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Homework 7
Exercise 3
       R code:
              cor.test(rock$area,rock$perm)
       output:
              Pearson's product-moment correlation
       data: rock$area and rock$perm
       t = -2.9305, df = 46, p-value = 0.005254
       alternative hypothesis: true correlation is not equal to 0
       95 percent confidence interval:
       -0.6118206 -0.1267915
       sample estimates:
          cor
       -0.396637
       Interpretation:
              The 95% confidence interval for rho ranged from -0.61 to -0.13 and does not
       overlap with 0. The p-value of 0.005 is well below the standard alpha level of 0.05. As
       such, the null hypothesis that the population correlation coefficient between area and
       perm is zero should be rejected.
Exercise 4
       R code: bfCorTest(rock$area,rock$perm)
       interpretation:
              The point estimate for rho is -0.345. the 95% HDI ranges from -0.614 up to -
       0.081 and does not overlap with 0. The Bayes Factor is 8.072781 ±0%, which is in favor
       of the alternative hypothesis that the population correlation coefficient is not equal to
       0.
Exercise 8
       R code: chisq.test(UCBAdmissions[,,1], correct=FALSE)
       Output:
              Pearson's Chi-squared test with Yates' continuity correction
       data: UCBAdmissions[, , 1]
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X-squared = 17.248, df = 1, p-value = 3.28e-05

Interpretation:

The reported valued of chi-square, 17.25 on one degree of freedom, has a corresponding p-value that is well below the standard alpha level. Thus, we reject the null hypothesis of independence between admission rates between males and females.

Exercise 9

R code: contingencyTableBF(UCBAdmissions[,,1], sampleType = 'poisson', posterior = FALSE)

Interpretation:

The Bayes factor of 1111.6:1 is in favor of the alternative hypothesis that the two factors are not independent of one another. Meaning that the admission rates between males and females are associated.

Exercise 10

R code:

ctBFout <- contingencyTableBF(UCBAdmissions[,,1], sampleType = 'poisson',
posterior = TRUE, iterations=10000)
summary(ctBFout)</pre>

2.5% 25% 50% 75% 97.5% lambda[1,1] 467.96 495.88 510.90 526.00 557.14 lambda[2,1] 279.48 300.85 312.74 324.50 348.38 lambda[1,2] 72.04 83.00 89.27 95.71 109.23 lambda[2,2] 12.13 16.75 19.54 22.64 29.46

95% HDI Difference in proportions between columns:

- Males that were admitted (lambda[1,1]): 467.96 to 557.14
- Males that were rejected (lambda[2,1]): 279.48 to 348.38
- Females that were admitted (lambda[1,2]): 72.04 to 109.23
- Females that were rejected (lambda[2,2]): 12.13 to 29.46