

Day - 18 _____ #100DaysOfML

```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
%matplotlib inline

df = pd.read_csv('Datasets/kag_risk_factors_cervical_cancer.csv')
pd.set_option('display.max_columns', 500)

df.replace('?', np.nan, inplace = True)
df.shape[0]

858

# null percentage
for i in df.columns:
    print( 'Null values in ', i , 'are', df[i].isnull().sum())

Null values in Age are 0
Null values in Number of sexual partners are 26
Null values in First sexual intercourse are 7
Null values in Num of pregnancies are 56
Null values in Smokes are 13
Null values in Smokes (years) are 13
Null values in Smokes (packs/year) are 13
Null values in Hormonal Contraceptives are 108
Null values in Hormonal Contraceptives (years) are 108
Null values in IUD are 117
Null values in IUD (years) are 117
Null values in STDs are 105
Null values in STDs (number) are 105
Null values in STDs:condylomatosis are 105
Null values in STDs:cervical condylomatosis are 105
Null values in STDs:vaginal condylomatosis are 105
Null values in STDs:vulvo-perineal condylomatosis are 105
Null values in STDs:syphilis are 105
Null values in STDs:pelvic inflammatory disease are 105
Null values in STDs:genital herpes are 105
Null values in STDs:molluscum contagiosum are 105
Null values in STDs:AIDS are 105
Null values in STDs:HIV are 105
Null values in STDs:Hepatitis B are 105
Null values in STDs:HPV are 105
Null values in STDs: Number of diagnosis are 0
Null values in STDs: Time since first diagnosis are 787
Null values in STDs: Time since last diagnosis are 787
```

```

Null values in Dx:Cancer are 0
Null values in Dx:CIN are 0
Null values in Dx:HPV are 0
Null values in Dx are 0
Null values in Hinselmann are 0
Null values in Schiller are 0
Null values in Citology are 0
Null values in Biopsy are 0

for i in df.columns:
    print( i , 'Null Percent = ', int(df[i].isnull().sum()/df.shape[0]
*100) )

Age Null Percent = 0
Number of sexual partners Null Percent = 3
First sexual intercourse Null Percent = 0
Num of pregnancies Null Percent = 6
Smokes Null Percent = 1
Smokes (years) Null Percent = 1
Smokes (packs/year) Null Percent = 1
Hormonal Contraceptives Null Percent = 12
Hormonal Contraceptives (years) Null Percent = 12
IUD Null Percent = 13
IUD (years) Null Percent = 13
STDs Null Percent = 12
STDs (number) Null Percent = 12
STDs:condylomatosis Null Percent = 12
STDs:cervical condylomatosis Null Percent = 12
STDs:vaginal condylomatosis Null Percent = 12
STDs:vulvo-perineal condylomatosis Null Percent = 12
STDs:syphilis Null Percent = 12
STDs:pelvic inflammatory disease Null Percent = 12
STDs:genital herpes Null Percent = 12
STDs:molluscum contagiosum Null Percent = 12
STDs:AIDS Null Percent = 12
STDs:HIV Null Percent = 12
STDs:Hepatitis B Null Percent = 12
STDs:HPV Null Percent = 12
STDs: Number of diagnosis Null Percent = 0
STDs: Time since first diagnosis Null Percent = 91
STDs: Time since last diagnosis Null Percent = 91
Dx:Cancer Null Percent = 0
Dx:CIN Null Percent = 0
Dx:HPV Null Percent = 0
Dx Null Percent = 0
Hinselmann Null Percent = 0
Schiller Null Percent = 0
Citology Null Percent = 0
Biopsy Null Percent = 0

```

```

# columns to be dropped
# STDs: Time since first diagnosis Null Percent = 91
# STDs: Time since last diagnosis Null Percent = 91

df.drop(columns= ['STDs: Time since first diagnosis','STDs: Time since
last diagnosis'],inplace = True)

df.info()

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 858 entries, 0 to 857
Data columns (total 34 columns):
#   Column                                     Non-Null Count  Dtype
---  -
0   Age                                       858 non-null    int64
1   Number of sexual partners              832 non-null    object
2   First sexual intercourse                851 non-null    object
3   Num of pregnancies                     802 non-null    object
4   Smokes                                 845 non-null    object
5   Smokes (years)                         845 non-null    object
6   Smokes (packs/year)                    845 non-null    object
7   Hormonal Contraceptives                 750 non-null    object
8   Hormonal Contraceptives (years)         750 non-null    object
9   IUD                                     741 non-null    object
10  IUD (years)                             741 non-null    object
11  STDs                                    753 non-null    object
12  STDs (number)                           753 non-null    object
13  STDs:condylomatosis                     753 non-null    object
14  STDs:cervical condylomatosis             753 non-null    object
15  STDs:vaginal condylomatosis              753 non-null    object
16  STDs:vulvo-perineal condylomatosis       753 non-null    object
17  STDs:syphilis                           753 non-null    object
18  STDs:pelvic inflammatory disease         753 non-null    object
19  STDs:genital herpes                     753 non-null    object
20  STDs:molluscum contagiosum               753 non-null    object
21  STDs:AIDS                               753 non-null    object
22  STDs:HIV                                753 non-null    object
23  STDs:Hepatitis B                         753 non-null    object
24  STDs:HPV                                753 non-null    object
25  STDs: Number of diagnosis                858 non-null    int64
26  Dx:Cancer                               858 non-null    int64
27  Dx:CIN                                   858 non-null    int64
28  Dx:HPV                                   858 non-null    int64
29  Dx                                       858 non-null    int64
30  Hinselmann                              858 non-null    int64
31  Schiller                                858 non-null    int64
32  Citology                                 858 non-null    int64
33  Biopsy                                  858 non-null    int64
dtypes: int64(10), object(24)
memory usage: 228.0+ KB

```

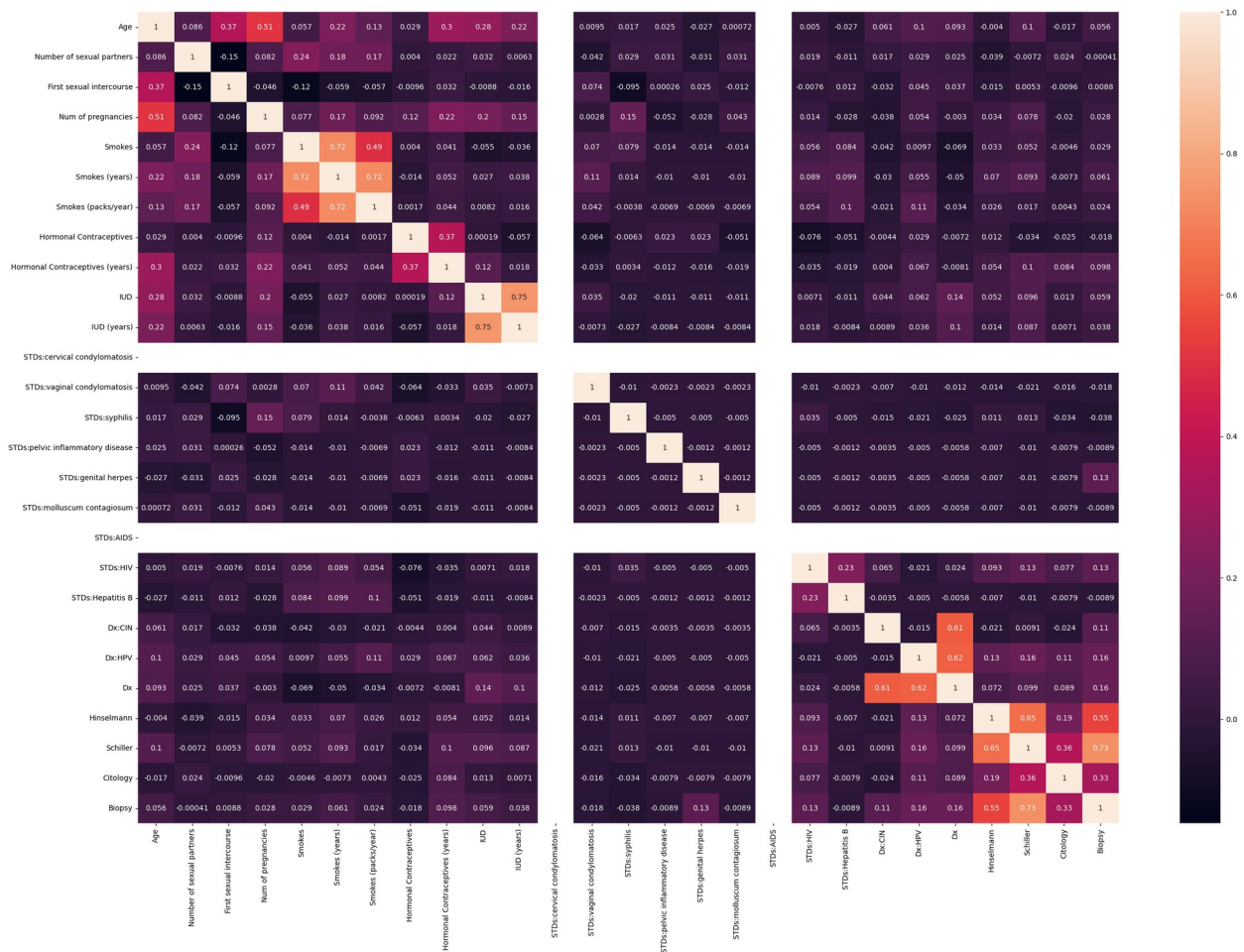
```
df['Age'].mean()

26.82051282051282

for i in df1.columns:
    df1[i] = df1[i].astype(float)

plt.figure(figsize=(30,20))
sns.heatmap(df1.corr(),annot= True)

<Axes: >
```



```
df1.drop(columns= ['STDs:condylomatosis','STDs:vulvo-perineal
condylomatosis','STDs:condylomatosis'],inplace = True)

df1.shape

(858, 27)

df1= df.copy())
```

```

X = df1.drop('Biopsy',axis =1)
y = df1['Biopsy']

from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(X, y,
test_size=0.33, random_state=42)

from sklearn.metrics import accuracy_score

from sklearn.linear_model import LogisticRegression
log_reg = LogisticRegression(max_iter= 1000)

log_reg.fit(X_train_scaled,y_train)

log_reg_pred = log_reg.predict(X_test_scaled)
print(accuracy_score(y_test,log_reg_pred))

0.9577464788732394

from sklearn.tree import DecisionTreeClassifier
clf = DecisionTreeClassifier()
clf.fit(X_train,y_train)
clf_pred = log_reg.predict(X_test)
print(accuracy_score(y_test,clf_pred))

0.9577464788732394

# Scaling
from sklearn.preprocessing import StandardScaler
sc = StandardScaler()
X_train_scaled = sc.fit_transform(X_train)
X_test_scaled = sc.transform(X_test)

from sklearn.svm import SVC
svc = SVC()
svc.fit(X_train_scaled,y_train)
svc_pred = svc.predict(X_test_scaled)
print(accuracy_score(y_test,svc_pred))

final_pred = []
def voting(models, X_test):
    for i in X_test.index:
        ones=0
        zeroes = 0
        input1 = X_test[X_test.index == i].values
        for mod in models:
            out = mod.predict(input1)
            if out == 0:
                zeroes = zeroes+1
            else:
                ones = ones +1
        if(ones > zeroes):

```

```

        final_pred.append(1)
    else:
        final_pred.append(0)
    return final_pred

```

```
voting_out = voting([svc,log_reg,knn,naive],X_test)
```

```
len(voting_out)
```

```
284
```

```
X_train.shape,y_train.shape,X_test.shape,y_test.shape,df1.shape
```

```
((574, 26), (574,), (284, 26), (284,), (858, 27))
```

```
print(accuracy_score(y_test,voting_out))
```

```
0.9366197183098591
```

```
X_test[X_test.index == 713].values.shape
```

```
(1, 26)
```

```
X_test
```

	Age	Number of sexual partners	First sexual intercourse \
713	16.0	1.0	16.0
604	23.0	3.0	17.0
120	33.0	1.0	16.0
208	27.0	4.0	16.0
380	18.0	3.0	15.0
...
422	18.0	2.0	15.0
764	23.0	1.0	15.0
477	38.0	2.0	19.0
41	37.0	2.0	18.0
530	21.0	4.0	15.0

	Num of pregnancies (packs/year) \	Smokes	Smokes (years)	Smokes
713	1.0	0.0	0.0	0.000
604	2.0	0.0	0.0	0.000
120	4.0	0.0	0.0	0.000
208	1.0	0.0	0.0	0.000
380	1.0	1.0	2.0	0.003

..
422	2.0	1.0	0.5	0.050
764	3.0	0.0	0.0	0.000
477	2.0	0.0	0.0	0.000
41	1.0	0.0	0.0	0.000
530	1.0	0.0	0.0	0.000
Hormonal Contraceptives Hormonal Contraceptives (years) IUD \				
713		0.0	0.00	0.0
604		0.0	0.00	0.0
120		0.0	0.00	0.0
208		1.0	0.67	0.0
380		1.0	0.58	0.0
..	
422		1.0	0.33	0.0
764		1.0	0.25	1.0
477		0.0	0.00	0.0
41		0.0	0.00	0.0
530		0.0	0.00	0.0
IUD (years) STDs:cervical condylomatosis STDs:vaginal condylomatosis \				
713	0.0		0.0	
0.0				
604	0.0		0.0	
0.0				
120	0.0		0.0	
0.0				
208	0.0		0.0	
0.0				
380	0.0		0.0	
0.0				
..	
...				
422	0.0		0.0	
0.0				
764	7.0		0.0	
0.0				
477	0.0		0.0	
0.0				
41	0.0		0.0	
0.0				
530	0.0		0.0	
0.0				

STDs:syphilis		STDs:pelvic inflammatory disease		STDs:genital herpes \	
713	0.0			0.0	
0.0					
604	0.0			0.0	
0.0					
120	0.0			0.0	
0.0					
208	0.0			0.0	
0.0					
380	0.0			0.0	
0.0					
..	
...					
422	0.0			0.0	
0.0					
764	0.0			0.0	
0.0					
477	0.0			0.0	
0.0					
41	0.0			0.0	
0.0					
530	0.0			0.0	
0.0					
STDs:molluscum contagiosum		STDs:AIDS	STDs:HIV	STDs:Hepatitis B	
\					
713	0.0	0.0	0.0	0.0	0.0
604	0.0	0.0	0.0	0.0	0.0
120	0.0	0.0	0.0	0.0	0.0
208	0.0	0.0	0.0	0.0	0.0
380	0.0	0.0	0.0	0.0	0.0
..
422	0.0	0.0	0.0	0.0	0.0
764	0.0	0.0	0.0	0.0	0.0
477	0.0	0.0	0.0	0.0	0.0
41	0.0	0.0	1.0	0.0	0.0
530	0.0	0.0	0.0	0.0	0.0

	Dx:CIN	Dx:HPV	Dx	Hinselmann	Schiller	Citology
713	0.0	0.0	0.0	0.0	0.0	0.0
604	0.0	0.0	0.0	0.0	0.0	0.0
120	0.0	0.0	0.0	0.0	0.0	0.0
208	0.0	0.0	0.0	0.0	0.0	0.0
380	0.0	0.0	0.0	0.0	0.0	0.0
..
422	0.0	0.0	0.0	1.0	0.0	0.0
764	0.0	0.0	0.0	0.0	0.0	0.0
477	0.0	0.0	0.0	0.0	0.0	0.0
41	1.0	0.0	1.0	0.0	1.0	0.0
530	0.0	0.0	0.0	0.0	1.0	1.0

[284 rows x 26 columns]

df

	Age	Number of sexual partners	First sexual intercourse	\
0	18		4.0	15.0
1	15		1.0	14.0
2	34		1.0	NaN
3	52		5.0	16.0
4	46		3.0	21.0
..
853	34		3.0	18.0
854	32		2.0	19.0
855	25		2.0	17.0
856	33		2.0	24.0
857	29		2.0	20.0

	Num of pregnancies	Smokes	Smokes (years)	Smokes (packs/year)	\
0		1.0	0.0	0.0	0.0
1		1.0	0.0	0.0	0.0
2		1.0	0.0	0.0	0.0
3		4.0	1.0	37.0	37.0
4		4.0	0.0	0.0	0.0
..	
853		0.0	0.0	0.0	0.0
854		1.0	0.0	0.0	0.0
855		0.0	0.0	0.0	0.0
856		2.0	0.0	0.0	0.0
857		1.0	0.0	0.0	0.0

	Hormonal Contraceptives (years)	Hormonal Contraceptives (years)	IUD	IUD
0		0.0	0.0	0.0
0.0				
1		0.0	0.0	0.0
0.0				
2		0.0	0.0	0.0

0.0			
3	1.0	3.0	0.0
0.0			
4	1.0	15.0	0.0
0.0			
..
...			
853	0.0	0.0	0.0
0.0			
854	1.0	8.0	0.0
0.0			
855	1.0	0.08	0.0
0.0			
856	1.0	0.08	0.0
0.0			
857	1.0	0.5	0.0
0.0			

	STDs	STDs (number)	STDs:condylomatosis	STDs:cervical
condylomatosis \				
0	0.0	0.0	0.0	
0.0				
1	0.0	0.0	0.0	
0.0				
2	0.0	0.0	0.0	
0.0				
3	0.0	0.0	0.0	
0.0				
4	0.0	0.0	0.0	
0.0				
..
.				
853	0.0	0.0	0.0	
0.0				
854	0.0	0.0	0.0	
0.0				
855	0.0	0.0	0.0	
0.0				
856	0.0	0.0	0.0	
0.0				
857	0.0	0.0	0.0	
0.0				

	STDs:vaginal	condylomatosis	STDs:vulvo-perineal	condylomatosis \
0		0.0		0.0
1		0.0		0.0
2		0.0		0.0
3		0.0		0.0
4		0.0		0.0

..
853	0.0	0.0
854	0.0	0.0
855	0.0	0.0
856	0.0	0.0
857	0.0	0.0

	STDs:syphilis	STDs:pelvic inflammatory disease	STDs:genital herpes
\			
0	0.0	0.0	0.0
1	0.0	0.0	0.0
2	0.0	0.0	0.0
3	0.0	0.0	0.0
4	0.0	0.0	0.0
..
853	0.0	0.0	0.0
854	0.0	0.0	0.0
855	0.0	0.0	0.0
856	0.0	0.0	0.0
857	0.0	0.0	0.0

	STDs:molluscum contagiosum	STDs:AIDS	STDs:HIV	STDs:Hepatitis B
STDs:HPV \				
0	0.0	0.0	0.0	0.0
0.0				
1	0.0	0.0	0.0	0.0
0.0				
2	0.0	0.0	0.0	0.0
0.0				
3	0.0	0.0	0.0	0.0
0.0				
4	0.0	0.0	0.0	0.0
0.0				
..
...				
853	0.0	0.0	0.0	0.0
0.0				
854	0.0	0.0	0.0	0.0
0.0				

855	0.0	0.0	0.0	0.0
0.0				
856	0.0	0.0	0.0	0.0
0.0				
857	0.0	0.0	0.0	0.0
0.0				

	STDs: Number of diagnosis	Dx:Cancer	Dx:CIN	Dx:HPV	Dx
Hinselmann \					
0	0	0	0	0	0
0					
1	0	0	0	0	0
0					
2	0	0	0	0	0
0					
3	0	1	0	1	0
0					
4	0	0	0	0	0
0					
..

...					
853	0	0	0	0	0
0					
854	0	0	0	0	0
0					
855	0	0	0	0	0
0					
856	0	0	0	0	0
0					
857	0	0	0	0	0
0					

	Schiller	Citology	Biopsy
0	0	0	0
1	0	0	0
2	0	0	0
3	0	0	0
4	0	0	0
..
853	0	0	0
854	0	0	0
855	0	1	0
856	0	0	0
857	0	0	0

[858 rows x 34 columns]

df[df.index == 9].values

```
array([[44, '3.0', '15.0', nan, '1.0', '1.266972909', '2.8', '0.0',
        '0.0', nan, nan, '0.0', '0.0', '0.0', '0.0', '0.0', '0.0',
        '0.0',
        '0.0', '0.0', '0.0', '0.0', '0.0', '0.0', '0.0', 0, 0, 0, 0,
0,
        0, 0, 0, 0]], dtype=object)
```

```
from sklearn.neighbors import KNeighborsClassifier
knn = KNeighborsClassifier()
knn.fit(X_train_scaled, y_train)
knn_pred = knn.predict(X_test_scaled)
print(accuracy_score(y_test, knn_pred))
# with scaled accurecy 0.9436619718309859
```

```
0.9401408450704225
```

```
from sklearn.naive_bayes import GaussianNB
naive = GaussianNB()
naive.fit(X_train, y_train)
naive_pred = naive.predict(X_test_scaled)
print(accuracy_score(y_test, naive_pred))
```

```
0.9366197183098591
```

```
C:\ProgramData\anaconda3\lib\site-packages\sklearn\base.py:420:
UserWarning: X does not have valid feature names, but GaussianNB was
fitted with feature names
  warnings.warn(
```

```
# voting_out = voting([svc, log_reg, knn, naive], X_test)
```

```
from sklearn.ensemble import RandomForestClassifier
rand_clf = RandomForestClassifier()
```

```
from sklearn.ensemble import RandomForestClassifier, VotingClassifier
eclf1 = VotingClassifier(estimators=[('svc', svc), ('log_reg',
log_reg), ('knn', knn), ('naive', naive), ('random', rand_clf)],
voting='hard')
```

```
eclf1 = eclf1.fit(X_train_scaled, y_train)
```

```
from sklearn.linear_model import LogisticRegression
log_reg = LogisticRegression()
```

```
voting_pred = eclf1.predict(X_test_scaled)
```

```
print(accuracy_score(y_test, voting_pred))
```

```
0.9577464788732394
```