

Classification of using Logistic Regression

In [1]: `pip install ucimlrepo`

Collecting ucimlrepo
 Downloading ucimlrepo-0.0.6-py3-none-any.whl (8.0 kB)
Installing collected packages: ucimlrepo
Successfully installed ucimlrepo-0.0.6

In [4]: *#importing libraries*
`import pandas as pd`
`from sklearn.model_selection import train_test_split`
`from sklearn.linear_model import LogisticRegression`
`from sklearn.preprocessing import StandardScaler`
`from sklearn.metrics import classification_report, confusion_matrix`

In [5]: `from ucimlrepo import fetch_ucirepo`

fetch dataset
`cervical_cancer_risk_factors = fetch_ucirepo(id=383)`

data (as pandas dataframes)
`X = cervical_cancer_risk_factors.data.features`
`y = cervical_cancer_risk_factors.data.targets`

metadata
`print(cervical_cancer_risk_factors.metadata)`

variable information
`print(cervical_cancer_risk_factors.variables)`

```
{'uci_id': 383, 'name': 'Cervical Cancer (Risk Factors)', 'repository_url': 'http
s://archive.ics.uci.edu/dataset/383/cervical+cancer+risk+factors', 'data_url': 'http
s://archive.ics.uci.edu/static/public/383/data.csv', 'abstract': 'This dataset focus
es on the prediction of indicators/diagnosis of cervical cancer. The features cover
demographic information, habits, and historic medical records.', 'area': 'Health and
Medicine', 'tasks': ['Classification'], 'characteristics': ['Multivariate'], 'num_in
stances': 858, 'num_features': 36, 'feature_types': ['Integer', 'Real'], 'demographi
cs': ['Age', 'Other'], 'target_col': None, 'index_col': None, 'has_missing_values':
'yes', 'missing_values_symbol': 'NaN', 'year_of_dataset_creation': 2017, 'last_updat
ed': 'Sun Mar 10 2024', 'dataset_doi': '10.24432/C5Z310', 'creators': ['Kelwin Ferna
ndes', 'Jaime Cardoso', 'Jessica Fernandes'], 'intro_paper': {'title': 'Transfer Lea
rning with Partial Observability Applied to Cervical Cancer Screening', 'authors':
'Kelwin Fernandes, Jaime S. Cardoso, Jessica C. Fernandes', 'published_in': 'Iberian
Conference on Pattern Recognition and Image Analysis', 'year': 2017, 'url': 'http
s://www.semanticscholar.org/paper/Transfer-Learning-with-Partial-Observability-to-F
ernandes-Cardoso/1c02438ba4dfa775399ba414508e9cd335b69012', 'doi': None}, 'additional
_info': {'summary': "The dataset was collected at 'Hospital Universitario de Caraca
s' in Caracas, Venezuela. The dataset comprises demographic information, habits, and
historic medical records of 858 patients. Several patients decided not to answer som
e of the questions because of privacy concerns (missing values).", 'purpose': None,
'funded_by': None, 'instances_represent': None, 'recommended_data_splits': None, 'se
nsitive_data': None, 'preprocessing_description': None, 'variable_info': '(int) Age
\r\n(int) Number of sexual partners\r\n(int) First sexual intercourse (age)\r\n(int)
Num of pregnancies\r\n(bool) Smokes\r\n(bool) Smokes (years)\r\n(bool) Smokes (pack
s/year)\r\n(bool) Hormonal Contraceptives\r\n(int) Hormonal Contraceptives (years)\r
\r\n(bool) IUD\r\n(int) IUD (years)\r\n(bool) STDs\r\n(int) STDs (number)\r\n(bool) ST
Ds:condylomatosis\r\n(bool) STDs:cervical condylomatosis\r\n(bool) STDs:vaginal cond
ylomatosis\r\n(bool) STDs:vulvo-perineal condylomatosis\r\n(bool) STDs:syphilis\r\n
(bool) STDs:pelvic inflammatory disease\r\n(bool) STDs:genital herpes\r\n(bool) STD
s:molluscum contagiosum\r\n(bool) STDs:AIDS\r\n(bool) STDs:HIV\r\n(bool) STDs:Hepati
tis B\r\n(bool) STDs:HPV\r\n(int) STDs: Number of diagnosis\r\n(int) STDs: Time sinc
e first diagnosis\r\n(int) STDs: Time since last diagnosis\r\n(bool) Dx:Cancer\r\n(b
ool) Dx:CIN\r\n(bool) Dx:HPV\r\n(bool) Dx\r\n(bool) Hinselmann: target variable\r\n
(bool) Schiller: target variable\r\n(bool) Cytology: target variable\r\n(bool) Biops
y: target variable', 'citation': None}}
```

	name	role	type	demographic \
0	Age	Feature	Integer	Age
1	Number of sexual partners	Feature	Continuous	Other
2	First sexual intercourse	Feature	Continuous	None
3	Num of pregnancies	Feature	Continuous	None
4	Smokes	Feature	Continuous	None
5	Smokes (years)	Feature	Continuous	None
6	Smokes (packs/year)	Feature	Continuous	None
7	Hormonal Contraceptives	Feature	Continuous	None
8	Hormonal Contraceptives (years)	Feature	Continuous	None
9	IUD	Feature	Continuous	None
10	IUD (years)	Feature	Continuous	None
11	STDs	Feature	Continuous	None
12	STDs (number)	Feature	Continuous	None
13	STDs:condylomatosis	Feature	Continuous	None
14	STDs:cervical condylomatosis	Feature	Continuous	None
15	STDs:vaginal condylomatosis	Feature	Continuous	None
16	STDs:vulvo-perineal condylomatosis	Feature	Continuous	None
17	STDs:syphilis	Feature	Continuous	None
18	STDs:pelvic inflammatory disease	Feature	Continuous	None
19	STDs:genital herpes	Feature	Continuous	None

20	STDs:molluscum contagiosum	Feature	Continuous	None
21	STDs:AIDS	Feature	Continuous	None
22	STDs:HIV	Feature	Continuous	None
23	STDs:Hepatitis B	Feature	Continuous	None
24	STDs:HPV	Feature	Continuous	None
25	STDs: Number of diagnosis	Feature	Integer	None
26	STDs: Time since first diagnosis	Feature	Continuous	None
27	STDs: Time since last diagnosis	Feature	Continuous	None
28	Dx:Cancer	Feature	Integer	None
29	Dx:CIN	Feature	Integer	None
30	Dx:HPV	Feature	Integer	None
31	Dx	Feature	Integer	None
32	Hinselmann	Feature	Integer	None
33	Schiller	Feature	Integer	None
34	Citology	Feature	Integer	None
35	Biopsy	Feature	Integer	None

	description	units	missing_values
0	None	None	no
1	None	None	yes
2	None	None	yes
3	None	None	yes
4	None	None	yes
5	None	None	yes
6	None	None	yes
7	None	None	yes
8	None	None	yes
9	None	None	yes
10	None	None	yes
11	None	None	yes
12	None	None	yes
13	None	None	yes
14	None	None	yes
15	None	None	yes
16	None	None	yes
17	None	None	yes
18	None	None	yes
19	None	None	yes
20	None	None	yes
21	None	None	yes
22	None	None	yes
23	None	None	yes
24	None	None	yes
25	None	None	no
26	None	None	yes
27	None	None	yes
28	None	None	no
29	None	None	no
30	None	None	no
31	None	None	no
32	None	None	no
33	None	None	no
34	None	None	no
35	None	None	no

Data Exploration

In [7]:

X.shape

Out[7]: (858, 36)

In [8]:

X.head()

Out[8]:

	Age	Number of sexual partners	First sexual intercourse	Num of pregnancies	Smokes	Smokes (years)	Smokes (packs/year)	Hormonal Contraceptives
0	18	4.0	15.0	1.0	0.0	0.0	0.0	0.0
1	15	1.0	14.0	1.0	0.0	0.0	0.0	0.0
2	34	1.0	NaN	1.0	0.0	0.0	0.0	0.0
3	52	5.0	16.0	4.0	1.0	37.0	37.0	1.0
4	46	3.0	21.0	4.0	0.0	0.0	0.0	1.0

5 rows × 36 columns

In [9]:

X.describe()

Out[9]:

	Age	Number of sexual partners	First sexual intercourse	Num of pregnancies	Smokes	Smokes (years)	Smol (packs/ye
count	858.000000	832.000000	851.000000	802.000000	845.000000	845.000000	845.0000
mean	26.820513	2.527644	16.995300	2.275561	0.145562	1.219721	0.4531
std	8.497948	1.667760	2.803355	1.447414	0.352876	4.089017	2.2266
min	13.000000	1.000000	10.000000	0.000000	0.000000	0.000000	0.0000
25%	20.000000	2.000000	15.000000	1.000000	0.000000	0.000000	0.0000
50%	25.000000	2.000000	17.000000	2.000000	0.000000	0.000000	0.0000
75%	32.000000	3.000000	18.000000	3.000000	0.000000	0.000000	0.0000
max	84.000000	28.000000	32.000000	11.000000	1.000000	37.000000	37.0000

8 rows × 36 columns

```
In [10]: #checks missing values
X.isnull().sum().sum()
```

```
Out[10]: 3622
```

```
In [11]: #checking categorical values
col_names = X.columns
```

```
In [12]: col_names
```

```
Out[12]: Index(['Age', 'Number of sexual partners', 'First sexual intercourse',
               'Num of pregnancies', 'Smokes', 'Smokes (years)', 'Smokes (packs/year)',
               'Hormonal Contraceptives', 'Hormonal Contraceptives (years)', 'IUD',
               'IUD (years)', 'STDs', 'STDs (number)', 'STDs:condylomatosis',
               'STDs:cervical condylomatosis', 'STDs:vaginal condylomatosis',
               'STDs:vulvo-perineal condylomatosis', 'STDs:syphilis',
               'STDs:pelvic inflammatory disease', 'STDs:genital herpes',
               'STDs:molluscum contagiosum', 'STDs:AIDS', 'STDs:HIV',
               'STDs:Hepatitis B', 'STDs:HPV', 'STDs: Number of diagnosis',
               'STDs: Time since first diagnosis', 'STDs: Time since last diagnosis',
               'Dx:Cancer', 'Dx:CIN', 'Dx:HPV', 'Dx', 'Hinselmann', 'Schiller',
               'Citology', 'Biopsy'],
              dtype='object')
```

```
In [13]: X.dtypes
```

```

Out[13]: Age                                int64
         Number of sexual partners          float64
         First sexual intercourse           float64
         Num of pregnancies                 float64
         Smokes                             float64
         Smokes (years)                    float64
         Smokes (packs/year)               float64
         Hormonal Contraceptives           float64
         Hormonal Contraceptives (years)   float64
         IUD                               float64
         IUD (years)                       float64
         STDs                              float64
         STDs (number)                     float64
         STDs:condylomatosis               float64
         STDs:cervical condylomatosis      float64
         STDs:vaginal condylomatosis       float64
         STDs:vulvo-perineal condylomatosis float64
         STDs:syphilis                     float64
         STDs:pelvic inflammatory disease  float64
         STDs:genital herpes               float64
         STDs:molluscum contagiosum        float64
         STDs:AIDS                         float64
         STDs:HIV                          float64
         STDs:Hepatitis B                  float64
         STDs:HPV                          float64
         STDs: Number of diagnosis         int64
         STDs: Time since first diagnosis  float64
         STDs: Time since last diagnosis   float64
         Dx:Cancer                         int64
         Dx:CIN                            int64
         Dx:HPV                            int64
         Dx                                int64
         Hinselmann                        int64
         Schiller                          int64
         Citology                          int64
         Biopsy                            int64
         dtype: object

```

```
In [15]: categorical_checker = X.select_dtypes(include=['object']).columns.tolist()
```

```

In [16]: if len(categorical_checker) > 0:
          print("Categorical columns:")
          print(categorical_checker)
        else:
          print("No categorical columns found in X.")

```

No categorical columns found in X.

No Categorical Values so Move on to Numerical Variables

Explore Numerical values

```
In [17]: df_X = pd.DataFrame(X)
```

```
In [18]: numerical = [var for var in df_X.columns if df_X[var].dtype != 'object']
```

```
In [19]: print('There are {} numerical variables\n'.format(len(numerical)))  
print('Numerical variables are: ', numerical)
```

There are 36 numerical variables

Numerical variables are: ['Age', 'Number of sexual partners', 'First sexual intercourse', 'Num of pregnancies', 'Smokes', 'Smokes (years)', 'Smokes (packs/year)', 'Hormonal Contraceptives', 'Hormonal Contraceptives (years)', 'IUD', 'IUD (years)', 'STDs', 'STDs (number)', 'STDs:condylomatosis', 'STDs:cervical condylomatosis', 'STDs:vaginal condylomatosis', 'STDs:vulvo-perineal condylomatosis', 'STDs:syphilis', 'STDs:pelvic inflammatory disease', 'STDs:genital herpes', 'STDs:molluscum contagiosum', 'STDs:AIDS', 'STDs:HIV', 'STDs:Hepatitis B', 'STDs:HPV', 'STDs: Number of diagnosis', 'STDs: Time since first diagnosis', 'STDs: Time since last diagnosis', 'Dx:Cancer', 'Dx:CIN', 'Dx:HPV', 'Dx', 'Hinselmann', 'Schiller', 'Citology', 'Biopsy']

Explore Numerical values Problems

Recheck missing values

```
In [20]: df_X[numerical].isnull().sum()
```

```

Out[20]: Age                                0
         Number of sexual partners          26
         First sexual intercourse           7
         Num of pregnancies                 56
         Smokes                             13
         Smokes (years)                    13
         Smokes (packs/year)               13
         Hormonal Contraceptives           108
         Hormonal Contraceptives (years)   108
         IUD                               117
         IUD (years)                       117
         STDs                              105
         STDs (number)                     105
         STDs:condylomatosis               105
         STDs:cervical condylomatosis      105
         STDs:vaginal condylomatosis       105
         STDs:vulvo-perineal condylomatosis 105
         STDs:syphilis                     105
         STDs:pelvic inflammatory disease  105
         STDs:genital herpes               105
         STDs:molluscum contagiosum        105
         STDs:AIDS                         105
         STDs:HIV                          105
         STDs:Hepatitis B                  105
         STDs:HPV                          105
         STDs: Number of diagnosis          0
         STDs: Time since first diagnosis   787
         STDs: Time since last diagnosis    787
         Dx:Cancer                         0
         Dx:CIN                            0
         Dx:HPV                            0
         Dx                                0
         Hinselmann                        0
         Schiller                          0
         Citology                          0
         Biopsy                            0
         dtype: int64

```

```

In [21]: #checking for outliers
         print(round(df_X[numerical].describe()),2)

```


	Age	Number of sexual partners	First sexual intercourse	\	
count	858.0	832.0	851.0		
mean	27.0	3.0	17.0		
std	8.0	2.0	3.0		
min	13.0	1.0	10.0		
25%	20.0	2.0	15.0		
50%	25.0	2.0	17.0		
75%	32.0	3.0	18.0		
max	84.0	28.0	32.0		

	Num of pregnancies	Smokes	Smokes (years)	Smokes (packs/year)	\	
count	802.0	845.0	845.0	845.0		
mean	2.0	0.0	1.0	0.0		
std	1.0	0.0	4.0	2.0		
min	0.0	0.0	0.0	0.0		
25%	1.0	0.0	0.0	0.0		
50%	2.0	0.0	0.0	0.0		
75%	3.0	0.0	0.0	0.0		
max	11.0	1.0	37.0	37.0		

	Hormonal Contraceptives	Hormonal Contraceptives (years)	IUD	\	
count	750.0	750.0	741.0		
mean	1.0	2.0	0.0		
std	0.0	4.0	0.0		
min	0.0	0.0	0.0		
25%	0.0	0.0	0.0		
50%	1.0	0.0	0.0		
75%	1.0	3.0	0.0		
max	1.0	30.0	1.0		

	STDs: Time since first diagnosis	STDs: Time since last diagnosis	\	
count	71.0	71.0		
mean	6.0	6.0		
std	6.0	6.0		
min	1.0	1.0		
25%	2.0	2.0		
50%	4.0	3.0		
75%	8.0	8.0		
max	22.0	22.0		

	Dx:Cancer	Dx:CIN	Dx:HPV	Dx	Hinselmann	Schiller	Citology	\	
count	858.0	858.0	858.0	858.0	858.0	858.0	858.0		
mean	0.0	0.0	0.0	0.0	0.0	0.0	0.0		
std	0.0	0.0	0.0	0.0	0.0	0.0	0.0		
min	0.0	0.0	0.0	0.0	0.0	0.0	0.0		
25%	0.0	0.0	0.0	0.0	0.0	0.0	0.0		
50%	0.0	0.0	0.0	0.0	0.0	0.0	0.0		
75%	0.0	0.0	0.0	0.0	0.0	0.0	0.0		
max	1.0	1.0	1.0	1.0	1.0	1.0	1.0		

	Biopsy
count	858.0
mean	0.0
std	0.0
min	0.0
25%	0.0

50%	0.0
75%	0.0
max	1.0

[8 rows x 36 columns] 2

Check for distribution of variables

```
In [23]: import pandas as pd
import matplotlib.pyplot as plt

numerical_vars = [
    'Age', 'Number of sexual partners', 'First sexual intercourse',
    'Num of pregnancies', 'Smokes (years)', 'Smokes (packs/year)',
    'Hormonal Contraceptives (years)', 'STDs (number)'
]

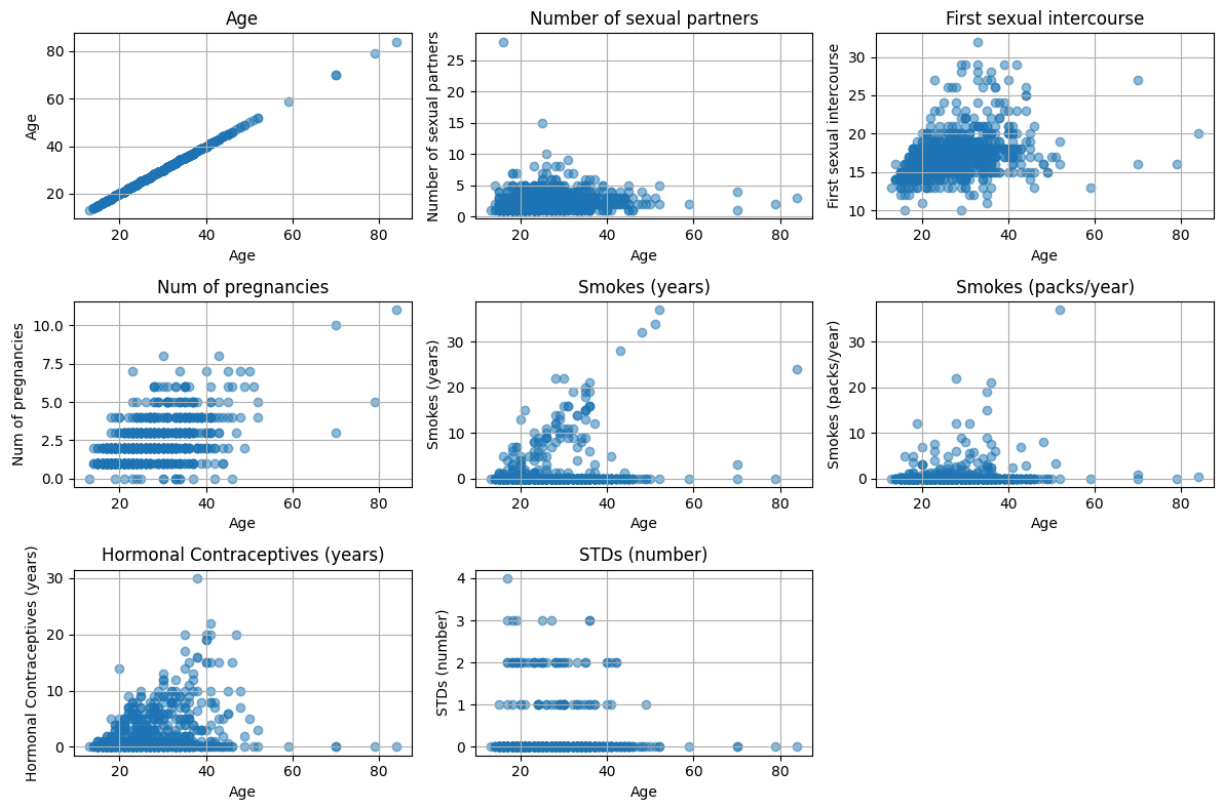
X_G = pd.DataFrame(X, columns=numerical_vars)

plt.figure(figsize=(12, 8))
for i, var in enumerate(numerical_vars, start=1):
    plt.subplot(3, 3, i)

    plt.scatter(df_X['Age'], df_X[var], alpha=0.5)

    plt.title(var)
    plt.xlabel('Age')
    plt.ylabel(var)
    plt.grid(True)

plt.tight_layout()
plt.show()
```



Declare feature vector and target variable

```
In [24]: X = df_X.drop(['Age'], axis = 1)
y = df_X['Age']
```

Split data into separate training and test set

```
In [25]: from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3, random_sta
```

```
In [26]: X_train.shape, X_test.shape
```

```
Out[26]: ((600, 35), (258, 35))
```

Feature Engineering

```
In [27]: X_train.dtypes
```

```

Out[27]: Number of sexual partners      float64
         First sexual intercourse      float64
         Num of pregnancies            float64
         Smokes                        float64
         Smokes (years)                float64
         Smokes (packs/year)           float64
         Hormonal Contraceptives       float64
         Hormonal Contraceptives (years) float64
         IUD                           float64
         IUD (years)                   float64
         STDs                          float64
         STDs (number)                 float64
         STDs:condylomatosis           float64
         STDs:cervical condylomatosis  float64
         STDs:vaginal condylomatosis   float64
         STDs:vulvo-perineal condylomatosis float64
         STDs:syphilis                 float64
         STDs:pelvic inflammatory disease float64
         STDs:genital herpes            float64
         STDs:molluscum contagiosum     float64
         STDs:AIDS                     float64
         STDs:HIV                      float64
         STDs:Hepatitis B              float64
         STDs:HPV                      float64
         STDs: Number of diagnosis      int64
         STDs: Time since first diagnosis float64
         STDs: Time since last diagnosis float64
         Dx:Cancer                     int64
         Dx:CIN                        int64
         Dx:HPV                        int64
         Dx                             int64
         Hinselmann                    int64
         Schiller                       int64
         Citology                       int64
         Biopsy                        int64
         dtype: object

```

```

In [28]: categorical = [col for col in X_train.columns if X_train[col].dtypes == '0']

categorical

```

```

Out[28]: []

```

```

In [29]: numerical = [col for col in X_train.columns if X_train[col].dtypes != '0']

numerical

```

```
Out[29]: ['Number of sexual partners',
          'First sexual intercourse',
          'Num of pregnancies',
          'Smokes',
          'Smokes (years)',
          'Smokes (packs/year)',
          'Hormonal Contraceptives',
          'Hormonal Contraceptives (years)',
          'IUD',
          'IUD (years)',
          'STDs',
          'STDs (number)',
          'STDs:condylomatosis',
          'STDs:cervical condylomatosis',
          'STDs:vaginal condylomatosis',
          'STDs:vulvo-perineal condylomatosis',
          'STDs:syphilis',
          'STDs:pelvic inflammatory disease',
          'STDs:genital herpes',
          'STDs:molluscum contagiosum',
          'STDs:AIDS',
          'STDs:HIV',
          'STDs:Hepatitis B',
          'STDs:HPV',
          'STDs: Number of diagnosis',
          'STDs: Time since first diagnosis',
          'STDs: Time since last diagnosis',
          'Dx:Cancer',
          'Dx:CIN',
          'Dx:HPV',
          'Dx',
          'Hinselmann',
          'Schiller',
          'Citology',
          'Biopsy']
```

```
In [33]: for col in numerical:

          if X_train[col].isnull().mean() > 0:

              missing_percentage = round(X_train[col].isnull().mean() * 100, 2)

              print(f"{col:<30} {missing_percentage:>10}% missing values")
```

Number of sexual partners	3.0% missing values
First sexual intercourse	0.67% missing values
Num of pregnancies	6.0% missing values
Smokes	1.5% missing values
Smokes (years)	1.5% missing values
Smokes (packs/year)	1.5% missing values
Hormonal Contraceptives	11.67% missing values
Hormonal Contraceptives (years)	11.67% missing values
IUD	12.67% missing values
IUD (years)	12.67% missing values
STDs	11.33% missing values
STDs (number)	11.33% missing values
STDs:condylomatosis	11.33% missing values
STDs:cervical condylomatosis	11.33% missing values
STDs:vaginal condylomatosis	11.33% missing values
STDs:vulvo-perineal condylomatosis	11.33% missing values
STDs:syphilis	11.33% missing values
STDs:pelvic inflammatory disease	11.33% missing values
STDs:genital herpes	11.33% missing values
STDs:molluscum contagiosum	11.33% missing values
STDs:AIDS	11.33% missing values
STDs:HIV	11.33% missing values
STDs:Hepatitis B	11.33% missing values
STDs:HPV	11.33% missing values
STDs: Time since first diagnosis	91.5% missing values
STDs: Time since last diagnosis	91.5% missing values

```
In [34]: for df1 in [X_train, X_test]:
         for col in numerical:
             col_median=X_train[col].median()
             df1[col].fillna(col_median, inplace=True)
```

```
In [35]: X_train[numerical].isnull().sum()
```

```

Out[35]: Number of sexual partners      0
         First sexual intercourse      0
         Num of pregnancies            0
         Smokes                        0
         Smokes (years)               0
         Smokes (packs/year)          0
         Hormonal Contraceptives      0
         Hormonal Contraceptives (years) 0
         IUD                          0
         IUD (years)                  0
         STDs                         0
         STDs (number)                0
         STDs:condylomatosis          0
         STDs:cervical condylomatosis 0
         STDs:vaginal condylomatosis  0
         STDs:vulvo-perineal condylomatosis 0
         STDs:syphilis                0
         STDs:pelvic inflammatory disease 0
         STDs:genital herpes          0
         STDs:molluscum contagiosum    0
         STDs:AIDS                    0
         STDs:HIV                     0
         STDs:Hepatitis B             0
         STDs:HPV                     0
         STDs: Number of diagnosis    0
         STDs: Time since first diagnosis 0
         STDs: Time since last diagnosis 0
         Dx:Cancer                    0
         Dx:CIN                       0
         Dx:HPV                       0
         Dx                             0
         Hinselmann                   0
         Schiller                      0
         Citology                      0
         Biopsy                       0
         dtype: int64

```

```

In [36]: X_test[numerical].isnull().sum()

```

```

Out[36]: Number of sexual partners      0
         First sexual intercourse      0
         Num of pregnancies            0
         Smokes                       0
         Smokes (years)               0
         Smokes (packs/year)          0
         Hormonal Contraceptives      0
         Hormonal Contraceptives (years) 0
         IUD                         0
         IUD (years)                 0
         STDs                        0
         STDs (number)               0
         STDs:condylomatosis         0
         STDs:cervical condylomatosis 0
         STDs:vaginal condylomatosis  0
         STDs:vulvo-perineal condylomatosis 0
         STDs:syphilis               0
         STDs:pelvic inflammatory disease 0
         STDs:genital herpes         0
         STDs:molluscum contagiosum   0
         STDs:AIDS                   0
         STDs:HIV                    0
         STDs:Hepatitis B            0
         STDs:HPV                    0
         STDs: Number of diagnosis    0
         STDs: Time since first diagnosis 0
         STDs: Time since last diagnosis 0
         Dx:Cancer                   0
         Dx:CIN                      0
         Dx:HPV                      0
         Dx                           0
         Hinselmann                  0
         Schiller                     0
         Citology                     0
         Biopsy                       0
         dtype: int64

```

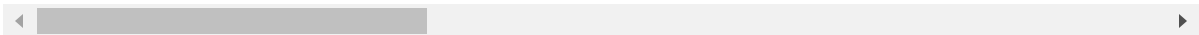
Feature Scaling

```
In [37]: X_train.describe()
```


Out[37]:

	Number of sexual partners	First sexual intercourse	Num of pregnancies	Smokes	Smokes (years)	Smokes (packs/year)	Hor Contract
count	600.000000	600.000000	600.000000	600.000000	600.000000	600.000000	600.000000
mean	2.478333	16.893333	2.276667	0.143333	1.252103	0.484163	0.000000
std	1.362335	2.567023	1.436510	0.350705	4.161544	2.351749	0.000000
min	1.000000	11.000000	0.000000	0.000000	0.000000	0.000000	0.000000
25%	2.000000	15.000000	1.000000	0.000000	0.000000	0.000000	0.000000
50%	2.000000	17.000000	2.000000	0.000000	0.000000	0.000000	1.000000
75%	3.000000	18.000000	3.000000	0.000000	0.000000	0.000000	1.000000
max	10.000000	29.000000	11.000000	1.000000	37.000000	37.000000	1.000000

8 rows × 35 columns



```
In [38]: cols = X_train.columns
```

```
In [39]: from sklearn.preprocessing import MinMaxScaler

scaler = MinMaxScaler()

X_train = scaler.fit_transform(X_train)

X_test = scaler.transform(X_test)
```

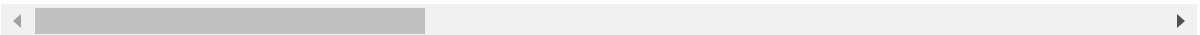
```
In [41]: X_train = pd.DataFrame(X_train, columns=[cols])
X_test = pd.DataFrame(X_test, columns=[cols])
```

```
In [42]: X_train.describe()
```

Out[42]:

	Number of sexual partners	First sexual intercourse	Num of pregnancies	Smokes	Smokes (years)	Smokes (packs/year)	Hor Contract
count	600.000000	600.000000	600.000000	600.000000	600.000000	600.000000	600.000000
mean	0.164259	0.327407	0.206970	0.143333	0.033841	0.013085	0.000000
std	0.151371	0.142612	0.130592	0.350705	0.112474	0.063561	0.000000
min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
25%	0.111111	0.222222	0.090909	0.000000	0.000000	0.000000	0.000000
50%	0.111111	0.333333	0.181818	0.000000	0.000000	0.000000	1.000000
75%	0.222222	0.388889	0.272727	0.000000	0.000000	0.000000	1.000000
max	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000

8 rows × 35 columns



Model training

```
In [43]: from sklearn.linear_model import LogisticRegression

logreg = LogisticRegression(solver='liblinear', random_state = 0)

logreg.fit(X_train, y_train)
```

```
Out[43]: LogisticRegression
LogisticRegression(random_state=0, solver='liblinear')
```

Predict Results

```
In [44]: y_pred_test = logreg.predict(X_test)

y_pred_test
```

```
Out[44]: array([26, 19, 18, 24, 18, 26, 18, 20, 21, 41, 19, 19, 23, 23, 19, 18, 19,
               18, 31, 23, 18, 23, 35, 30, 19, 23, 34, 18, 23, 19, 23, 19, 35, 19,
               19, 28, 19, 36, 19, 19, 18, 21, 21, 19, 26, 18, 19, 23, 26, 34, 26,
               19, 23, 19, 18, 24, 19, 18, 19, 34, 35, 19, 19, 17, 19, 18, 19, 25,
               19, 21, 28, 18, 23, 18, 18, 27, 27, 35, 25, 19, 18, 19, 19, 31, 19,
               24, 21, 18, 24, 19, 24, 18, 19, 19, 19, 19, 19, 18, 27, 19, 19, 24,
               28, 26, 19, 19, 28, 19, 40, 24, 18, 17, 19, 33, 19, 34, 18, 18, 18,
               24, 18, 21, 23, 23, 26, 19, 21, 21, 26, 19, 23, 30, 24, 19, 25, 25,
               34, 19, 25, 19, 18, 18, 19, 25, 18, 18, 34, 19, 19, 18, 19, 18, 18,
               19, 23, 18, 26, 19, 24, 25, 19, 18, 24, 25, 18, 19, 19, 23, 19, 25,
               24, 18, 23, 34, 19, 23, 21, 17, 19, 19, 35, 34, 18, 26, 21, 23, 20,
               30, 19, 18, 18, 19, 30, 19, 24, 20, 18, 21, 19, 20, 30, 19, 19, 18,
               19, 24, 19, 19, 27, 19, 23, 18, 26, 24, 19, 30, 34, 19, 20, 26, 19,
               19, 18, 40, 18, 34, 19, 18, 18, 18, 18, 18, 19, 18, 19, 19, 23, 19,
               19, 18, 27, 18, 18, 34, 35, 23, 19, 19, 25, 30, 27, 26, 23, 35, 21,
               18, 19, 31])
```

```
In [45]: logreg.predict_proba(X_test)[: ,0]
```

```
Out[45]: array([0.00257353, 0.00399272, 0.0100894 , 0.00281407, 0.01054731,
0.00301097, 0.0108993 , 0.00401071, 0.00698407, 0.00197939,
0.0039962 , 0.00376588, 0.00268822, 0.00267909, 0.00377783,
0.01188848, 0.00367413, 0.01062505, 0.00177621, 0.0028448 ,
0.01205777, 0.00314333, 0.00324846, 0.00817091, 0.00369901,
0.0024679 , 0.00931322, 0.01211857, 0.00331648, 0.00371361,
0.00361802, 0.00389594, 0.0022301 , 0.00377806, 0.00389483,
0.00318388, 0.00354974, 0.00183991, 0.00362241, 0.00409199,
0.01109818, 0.00245209, 0.00244971, 0.00423392, 0.00964493,
0.00716898, 0.00379468, 0.00236979, 0.00299913, 0.00338255,
0.00262294, 0.00389388, 0.00312507, 0.00370023, 0.01002922,
0.00371741, 0.00362241, 0.01253573, 0.00198429, 0.00831954,
0.00295478, 0.00375978, 0.00341799, 0.00432336, 0.00379353,
0.00279343, 0.0036232 , 0.00274162, 0.00376753, 0.00160651,
0.00281734, 0.00323203, 0.00193474, 0.01192904, 0.00818507,
0.00668169, 0.00811841, 0.00192768, 0.00302717, 0.00367362,
0.00819972, 0.0039632 , 0.00389597, 0.00193123, 0.00381839,
0.00311583, 0.00375742, 0.01163531, 0.00329315, 0.00386511,
0.00363324, 0.01143476, 0.00375644, 0.00406183, 0.00395334,
0.00390253, 0.00409195, 0.00748637, 0.00843297, 0.00426326,
0.00409819, 0.00375328, 0.00337207, 0.00234114, 0.00356334,
0.00386127, 0.00307698, 0.00368968, 0.00160235, 0.00297859,
0.01211857, 0.00709824, 0.0039921 , 0.00261502, 0.00393049,
0.0032861 , 0.01114771, 0.01020928, 0.01063606, 0.0027868 ,
0.01045774, 0.00260124, 0.00154839, 0.00251186, 0.00281193,
0.00399535, 0.00202947, 0.00297378, 0.0031609 , 0.00374543,
0.00256887, 0.00262858, 0.00367052, 0.00371996, 0.00330418,
0.00326767, 0.00347829, 0.00412538, 0.004063 , 0.00347878,
0.01253573, 0.00442786, 0.00386127, 0.00313026, 0.01119107,
0.01192904, 0.00622656, 0.00358372, 0.00382706, 0.01138947,
0.00347308, 0.00181484, 0.01086708, 0.00352611, 0.00271463,
0.00589394, 0.00303631, 0.00400982, 0.00377865, 0.00272063,
0.00397087, 0.01063495, 0.00172006, 0.00139274, 0.01211857,
0.00385998, 0.00382622, 0.00276962, 0.0036893 , 0.00287509,
0.00331733, 0.01119107, 0.00247816, 0.00901803, 0.00355445,
0.00284556, 0.00247073, 0.00739079, 0.00385014, 0.00405102,
0.00231681, 0.00346085, 0.01061802, 0.00325816, 0.00535199,
0.0032561 , 0.0028696 , 0.00889089, 0.0037197 , 0.01167532,
0.00872058, 0.00421804, 0.00165302, 0.00422237, 0.00341956,
0.00260314, 0.01088185, 0.00252159, 0.00380342, 0.00287363,
0.00905023, 0.00377161, 0.00409195, 0.01129274, 0.00354895,
0.00345177, 0.00340351, 0.00385781, 0.0069115 , 0.0040011 ,
0.00231112, 0.01032239, 0.00325576, 0.00347078, 0.00358387,
0.00215412, 0.00867153, 0.00201578, 0.00284118, 0.00246355,
0.0041833 , 0.00368229, 0.01215939, 0.00494756, 0.00872203,
0.00242668, 0.00394467, 0.01238621, 0.01113286, 0.01167532,
0.00794232, 0.00368802, 0.00405972, 0.01033033, 0.00400732,
0.00340279, 0.00337131, 0.00368989, 0.00371361, 0.01139514,
0.00314854, 0.01113317, 0.00769975, 0.00944234, 0.00343343,
0.00387602, 0.00332257, 0.00363648, 0.00219793, 0.00302444,
0.00816752, 0.00253343, 0.00353349, 0.00291908, 0.00229916,
0.00998748, 0.00366023, 0.00197514])
```

```
In [46]: logreg.predict_proba(X_test)[: ,1]
```

```
Out[46]: array([0.00506526, 0.00831363, 0.01133216, 0.00511732, 0.01312885,
0.00628249, 0.01277106, 0.00327126, 0.00802251, 0.00329502,
0.00829591, 0.00825 , 0.00483418, 0.00475953, 0.00791952,
0.01395741, 0.00801414, 0.01201613, 0.00299856, 0.00505894,
0.01403951, 0.00614599, 0.00282286, 0.00986657, 0.00794252,
0.00459406, 0.01029969, 0.01427534, 0.00676839, 0.00774996,
0.00758795, 0.00774025, 0.0037773 , 0.00760526, 0.00774599,
0.00668483, 0.00712003, 0.0029705 , 0.00762487, 0.00852288,
0.01331499, 0.00428484, 0.00453113, 0.00854162, 0.01016459,
0.00796022, 0.00782504, 0.0042218 , 0.00654752, 0.00648468,
0.00572759, 0.00791082, 0.00541788, 0.00760288, 0.01126262,
0.00730486, 0.00762487, 0.0142366 , 0.00383479, 0.00951155,
0.00610509, 0.00770442, 0.00750834, 0.00407335, 0.00785004,
0.00536282, 0.00761552, 0.00537021, 0.0082452 , 0.00264583,
0.00588868, 0.00588641, 0.00371077, 0.01416907, 0.00874983,
0.00732669, 0.00881835, 0.00324628, 0.00665879, 0.00789032,
0.00875446, 0.00813072, 0.00807307, 0.00363125, 0.00799555,
0.00625326, 0.00712481, 0.01421858, 0.00654085, 0.00790305,
0.00715968, 0.0134906 , 0.00747273, 0.00826188, 0.00791843,
0.00767994, 0.00818425, 0.00812101, 0.00919319, 0.00896873,
0.00816824, 0.00746484, 0.0075591 , 0.00489178, 0.00762601,
0.00792279, 0.00711529, 0.00758282, 0.00251099, 0.00560808,
0.01427534, 0.00730102, 0.00831633, 0.00502763, 0.00790184,
0.00612761, 0.01254777, 0.01338658, 0.01256611, 0.00509296,
0.01328321, 0.00457991, 0.00229808, 0.00464869, 0.00547328,
0.0084214 , 0.00319268, 0.00542808, 0.00620055, 0.00757583,
0.00516929, 0.00498859, 0.00712622, 0.00742809, 0.00681879,
0.0070041 , 0.00649831, 0.00836625, 0.00613904, 0.00754386,
0.0142366 , 0.00407309, 0.00792279, 0.00690929, 0.01274492,
0.01416907, 0.00604704, 0.00736218, 0.00764123, 0.01387179,
0.00749749, 0.0028124 , 0.0131464 , 0.00791689, 0.00492715,
0.00604165, 0.0061462 , 0.007823 , 0.00727651, 0.00595695,
0.00790514, 0.012713 , 0.00285238, 0.00206033, 0.01427534,
0.00792824, 0.00773152, 0.00494495, 0.00803479, 0.00705039,
0.00611255, 0.01274492, 0.00456316, 0.00971078, 0.00721604,
0.00504609, 0.00402121, 0.00742429, 0.00825582, 0.00836756,
0.00436999, 0.006563 , 0.01239852, 0.00664143, 0.00524587,
0.00706436, 0.00521485, 0.01049036, 0.00741639, 0.01323309,
0.00874256, 0.00828443, 0.00275227, 0.00857369, 0.00720588,
0.00529287, 0.01331928, 0.00481397, 0.00774532, 0.00521352,
0.00985906, 0.00803079, 0.00818425, 0.01403381, 0.0075455 ,
0.00677569, 0.00742197, 0.00847059, 0.00748735, 0.00825633,
0.00444617, 0.01254855, 0.00662291, 0.00703836, 0.00736605,
0.00382976, 0.0100292 , 0.00383995, 0.00491749, 0.00503272,
0.00839919, 0.00747692, 0.01449089, 0.00472945, 0.00931414,
0.00480535, 0.00848652, 0.01418315, 0.01293739, 0.01323309,
0.0083658 , 0.00690966, 0.00828643, 0.01164182, 0.00777119,
0.00814893, 0.00689767, 0.00760981, 0.00774996, 0.0132877 ,
0.00619931, 0.01351407, 0.00831133, 0.01051104, 0.00700143,
0.00799463, 0.00783646, 0.00755754, 0.0039613 , 0.00585141,
0.00977211, 0.0047226 , 0.0028935 , 0.00644094, 0.00392189,
0.01181859, 0.00743373, 0.00394042])
```

Check accuracy score

```
In [47]: from sklearn.metrics import accuracy_score

print ('Model accuracy score: {0:0.4f}'.format(accuracy_score(y_test, y_pred_test))
```

Model accuracy score: 0.0543

```
In [48]: y_pred_train = logreg.predict(X_train)

y_pred_train
```

```
Out[48]: array([25, 23, 21, 19, 18, 18, 24, 31, 40, 35, 19, 38, 19, 19, 24, 18, 19,
                28, 34, 18, 34, 18, 23, 18, 19, 18, 19, 23, 35, 35, 21, 19, 26, 19,
                24, 19, 30, 23, 36, 23, 19, 18, 19, 36, 30, 35, 34, 19, 19, 19, 23,
                18, 18, 19, 24, 18, 19, 18, 19, 23, 19, 35, 18, 19, 18, 21, 18, 27,
                19, 18, 35, 30, 18, 18, 40, 19, 30, 24, 24, 23, 18, 23, 23, 19, 19,
                27, 18, 18, 18, 19, 24, 18, 18, 23, 27, 23, 23, 18, 24, 20, 27, 24,
                19, 27, 41, 18, 19, 30, 30, 19, 23, 19, 35, 18, 24, 19, 20, 18, 18,
                24, 23, 18, 19, 30, 18, 19, 27, 19, 19, 17, 19, 21, 19, 25, 19, 37,
                35, 19, 26, 19, 35, 19, 36, 19, 31, 18, 24, 19, 24, 19, 18, 21, 18,
                34, 20, 19, 19, 23, 18, 18, 23, 17, 18, 23, 19, 30, 19, 19, 19, 19,
                27, 27, 23, 18, 18, 24, 23, 23, 19, 19, 24, 18, 23, 35, 19, 18, 18,
                28, 18, 34, 20, 31, 19, 19, 20, 19, 19, 19, 19, 18, 18, 18, 19, 19,
                18, 23, 23, 30, 35, 18, 19, 18, 18, 21, 24, 34, 21, 33, 18, 19, 19,
                19, 19, 30, 26, 18, 24, 18, 18, 18, 37, 35, 25, 35, 18, 24, 19, 18,
                19, 19, 18, 19, 18, 24, 19, 23, 23, 18, 19, 27, 19, 19, 30, 23, 34,
                23, 18, 35, 18, 23, 19, 19, 18, 18, 19, 19, 18, 26, 30, 19, 19, 19,
                26, 18, 18, 23, 20, 28, 24, 34, 23, 19, 27, 19, 19, 19, 33, 38, 18,
                18, 35, 19, 26, 24, 20, 18, 30, 19, 18, 19, 18, 35, 18, 23, 23, 19,
                19, 24, 18, 18, 34, 18, 23, 19, 19, 18, 21, 20, 18, 21, 19, 24, 19,
                19, 19, 19, 35, 18, 35, 18, 19, 18, 35, 23, 35, 19, 19, 41, 24,
                19, 24, 18, 19, 19, 28, 23, 35, 19, 19, 19, 23, 21, 19, 23, 19, 23,
                18, 19, 19, 28, 19, 23, 18, 26, 24, 23, 34, 24, 18, 38, 19, 18, 19,
                35, 18, 30, 18, 34, 24, 18, 24, 19, 18, 28, 19, 19, 23, 24, 23, 23,
                19, 23, 19, 26, 19, 19, 19, 19, 20, 19, 19, 18, 23, 18, 19, 19, 24,
                23, 24, 18, 19, 21, 18, 37, 18, 27, 18, 26, 19, 19, 35, 25, 19, 19,
                30, 19, 18, 27, 35, 19, 19, 19, 35, 18, 19, 23, 28, 36, 19, 18, 18,
                19, 23, 23, 19, 18, 19, 23, 21, 19, 18, 18, 19, 18, 19, 19, 41, 26,
                20, 19, 19, 23, 24, 20, 19, 18, 23, 18, 19, 18, 18, 21, 18, 19, 18,
                18, 41, 23, 19, 25, 20, 18, 18, 24, 18, 18, 18, 19, 23, 18, 19, 19,
                19, 26, 38, 34, 19, 26, 19, 19, 19, 27, 18, 19, 31, 18, 17, 18, 18,
                20, 18, 34, 25, 19, 23, 18, 30, 19, 21, 19, 34, 21, 25, 18, 18, 19,
                18, 23, 26, 19, 19, 30, 18, 19, 19, 38, 18, 28, 19, 34, 30, 19, 35,
                20, 19, 19, 18, 18, 19, 19, 23, 18, 18, 35, 18, 18, 19, 19, 24, 23,
                19, 20, 23, 18, 34, 18, 20, 23, 20, 28, 18, 21, 19, 19, 17, 41, 23,
                19, 23, 24, 19, 27, 18, 27, 19, 18, 18, 19, 19, 24, 23, 19, 18, 26,
                20, 18, 24, 35, 19])
```

```
In [52]: #confusion matrix
from sklearn.metrics import confusion_matrix

cm = confusion_matrix(y_test, y_pred_test)
```

```

print('Confusion matrix\n\n', cm)

print('\nTrue Positives(TP) =', cm[0,0])

print('\nTrue Negatives(TN) =', cm[1,1])

print('\nFalse Positives(FP) =', cm[0,1])

print('\nFalse Negatives(FN) =', cm[1,0])

```

Confusion matrix

```

[[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]]

```

True Positives(TP) = 0

True Negatives(TN) = 0

False Positives(FP) = 0

nFalse Negatives(FN) = 0

```

In [51]: #classification matrix
from sklearn.metrics import classification_report

print(classification_report(y_test, y_pred_test))

```

	precision	recall	f1-score	support
14	0.00	0.00	0.00	2
15	0.00	0.00	0.00	3
16	0.00	0.00	0.00	9
17	0.33	0.08	0.13	12
18	0.04	0.18	0.06	11
19	0.06	0.42	0.11	12
20	0.00	0.00	0.00	12
21	0.17	0.13	0.15	15
22	0.00	0.00	0.00	10
23	0.05	0.06	0.05	17
24	0.07	0.11	0.08	9
25	0.10	0.07	0.08	15
26	0.00	0.00	0.00	12
27	0.00	0.00	0.00	10
28	0.00	0.00	0.00	15
29	0.00	0.00	0.00	17
30	0.00	0.00	0.00	10
31	0.00	0.00	0.00	8
32	0.00	0.00	0.00	4
33	0.00	0.00	0.00	10
34	0.00	0.00	0.00	4
35	0.14	0.14	0.14	7
36	0.00	0.00	0.00	6
37	0.00	0.00	0.00	5
38	0.00	0.00	0.00	4
39	0.00	0.00	0.00	4
40	0.00	0.00	0.00	3
41	0.00	0.00	0.00	3
42	0.00	0.00	0.00	1
44	0.00	0.00	0.00	2
45	0.00	0.00	0.00	3
50	0.00	0.00	0.00	1
51	0.00	0.00	0.00	1
59	0.00	0.00	0.00	1
accuracy			0.05	258
macro avg	0.03	0.04	0.02	258
weighted avg	0.04	0.05	0.04	258


```

/usr/local/lib/python3.10/dist-packages/sklearn/metrics/_classification.py:1344: Und
efinedMetricWarning: Precision and F-score are ill-defined and being set to 0.0 in l
abels with no predicted samples. Use `zero_division` parameter to control this behav
ior.
    _warn_prf(average, modifier, msg_start, len(result))
/usr/local/lib/python3.10/dist-packages/sklearn/metrics/_classification.py:1344: Und
efinedMetricWarning: Precision and F-score are ill-defined and being set to 0.0 in l
abels with no predicted samples. Use `zero_division` parameter to control this behav
ior.
    _warn_prf(average, modifier, msg_start, len(result))
/usr/local/lib/python3.10/dist-packages/sklearn/metrics/_classification.py:1344: Und
efinedMetricWarning: Precision and F-score are ill-defined and being set to 0.0 in l
abels with no predicted samples. Use `zero_division` parameter to control this behav
ior.
    _warn_prf(average, modifier, msg_start, len(result))

```

```

In [53]: TP = cm[0, 0]
        TN = cm[1, 1]
        FP = cm[0, 1]
        FN = cm[1, 0]

        classification_accuracy = (TP + TN) / float(TP + TN + FP + FN)

        print('Classification accuracy: {:.4f}'.format(classification_accuracy))

```

Classification accuracy: nan

```

<ipython-input-53-b5213b263dc3>:6: RuntimeWarning: invalid value encountered in divi
de
    classification_accuracy = (TP + TN) / float(TP + TN + FP + FN)

```

```

In [54]: precision = TP / float(TP + FP)

        print('Precision : {0:0.4f}'.format(precision))

```

Precision : nan

```

<ipython-input-54-de8ba741fd3c>:1: RuntimeWarning: invalid value encountered in divi
de
    precision = TP / float(TP + FP)

```

```

In [55]: recall = TP / float(TP + FN)

        print('Recall or Sensitivity : {0:0.4f}'.format(recall))

```

Recall or Sensitivity : nan

```

<ipython-input-55-4541e477f8ab>:1: RuntimeWarning: invalid value encountered in divi
de
    recall = TP / float(TP + FN)

```

```

In [56]: true_positive_rate = TP / float(TP + FN)

        print('True Positive Rate : {0:0.4f}'.format(true_positive_rate))

```

True Positive Rate : nan

```

<ipython-input-56-934b41082672>:1: RuntimeWarning: invalid value encountered in divi
de
    true_positive_rate = TP / float(TP + FN)

```

```
In [57]: false_positive_rate = FP / float(FP + TN)

print('False Positive Rate : {0:0.4f}'.format(false_positive_rate))
```

False Positive Rate : nan

<ipython-input-57-d365adb81363>:1: RuntimeWarning: invalid value encountered in divide

```
false_positive_rate = FP / float(FP + TN)
```

```
In [58]: specificity = TN / (TN + FP)

print('Specificity : {0:0.4f}'.format(specificity))
```

Specificity : nan

<ipython-input-58-9df300ba775b>:1: RuntimeWarning: invalid value encountered in scalar divide

```
specificity = TN / (TN + FP)
```

Adjusting the threshold level

```
In [59]: y_pred_prob = logreg.predict_proba(X_test)[0:10]

y_pred_prob
```

```
Out[59]: array([[0.00257353, 0.00506526, 0.00894116, 0.00929437, 0.01100428,
0.02189776, 0.03231865, 0.05074597, 0.0318772 , 0.03835678,
0.05979673, 0.05652839, 0.06254897, 0.07750053, 0.05260326,
0.04367154, 0.02192095, 0.04202645, 0.03056631, 0.03577554,
0.05040407, 0.02729505, 0.04597197, 0.0360051 , 0.03070043,
0.00773785, 0.01179163, 0.01762867, 0.01311988, 0.00883457,
0.00602795, 0.01587491, 0.00635549, 0.00436779, 0.00325353,
0.00379094, 0.00353365, 0.00334671, 0.00362875, 0.00272612,
0.00259128],
[0.00399272, 0.00831363, 0.03609807, 0.02620335, 0.02704087,
0.04777543, 0.08182183, 0.04987633, 0.04954438, 0.04200428,
0.05677125, 0.05288797, 0.04746386, 0.04653228, 0.03662504,
0.03719159, 0.02345649, 0.03311216, 0.03239921, 0.02964388,
0.02460153, 0.02989584, 0.02654978, 0.02319232, 0.01613866,
0.00769372, 0.00876181, 0.00878386, 0.01448556, 0.00780414,
0.00860648, 0.00759226, 0.00889237, 0.00615283, 0.0046633 ,
0.0060235 , 0.00560274, 0.00460054, 0.00374098, 0.00397538,
0.0034878 ],
[0.0100894 , 0.01133216, 0.06917836, 0.04244925, 0.04846814,
0.15780828, 0.02361809, 0.0406979 , 0.04458707, 0.01598541,
0.03470736, 0.02791428, 0.05325171, 0.02496876, 0.01948394,
0.01574266, 0.01164744, 0.03532278, 0.01903598, 0.02130706,
0.02795675, 0.01654505, 0.02337171, 0.01317024, 0.01021362,
0.01913197, 0.01075923, 0.0173256 , 0.01043394, 0.01050614,
0.01100065, 0.01235151, 0.0088414 , 0.01243563, 0.01485078,
0.00695096, 0.01003884, 0.00786467, 0.01037726, 0.00991249,
0.00836553],
[0.00281407, 0.00511732, 0.0107005 , 0.00977665, 0.00772834,
0.00906614, 0.01404168, 0.01049944, 0.0187219 , 0.02946667,
0.0519206 , 0.06672986, 0.01548925, 0.02245009, 0.01449478,
0.06488373, 0.02435788, 0.05895656, 0.02901299, 0.03750333,
0.04387679, 0.06610817, 0.0468129 , 0.05456425, 0.03458407,
0.02694158, 0.02047828, 0.03882848, 0.06301454, 0.0140146 ,
0.02559373, 0.00505839, 0.01332178, 0.00573607, 0.0047805 ,
0.01116771, 0.00405674, 0.00596048, 0.00567754, 0.00296886,
0.00272275],
[0.01054731, 0.01312885, 0.02558225, 0.02584192, 0.04901366,
0.06339481, 0.0287722 , 0.04060529, 0.04861127, 0.02531803,
0.0470696 , 0.03358698, 0.03607685, 0.03287692, 0.05027265,
0.02572361, 0.02362664, 0.03158231, 0.02311375, 0.01813953,
0.02466383, 0.03207744, 0.03229352, 0.02612535, 0.02346675,
0.01007846, 0.01659781, 0.0179266 , 0.01700269, 0.01485147,
0.01527205, 0.01748044, 0.01071097, 0.01450441, 0.00835209,
0.00892269, 0.01162729, 0.01034523, 0.01326837, 0.01113003,
0.01041808],
[0.00301097, 0.00628249, 0.01467561, 0.0128878 , 0.01521758,
0.02886378, 0.04804109, 0.04420596, 0.03764325, 0.03666953,
0.05876453, 0.05601355, 0.06101961, 0.06727193, 0.04954531,
0.04632431, 0.02445255, 0.03923192, 0.03494606, 0.03392672,
0.03827367, 0.02986914, 0.0435277 , 0.03178577, 0.02537132,
0.0076255 , 0.01075573, 0.01301053, 0.01420212, 0.00842915,
0.00743243, 0.01158656, 0.00744534, 0.0050201 , 0.00371695,
0.00469437, 0.00435505, 0.00390935, 0.00377208, 0.00320467,
0.0030179 ],
[0.0108993 , 0.01277106, 0.02649481, 0.02995219, 0.04992006,
0.06329829, 0.0253621 , 0.04745813, 0.04782545, 0.02936823,
```

```

0.04891048, 0.0341762 , 0.02960972, 0.02994064, 0.04719404,
0.02321735, 0.02139433, 0.03203769, 0.02066678, 0.01758341,
0.02728984, 0.03226241, 0.02782497, 0.0265793 , 0.02301641,
0.010665 , 0.01676969, 0.02027387, 0.01714669, 0.01504276,
0.01499303, 0.01869575, 0.01074177, 0.01523498, 0.00865332,
0.00895877, 0.0116124 , 0.01026935, 0.01385533, 0.01135745,
0.01067668],
[0.00401071, 0.00327126, 0.00528848, 0.00614952, 0.05378486,
0.14014187, 0.02565009, 0.15199161, 0.06373131, 0.01210715,
0.05115941, 0.01002655, 0.01397046, 0.00669747, 0.00356197,
0.05350392, 0.01951351, 0.01995641, 0.01159611, 0.00232678,
0.04931752, 0.01271681, 0.03766907, 0.01686448, 0.02662826,
0.00943711, 0.00537729, 0.06478945, 0.01140073, 0.02396362,
0.00420892, 0.00449774, 0.00248091, 0.00401404, 0.0090517 ,
0.01364493, 0.00579792, 0.01539647, 0.00770197, 0.00410186,
0.0124997 ],
[0.00698407, 0.00802251, 0.0067231 , 0.02747781, 0.0329448 ,
0.03378263, 0.01925299, 0.02757315, 0.11100597, 0.05219863,
0.017278 , 0.01827968, 0.03317279, 0.01229916, 0.04051347,
0.05073459, 0.01921546, 0.0236776 , 0.00834538, 0.00694485,
0.04629445, 0.03121206, 0.05761897, 0.01050183, 0.05823635,
0.03258692, 0.01788441, 0.03045571, 0.01289743, 0.00779571,
0.00946373, 0.01121243, 0.00654281, 0.00963927, 0.0182577 ,
0.02026957, 0.00770775, 0.02232498, 0.00960439, 0.00792822,
0.01513867],
[0.00197939, 0.00329502, 0.00431781, 0.00446281, 0.00371306,
0.0041456 , 0.00595496, 0.00769956, 0.01118166, 0.02451003,
0.04094198, 0.05554524, 0.0140117 , 0.0180278 , 0.01179027,
0.05600174, 0.02184583, 0.0770507 , 0.02227597, 0.0424647 ,
0.04502056, 0.06415137, 0.06103282, 0.06529298, 0.03424272,
0.03691899, 0.01936133, 0.05971053, 0.09917713, 0.01321761,
0.02144522, 0.00590487, 0.0105633 , 0.00458077, 0.00430564,
0.00823803, 0.00263396, 0.00495322, 0.0042387 , 0.00201476,
0.00177965]]))

```

In this exercise, we used a confusion matrix to evaluate the performance of a classification model. Even though we faced difficulties and had limited time, we learned important lessons. True positives (TP), true negatives (TN), false positives (FP), and false negatives (FN) were all counted in the confusion matrix. To evaluate the efficacy of the model, we computed important metrics such as recall (sensitivity) and classification accuracy. But due to time constraints, certain scheduled tasks—like visualizing the confusion matrix—were not finished. In order to improve predicted accuracy and reliability going forward, more model improvement and modification are advised. The significance of iterative model evaluation and improvement in machine learning is emphasized by this work.