**EDA ON HABERMAN DATASET** In [2]: import numpy as np # linear algebra import pandas as pd # data processing, CSV file I/O (e.g. pd.read\_csv) import seaborn as sns # data visualization library import matplotlib.pyplot as plt In [3]: data = pd.read\_csv(r"C:\Users\RAVI KUMAR\Desktop\ASSIGNMENTS APPLIED ML\haberman.csv") In [3]: data.head() Out[3]: age year nodes status **0** 30 1 1 30 62 1 **2** 30 65 1 1 31 59 **4** 31 65 1 In [4]: data.tail() Out[4]: age year nodes status **301** 75 0 **302** 76 67 1 77 2 78 65 1 304 In [5]: print(data.shape) (306, 4)In [6]: print(data.columns) Index(['age', 'year', 'nodes', 'status'], dtype='object') There are no missing values in this data set. All the columns are of the integer data type. data.describe() In [13]: Out[13]: nodes status year count 306.000000 306.000000 306.000000 306.000000 62.852941 mean 52.457516 4.026144 1.264706 3.249405 std 10.803452 7.189654 0.441899 30.000000 58.000000 0.000000 1.000000 44.000000 0.000000 1.000000 60.000000 63.000000 52.000000 1.000000 1.000000 2.000000 60.750000 65.750000 4.000000 75% 83.000000 69.000000 52.000000 Patients are of Minimum age 30 and maximum age 83 years. minimum year of operation is 58 and maximum is 69. In [8]: data["status"].value\_counts() Out[8]: 1 225 Name: status, dtype: int64 status 1 means YES (survived) status 2 means NO or Dead :-( **Imbalanced dataset** In [12]: data.plot(kind="scatter", x="year", y="status") plt.show() 1.8 16 14 1.2 1.0 In [21]: sns.set\_style("whitegrid"); sns.FacetGrid(data, hue="status",height=5)\ .map(plt.scatter, "age", "nodes")\ .add\_legend(); plt.show(); 30 Patients with 0 nodes are more likely to survive irrespective of their age. There are hardly any patients who have nodes more than 25. Patients aged more than 50 with nodes more than 10 are less likely to survive. In [17]: sns.set\_style("whitegrid"); sns.pairplot(data, hue="status",height=5); plt.show() 57.5 60.0 62.5 65.0 67.5 70.0 72.5 **Histogram & PDF** In [4]: sns.FacetGrid(data, hue="status", height=6)\ .map(sns.distplot, "age")\ .add\_legend(); plt.show(); 0.040 0.035 0.030 0.025 status 0.020 1 2 0.015 0.010 0.005 100 40 50 60 70 80 There is major overlapping observed. This graph only tells how many of the operations were successful and how many weren't. This cannot be a parameter to decide the patient's survival chances. However, it can be observed that in the years 1960 and 1965 there were more unsuccessful operations. In [5]: sns.FacetGrid(data, hue="status", height=6)\ .map(sns.distplot, "nodes")\ .add\_legend(); plt.show(); 0.5 0.4 0.3 status 1 0.2 0.1 nodes Patients with no nodes or 1 node are more likely to survive. There are very few chances of surviving if there are 25 or more nodes. In [7]: haber\_survived=data.loc[data["status"]==1] haber\_dead=data.loc[data["status"]==2] In [9]: #PDF counts, bin\_edges=np.histogram(haber\_survived["nodes"], bins=10, density=True) pdf=counts/sum(counts) print(pdf) print(bin\_edges) #CDF cdf=np.cumsum(pdf) plt.plot(bin\_edges[1:], pdf) plt.plot(bin\_edges[1:], cdf) plt.xlabel('nodes') plt.show(); [0.83555556 0.08 0.02222222 0.02666667 0.01777778 0.00444444 0.00888889 0. 0. 0.00444444] [ 0. 4.6 9.2 13.8 18.4 23. 27.6 32.2 36.8 41.4 46. ] 1.0 0.8 0.6 0.4 0.2 0.0 10 20 30 nodes 83.55% of the patients who have survived had nodes in the range of 0-Lesser number of nodes does result in more survival rates. In [43]: print("\nSurvived") print("mean :" + str(np.mean(haber\_survived["year"]))) print("median : " + str( np.median(haber\_survived["year"]))) print("standard deviation: " + str( np.std(haber\_survived["year"]))) print("\nDead") print("mean :" + str(np.mean(haber\_dead["year"]))) print("median :" + str(np.median(haber\_dead["year"]))) print("standard deviation: " + str( np.std(haber\_dead["year"]))) Survived mean :62.862222222222 median : 63.0 standard deviation: 3.2157452144021956 Dead mean :62.82716049382716 median :63.0 standard deviation: 3.3214236255207883 mean , medians and standard deviations for age and year are almost same for both the survived and dead patients In [46]: # Mean absolute deviation[MAD] from statsmodels import robust print(robust.mad(haber\_survived["age"])) 13.343419966550417 **Boxplot** In [10]: sns.boxplot(x="status", y="year", data=data) plt.show() sns.boxplot(x="status", y="age", data=data) plt.show() sns.boxplot(x="status", y="nodes", data=data) plt.show() 68 66 62 60 58 status 80 70 60 50 40 30 status 50 40 nodes 30 20 10 status ViolinPlot In [11]: sns.violinplot(x="status", y="year", data=data, height=6) plt.show() sns.violinplot(x="status", y="age", data=data, height=6) sns.violinplot(x="status", y="nodes", data=data, height=6) plt.show() 72.5 70.0 67.5 65.0 62.5 60.0 57.5 55.0 i status 90 80 70 60 50

## 50 40 30 20 10

did not survive.

classes of patients.

In [ ]:

status

status

cannot always guarantee survival.

Patients with more than 1 nodes are not likely to survive.

A large percentage of patients who survived had 0 nodes. Yet there is a small percentage of patients who had no positive axillary nodes died within 5 years of operation, thus an absence of positive axillary nodes

There were comparatively more people who got operated in the year 1965

There were comparatively more people in the age group 45 to 65 who did not survive. Patient age alone is not an important parameter in determining the survival of a patient.

The box plots and violin plots for age and year parameters give similar results with a substantial overlap of data points. The overlap in the box plot and the violin plot of nodes is less compared to other features but the overlap still exists and thus it is difficult to set a mark to classify both

40

30

20

60

-10

**Density plot** In [53]: sns.jointplot(x="year",y="age", data=haber\_survived, kind="kde", height=6) plt.show()

70 60

80 40 30 67.5 55.0 57.5 60.0 70.0 62.5 65.0 From 1960 to 1962, more operations done on the patients in the age group 45 to 55.

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In [ ]:
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