

## Statistics: Homework 3

10.5 Given  $X_1, \dots, X_n \sim \text{Uniform}(0, \theta)$  and  $Y = \max\{X_1, \dots, X_n\}$ , we have the cdf of  $Y$  to be  $F_Y(y) = (y/\theta)^n$  for  $y \in [0, 1/2]$ .

(a) When we choose to reject  $H_0$  when  $Y > c$ , the power function is  $\beta(\theta) = 1 - (c/\theta)^n$ ,  $c \in [0, 1/2]$ .

(b) Given size of the test to be .05, we need to solve,

$$1 - (2c)^n = .05$$

which gives us a solution of  $c = 1/2(.95)^{1/n}$

(c) The size,  $\alpha = \beta(1/2) = 1 - (2c)^n$ ,  $c \in [0, 1/2]$ . Thus, when  $n = 20, Y = .48$ , the p-value is

$$\inf\{\alpha : X^n \in R_\alpha\} = 1 - (2 \times .48)^{20} = 0.557997566$$

We would conclude that we do not reject  $H_0$  with an approximate probability of 0.56, which does not give a strong evidence to reject  $H_0$

(d) When  $n = 20, Y = .52$ , using the  $\alpha$  formula in (c) gives us  $1 - (2 \times .52)^{20} = -1.19112314$ . But the given  $Y = .52 > 1/2$  which is out of the defined boundaries of the size, i.e.  $F_Y(0.52; \theta = 1/2) = 0$ . Hence the p-value is 0. This allows us to conclude that  $H_0$  is to be rejected as the p-value always lies in the criteria region; a very strong reason to reject  $H_0$ .

10.7b Let  $H_0 : F_T = F_S$  and  $H_1 : F_T \neq F_S$ , where the subscripts denote Twain and Snodgrass respectively. The observed value of the test statistic given by the absolute difference of their means,  $|\bar{T} - \bar{S}|$  is

$$|0.231875 - 0.2097| = 0.022175$$

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Have to do some simulation here.

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Under this p-value, do we reject  $H_0$  at a 5 percent level? How about 2.5 percent level?

10.8 (a) The size of this test with rejection region  $R$  is

$$\begin{aligned} \mathbb{P}(T(X^n) > c | \theta = 0) &= \mathbb{P}(\bar{X}_n > c) \\ &= \mathbb{P}(Z > \sqrt{nc}), \quad Z \text{ is the standard normal distribution} \\ &= 1 - \Phi(\sqrt{nc}), \quad \Phi \text{ is the cdf of the standard normal} \end{aligned}$$

where by Central Limit Theorem,  $\bar{X}_n \sim N(0, 1/\sqrt{n})$ . Thus given size  $\alpha$ , the  $c$  is  $\Phi^{-1}(1 - \alpha)/\sqrt{n}$

(b) Under  $H_1 : \theta = 1$ , the power is  $\beta(1) = \mathbb{P}(T(X^n) > c | \theta = 1) = 1 - \Phi(\sqrt{n}(c - 1))$ . Thus when  $n \rightarrow \infty$ ,  $\sqrt{n}(c - 1) \rightarrow \infty$  for  $c \neq 1$  which then  $1 - \Phi(\sqrt{n}(c - 1)) \rightarrow 1$ .

(c)

10.12 (a) We known that the MLE for  $\lambda$  is  $\bar{X}_n = n^{-1} \sum_{i=1}^n X_i$ . The Fisher information  $I_n(\lambda)$  is

$$I_n(\lambda) = nI(\lambda) = -n\mathbb{E}_\lambda \left( \frac{\partial^2 f_X(X; \lambda)}{\partial \lambda^2} \right) = -n\mathbb{E}_\lambda \left( -\frac{X}{\lambda^2} \right) = \frac{n}{\lambda}$$

thus by the property of MLE,

$$\frac{\bar{X}_n - \lambda}{\hat{\text{se}}} \rightsquigarrow N(0, 1)$$

thus the size of of the Wald test

$$\mathbb{P} \left( \left| \frac{\bar{X}_n - \lambda_0}{\sqrt{\lambda_0/n}} \right| > z_{\alpha/2} \right)$$

(b)

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```

import numpy as np
from scipy.stats import norm
def poisson_sample(l, n):
    """
    Generates n Poisson distributed samples with parameter l.
    """
    return np.random.poisson(lam = l, size = n)
def wald_test(sample, n = 20, alpha = .05, null_lambda = 1):
    """
    Performs Wald test and returns p-value.
    """
    xbar = np.mean(sample)
    test_statistic = np.absolute((xbar - null_lambda) / (null_lambda / n) ** 0.5)
    return 2 * (1 - norm.cdf(test_statistic))
def multwald(l = 1, n = 20, alpha = .05, null_lambda = 1, B = 10000):
    """
    Performs Wald test B times and return proportion of test where null hypothesis is
    rejected.
    """
    count = 0
    for i in np.arange(B):
        sample = poisson_sample(l, n)
        if wald_test(sample) < alpha:
            count += 1

    return count/B
multwald()

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From performing the simulation of Wald 10000 times, the proportion of null rejected is 0.0564 which is very close to the type I error rate of  $\alpha$ .

### 11.3 The posterior density

$$f(\theta|x^n) \propto \mathcal{L}_n(\theta)f(\theta)$$

$$f(\theta|x^n) \propto (1/\theta)^n(1/\theta)$$

Thus the posterior density is a uniform distribution on  $(a, b)$  where  $b - a = \theta^n$ .

### 11.4 (a) The likelihood function where $\theta = (p_1, p_2)$ , $X_i \sim \text{Bernoulli}(p_1)$ and $Y_i \sim \text{Bernoulli}(p_2)$ is

$$\mathcal{L}(\theta) = p_1^{\sum_{i=1}^n X_i} (1 - p_1)^{n - \sum_{i=1}^n X_i} p_2^{\sum_{i=1}^m Y_i} (1 - p_2)^{m - \sum_{i=1}^m Y_i}$$

$$\text{with log-likelihood, } \ell(\theta) = \sum_{i=1}^n X_i \log p_1 + \left(n - \sum_{i=1}^n X_i\right) \log(1 - p_1) + \sum_{i=1}^m Y_i \log p_2 + \left(m - \sum_{i=1}^m Y_i\right) \log(1 - p_2)$$

differentiating with respect to  $p_1$  and  $p_2$  to get the MLE,

$$\frac{\partial \ell}{\partial p_1} = \frac{\sum_{i=1}^n X_i}{p_1} - \frac{(n - \sum_{i=1}^n X_i)}{1 - p_1}$$

$$\frac{\partial \ell}{\partial p_2} = \frac{\sum_{i=1}^m Y_i}{p_2} - \frac{(m - \sum_{i=1}^m Y_i)}{1 - p_2}$$

we get  $\hat{p}_1 = \sum X_i/n$  and  $\hat{p}_2 = \sum Y_i/m$  when we solve for the above to be equal to 0. Using the multiparameter delta method, with  $\tau = g(\theta) = p_2 - p_1$ , we have  $\hat{\tau} = \hat{p}_2 - \hat{p}_1$ . We then require  $\Delta \hat{g}$  and  $J_n(\hat{\theta})$  to evaluate  $\hat{\text{se}}(\hat{\tau})$ . It is easy to see that  $\Delta \hat{g} = (-1 \ 1)^T$  and

$$I_n(\theta) = \begin{pmatrix} \mathbb{E}_{p_1} \left( \frac{\sum X_i}{p_1^2} + \frac{(n - \sum X_i)}{(1 - p_1)^2} \right) & 0 \\ 0 & \mathbb{E}_{p_1} \left( \frac{\sum Y_i}{p_2^2} + \frac{(m - \sum Y_i)}{(1 - p_2)^2} \right) \end{pmatrix}$$

$$= \begin{pmatrix} \frac{n}{p_1} + \frac{n}{(1 - p_1)} & 0 \\ 0 & \frac{m}{p_2} + \frac{m}{1 - p_2} \end{pmatrix}$$

$J$

- (b) Using parametric bootstrap, we have MLE of  $p_1$  and  $p_2$  to be  $\hat{p}_1 = 3/5$  and  $\hat{p}_2 = 4/5$  respectively and thus MLE of  $\tau$  to be  $1/5$ . The parametric bootstrap requires sampling from  $X_P \sim \text{Bernoulli}(3/5)$  and  $X_T \sim \text{Bernoulli}(4/5)$ , where the subscripts denote placebo and treatment respectively. Using 1000 simulations, we get a standard error of 0.0895209919516.

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```
import numpy as np
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mle_p1 = 3/5
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mle_p2 = 4/5
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mle_tau = mle_p2 - mle_p1
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n = 100000
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```
se2_boot = 0
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for i in np.arange(n):
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    p1_mean = np.mean(np.random.binomial(1, mle_p1, size = 50))
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    p2_mean = np.mean(np.random.binomial(1, mle_p2, size = 50))
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```
    se2_boot += ((p2_mean - p1_mean) - mle_tau) ** 2
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se_boot = np.sqrt(se2_boot/n)
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print (se_boot)
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A 90% confidence interval will then be  $0.2 \pm 0.148$

(c)

(d)

(e)