PSET 4 (1)

April 24, 2018

1 Homework Problem Set 4

Done by Adam Ilyas 1002010

```
In [1]: import pandas as pd
        import numpy as np

        import scipy.stats as stats
        from scipy.misc import comb
```

1.1 Question 1.

Refer to the spreadsheet for the corneal thickness data of glaucoma patients

```
In [2]: data = pd.read_excel("stats2018_PS4.xlsx")
        data
```

Out[2]:

	Person	Glaucoma	No Glaucoma
0	1	488	484
1	2	478	478
2	3	480	492
3	4	426	444
4	5	440	436
5	6	410	398
6	7	458	464
7	8	460	476

(a) Do the sign test to determine if the corneal thickness differs between an eye affected with glaucoma and an unaffected eye. Use = 0.05.

$h_0 : m = 0$

$h_A : m \neq 0$

```
In [3]: data["difference"] = data["Glaucoma"] - data["No Glaucoma"]
        data
```

Out[3]:

	Person	Glaucoma	No Glaucoma	difference
0	1	488	484	4
1	2	478	478	0

```
2       3       480            492          -12
3       4       426            444          -18
4       5       440            436            4
5       6       410            398           12
6       7       458            464           -6
7       8       460            476          -16
```

```
In [4]: s_plus = len([i for i in data["difference"] if i>0])
        s_minus = len([i for i in data["difference"] if i<0])
        print("s_plus: {}\ns_minus: {}".format(s_plus,s_minus))
```

```
s_plus: 3
s_minus: 4
```

```
In [5]: n = s_plus + s_minus # 7
        alpha = 0.05
        # probability of getting 3 or fewer s plus
        p_plus = sum([comb(n, k)*0.5**n for k in range(0, s_plus+1)]) # sum for case 0, 1, 2,

        def test_hypo(p_value, alpha, h_0):
            if p_value > alpha:
                print("Since p_value ({}) > alpha ({}),\nWe have insufficient evidence to reje
                      .format(p_value, alpha,h_0))
            elif p_value <= alpha:
                print("Since p_value ({}) < alpha ({}),\nWe have insufficient evidence to accep
                      .format(p_value, alpha,h_0))

        test_hypo(p_plus, alpha, "corneal thickness differs")
```

```
Since p_value (0.5) > alpha (0.05),
We have insufficient evidence to reject the hypothesis that corneal thickness differs
```

```
In [6]: # or you can use s_minus as show here
        # probability of getting 4 or more s_minus (4,5,6,7)
        p_minus = sum([comb(n, k)*0.5**n for k in range(s_minus, n+1)]) # sum for case 4, 5, 6

        test_hypo(p_minus, alpha, "corneal thickness differs")
```

```
Since p_value (0.5) > alpha (0.05),
We have insufficient evidence to reject the hypothesis that corneal thickness differs
```

(b) Repeat part (a) using the Wilcoxon signed rank test. Do the two tests always give the same result when applied to the same data?

```
In [7]: data["absolute"] = abs(data["difference"])
        data
```

Out[7]:

	Person	Glaucoma	No Glaucoma	difference	absolute
0	1	488	484	4	4
1	2	478	478	0	0
2	3	480	492	-12	12
3	4	426	444	-18	18
4	5	440	436	4	4
5	6	410	398	12	12
6	7	458	464	-6	6
7	8	460	476	-16	16

In [8]:
```
data["rank"] = data["absolute"].rank()
data
```

Out[8]:

	Person	Glaucoma	No Glaucoma	difference	absolute	rank
0	1	488	484	4	4	2.5
1	2	478	478	0	0	1.0
2	3	480	492	-12	12	5.5
3	4	426	444	-18	18	8.0
4	5	440	436	4	4	2.5
5	6	410	398	12	12	5.5
6	7	458	464	-6	6	4.0
7	8	460	476	-16	16	7.0

In [13]:
```
w_plus = sum([data["rank"].iloc[index] for index in data.index if data["difference"].i
w_plus

w_minus = sum([data["rank"].iloc[index] for index in data.index if data["difference"]
w_minus

print("W+: {}\nW-: {}".format(w_plus, w_minus))
```

```
W+: 10.5
W-: 24.5
```

In [15]:
```
# w_plus follows approx a normal distribution with miu and sigma
N = len(data.index)
miu = N*(N+1)/4
sigma = ( N*(N+1)*(2*N+1)/24 )**0.5
test_statistic_minus = ( w_minus - miu ) / sigma
print("miu: {}\nsigma: {}\ntest-statistic: {}".format(miu,sigma, test_statistic_minus

p_value = 1 - stats.norm.cdf(test_statistic_minus)

test_hypo(p_value, alpha, "corneal thickness differs")
```

```
miu: 18.0
sigma: 7.14142842854285
test-statistic: 0.9101820546182063
```

```
Since p_value (0.1813632532425491) > alpha (0.05),
We have insufficient evidence to reject the hypothesis that corneal thickness differs
```

```
In [16]: # w_minus follows approx a normal distribution with miu and sigma
         N = len(data.index)
         miu = N*(N+1)/4
         sigma = ( N*(N+1)*(2*N+1)/24 )**0.5
         test_statistic = ( w_plus - miu ) / sigma
         print("miu: {}\nsigma: {}\ntest-statistic: {}".format(miu,sigma, test_statistic))

         p_value = stats.norm.cdf(test_statistic)

         test_hypo(p_value, alpha, "corneal thickness differs")
```

```
miu: 18.0
sigma: 7.14142842854285
test-statistic: -1.0502100630210074
Since p_value (0.1468107719644529) > alpha (0.05),
We have insufficient evidence to reject the hypothesis that corneal thickness differs
```

No both test will not always give the same value. For Wilcoxon Signed Rank test, additional assumption of mean == median is made. Thus, it depends on whether the population is symmetric.

1.2 Question 2.

In ANOVA for single factor experiments, define MST = SST/(N 1). Is it possible that MST = MSA + MSE? Fully justify your answer.

We know that Mean Square Total

$$MST = \frac{SST}{N-1}$$

And we know that Mean Square Error

$$MSE = \frac{SSE}{N-k}$$

If MST = MSA + MSE, then we would have:

$$\frac{SST}{N-1} = \frac{SSA}{k-1} + \frac{SSE}{N-k} = \frac{SSA+SSE}{(k-1)-(N-k)}$$

multiply both sides by $(k-1)-(N-K)$ (which is) we get:

$$SSA + \frac{SSA \times (N-k)}{k-1} + SSE + \frac{SSE \times (k-1)}{N-k} = SSA + SSE$$

$$\frac{SSA \times (N-k)}{k-1} + \frac{SSE \times (k-1)}{N-k} = 0$$

Therefore it is not possible for MST = MSA + MSE

	Water salinity at three sites		
	37.54	40.17	39.04
	37.01	40.8	39.21
	36.71	39.76	39.05
	37.03	39.7	38.24
	37.32	40.79	38.53
	37.01	40.44	38.71
	37.03	39.79	38.89
	37.7	39.38	38.66
	37.36		38.51
	36.75		40.08
	37.45		
	38.85		
mean	37.31333	40.10375	38.892
grand mean	38.58367		
SSA	38.80088		

title

1.2.1 Question 3.

Water salinity measurements at three sites are given in the spreadsheet, and an ANOVA table is produced. However, one entry (marked by X) has been accidentally deleted.

```
In [ ]: # from excel
        site1 = [37.54, 37.01, 36.71, 37.03, 37.32, 37.01, 37.03, 37.7, 37.36, 36.75, 37.45] #
        site2 = [40.17, 40.8, 39.76, 39.7, 40.79, 40.44, 39.79, 39.38]
        site3 = [39.04, 39.21, 39.05, 38.24, 38.53, 38.71, 38.89, 38.66, 38.51, 40.08]
```

From excel: P-value (4.00865E-11) <<<< F-crit (3.354130829). Thus there is sufficient evidence to reject the null hypothesis that mean salinity of water of the three sites are the same.

(b) Find X with help from the ANOVA table. (Hint: you can do this using any method you like, but check your answer.)

1.2.2 Question 4.

Refer to the sugar content example given in the spreadsheet. Use the Bonferroni method to determine which shelves have significantly different mean sugar content. Use = 0.05.

```
In [44]: sugar = pd.read_excel("stats2018_PS4.xlsx", sheetname=2, skiprows=1)
         sugar = sugar.set_index("Unnamed: 0")
         sugar

Out[44]:             Shelf 1  Shelf 2  Shelf 3
         Unnamed: 0
         n            20.000   20.000   20.000
         mean          4.800    9.850    6.100
         sd            2.138    1.985    1.865

In [56]: SSE = sum([(sugar[i]["n"]-1)*sugar[i]["sd"]**2 for i in sugar.columns])
         MSE = SSE/ (sum([sugar[i]["n"] for i in sugar.columns]) - 3 )
         print("SSE: {}\nMSE: {}".format(SSE, MSE))
```

```
SSE: 227.800386
MSE: 3.996498
```

$$SSE = \sum_{i=1}^{3}(n_i - 1) \times s_i^2$$

$$MSE = \frac{SSE}{N - K}$$

where N: total size, K: Number of predictors (3)

```
In [59]: def bonferroni_confidence_interval(alpha, k, N, MSE, n1, n2, mean1, mean2):
             m = comb(k,2)
             LHS = abs(mean1 - mean2)
             RHS = stats.t.ppf(1-alpha/(2*m), df=N-k) * MSE**0.5 * (1/n1+1/n2)**0.5
             if LHS > RHS:
                 print("LHS: {} RHS: {} (REJECT)".format(LHS, RHS))
             else:
                 print("LHS: {} RHS: {}".format(LHS,RHS))

         #test function
         bonferroni_confidence_interval(alpha=0.05, k=3, N=60, MSE=MSE, n1=20, n2=20,
                                        mean1=sugar["Shelf 1"]["mean"], mean2=sugar["Shelf 2"]
```

```
LHS: 5.05 RHS: 1.5593867622836817 (REJECT)
```

```
In [64]: m = comb(3,2) # m = k choose 2 where k => number of predictors (3)


         for i in sugar.columns:
             for j in sugar.columns:
                 if i == j:
                     continue
                 else:
                     # perform pairwise
                     print()
                     print(i, j)
                     bonferroni_confidence_interval(alpha=0.05, k=3, N=60, MSE=MSE, n1=20, n2=
                                        mean1=sugar[i]["mean"], mean2=sugar[j]["mean"])
```

```
Shelf 1 Shelf 2
LHS: 5.05 RHS: 1.5593867622836817 (REJECT)

Shelf 1 Shelf 3
LHS: 1.2999999999999998 RHS: 1.5593867622836817
```

		Biological parents' socioeconomic status		
		Mean	High	Low
Adoptive parents'		High	120.5	102.5
socioeconomic status		Low	107.5	90.25

title

```
Shelf 2 Shelf 1
LHS: 5.05 RHS: 1.5593867622836817 (REJECT)

Shelf 2 Shelf 3
LHS: 3.75 RHS: 1.5593867622836817 (REJECT)

Shelf 3 Shelf 1
LHS: 1.2999999999999998 RHS: 1.5593867622836817

Shelf 3 Shelf 2
LHS: 3.75 RHS: 1.5593867622836817 (REJECT)
```

1.2.3 Question 5.

Refer to the spreadsheet 'IQ', which records some adopted children's IQ with the socioeconomic status of their biological parents as well as adoptive parents.

(a) Sketch a line chart for the cell means, and from it comment on whether there is any significant interaction.

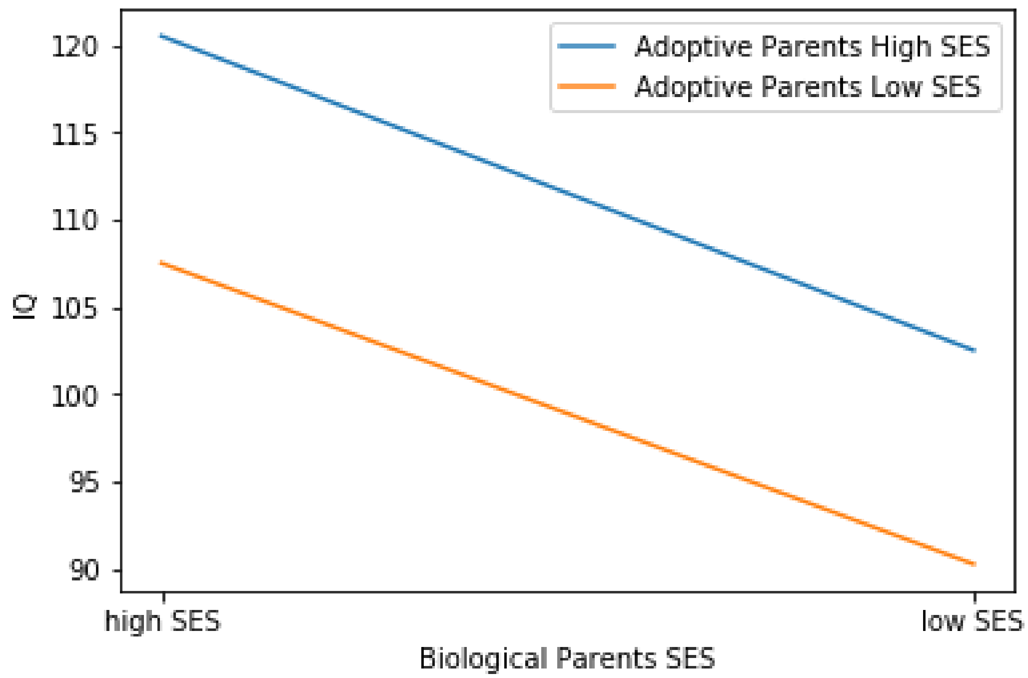
```
In [79]: adoptive_high = [120.5,102.5]
         adoptive_low = [107.5,90.25]

         plt.plot(adoptive_high, label="Adoptive Parents High SES")
         plt.plot(adoptive_low, label = "Adoptive Parents Low SES")
         plt.xlabel("Biological Parents SES")
         plt.ylabel("IQ")
         plt.legend()
         plt.xticks([0,1],["high SES","low SES"])
         plt.show()
```

ANOVA

Source of Variation	*SS*	*df*	*MS*	*F*	*P-value*	*F crit*
Sample	1275.125	1	1275.125	7.68561	0.009786	4.195972
Columns	2485.125	1	2485.125	14.97869	0.000594	4.195972
Interaction	1.125	1	1.125	0.006781	0.934958	4.195972
Within	4645.5	28	165.9107			
Total	8406.875	31				

title



Since lines do not cross, there are no interaction

(b) Construct an ANOVA table for this two-factor experiment. What conclusions can you draw from it?

As the first 2 F statistic are higher than the critical value hence, there is not enough evidence to reject the null hypothesis that:

1) The means of biological high ses and low ses are the same

2) The means of adopted high ses and low ses are the same

However, there is enough evidence to reject hypothesis that:

3) No interaction between adopted and biological.

In conclusion, the affluence of your family (SES) has some correlation with the IQ and However, whether you are adopted or not should not have great influence on your IQ

1.2.4 Question 6.

Suppose x is the number of iid Bernoulli trials with success probability p required to achieve the first success. Show that the MLE of p equals p = 1/x

p(success on 1st try) = p
p(success on 2nd try) = $(1-p)p$
p(success on 3rd try) = $(1-p)^2 p$
p(success on x^{th} try) = $(1-p)^{x-1}p$
Thus, the max likelihood function is defined as:

$$L(p) = (1-p)^{x-1}p$$

$$\ln L(p) = (x-1)\ln(1-p) + \ln p$$

$$\frac{d}{dp}\ln L(p) = (x-1)\frac{-1}{1-p} + \frac{1}{p}$$

To find the minimum, we equate $\frac{d}{dp}$ to 0

$$(x-1)\frac{-1}{1-p} + \frac{1}{p} = 0$$

$$\frac{1}{p} = \frac{x-1}{1-p}$$

$$1-p = (x-1)p$$

$$p = \frac{1}{x}$$

1.2.5 Question 7.

Show that the gamma distribution is a conjugate prior for the Poisson distribution. In particular, suppose that $x_1, ..., x_n$ is a random sample from a Poisson distribution

$$f(x|\theta) = \frac{e^{-\theta}\theta^x}{x!}, \forall\, x = 0, 1, 2, ...$$

and the prior on θ is Gamma(α, β) distribution

$$\pi(\theta) = \frac{1}{\Gamma(\alpha)}\beta^\alpha\theta^{\alpha-1}e^{-\beta\theta}$$

(a) Show that the posterior distribution of θ is Gamma($\alpha + \sum_i x_i, \beta + n$)

$$P(\theta|x) \propto P(x|\theta)P(\theta)$$

$$P(\theta|x) = \prod_{i=0}^{n}(\frac{e^{-\theta}}{x_i!})\frac{1}{\Gamma\alpha}\beta^\alpha\theta^{\alpha-1}e^{-\beta\theta}$$

$$P(\theta|x) \propto (\theta^{\alpha-1}e^{-\beta\theta})\prod_{i=1}^{n}(e^{-\theta}\theta^{x_i})$$

$$P(\theta|x) = e^{-n\theta}\theta\sum_i x_i(\theta^{\alpha-1})(e^{-\beta\theta})$$

$$P(\theta|x) = e^{-(\beta+n)(\theta)}\theta(\alpha-1)+\sum_i x_i$$

$$P(\theta|x) \propto (\beta+n)^{\alpha+\sum_i x_i}(e^{-(\beta+n)\theta})(\theta^{(\alpha-1)+\sum_i x_i})$$

$$= Gamma(\alpha+\sum_{i=0} n,\ \beta+n)$$

(b) Interpret how the posterior mean of θ

$$E(\theta|x_1, ..., x_n) = \frac{\alpha+\sum_i x_i}{\beta+n}$$

depends on n. What happens to this estimate as $n \to \infty$?

as $n \to \infty$

the mean $\to \frac{\sum_i x_i}{n} = \bar{x}$

Thus, it shows that the expected mean of the Poisson Distribution = sample mean as n tends to infinity