MT18049_A4 about:srcdoc

Assignment 4

Question 1

Imports

```
In [1]: import pandas as pd
import matplotlib.pyplot as plt
```

Reading Data

```
In [2]: df = pd.read_table('Data/divorce_raw.raw', sep="\s+", header=None)
    df.set_axis(['id', 'heduc', 'heblack', 'mixed', 'years', 'div'], axis=1, inplace=Tr
    ue)
```

Dataset Description

id: a couple number

heduc: education of the husband - 0 -> less than 12 years, 1 -> 12 to 15 years, 2 -> 16 or more years.

heblack: 1 if the husband is black.

mixed: 1 if husband and wife have different ethnicity, else 0.

years: duration of marriagediv: 1 for divorce; 0 for censoring

For survival analysis, 'heblack' and 'mixed' columns will be dropped.

Three groups are considered, described by the 'heduc' column.

```
In [3]: del df['heblack']; del df['mixed']
```

Rounding years to nearest integer

```
In [4]: df.years = df.years.round()
df = df.astype({'years': int})
```

Removing zero values

```
In [5]: df = df[df.years != 0]
```

Separating data into three groups based on the education of husband

MT18049_A4 about:sredoc

```
In [6]: df0 = df[df['heduc'] == 0]; del df0['heduc']; df0 = df0.sort_values(by=['years']);
    df1 = df[df['heduc'] == 1]; del df1['heduc']; df1 = df1.sort_values(by=['years']);
    df2 = df[df['heduc'] == 2]; del df2['heduc']; df2 = df2.sort_values(by=['years']);
```

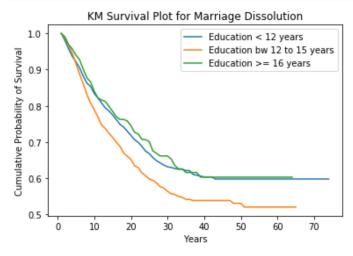
Kaplan-Meier Survival Plot

km df 2 = KMatrix(df2)

```
In [7]: def calcMDC(df, i):
             m = 0; d = 0; c = 0;
             for j, row in df.iterrows():
                 if df.at[j, 'years'] > i:
                     m += 1
                 elif df.at[j, 'years'] == i:
                     m += 1
                     if df.at[j, 'div'] == 1:
                         d += 1
                     else:
                        c += 1
             return m, d, c
In [8]: def calcCP(df):
             cp = [df.iloc[0]];
             for i, d in enumerate(df):
                 if i > 0:
                     cp.append(d*cp[i-1])
             return cp
In [9]: def KMatrix(df):
             max val = df['years'].max()
             columns = ['Year', '#_of_couples_@ y', '#_of_divorces_@ y', '#_of_censored_coup
         les', 'Prob_D', 'Comp_Prob_D']
            km_df = pd.DataFrame(columns=columns)
             for y in range(max val+1):
                 m, d, c = calcMDC(df, y) #M=Married, D=Divorced, C=Censored
                 km_df.loc[y] = [y+1, m, d, c, d/m, 1-(d/m)]
             # Calculate cumulative probability
             cum P = calcCP(km df['Comp Prob D'])
             km_df['C_Prob'] = cum_P
             return km df
In [10]: km df 0 = KMatrix(df0)
         km df 1 = KMatrix(df1)
```

MT18049_A4 about:sredoc

```
In [11]: plt.plot(km_df_0['Year'], km_df_0['C_Prob'])
    plt.plot(km_df_1['Year'], km_df_1['C_Prob'])
    plt.plot(km_df_2['Year'], km_df_2['C_Prob'])
    plt.xlabel("Years")
    plt.ylabel("Cumulative Probability of Survival")
    plt.title("KM Survival Plot for Marriage Dissolution")
    plt.legend(['Education < 12 years', 'Education bw 12 to 15 years', 'Education >= 16
    years'])
    plt.show()
```



Log-rank Test

For this test, only two groups ('Education bw 12 to 15 years' and 'Education >= 16 years') shall be considered.

```
In [12]: def LogRankTest(df1, df2):
                                  cdf = pd.concat([df1, df2], axis=1)
                                  cdf = cdf.assign(TOT RSKS = cdf.N of couples 1 + cdf.N of couples 2)
                                  cdf = cdf.assign(TOT EVNTS = cdf.N of divorces 1 + cdf.N of divorces 2)
                                  cdf = cdf.assign(EXP_EVNTS_1 = cdf.N_of_couples_1*(cdf.TOT_EVNTS/cdf.TOT_RSKS))
                                  cdf = cdf.assign(EXP EVNTS 2 = cdf.N of couples 2*(cdf.TOT EVNTS/cdf.TOT RSKS))
                                  return list(cdf.sum(axis=0, skipna=True))
In [13]: df1 mod = km df 1; df2 mod = km df 2;
                        df1 mod.drop(['Year', '# of censored couples', 'Prob D', 'Comp Prob D', 'C Prob'],
                        axis=1, inplace=True)
                        df1 mod.columns = ['N of couples 1', 'N of divorces 1']
                        df2 mod.drop(['Year', '# of censored couples', 'Prob D', 'Comp Prob D', 'C Prob'],
                        axis=1, inplace=True)
                        df2 mod.columns = ['N of couples 2', 'N of divorces 2']
In [14]: res list = LogRankTest(df1 mod, df2 mod)
                        chi sq = (((res list[1] - res list[6])**2)/res list[6]) + (((res list[3] - res list[6])**2)/res list[6]) + (((res list[6] - res list[6] - re
                        [7])**2)/res list[7])
                        print("Value of Chi-Square: " + str(chi_sq))
                        print("Since value of chi-square is greater than 3.84, null hypthesis is rejected.
                        There is significant evidence that the two survival curves are different.")
                       Value of Chi-Square: 8.446842420406547
                        Since value of chi-square is greater than 3.84, null hypthesis is rejected. Ther
```

3 of 6 08-11-2019, 05:24

e is significant evidence that the two survival curves are different.

MT18049_A4 about:sredoc

Median Survival

From the above graph, median survival (survival probability of 50%) for the groups are:

```
Education < 12 years = 25 years
Education bw 12 and 15 years = 18 years
Education >= 16 years = 30 years
```

Question 2

Imports

```
In [15]: import numpy as np
```

Generate Data

```
In [16]: grp1 = np.random.exponential(5, 100).round()
         grp2 = np.random.exponential(8, 100).round()
In [17]: grp1_mod = [x if x != 0 else 1.0 for x in grp1]
         grp1_mod = list(map(int, grp1_mod))
         grp2_mod = [x if x != 0 else 1.0 for x in grp2]
         grp2_mod = list(map(int, grp2_mod))
In [18]: def censorData(data):
            max val = max(data)
             df = pd.DataFrame(columns=['death_after', 'status']) # death_after -> Death
         after no. of days, status -> 1 - record censored, 0 - not censored
             censor = np.random.choice([0, 1], 100, [0.9, 0.1])
             for d in range(100):
                 df.loc[d] = [data[d], censor[d]]
             return df
In [19]: df1 = censorData(grp1_mod)
         df2 = censorData(grp2_mod)
```

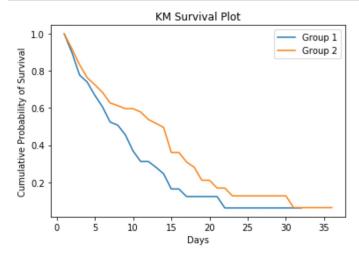
KM Plot

MT18049_A4 about:srcdoc

```
In [21]: def KMChart(df):
    max_val = df['death_after'].max()
    columns = ['day', 'current', 'deaths', 'censored', 'p', 'p_dash']
    km_df = pd.DataFrame(columns=columns)
    for y in range(max_val+1):
        c, d, cn = calcRecord(df, y)
        km_df.loc[y] = [y+1, c, d, cn, d/c, 1-(d/c)]
    # Calculate cumulative probability
    cum_P = calcCP(km_df['p_dash'])
    km_df['P'] = cum_P
    return km_df
```

```
In [22]: km_df_1 = KMChart(df1)
km_df_2 = KMChart(df2)
```

```
In [23]: plt.plot(km_df_1['day'], km_df_1['P'])
    plt.plot(km_df_2['day'], km_df_2['P'])
    plt.xlabel("Days")
    plt.ylabel("Cumulative Probability of Survival")
    plt.title("KM Survival Plot")
    plt.legend(['Group 1', 'Group 2'])
    plt.show()
```



Log-rank Test

MT18049_A4 about:srcdoc

```
In [24]: def LogRankTest2(df1, df2):
                                 cdf = pd.concat([df1, df2], axis=1)
                                  cdf = cdf.assign(TOT RSKS = cdf.current 1 + cdf.current 2)
                                  cdf = cdf.assign(TOT_EVNTS = cdf.deaths_1 + cdf.deaths_2)
                                   cdf = cdf.assign(EXP_EVNTS_1 = cdf.current_1*(cdf.TOT_EVNTS/cdf.TOT_RSKS))
                                   cdf = cdf.assign(EXP EVNTS 2 = cdf.current 2*(cdf.TOT EVNTS/cdf.TOT RSKS))
                                   return list(cdf.sum(axis=0, skipna=True))
In [25]: df1_mod = km_df_1; df2_mod = km_df_2;
                        df1 mod.drop(['day', 'censored', 'p', 'p dash', 'P'], axis=1, inplace=True)
                         df1 mod.columns = ['current 1', 'deaths 1']
                         df2 mod.drop(['day', 'censored', 'p', 'p dash', 'P'], axis=1, inplace=True)
                         df2 mod.columns = ['current 2', 'deaths 2']
In [27]: res_list = LogRankTest2(df1_mod, df2_mod)
                        chi sq = (((res list[1] - res list[6])**2)/res list[6]) + (((res list[3] - res list[6])**2)/res list[6]) + (((res list[6] - res list[6])**2)/res list[6]) + (((res list[6] - res list[6] - re
                         [7]) **2) / res list[7])
                        print("Value of Chi-Square: " + str(chi sq))
                        print("Since value of chi-square is greater than 3.84, null hypthesis is rejected.
                        There is significant evidence that the two survival curves are different.")
                        Value of Chi-Square: 4.035041866257284
                        Since value of chi-square is greater than 3.84, null hypthesis is rejected. Ther
                        e is significant evidence that the two survival curves are different.
```

References

- Dataset Lillard and Panis (2000), aML Multilevel Multiprocess Statistical Software, Release 1.0, EconWare, LA, California.
- 2. Comparing Survival Curves http://sphweb.bumc.bu.edu/otlt/MPH-Modules/BS/BS704_Survival/BS704_Survival5.html)

 (http://sphweb.bumc.bu.edu/otlt/MPH-Modules/BS/BS704_Survival5.html)
- 3. Survival Analysis Tutorial https://www.youtube.com/watch?v=tiCyQp29nwA&list=WL&index=5&t=0s)

 (https://www.youtube.com/watch?v=tiCyQp29nwA&list=WL&index=5&t=0s)