

```
##      cm      ease      treatment oc complications      BMI
## 1 172 Difficult Traditional Sitting 0          None 39.21038
## 2 176      Easy   Hamstring Stretch 0          None 27.76343
## 3 157 Difficult Traditional Sitting 0          None 29.21011
## 4 169      Easy   Hamstring Stretch 2          None 22.05805
## 5 163 Impossible Traditional Sitting 0          None 42.90715
```

```
mean(EPIDURALF$ease == "Easy" & EPIDURALF$BMI < 25) * 100
```

```
## [1] 9.064327
```

11. Use a for loop to convert a sequence of temperatures (18 to 28 by 2) from degrees centigrade to degrees fahrenheit.

```
for (celsius in seq(from = 18, to = 28, by = 2)) {
  print(c(celsius, 9/5 * celsius + 32))
}
```

```
## [1] 18.0 64.4
## [1] 20 68
## [1] 22.0 71.6
## [1] 24.0 75.2
## [1] 26.0 78.8
## [1] 28.0 82.4
```