1.
-Remember that x=0,...,30, don't forget x=0! Take x=0 into account in the indexing.
-The alternative hypothesis is two-sided, so the null hypothesis can be rejected with low OR high values!
-The distribution is symmetric.

2.
a)
-Remember to use set.seed(0511) so that the results will be comparable to the model solution
-rnorm takes standard deviation as a parameter instead of variance
-With replicates we mean study subjects, for example patients. 8 individuals from both groups A and B from which we measure the gene expression levels.
-For each group, generate matrix of size Number of genes x Number of replicates filled with random numbers

b)
-Perform testing for **each gene**, you should end up with 100 p-values
-Use var.equal=TRUE with t.test function

c)
-The idea in Bonferroni correction: multiply the original p-values with the total number of p-values to be adjusted, find minimum of that and 1
-You can compare the results from your implementation to p.adjust(.., method="bonferroni")

d)
-You can compare the results from your implementation with p.adjust(.., method="BH")
-Remember to return the p-values in the original order!
-The steps in B-H correction:
    1. order the p-values from smallest to largest
    2. store the original order of the p-values
    3. calculate the q_k values
    4. make sure that the corrected values do not decrease when k increases
    5. return the corrected p-values (make sure they are <=1) in their original order

e)
-20 rows with mu_a =/= mu_b
-80 rows with mu_a=mu_b

f)
-See ?t.test for how to set the alternative hypothesis
-Use var.equal=TRUE with t.test function
-Which one of the corrections, Bonferroni or B-H gives less significant p-values? Comment on your findings.

g)
-See 43/45 for FDR
    1) Average FDR

2) Average FWER
3) 0.05

FDR for one gene = p value * number genes/ (p value* number of genes + 20)
Average FDR = sum (FDR for one gene) / 100

Average FWER =
1) one or more false discovery (reject the null hypothesis p value < 0.05)
2) gene pvalue < 0.05 non differential genes (80) 1
   differential gene (20) 0
   p value > 0.05 0
   1+1+0+ 1 ….. +1/100