Exercise #3 Survival Analysis Exercise

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Imports

```
In [21]: import pandas as pd
    from lifelines import KaplanMeierFitter
    import matplotlib.pyplot as plt
    from IPython.display import IFrame
    import seaborn as sns
    from lifelines.statistics import logrank_test, multivariate_logrank_test
```

Load and Clean Data

```
Out[22]:
              subject days dead
           0
                         1
                                1
           1
                   В
           2
                   C
                         5
                                0
           3
                         5
                   D
           4
                   Ε
                         7
                                1
           5
                        10
                                0
           6
                   G
                        10
                                0
           7
                        12
           8
                    Τ
                        14
                                1
                        16
                                0
```

```
In [23]: # Second database needed
long_df = pd.read_csv('./data/long_events_data.csv')
#rename group column
```

```
long_df.rename(columns={'Group#':'Group'}, inplace=True)
# Let's Look
long_df.head()
```

Out[23]: Group time event 0 681 0 1 1 602 0 2 996 0 3 1 1162 0 4 833 0

- 1. You are analyzing a 16 day study of patients who have Krusty the Clown disease. Your data includes a subject ID, their survival time and a status. A status of 0 means they are alive while a status of 1 means they died of the disease.
- a. Construct a survival table similar to the one in the lecture for the data. You will show your work within the table if there is some division like 1/5 then show that like 1/5=.2 and if there is some multiplication then show the numbers being multiplied and the result e.g. .1 * 4 = 0.4

```
In [25]: from IPython.display import Image

# Display an image with its filename
Image(filename='./data/surv_an.png')
```

Out[25]: @ RISK Gensord Ad:05 10 B dies Cdrops 9-1 Ddies 5 6 dies 8-1-1 7 F+G 10 Hdies 12 3-1 I Idies 14 1 3 Right 2-1 Consoled

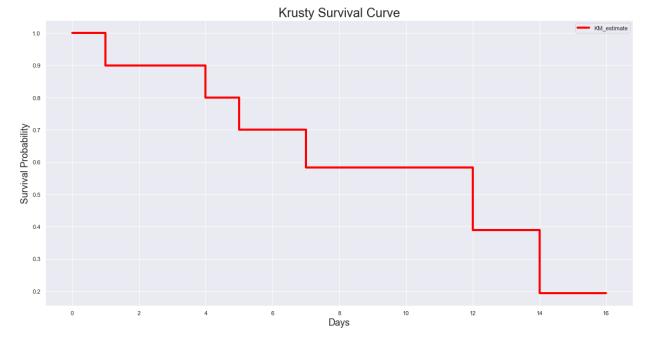
b. Plot a survival curve for the probabilities you generate in part a.

```
In [20]: #this looks better
sns.set(style="darkgrid")
plt.figure(figsize=(20,10))

# Instantiate
kmf = KaplanMeierFitter()

# Fit
kmf.fit(durations=short_df['days'], event_observed=short_df['dead'])

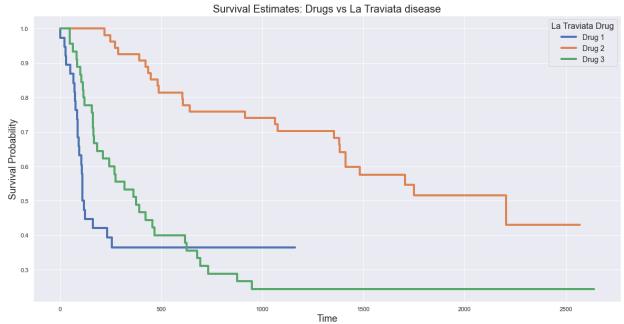
# Plot
kmf.plot_survival_function(ci_show=False, color='red', lw=4)
plt.title('Krusty Survival Curve', fontsize=24)
plt.xlabel('Days', fontsize=18)
plt.ylabel('Survival Probability',fontsize=18)
plt.show();
```



- 2. You are studying three different new drugs that may help slow the progress of La Traviata disease which compels people to sing opera until they exhaust themselves and die. Do the following:
- a. Draw a survival plot that shows the survival curves for all three drugs.

```
In [15]: # make Look nice
   plt.figure(figsize=(20,10))
   sns.set(style="darkgrid")
```

```
#instantiate 3 dif
kmf1 = KaplanMeierFitter()
kmf2 = KaplanMeierFitter()
kmf3 = KaplanMeierFitter()
# split drugs up
group1 = long df[long df['Group'] == 1]
group2 = long_df[long_df['Group'] == 2]
group3 = long_df[long_df['Group'] == 3]
# Fit
kmf1.fit(durations=group1['time'], event_observed=group1['event'])
kmf2.fit(durations=group2['time'], event_observed=group2['event'])
kmf3.fit(durations=group3['time'], event_observed=group3['event'])
# PLot
ax = kmf1.plot survival function(ci show=False, label='Drug 1',lw=4)
kmf2.plot_survival_function(ax=ax, ci_show=False, label='Drug 2',lw=4)
kmf3.plot survival function(ax=ax, ci show=False, label='Drug 3',lw=4)
# Add Legend + Customize
plt.xlabel('Time', fontsize=18)
plt.ylabel('Survival Probability', fontsize=18)
plt.title('Survival Estimates: Drugs vs La Traviata disease', fontsize=20)
plt.legend(title='La Traviata Drug', fontsize=14, title_fontsize=16)
plt.show();
```



b. Test to see if overall there is an effect of any of the drugs on survival taken as a global set.

```
In [18]: # Multivar Logrank
    print('H0: Groups have identical hazard functions')
    result = multivariate_logrank_test(
```

```
event_durations=long_df['time'],
    groups=long_df['Group'],
    event_observed=long_df['event']
)

alpha = .05

print(f'\ntest stat: {result.test_statistic:.3}')
print(f'p val: {result.p_value:.3}')

if result.p_value < alpha:
    print('\nReject H0. Groups DO NOT have identical hazard functions')
else:
    print('Cannot Reject H0')</pre>
H0: Groups have identical hazard functions
```

test stat: 25.7 p val: 2.67e-06

Reject H0. Groups DO NOT have identical hazard functions

c. Compare the survival curves for each of the three drugs with each other (three comparisons) and see if any if the curves are different from each other. Note that you should be sure to adjust for multiple group comparisons.

```
In [19]: # Log-rank test
                                                    print('H0: Groups have identical hazard functions\n')
                                                     compare_1_2 = logrank_test(group1['time'], group2['time'], event_observed_A=group1['event_observed_A=group1['event_observed_A=group1['event_observed_A=group1['event_observed_A=group1['event_observed_A=group1['event_observed_A=group1['event_observed_A=group1['event_observed_A=group1['event_observed_A=group1['event_observed_A=group1]'event_observed_A=group1['event_observed_A=group1]'event_observed_A=group1['event_observed_A=group1]'event_observed_A=group1['event_observed_A=group1]'event_observed_A=group1['event_observed_A=group1]'event_observed_A=group1['event_observed_A=group1]'event_observed_A=group1['event_observed_A=group1]'event_observed_A=group1['event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1['event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_o
                                                     compare_1_3 = logrank_test(group1['time'], group3['time'], event_observed_A=group1['event_observed_A=group1['event_observed_A=group1['event_observed_A=group1['event_observed_A=group1['event_observed_A=group1['event_observed_A=group1['event_observed_A=group1['event_observed_A=group1['event_observed_A=group1['event_observed_A=group1['event_observed_A=group1['event_observed_A=group1]'event_observed_A=group1['event_observed_A=group1['event_observed_A=group1]'event_observed_A=group1['event_observed_A=group1]'event_observed_A=group1['event_observed_A=group1]'event_observed_A=group1['event_observed_A=group1]'event_observed_A=group1['event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_observed_A=group1]'event_o
                                                     compare 2 3 = logrank test(group2['time'], group3['time'], event observed A=group2['ev
                                                     # grab p-values
                                                     p_values = pd.Series([compare_1_2.p_value, compare_1_3.p_value, compare_2_3.p_value],
                                                    # Adjusting for multiple comparison
                                                     p adjusted = p values * 3 # Multiplying by the number of comparisons
                                                     # results
                                                    print("Adjusted p-values for multiple comparisons:\n")
                                                    print(p adjusted)
                                                     print('\nReject H0 in all cases. Each group has a unique hazard function')
                                                   H0: Groups have identical hazard functions
                                                    Adjusted p-values for multiple comparisons:
                                                    1 vs 2 9.824754e-07
                                                    1 vs 3 1.141928e+00
                                                    2 vs 3 1.210205e-04
                                                    dtype: float64
```

Reject H0 in all cases. Each group has a unique hazard function