Math4397/6397
Problem Set 11, due Thursday Dec 3

Problem 1. Refer to the data from Problem 2 in Set 10. Re-use your computations for the tables to perform Fisher's test against having an unequal mortality rate in the two groups (two-sided). Compare the p-value resulting from this test with that from a test based on the χ^2-statistic.

Using the probabilities for the tables for Problem 2 in Set 10 with a two-sided Fisher test means we add the probabilities for all tables which have a probability at most equal to that of the observed one. This gives a p-value

$$p = 0.0202 + 0.1297 + 0.3026 + 0.1736 + 0.0424 + 0.0037 = 0.672\,.$$

We compare this with the χ^2-statistic. The test statistic is

$$TS = \frac{(2 - 2.65)^2}{2.65} + \frac{(4 - 3.35)^2}{3.35} + \frac{(13 - 12.35)^2}{12.35} + \frac{(15 - 15.65)^2}{15.65} = 0.34\,.$$

This gives the p-value $p = 0.56$, which is quite a bit smaller than the result of the exact test. Fortunately, the conclusion would be the same: we retain H_0.

Problem 2. A small study was done to compare how well students with different majors do in an introductory statistics course. Seven majors were found: biology, psychology, sociology, business, education, meteorology and economics. At the end of the course, the students were given a special test to measure their understanding of basic statistics. Then a series of t-tests were performed to compare *every pair* of majors. Thus, biology and psychology majors were compared, biology and sociology majors, psychology and sociology majors, etc., for a total of 21 t-tests.

Simulate this study assuming all majors do about the same. Assume there are 20 students in each major, and that scores on the test have a normal distribution with mean $\mu = 12$ and standard deviation $\sigma = 2$. Use the computer to generate random test scores that are normally distributed for biology majors, then do it a second time to get a sample for psychology majors and so on, for 7 samples (one for each major).

a. List the 21 pairs of majors and perform the 21 t-tests.

We use the code:

```
n <- 20
majors <- 7
dat <- matrix(rnorm(n * majors, mean = 12, sd = 2), n, majors)
results <- sapply(1 : (ncol(dat) - 1),
                  function(i){
                    sapply((i + 1): ncol(dat),
                           function(j){
                             t.test(dat[,i], dat[,j])$p.value
```

```
                              }
                         )
                    }
                 )
         sum(unlist(results) <= .1)
```

b. In how many of the tests did you reject the null hypothesis at $\alpha = 0.10$?

The number of positives is 5.

c. Use the Bonferroni procedure to pick a significance level α^* for each comparison so that the probability of a familywise error under the null hypothesis is no larger than 0.1. Perform the tests and report.

We use $\alpha^* = 0.1/21$. Adding a line `sum(unlist(results) <= .1/21)` results in one remaining rejection instead of five. We would still (falsely) reject the null hypothesis.

Problem 3. Researchers comparing fMRI signals between a resting state and a active state in 10 different regions of the brain, found the following p-values resulting from a test for equal activity:

Region	1	2	3	4	5	6	7	8	9	10
P-value	.081	.011	.053	.0140	.016	.045	.046	.050	.003	.053

a. Controlling the FWE of .05, which regions would be rejected? There are 10 tests and we want a FWER of .05. Reject all tests for which the P-value is less that .05 / 10 = .005. The only region which we reject is no. 9. Consequently, we reject the null hypothesis that the fMRI data of a resting brain shows equal activity levels compared to an active brain.

b. Controlling the FDR at .05, which regions would be rejected? (Interpret your results.)

Test	i	Pvalue	kp_i/i	min
9	1	.003	.030	.030
2	2	.011	.055	.040
4	3	.014	.047	.040
5	4	.016	.040	.040
6	5	.045	.090	.059
7	6	.046	.077	.059
8	7	.050	.071	.059
10	8	.053	.066	.059
3	9	.053	.059	.059
1	10	.081	.081	.081

So tests 9, 2, 4 and 5 would be rejected at a FDR of .05. Rememeber that we are controlling the expected percentage of falsely rejected hypotheses at 5%, which means we would expect 0.5 false discoveries.

Problem 4. **For students enrolled in Math6397 only.** In the new teams, work out the solution to Project 3, linked from the course webpage.

- Since flies are being consumed, the total number of flies changes between the different time periods.

  We do a χ^2-test with the data

Time	Consumed	Alive	Total
<48	43	167	210
48-96	16	151	167
96-144	13	138	151
144-192	12	126	138
Sum	84	582	666

  with 3 degrees of freedom whcih gives $p = 0.00062$, so we can reject the hypothesis that the survival probability stays constant.

- Now we create contingency tables for the time periods.

	Consumed	Survive	Total
Light	16	89	105
Heavy	27	78	105
Total	43	167	210

  Table 1: Contingency table for 0-48 hours

  We apply the chi-squared test to the first table, because the expected values are all above 5 (large counts). This gives a p-value 0.0600 for the two-sided test. Knowing that the chi-square value is large for both extremes (mortality of heavy flies larger or smaller than expected) we have to divide this by two because we only want to count the extreme tables on one side. Thus, our p-value is 0.03.

	Consumed	Survive	Total
Light	6	83	89
Heavy	10	68	78
Total	16	151	167

  Table 2: Contingency table for 48-96 hours

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For the second table, we use the Fisher test with the simulated p-value to get $p = 0.143$.

	Consumed	Survive	Total
Light	7	76	83
Heavy	6	62	68
Total	13	138	151

Table 3: Contingency table for 96-144 hours

For the third table, Fisher's test gives $p = 0.578$.

	Consumed	Survive	Total
Light	5	71	76
Heavy	7	55	62
Total	12	126	138

Table 4: Contingency table for 144-192 hours

For the last one, Fisher's text gives $p = 0.25$.

Now we perform the Bonferroni procedure. Since we have 4 tables, we have $\alpha^* = \alpha/4 = 0.125$. Since none of the tables has produced a p-value below this level, we retain H_0.