

Ch2. Vectors

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1. more on vectors

Scalar: the vector whose length is 1

```
# define new scalar
x <- 1
is.vector(x)
```

```
## [1] TRUE
```

```
# built-in scalar
pi
```

```
## [1] 3.141593
```

```
print(pi, 16)
```

```
## [1] 3.141592653589793
```

Scalar example 1: Fibonacci sequence

```
# define the function
f <- vector(length = 10)
f[1] <- 1
f[2] <- 1

for (i in 3:10) f[i] <- f[i - 1] + f[i - 2]

f
```

```
## [1] 1 1 2 3 5 8 13 21 34 55
```

Matrix: 2nd dimension vector

```
# matrix(a vector, the length of row, the length of column, by row or not)
# example: convert a vector with length 12 to a 4 x 3 matrix
# default is 'column-wise' or 'by column'
M <- matrix(1:12, nrow = 4, ncol = 3)

M
```

```
##      [,1] [,2] [,3]
## [1,]    1    5    9
## [2,]    2    6   10
```

```
## [3,] 3 7 11
## [4,] 4 8 12
```

```
# 'row-wise' or 'by row'
```

```
M.1 <- matrix(1:12, nrow = 4, ncol = 3, byrow = T)
```

```
M.1
```

```
##      [,1] [,2] [,3]
## [1,] 1    2    3
## [2,] 4    5    6
## [3,] 7    8    9
## [4,] 10   11   12
```

```
# recycling (when the length of source vector is smaller than the length that a matrix needs)
```

```
M.2 <- matrix(1:10, nrow = 4, ncol = 3)
```

```
## Warning in matrix(1:10, nrow = 4, ncol = 3): data length [10] is not a sub-
## multiple or multiple of the number of rows [4]
```

```
M.2
```

```
##      [,1] [,2] [,3]
## [1,] 1    5    9
## [2,] 2    6   10
## [3,] 3    7    1
## [4,] 4    8    2
```

```
M.3 <- matrix(c(1:10, 1, 2), nrow = 4, ncol = 3)
```

```
M.3
```

```
##      [,1] [,2] [,3]
## [1,] 1    5    9
## [2,] 2    6   10
## [3,] 3    7    1
## [4,] 4    8    2
```

Indexing

```
f
```

```
## [1] 1 1 2 3 5 8 13 21 34 55
```

```
f[10]
```

```
## [1] 55
```

```
f[3:10]
```

```
## [1] 2 3 5 8 13 21 34 55
```

```
# except the first and second elements
```

```
f[-c(1,2)]
```

```
## [1] 2 3 5 8 13 21 34 55
```

```
# call specific elements
```

```
f[c(2, 4, 6, 8, 10)]
```

```
## [1] 1 3 8 21 55
```

2. Special function, special value, and filtering

seq()

```
# seq(from, to, by = n)  
seq(0, 10, by = 2.5)
```

```
## [1] 0.0 2.5 5.0 7.5 10.0
```

```
# seq(from, to, length = n)  
seq(0, 10, length = 10)
```

```
## [1] 0.000000 1.111111 2.222222 3.333333 4.444444 5.555556 6.666667  
## [8] 7.777778 8.888889 10.000000
```

rep()

```
# rep(x, times = k) x can be a scalar or vector  
rep(0, times = 10)
```

```
## [1] 0 0 0 0 0 0 0 0 0 0
```

```
rep(NA, 10)
```

```
## [1] NA NA NA NA NA NA NA NA NA NA
```

```
rep(c(1, 2, 3), 2)
```

```
## [1] 1 2 3 1 2 3
```

```
# k also can be a vector
```

```
rep(c(1, 2, 3), c(1, 2, 3)) # 1 is repeated 1 time, 2 is repeated 2 times, and 3 is repeated 3 times
```

```
## [1] 1 2 2 3 3 3
```

NULL: not exist / NA: not available

```
# NULL is 'nothing'  
x <- c(1, 2, NULL, 6) # put 4 things
```

```
x
```

```
## [1] 1 2 6
```

```
mean(x)
```

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

```
length(x) # but the length is 3 in that there's one NULL out of four elements
```

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

```
# NA is not 'nothing' but just 'not available' - missing
```

```
x <- c(1, 2, NA, 6) # put 4 things
```

```
x
```

```
## [1] 1 2 NA 6
```

```
mean(x) # the average value can not be calculated

## [1] NA

length(x) # and the length is 4

## [1] 4

mean(x, na.rm = T) # omit NA and calculate the average value

## [1] 3
```

Filtering

```
# define a vector
z <- c(1, 8, 9, 2, 7, 10, 5, 6, 4, 3)

index <- (z %% 2) == 1
index

## [1] TRUE FALSE TRUE FALSE TRUE FALSE TRUE FALSE FALSE TRUE

z[index]

## [1] 1 9 7 5 3

z[(z %% 2) == 1]

## [1] 1 9 7 5 3

subset(z, (z %% 2) == 1)

## [1] 1 9 7 5 3
```

3. ifelse(), identical(), all(), names()

ifelse(): yes or no

```
# ifelse(test, yes, no) / test, yes, and no are all vectors

# example: if x > 0, then print x. Otherwise, print 2x
x <- c(-0.6, 0.2, -0.8, 1.6, 0.3, -0.8, 0.5, 0.7, 0.6, -0.3)

x.1 <- ifelse(x > 0, x, 2 * x)
x.1

## [1] -1.2 0.2 -1.6 1.6 0.3 -1.6 0.5 0.7 0.6 -0.6

rbind(x, x.1)

##      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10]
## x    -0.6 0.2 -0.8 1.6 0.3 -0.8 0.5 0.7 0.6 -0.3
## x.1 -1.2 0.2 -1.6 1.6 0.3 -1.6 0.5 0.7 0.6 -0.6

# ifelse() help us to make simpler code

# basic code with 'for'
x.1 <- x
for (i in 1:length(x)) {
```

```

  if (x[i] > 0) x.1[i] <- x[i] else x.1[i] <- 2 * x[i]
}

rbind(x, x.1)

##      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10]
## x    -0.6  0.2 -0.8  1.6  0.3 -0.8  0.5  0.7  0.6  -0.3
## x.1 -1.2  0.2 -1.6  1.6  0.3 -1.6  0.5  0.7  0.6  -0.6

```

identical()

```

# k1:k3 and c(k1, k2, k3) are different
x <- 1:3 # integer
y <- c(1, 2, 3) # numeric

identical(x, y)

```

```

## [1] FALSE

# c(k1, k2, k3) and seq(k1, k2, 1) are same
z <- seq(1, 3, 1) # numeric

identical(y, z)

```

```
## [1] TRUE
```

all(): Do all the things in specific vector satisfy the condition? Yes or no

```

# it returns TRUE only when all elements satisfy the condition
all(x == y)

```

```

## [1] TRUE

# x is integer vector but it is converted to numeric so can be compare with y.

```

names() <- : assign specific names to each element

```

era <- c(5, 4, 3, 4, 5, 6)
names(era) # NULL

## NULL

# assign names
# paste is combine two character strings paste(c, c, sep = "separator")
names(era) <- paste("y", 2001:2006, sep = ".")

era

## y.2001 y.2002 y.2003 y.2004 y.2005 y.2006
##      5      4      3      4      5      6

era[2] # indexing with the order

## y.2002
##      4

```

```
era["y.2002"] # indexing with the name
```

```
## y.2002  
##      4
```

4. arithmetic and relation operators

application: run lengths

```
# define the binomial sample  
set.seed(1)  
z <- rbinom(20, 1, 0.5)
```

```
z
```

```
## [1] 0 0 1 1 0 1 1 1 1 0 0 0 1 0 1 0 1 1 0 1
```

```
# If the difference between two elements are same, run. otherwise, run is over.
```

```
n <- length(z)  
d <- z[2:n] - z[1:(n-1)]  
d
```

```
## [1] 0 1 0 -1 1 0 0 0 -1 0 0 1 -1 1 -1 1 0 -1 1
```

```
sum(d != 0) + 1 # how many 'run's are there?
```

```
## [1] 12
```

```
index <- c(which(d != 0), length(z))  
index
```

```
## [1] 2 4 5 9 12 13 14 15 16 18 19 20
```

```
c(index[1], diff(index))
```

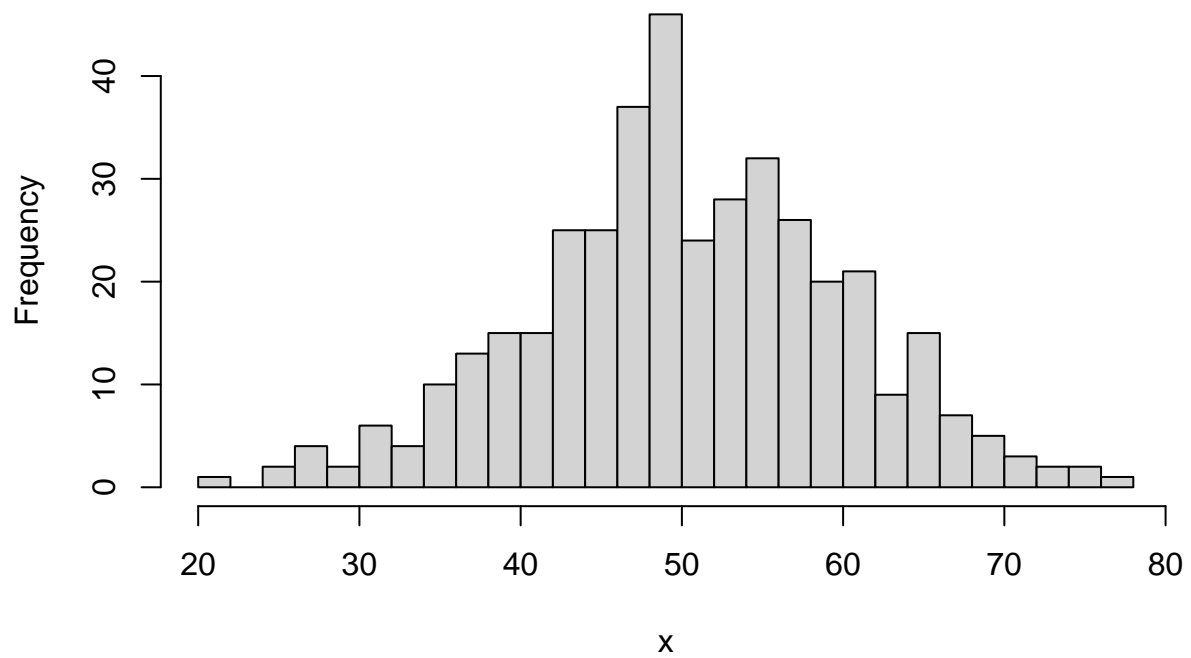
```
## [1] 2 2 1 4 3 1 1 1 1 2 1 1
```

5. random number generation

normal distribution

```
n <- 400  
set.seed(1)  
x <- rnorm(n, 50, 10)  
  
hist(x, nclass = 20, main = "normal(50,10) distribution")
```

normal(50,10) distribution

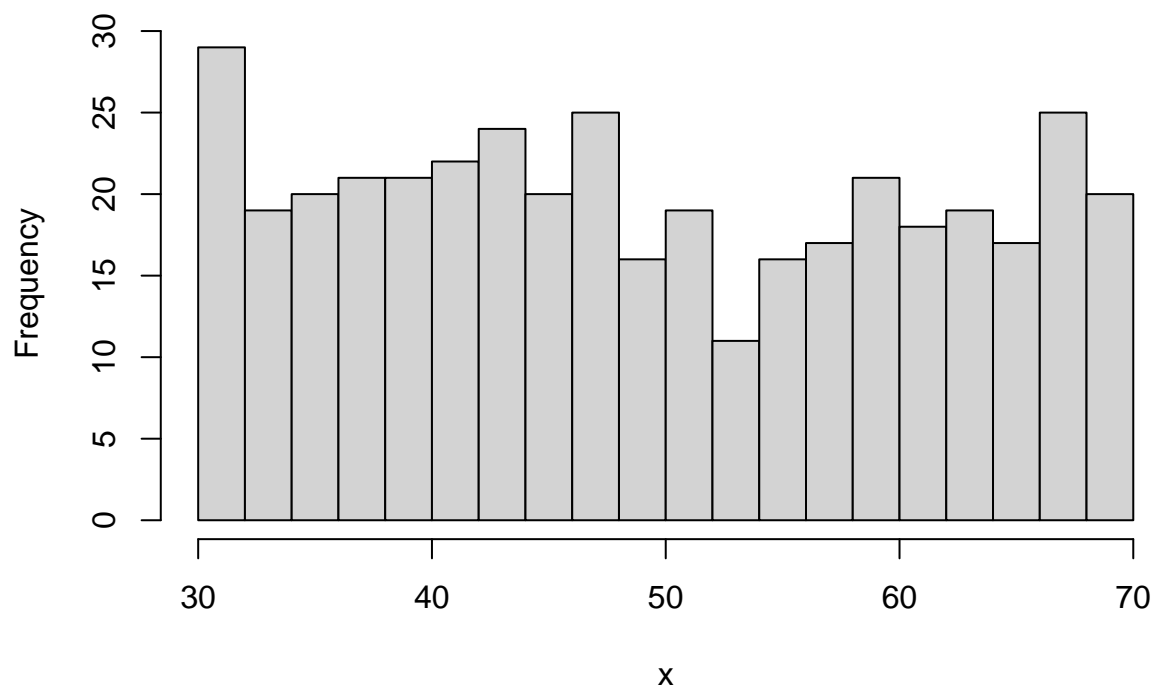


uniform distribution

```
n <- 400
x <- runif(n, 30, 70)

hist(x, nclass = 20, main = "uniform(30, 70) distribution")
```

uniform(30, 70) distribution

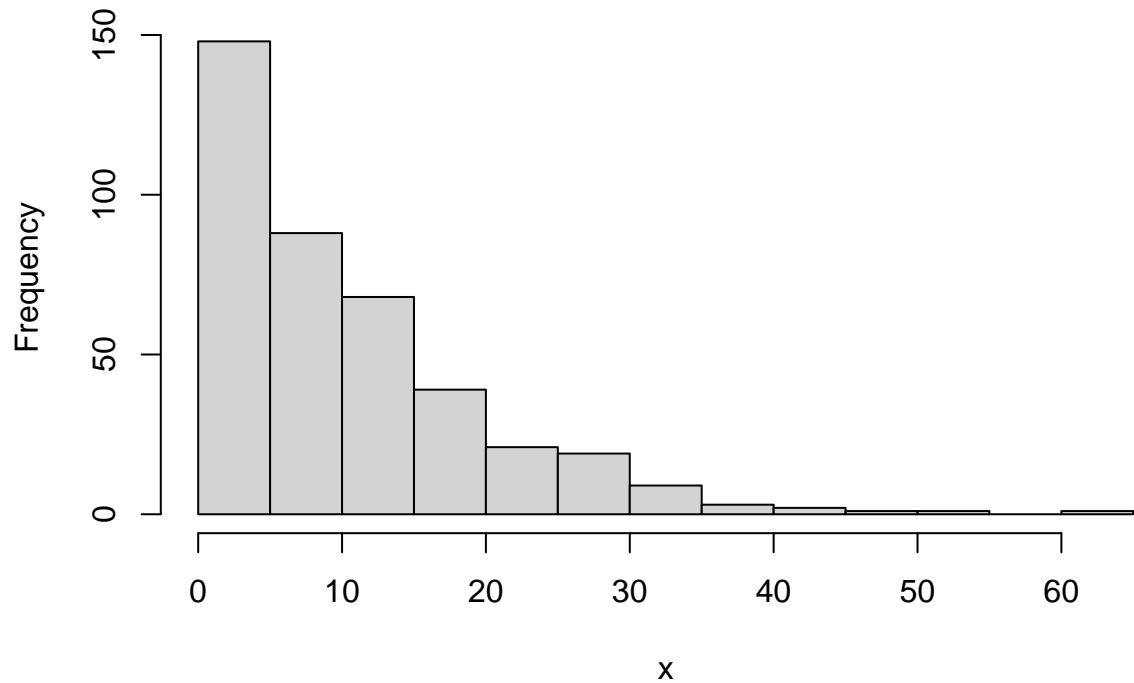


exponential distribution

```
n <- 400
x <- rexp(n, 0.1)

hist(x, nclass = 20, main = "exponential(0.1) distribution")
```


exponential(0.1) distribution

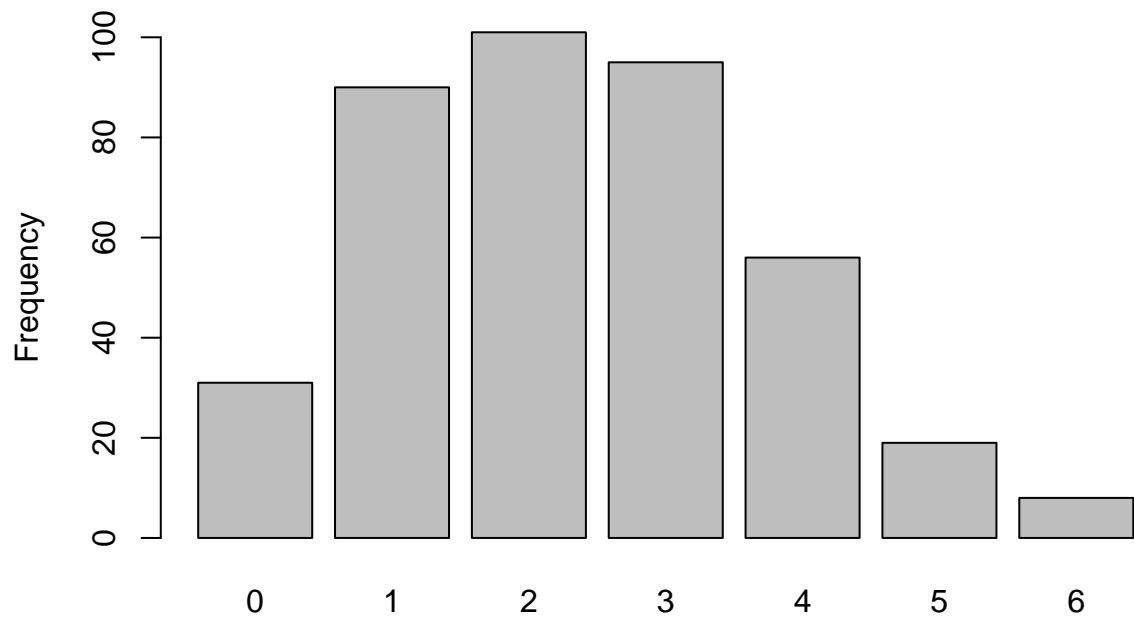


mial distribution

```
n <- 400
x <- rbinom(n, 10, 0.25)

barplot(table(x), ylab = "Frequency", main = "binomial(10, 0.25) distribution")
```

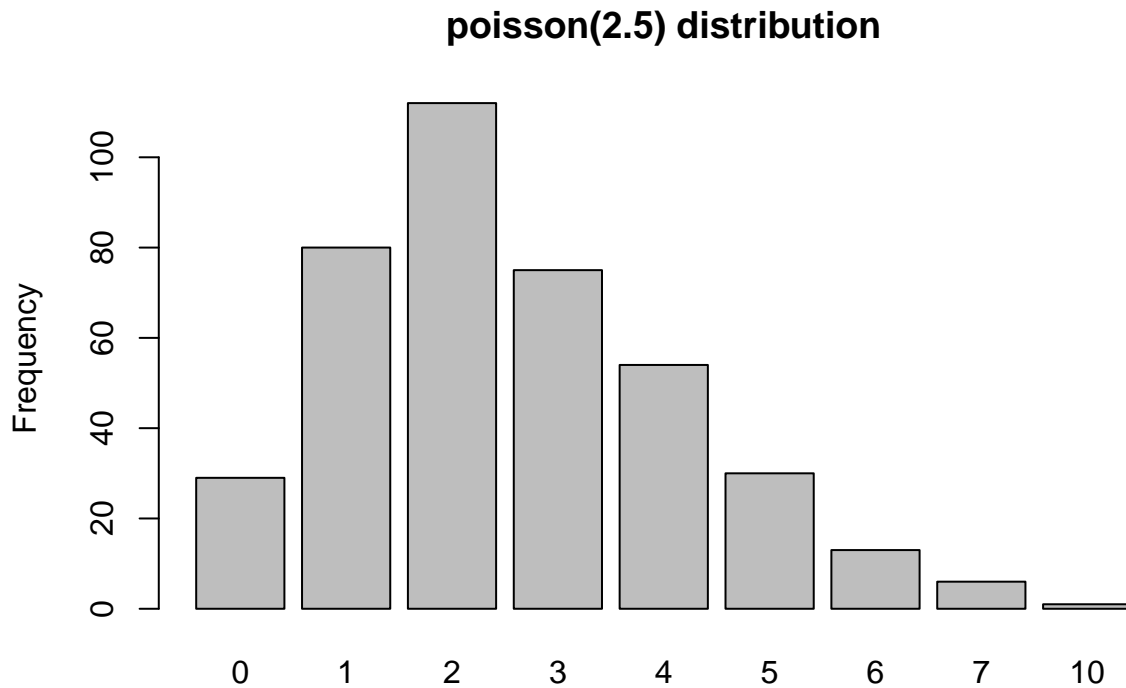
binomial(10, 0.25) distribution



Poisson distribution

```
n <- 400
x <- rpois(n, 2.5)

barplot(table(x), main = "poisson(2.5) distribution", ylab = "Frequency")
```



Random sampling from finite population: sample()

ex

```
# n = 10, without replacement -> random permutatin
sample(LETTERS[1:10])
```

```
## [1] "I" "H" "J" "B" "G" "C" "E" "A" "F" "D"
```

```
# n = 10, with replacement
sample(LETTERS[1:10], replace = T)
```

```
## [1] "H" "B" "A" "G" "H" "F" "E" "H" "J" "I"
```