# Data Mining and Machine Learning in Bioinformatics

## Exercise Series 3

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## Task 4

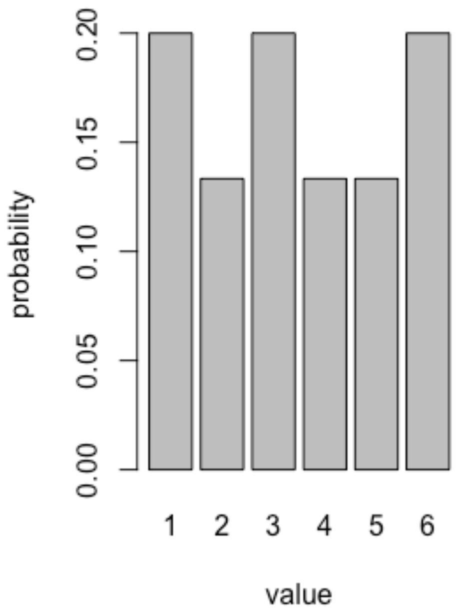
#### CODE

```
# Parameters
#   m: sample matrix
#   p: probability vector
#   n: number of trials
multinom <- function(m, p, n) {
  #   - the expectation value
  ex <- p*n
  print ('=============================')
  print ('Expectation Value')
  print (ex)

  #   - the population variance/covariance matrix
  var_m<-n*p*(1-p)
  print ('=============================')
  print ('Population variance')
  print (var_m)

  cov_m<-matrix(0,ncol=6,nrow=6)
  for (i in 1:length(p)) {
    for (j in 1:length(p)) {
      #print (-1 * n * i * j)
      cov_m[i,j] <- (-1 * n * p[i] * p[j])
    }
  }
  print ('=============================')
```

```
  print ('Population covariance matrix')
  print (cov_m)

  #   - the sample mean (R functions apply and mean)
  print ('=============================')
  print ('Sample Mean')
  print (apply(m, 2, mean))
  #apply(m,1,function(x) sum(x*c(1,2,3,4,5,6))/n)

  #   - the sample covariance matrix (R function cov)
  print ('=============================')
  print ('Sample Covariance Matrix')
  print (cov(m))

  #   - the value of the probability mass function for each sample (Tip: you can u
se R function dmultinom)
  print ('=============================')
  print ('Value of the probability mass function')
  print (apply(m, 1, function(x) dmultinom(x, prob=p)))

  # visualizing p
  barplot(p, xlab = "value", ylab="probability", axisnames = T, names.arg = c(1,2,
3,4,5,6))
}


# probability vector
p <- c(0.2,0.4/3,0.2,0.4/3,0.4/3,0.2)
# number of trials
n <- 10
# sample matrix - 50 random drawings from the multinomial distribution, transpose
the matrix (row=sample vector)
m<-t(rmultinom(50, n, p))

multinom(m,p,n)
```

### RESULT

```
[1] "=============================="
[1] "Expectation Value"
[1] 2.000000 1.333333 2.000000 1.333333 1.333333 2.000000

[1] "=============================="
[1] "Population variance"
[1] 1.600000 1.155556 1.600000 1.155556 1.155556 1.600000

[1] "=============================="
[1] "Population covariance matrix"
           [,1]       [,2]       [,3]       [,4]       [,5]       [,6]
[1,] -0.4000000 -0.2666667 -0.4000000 -0.2666667 -0.2666667 -0.4000000
[2,] -0.2666667 -0.1777778 -0.2666667 -0.1777778 -0.1777778 -0.2666667
[3,] -0.4000000 -0.2666667 -0.4000000 -0.2666667 -0.2666667 -0.4000000
[4,] -0.2666667 -0.1777778 -0.2666667 -0.1777778 -0.1777778 -0.2666667
[5,] -0.2666667 -0.1777778 -0.2666667 -0.1777778 -0.1777778 -0.2666667
[6,] -0.4000000 -0.2666667 -0.4000000 -0.2666667 -0.2666667 -0.4000000

[1] "=============================="
[1] "Sample Mean"
[1] 2.40 1.28 2.04 1.10 1.26 1.92

[1] "=============================="
[1] "Sample Covariance Matrix"
           [,1]        [,2]        [,3]        [,4]          [,5]          [,6]
[1,]  2.2448980 -0.62448980 -0.26122449 -0.14285714 -0.3510204082 -0.8653061224
[2,] -0.6244898  1.06285714 -0.01142857 -0.08979592 -0.3191836735 -0.0179591837
[3,] -0.2612245 -0.01142857  1.34530612 -0.10612245 -0.4800000000 -0.4865306122
[4,] -0.1428571 -0.08979592 -0.10612245  0.94897959 -0.3122448980 -0.2979591837
[5,] -0.3510204 -0.31918367 -0.48000000 -0.31224490  1.4616326531  0.0008163265
[6,] -0.8653061 -0.01795918 -0.48653061 -0.29795918  0.0008163265  1.6669387755

[1] "=============================="
[1] "Value of the probability mass function"
[1] 8.601600e-04 7.645867e-05 7.645867e-04 1.146880e-03 4.587520e-03 2.293760e-03
3.058347e-03 2.293760e-03 9.061768e-05
[10] 2.293760e-03 3.398163e-04 1.019449e-03 3.058347e-03 7.645867e-04 1.146880e-03
 8.601600e-04 5.097244e-04 3.058347e-03
[19] 1.529173e-03 1.529173e-03 1.529173e-03 3.440640e-04 8.601600e-04 1.146880e-03
 6.881280e-04 1.529173e-03 1.019449e-03
[28] 2.548622e-04 1.529173e-03 1.146880e-03 5.734400e-05 1.699081e-04 1.146880e-03
 1.146880e-03 1.019449e-03 1.146880e-03
[37] 1.019449e-03 4.587520e-04 4.530884e-04 3.398163e-04 8.601600e-04 2.548622e-04
 1.529173e-03 1.529173e-03 1.146880e-03
[46] 1.699081e-04 2.293760e-04 2.293760e-03 4.530884e-04 1.359265e-04
```




**Discussion**

Everytime we draw random samples, it differed mean, variance and covariances. With bigger number of samples, we get more closed results to the theoretically expected results.