Stat 342: HW 2 Key

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1. (a) The pdf of Y, the maximum order statistic is

$$f_Y(y) = \frac{n!}{(n-1)!(n-n)!}(\frac{y}{\theta})^{n-1}(1-\frac{y}{\theta})^{n-n}\frac{1}{\theta} = \frac{ny^{n-1}}{\theta^n}$$

Thus, the power function $p(\theta)$ is

$$p(\theta) = P_\theta[Y > c] = \int_c^\theta \frac{ny^{n-1}}{\theta^n}dy = (\frac{y}{\theta})^n|_c^\theta = 1 - (\frac{c}{\theta})^n$$

(b)

$$\alpha = 0.05 = P_{\theta=0.5}[Y > c]$$
$$= \int_c^{0.5} \frac{ny^{n-1}}{0.5^n}dy$$
$$= \frac{y^n}{0.5^n}|_c^{0.5}$$
$$= 1 - \frac{c^n}{0.5^n}$$

Thus,

$$0.05 = 1 - \frac{c^n}{0.5^n} \longrightarrow c = ((0.95)*0.5^n)^{1/n}$$

(c)

$$p = P_{\theta=0.5}[Y > 0.48]$$
$$= \int_{0.48}^{0.5} \frac{20y^{19}}{0.5^{20}}dy$$
$$= 0.558$$

Since our p-value is large, we fail to reject the null hypothesis.

(d) If $Y = 0.52$, no integral is needed. This event has probability 0 under the null hypothesis, so the p-value is 0. Thus, we reject the null hypothesis.

2. (a) The size α Wald test rejects H_0 when

$$|\hat{\lambda} - \lambda_0| \geq z_{\alpha/2}\hat{SE}$$

where $\hat{\lambda} = \frac{\sum x_i}{n}$ for n independent Poisson(λ) random variables and

$$\hat{SE} = \sqrt{\frac{\hat{\lambda}}{n}} = \sqrt{\frac{\sum x_i}{n^2}} = \frac{\sqrt{x_i}}{n}$$

Thus, the size α Wald test rejects H_0 when

$$|\frac{\sum x_i}{n} - \lambda_0| \geq z_{\alpha/2}\frac{\sqrt{x_i}}{n}$$

(b) The following is an example of R code that can simulate this Wald test. In my realization, I found a Type I error rate of 0.0511, which is close to 0.05.

```
lambda0<-1
n=20
alpha=0.05

numExperiments<-100000
trues<-0
for(i in 1:numExperiments){
  data<-rpois(n,lambda=lambda0)
  if(abs(sum(data)/n - 1) >= qnorm(1-0.05/2)*sqrt(sum(data))/n){
    trues <- trues+1
  }
}

trues/numExperiments
```

3.
$$\lambda = \frac{L(\theta_1)|x)}{L(\theta_0)|x)} = (\frac{\sigma_0}{\sigma_1})^n \exp[-\sum x_i^2(\frac{1}{\sigma_1^2} - \frac{1}{\sigma_0^2})]$$

The most powerful test rejects iff $\lambda > k$.

Since $\sigma_1^2 < \sigma_0^2$, we know that $-(\frac{1}{\sigma_1^2} - \frac{1}{\sigma_0^2})$ is a decreasing function of $\sum x_i^2$. Thus, the rejection region is $\sum x_i^2 \leq k$. Now, under $H_0 : \sigma = \sigma_0$,

$$\sum x_i^2/\sigma_0^2 \sim \chi_n^2$$

and therefore to ensure a size of α, we need to choose $k = \sigma_0^2 \times \chi_{1-\alpha,n}^2$ where $\chi_{1-\alpha,n}^2$ is the $(1-\alpha)$ percentile of the χ^2 distribution with n degrees of freedom.

Note that the rejection region obtained is free of σ_1. Thus, for all $\sigma_1 \in R$ such that $\sigma_1^2 < \sigma_0^2$, the test remains the same. This proves that the test is uniformly most powerful.

4. **a)** There appears to be a non-linear association.

**Number of Lymph Nodes Examined
by Patient, Doctor A vs. Doctor B**
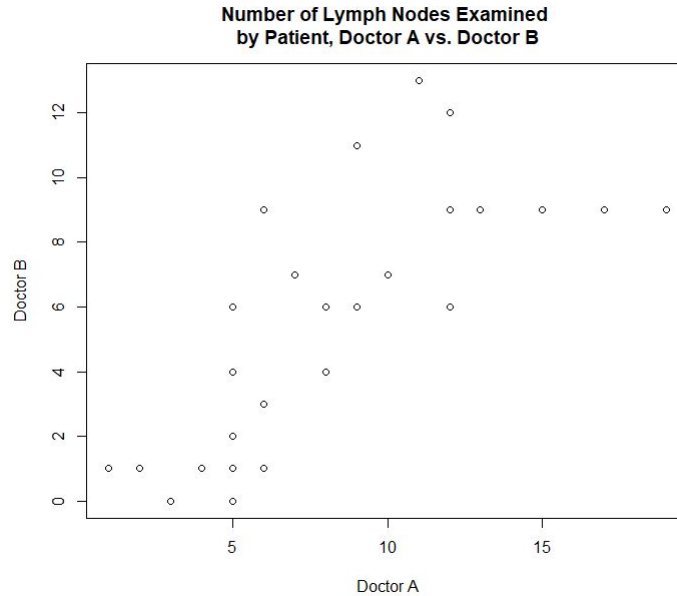
b) (Various options). Based on the nature of the data, a paired t-test is good option. Let μ_d be the population mean difference between the number of lymph nodes observed by two doctors, if both observe all potential patients. We will test the hypothesis $H_0 : \mu_d = 0$ vs $H_1 : \mu_d \neq 0$. Let $d_i = x_i - y_i$ for $i \in 1, \ldots, n$, and $\bar{d} = \frac{\sum d_i}{n}$. Since we wish to see if there is a systematic difference (in either direction), a two-sided test is appropriate.

The T-statistic will be

$$T = \frac{\bar{d} - 0}{s_d / \sqrt{n}}$$

and we will reject when

$$|T| > t_{n-1, 1-\alpha/2}$$

c) For our data, the test statistic is $T = 5.5$ with corresponding p-value 5.12×10^{-6}. See code below:

```
# Simple Plot of the Data
plot(arc$DoctorA, arc$DoctorB,
     main="Number of Lymph Nodes Examined \nby Patient, Doctor A vs. Doctor B",
     xlab="Doctor A", ylab="Doctor B")

# View Arguments for T Test
?t.test

tstat<-mean(arc$DoctorA-arc$DoctorB)/
     (sd(arc$DoctorA-arc$DoctorB)/sqrt(length(arc$DoctorA)))
pvalue<-(1-pt(tstat,df=31))*2
print(tstat)
print(pvalue)

# Perform Paired Difference T-Test Two Ways: Results are the Same!!
t.test(arc$DoctorA-arc$DoctorB,
     alternative="two.sided",mu=0,conf.level=0.95)
t.test(arc$DoctorA, arc$DoctorB,
     alternative="two.sided",mu=0,conf.level=0.95,
     paired=TRUE)
```

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```
          Paired t-test

data:   arc$DoctorA and arc$DoctorB
t = 5.5, df = 31, p-value = 5.12e-06
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 1.730243 3.769757
sample estimates:
mean of the differences
                2.75
```

Thus, we have enough evidence to reject H_0 at the 0.05 level.

d) If this experiment were repeated with different doctors, we would not necessarily get the same result. Thus, failing to reject the null hypothesis is not equivalent to accepting the null hypothesis. This experiment is not highly reproducible.

5. **a)** In the H_0 parameter space, the MLEs are

$$\hat{p}_{0,i} = \frac{m_i}{n}$$

In the unrestricted parameter space $H_0 \cup H_1$, the MLEs are

$$\hat{p}_{0,i} = \frac{x_i}{n}$$

Thus,

$$\lambda(x) = \frac{\frac{n!}{x_1! x_2! \dots x_5!} \prod_{i=1}^{5} \left(\frac{m_i}{n}\right)^{x_i}}{\frac{n!}{x_1! x_2! \dots x_5!} \prod_{i=1}^{5} \left(\frac{x_i}{n}\right)^{x_i}}$$

$$= \prod_{i=1}^{5} \left(\frac{n m_i}{n x_i}\right)^{x_i}$$

$$= \prod_{i=1}^{5} \left(\frac{m_i}{x_i}\right)^{x_i}$$

$$2 \log(\lambda(x)) = 2 \sum_{i=1}^{5} x_i \log\left(\frac{m_i}{x_i}\right)$$

$$-2 \log(\lambda(x)) = 2 \sum_{i=1}^{5} x_i \log\left(\frac{x_i}{m_i}\right)$$

since $\log(\frac{m_i}{x_i}) = \log(m_i) - \log(x_i)$, so $(-1) \log(\frac{m_i}{x_i}) = \log(x_i) - \log(m_i) = \log(\frac{x_i}{m_i})$

b) ν is the difference in the number of free parameters specified between the null and alternative spaces. The null space specifies 1 free parameter, and the alternative 4. Thus, $\nu = 4 - 1 = 3$.

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