# Consulting Homework 1

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# R Lab 1

### Ex. 1 & 2

Add a red horizontal line at mean(y1) and a blue horizontal line at mean(y2). Move the legend up on the graph so it looks better and add red and blue points in front of the text.

```
# Code below copied from R Lab 1 document.

# Create 3 vectors of length 8

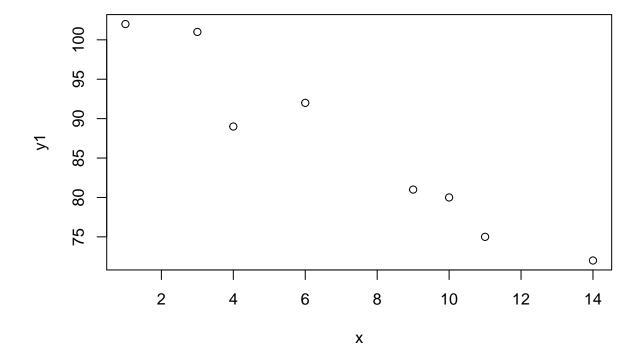
x <- c(1,3,4,6,9,10,11,14)

y1 <- c(102,101,89,92,81,80,75,72)

y2 <- c(88,85,81,80,76,71,66,64)

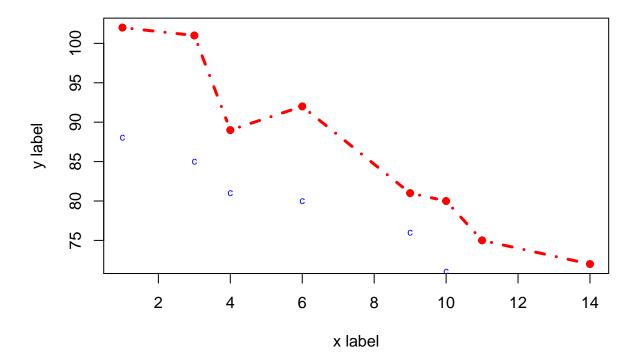
### Basic x-y graph

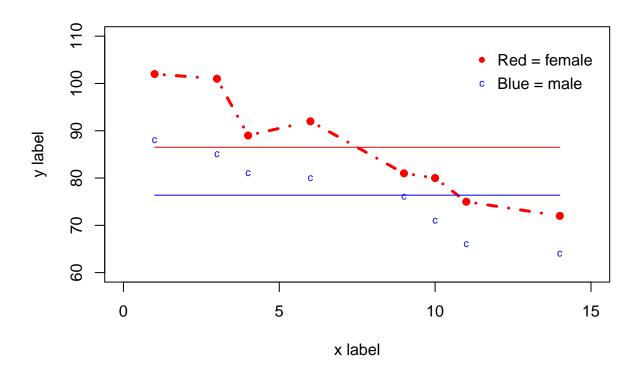
plot(x, y1)
```



```
### Useful options to plot
### Documentation in Help menu
### ?par gives options
plot(x, y1, xlab='x label', ylab='y label', pch=19, type="b", cex=.7, col="red", lty=4, lwd=3)
```

```
### Adding things to a plot
points(x, y2, pch="circle", cex=.7, col="blue")
```





## R Lab 2

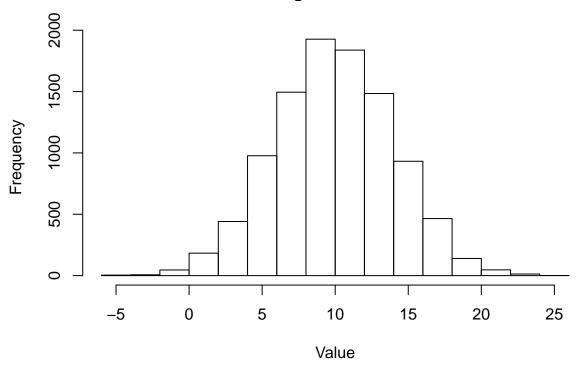
### Ex. 1

```
Use rep and seq to create c(.2,.2,.4,.4,.6,.6,.2,.2,.4,.4,.6,.6,.2,.2,.4,.4,.6,.6)
# Make the sequence we're aiming for.
goal \leftarrow c(.2, .2, .4, .4, .6, .6, .2, .2, .4, .4, .6, .6, .2, .2, .4, .4, .6, .6)
# Use seq() to create c(0.2, 0.4, 0.6).
seq < - seq(.2, .6, by = 0.2)
# Use rep() to repeat each element in seq twice.
seq \leftarrow rep(seq, each = 2)
# Use rep() again to repeat the whole list three times.
seq <- rep(seq,times = 3)</pre>
# Show the sequence
seq
## [1] 0.2 0.2 0.4 0.4 0.6 0.6 0.2 0.2 0.4 0.4 0.6 0.6 0.2 0.2 0.4 0.4 0.6 0.6 0.2 0.2 0.4 0.4 0.6
## [18] 0.6
# Double check that it matches the goal sequence.
seq == goal
## [15] TRUE TRUE TRUE TRUE
```

# Ex. 2

```
# Generate a sample of 10000 normal values with mean 10 and sd 4.
r.norm <- rnorm(n = 10000, mean = 10, sd = 4)
# Make a histogram of the values.
hist(r.norm,xlab = "Value")</pre>
```

# Histogram of r.norm



```
# Check that the empirical mean and SD match those used to generate the sample.
mean(r.norm)

## [1] 9.950444

sd(r.norm)

## [1] 4.010926

# For X-N(10, 16), find Pr(X > 18).
pnorm(18,mean = 10,sd = 4,lower.tail = FALSE)

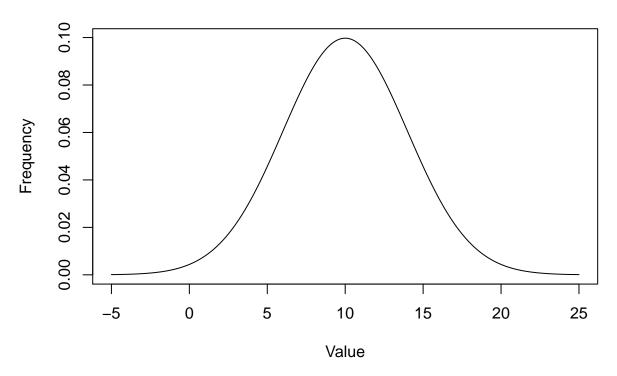
## [1] 0.02275013

# For X-N(10, 16), find the value so that 97.5% of the distribution is less than that value.
qnorm(0.975,mean = 10,sd = 4)

## [1] 17.83986

# Make a smooth line graph of the N(10, 16) density.
x <- seq(-5,25, by = 0.1)
y <- dnorm(x, mean = 10, sd = 4)
plot(x, y, type="l", main = "Normal Distribution (10, 16)", ylab = "Frequency", xlab = "Value")</pre>
```

# Normal Distribution (10, 16)



Ex. 3

With a shape parameter k and a scale parameter s, for a Gamma distribution:

$$\mu=ks=10$$
 and  $\sigma^2=ks^2=16$ 

So:

$$k = \frac{100}{16}$$
 and  $s = \frac{16}{10}$ 

```
# Generate a sample of 10000 values from a Gamma distribution with mean 10 and sd 4.

r.gamma <- rgamma(n = 10000, shape = 25/4, scale = 8/5)

# Verify empirically that your sample mean and sd are close to 10 and 4.

mean(r.gamma)
```

```
## [1] 10.00416
```

sd(r.gamma)

## [1] 3.987558

## R Lab 3

#### Ex. 1

Explain (1 sentence each) what each of these statements does:

a. x[c(3:7)-2]: This command selects elements (3-2), (4-2), (5-2), (6-2), and (7-2), (i.e. elements 1 - 5) from the vector x.

```
## [1] 1 3 4 6 9 10 11 14
x[c(3:7)-2]
```

```
## [1] 1 3 4 6 9
```

b. x[c(3:7)]-2: This takes elements 3 - 7 of vector x, and subtracts 2 from each value.

```
x[c(3:7)]
```

```
## [1] 4 6 9 10 11
x[c(3:7)]-2
```

```
## [1] 2 4 7 8 9
```

c. xy.mat[14, ]: THis takes row 14 and all columns of the matrix xy.mat (subsetting row 8 is shown below, since there are only 8 rows of our matrix).

```
xy.mat[8, ]
## x y1 y2
## 14 72 64
  d. xy.mat[c(2:4)]: This takes the values in column 1, rows 2, 3, and 4.
xy.mat[c(2:4)]
```

```
## [1] 3 4 6
```

e. cbind(x, lab): This takes the vectors x and lab, and turns them into a matrix where each vector is a column.

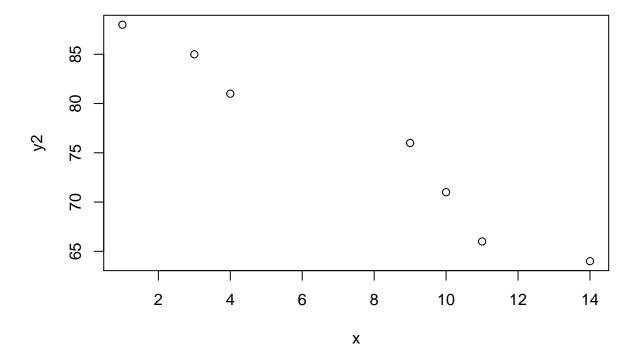
```
cbind(x, lab)
```

```
##
              lab
        х
## [1,] "1"
## [2,]
        "3"
              "b"
        "4"
              "c"
        "6"
              "d"
## [5,]
       "9"
## [6,] "10" "f"
## [7,] "11" "g"
## [8,] "14" "h"
```

### Ex. 2

Using the object xy.mat and not making any new assignments (don't use <-), graph y2 versus x, omitting the 4th row, and with axis labels "y2" and "x".

```
xy.mat
##
         x y1 y2
## [1,]
         1 102 88
## [2,]
         3 101 85
## [3,]
         4
            89 81
   [4,]
         6
            92 80
   [5,]
##
         9
            81 76
## [6,] 10
            80 71
## [7,] 11
            75 66
## [8,] 14
            72 64
plot(xy.mat[c(1:3,5:8),1], xy.mat[c(1:3,5:8),3], xlab = "x", ylab = "y2")
```



## Ex. 3

Suppose y1 and y2 are measures of an outcome at times 1 and 2 for 8 subjects. So cbind(y1,y2) is the 'wide' form of the dataset. Create the 'long' form of the dataset, with 16 rows and 3 columns: a column for y, one for time, and one for subject id.

```
# Make an empty matrix.
mat <- matrix(NA, ncol=3, nrow=16)
# Name the columns.
colnames(mat) <- c("subjectid", "time", "outcome")
# Fill in subject ids (from vector x).
mat[,1] <- rep(x,times = 2)</pre>
```

```
# Fill in times 1 and 2.
mat[,2] <- c(rep(1,times = 8),rep(2,times = 8))
# Fill in outcomes data from y1 and y2.
mat[,3] <- c(y1,y2)
# Show the matrix.
print.data.frame(as.data.frame(mat),row.names = FALSE)</pre>
```

##	subjectid	time	outcome
##	1	1	102
##	3	1	101
##	4	1	89
##	6	1	92
##	9	1	81
##	10	1	80
##	11	1	75
##	14	1	72
##	1	2	88
##	3	2	85
##	4	2	81
##	6	2	80
##	9	2	76
##	10	2	71
##	11	2	66
##	14	2	64