Hands-on Activity 11.2 Classification using Logistic Regression

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Import libraries, dataset and install ucimlrepo package

```
import pandas as pd
import numpy as np
import seaborn as sns
\stackrel{\cdot}{\text{import matplotlib.pyplot as plt}}
import seaborn as sns
%matplotlib inline
from scipy import stats
from sklearn.model_selection import train_test_split
from sklearn.linear_model import LogisticRegression
from sklearn.preprocessing import StandardScaler
from sklearn import metrics
from sklearn.linear_model import LinearRegression
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
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
print(cervical_cancer_risk_factors.metadata)
# variable information
print(cervical_cancer_risk_factors.variables)
            STDs:pelvic inflammatory disease Feature Continuous STDs:genital herpes Feature Continuous STDs:molluscum contagiosum Feature Continuous
                   STDs:AIDS Feature
      21
                                                                   Continuous
                                                                                         None
      22
23
                               STDs:HIV Feature
STDs:Hepatitis B Feature
                                                                   Continuous
                                                                                         None
             STDs: Number of diagnosis Feature Continuous
STDs: Time since first diagnosis Feature Continuous
                                                                                         None
              STDs: Time since last diagnosis Feature Continuous
                                         Dx:Cancer Feature
Dx:CIN Feature
                                                                      Integer
      28
29
30
31
32
33
                                                                       Integer
                                                                                         None
                                             Dx:HPV Feature
Dx Feature
                                                                      Integer
Integer
                                        Hinselmann
Schiller
                                                       Feature
Feature
                                                                      Integer
Integer
                                           Citology Feature
                                                                      Integer
                                                                                         None
                                              Biopsy Feature
                                                                      Integer
          description units missing_values
                  None None
                                              yes
                  None None
                  None None
                  None None
```

Data Wrangling/cleaning & Perform Exploratory Data Analysis

cancer = pd.concat([X,y], axis = 1)

	Age	Number of sexual partners	First sexual intercourse	Num of pregnancies	Smokes	Smokes (years)	Smokes (packs/year)	Hormonal Contraceptives	Hormonal Contraceptives (years)	IUD	•••	di
0	18	4.0	15.0	1.0	0.0	0.0	0.0	0.0	0.00	0.0		
1	15	1.0	14.0	1.0	0.0	0.0	0.0	0.0	0.00	0.0		
2	34	1.0	NaN	1.0	0.0	0.0	0.0	0.0	0.00	0.0		
3	52	5.0	16.0	4.0	1.0	37.0	37.0	1.0	3.00	0.0		
4	46	3.0	21.0	4.0	0.0	0.0	0.0	1.0	15.00	0.0		
853	34	3.0	18.0	0.0	0.0	0.0	0.0	0.0	0.00	0.0		
854	32	2.0	19.0	1.0	0.0	0.0	0.0	1.0	8.00	0.0		
855	25	2.0	17.0	0.0	0.0	0.0	0.0	1.0	0.08	0.0		
856	33	2.0	24.0	2.0	0.0	0.0	0.0	1.0	0.08	0.0		
857	29	2.0	20.0	1.0	0.0	0.0	0.0	1.0	0.50	0.0		•

cancer.head()

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

cancer.tail()

	Age	Number of sexual partners	First sexual intercourse	Num of pregnancies	Smokes	Smokes (years)	Smokes (packs/year)	Hormonal Contraceptives	Hormonal Contraceptives (years)	IUD	 di
853	34	3.0	18.0	0.0	0.0	0.0	0.0	0.0	0.00	0.0	
854	32	2.0	19.0	1.0	0.0	0.0	0.0	1.0	8.00	0.0	
855	25	2.0	17.0	0.0	0.0	0.0	0.0	1.0	0.08	0.0	
856	33	2.0	24.0	2.0	0.0	0.0	0.0	1.0	0.08	0.0	
857	29	2.0	20.0	1.0	0.0	0.0	0.0	1.0	0.50	0.0	 >

cancer.describe(include='all')

	Age	Number of sexual partners	First sexual intercourse	Num of pregnancies	Smokes	Smokes (years)	Smokes (packs/year)	Hormonal Contraceptives	Hormo Contracepti (yea
count	858.000000	832.000000	851.000000	802.000000	845.000000	845.000000	845.000000	750.000000	750.000
mean	26.820513	2.527644	16.995300	2.275561	0.145562	1.219721	0.453144	0.641333	2.256
std	8.497948	1.667760	2.803355	1.447414	0.352876	4.089017	2.226610	0.479929	3.764
min	13.000000	1.000000	10.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000
25%	20.000000	2.000000	15.000000	1.000000	0.000000	0.000000	0.000000	0.000000	0.000
50%	25.000000	2.000000	17.000000	2.000000	0.000000	0.000000	0.000000	1.000000	0.500
75%	32.000000	3.000000	18.000000	3.000000	0.000000	0.000000	0.000000	1.000000	3.000
max	84.000000	28.000000	32.000000	11.000000	1.000000	37.000000	37.000000	1.000000	30.000
8 rows × 36 columns									

cancer.info()

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 858 entries, 0 to 857
Data columns (total 36 columns):
Column
------0 Age
1 Number of sexual partners

Non-Null Count Dtype 858 non-null int64 832 non-null float64

```
First sexual intercourse
                                                      851 non-null
                                                                         float64
           Num of pregnancies
                                                      802 non-null
                                                                         float64
           Smokes
Smokes (years)
                                                      845 non-null
                                                                         float64
float64
                                                      845 non-null
           Smokes (packs/year)
Hormonal Contraceptives
                                                      845 non-null
                                                                         float64
                                                      750 non-null
                                                                         float64
           Hormonal Contraceptives (years)
                                                      750 non-null
                                                                         float64
                                                                         float64
                                                      741 non-null
       10
           IUD (years)
                                                      741 non-null
                                                                         float64
           STDs (number)
      12
                                                      753 non-null
                                                                         float64
                                                      753 non-null
753 non-null
           STDs:condylomatosis
                                                                         float64
           STDs:cervical condvlomatosis
                                                                         float64
           STDs:vaginal condylomatosis
                                                      753 non-null
                                                                         float64
           STDs:syphilis
       16
                                                      753 non-null
                                                                         float64
                                                      753 non-null
                                                                         float64
           STDs:pelvic inflammatory disease
                                                      753 non-null
       18
                                                                         float64
       19
20
           STDs:genital herpes
STDs:molluscum contagiosum
                                                      753 non-null
753 non-null
                                                                         float64
float64
           STDs:AIDS
STDs:HIV
      21
                                                      753 non-null
                                                                         float64
                                                      753 non-null
                                                                         float64
      23
           STDs:Hepatitis B
                                                      753 non-null
                                                                         float64
            STDs:HPV
                                                                         float64
           STDs:HPV
STDs: Number of diagnosis
STDs: Time since first diagnosis
STDs: Time since last diagnosis
      25
                                                      858 non-null
                                                                         int64
                                                      71 non-null
71 non-null
                                                                         float64
       27
                                                                         float64
       29
           Dx:CTN
                                                      858 non-null
                                                                         int64
           Dx:HPV
                                                      858 non-null
858 non-null
                                                                         int64
       31
           Dx
                                                                         int64
                                                      858 non-null
858 non-null
                                                                         int64
int64
           Hinselmann
           Schiller
                                                     858 non-null
858 non-null
                                                                         int64
int64
           Citology
       35
     35 Biopsy
dtypes: float64(26), int64(10)
     memory usage: 241.4 KB
cancer.isna().sum()
      Number of sexual partners
     First sexual intercourse
     Num of pregnancies
Smokes
     Smokes (years)
Smokes (packs/year)
     Hormonal Contraceptives
                                                  108
     Hormonal Contraceptives (years)
     IUD
                                                  117
      IUD (years)
     STDs
STDs (number)
                                                  105
     STDs:condylomatosis
STDs:cervical condylomatosis
                                                  105
      STDs:vaginal condvlomatosis
                                                  105
      STDs:vulvo-perineal condylomatosis
     STDs:pelvic inflammatory disease
STDs:genital herpes
                                                  105
     STDs:molluscum contagiosum
STDs:AIDS
                                                  105
     STDs:HIV
                                                  105
      STDs:Hepatitis B
     STDs:HPV
                                                  105
      STDs: Number of diagnosis
     Dx:Cancer
     Dx:HPV
     Hinselmann
     Schiller
Citology
     Biopsy
dtype: int64
cancer.dropna(subset=['First sexual intercourse','Number of sexual partners',
                     'Smokes (years)'],inplace = True)
def pdf(x):
    mean = np.mean(x)
    print(mean)
    std = np.std(x)
    print(std)
    y_out = 1/(std * np.sqrt(2 * np.pi)) * np.exp( - (x - mean)**2 / (2 * std**2))
    return y_out
coltoint = {'Number of sexual partners': int,
                        'Num of pregnancies' : int}
cancer = cancer.astype(coltoint)
cancer.isna().sum()
     Age
Number of sexual partners
     First sexual intercourse
      Num of pregnancies
     Smokes
     Smokes (years)
     Smokes (packs/year)
Hormonal Contraceptives
Hormonal Contraceptives (years)
      TUD
                                                  101
      IUD (years)
     STDs
STDs (number)
                                                   90
     STDs:condylomatosis
                                                   90
     STDs:cervical condylomatosis
```

```
STDs:vaginal condylomatosis
      STDs:vulvo-perineal condylomatosis
      STDs:syphilis
STDs:pelvic inflammatory disease
      STDs:genital herpes
                                                          90
       STDs:molluscum contagiosum
      STDs · ATDS
                                                          90
       STDs:HIV
       STDs:Hepatitis B
      STDs: Number of diagnosis
       Dx:Cancer
      Dx:CIN
      Dx:HPV
       Hinselmann
      Schiller
       Citology
       Biopsy
      dtype: int64
# removing unnecessary columns for easy access data
'STDs:syphilis','STDs:pelvic inflammatory disease',
                'STDs:genital herpes','STDs:molluscum contagiosum',
'STDs:AIDS','STDs:HIV','STDs:Hepatitis B',
'STDs:HPV', 'First sexual intercourse' ],inplace = True)
      KevError
                                                              Traceback (most recent call last)
      <ipython-input-48-d3fed2252223> in <cell line: 2>()
      1 # removing unnecessary columns for easy access data
----> 2 cancer.drop(columns= ['STDs:condylomatosis', 'STDs:cervical condylomatosis',
3 'STDs:vaginal condylomatosis', 'STDs:vulvo-perineal condylomatosis',
4 'STDs:syphilis','STDs:pelvic inflammatory disease',
                                 'STDs:genital herpes', 'STDs:molluscum contagiosum',
                                                    🗘 3 frames
      \underline{/usr/local/lib/python 3.10/dist-packages/pandas/core/indexes/base.py} \ \ in \ drop(self, \ labels, \ errors)
                           6697
          6698
                           indexer = indexer[~mask]
return self.delete(indexer)
          6700
      KeyError: "['STDs:condylomatosis', 'STDs:cervical condylomatosis', 'STDs:valvo-perineal
condylomatosis', 'STDs:syphilis', 'STDs:pelvic inflammatory disease', 'STDs:genital herpes', 'STDs:molluscum
contagiosum', 'STDs:AIDS', 'STDs:HIV', 'STDs:Hepatitis B', 'STDs:HPV'] not found in axis"
\# because of the column "STDs: Time since first diagnosis" and "STDs: Time since last diagnosis" \# has a great amount of non-null values I will remove these columns
cancer = cancer.drop(columns=['STDs: Time since first diagnosis','STDs: Time since last diagnosis'])
cancer
```

Number First Hormonal Smokes Hormonal Contraceptives IUD ... ST Smokes Age sexual sexual pregnancies (years) (packs/year) Contraceptives intercourse (years) partners 0 18 4.0 0.0 0.0 0.0 0.0 0.00 0.0 15 1.0 1.0 0.0 0.0 0.0 0.0 0.00 0.0 2 34 1.0 1.0 0.0 0.0 0.0 0.0 0.00 0.0 NaN 3 52 5.0 4.0 1.0 37.0 37.0 1.0 3.00 0.0 3.0 0.0 4 46 21.0 4.0 0.0 0.0 1.0 15.00 0.0 853 34 3.0 18.0 0.0 0.0 0.0 0.0 0.00 0.0 0.0 854 32 2.0 19.0 1.0 0.0 0.0 0.0 1.0 8.00 0.0 855 2.0 17.0 0.0 0.0 0.0 0.0 1.0 0.08 0.0 856 33 2.0 24 0 2.0 0.0 0.0 0.0 1.0 0.08 0.0 **857** 29 2.0 20.0 1.0 0.0 0.0 0.0 1.0 0.50 0.0

```
for col in cancer.columns:
   if cancer[col].isna().sum() > 0:
        print(f'{col}\n'
        f'mean: {cancer[col].mean()}\n'
        \verb|f'median:{cancer[col].median()}\| \\
        f'mode: {stats.mode(cancer[col])}\n')
     Hormonal Contracentives
     mean: 0.6459197786998617
     median:1.0
     mode: ModeResult(mode=1.0, count=467)
     mean: 0.11360448807854137
    median:0.0
mode: ModeResult(mode=0.0, count=632)
     STDs
     mean: 0.10359116022099447
     median:0.0
     mode: ModeResult(mode=0.0, count=649)
```

```
# filling nan values into mean and median values
cancer['Num of pregnancies'] = cancer['Num of pregnancies'].fillna(cancer[col].mean())
cancer['IUD (years)'] = cancer['IUD (years)'].fillna(cancer[col].mean())
cancer['IUD'] = cancer['IUD'].fillna(cancer[col].mean())
cancer['STDs (number)'] = cancer['STDs (number)'].fillna(cancer[col].mean())
cancer['STDs'] = cancer['STDs'].fillna(cancer[col].mean())
cancer['Hormonal Contraceptives'] = cancer['Hormonal Contraceptives'].fillna(cancer[col].mean())
cancer['Hormonal Contraceptives (years)'] = cancer['Hormonal Contraceptives (years)'].fillna(cancer[col].median())
correlation_matrix = cancer.corr()
sns.set(style='white')
plt.figure(figsize=(14, 12))
sns.heatmap(correlation_matrix, annot=True, cmap='coolwarm', fmt=".2f")
                                                                                                                                                        1.0
                                 Number of sexual partners
                                      <mark>0.37-</mark>0.15<mark>1.00-</mark>0.040.12-0.050.060.05 0.03-0.02-0.030.00 0.02-0.000.05-0.030.03 0.02-0.01-0.00-0.010.0
                                       <mark>0.50</mark> 0.09-0.04 <mark>1.00</mark> 0.07 0.17 0.09 0.15 0.22 0.18 0.14 0.05 0.01 0.04 0.05 <mark>-</mark>0.07 0.06-0.020.03 0.07 -0.010.0
                   Num of pregnancies
                                                                                                                                                       - 0.8
                                         05 <mark>0.24</mark>-0.12 <mark>0.07 <mark>1.00 0.72 0.49</mark>-0.010.04-0.060.040.11 0.10 0.09-0.01-0.040.01-0.070.02 0.04-0.010.0</mark>
                                      0.22 0.18 0.05 <mark>0.17 0.72 1.00 0.73 -</mark>0.000.05 0.03 0.04 0.07 0.08 0.07 0.06-0.030.06-0.050.04 0.08 -0.010.0
                       Smokes (years)
                                       <mark>0.13 0.17-</mark>0.06 0.09 <mark>0.49 0.73 1.00</mark> 0.01 0.04 0.01 0.02 0.03 0.03 0.03 0.11-0.02 0.11-0.030.02 0.01 0.00 0.0
                                        Hormonal Contraceptives
                                                                                                                                                       - 0.6
       Hormonal Contraceptives (years) 0.30 0.02 0.03 0.22 0.04 0.05 0.04 0.48 1.00 0.10 0.01 -0.00-0.00-0.02 0.06 0.00 0.06-0.01 0.06 0.10 0.08 0.
                                 NUD 0.28 0.03-0.02 0.18 0.060.03 0.01 0.04 0.10 1.00 0.75 0.04 0.05 0.03 0.09 0.05 0.04 0.12 0.05 0.08 0.01 0.0
                                      0.21 0.00-0.03 0.14 0.040.04 0.02 -0.010.01 0.75 1.00 0.01 0.02 0.01 0.08 0.01 0.01 0.08 0.02 0.08 0.01 0.0
                                        - 0.4
                                        .00 0.01 0.0<u>2</u> 0.01 0.10 0.08 0.03 -0.02-0.000.05 0.02 <mark>0.92 1.00 0.89</mark>-0.01-0.01-0.01-0.020.07 0.13 0.07 0.1
                       STDs (number)
                                        .01 0.03-0.000.04 0.09 0.07 0.03-0.02-0.020.03 0.01 <mark>0.91 0.89 1.00-</mark>0.010.01-0.010.00 0.07 0.13 0.06 0.1
            STDs: Number of diagnosis
                                         10 0.02 0.05 0.05 <mark>-0.01 0.06 0.11 0.04 0.06 0.09 0.08 0.01 -0.01-0.01 <mark>1.00</mark>-0.02 <mark>0.88 0.65</mark> 0.14 0.14 0.12 0.17</mark>
                                                                                                                                                       - 0.2
                                         6 0.02-0.03-0.07-0.04-0.03-0.02-0.000.00 0.05 0.01 0.01-0.010.01-0.02<mark>1.00</mark>-0.02<mark>0.62</mark>-0.020.01-0.020
                              Dx:HPV
                                         09 0.03 0.03 0.06 0.01 0.06 0.11 0.04 0.06 0.04 0.01 0.01-0.01-0.01<mark>0.88</mark>-0.02 <mark>1.00 0.60</mark> 0.14 0.14 0.12 0.17
                                        Dχ
                          Hinselmann
                                        0.01-0.040.010.03 0.02 0.04 0.02 0.07 0.06 0.05 0.02 0.04 0.07 0.07 <mark>0.14</mark>-0.02<mark>0.14</mark> 0.08 <mark>1.00 0.64 0.17 0.53</mark>
                                                                                                                                                       - 0.0
                                        0.020.02-0.01-0.01-0.01-0.010.00 0.01 0.08 0.01 0.01 0.06 0.07 0.06 <mark>0.12-</mark>0.02<mark>0.12 0.09 0.17 0.36 1.00</mark>0.32
                             Citology
                                        .05-0.<u>0</u>00.01 0.01 <u>0.</u>02 0.04 0.02 0.05 0.10 0.06 0.04 0.10 0.10 0.09 <mark>0.17</mark> 0.11 0.17 0.17 <mark>0.53</mark> 0.73 <mark>0.32 1.00</mark>
                              Biopsy
                                                                                                                Dx:HPV
                                                                                                       Dx:Cancer
                                                     Num of pregnancies
                                                                            Contraceptives (years)
                                                                                     IUD (years)
                                            mber of sexual partners
                                                sexual intercourse
                                                                   Smokes (packs/year
                                                                       Contraceptives
                                                                                              STDs (
```

Training

```
X = cancer.drop(columns = 'Biopsy')
y = cancer['Biopsy']

X_train, X_test, y_train, y_test = train_test_split(X,y,test_size = 0.3, random_state = 21)
X_train
```

	Age	Number of sexual partners	First sexual intercourse	Num of pregnancies	Smokes	Smokes (years)	Smokes (packs/year)	Hormonal Contraceptives	Hormonal Contraceptives (years)	IUD	 ST
580	17	2	15.0	1	0.0	0.0	0.0	1.0	0.33	0.0	 -
733	31	2	18.0	4	0.0	0.0	0.0	1.0	3.00	0.0	 1
831	40	3	23.0	2	0.0	0.0	0.0	0.0	0.00	0.0	
604	23	3	17.0	2	0.0	0.0	0.0	0.0	0.00	0.0	 -
59	35	3	17.0	4	0.0	0.0	0.0	1.0	7.00	1.0	
126	31	2	19.0	2	0.0	0.0	0.0	0.0	0.00	0.0	 - 1
390	20	2	17.0	1	0.0	0.0	0.0	1.0	0.08	0.0	 - 1
52	36	5	17.0	3	0.0	0.0	0.0	1.0	0.50	0.0	 - 1
813	20	1	17.0	0	0.0	0.0	0.0	1.0	1.00	0.0	 -
218	28	3	17.0	4	0.0	0.0	0.0	1.0	1.00	0.0	 -
4											>

X_test

	Age	Number of sexual partners	First sexual intercourse	Num of pregnancies	Smokes	Smokes (years)	Smokes (packs/year)	Hormonal Contraceptives	Hormonal Contraceptives (years)	IUD	
69	35	5	23.0	2	0.0	0.0	0.00	1.000000	0.33	0.000000	-
701	29	2	17.0	0	0.0	0.0	0.00	0.065111	0.00	0.065111	
538	24	3	18.0	2	0.0	0.0	0.00	1.000000	0.16	0.000000	
676	70	4	27.0	3	1.0	3.0	0.75	0.000000	0.00	0.000000	
448	17	3	16.0	1	0.0	0.0	0.00	1.000000	0.25	0.000000	
406	17	1	17.0	1	0.0	0.0	0.00	0.000000	0.00	0.000000	
429	18	1	15.0	2	0.0	0.0	0.00	1.000000	0.08	0.000000	
455	18	1	16.0	2	0.0	0.0	0.00	0.000000	0.00	0.000000	
486	28	2	20.0	2	0.0	0.0	0.00	1.000000	1.00	0.000000	
183	28	2	18.0	3	0.0	0.0	0.00	0.000000	0.00	0.000000	
4											>

```
y_train

580 0
733 0
831 0
604 0
59 0
...
126 0
390 0
52 0
813 0
218 0
Name: Biopsy, Length: 569, dtype: int64
```

y_test

Linear Regression

model = LinearRegression()

model.fit(X_train, y_train)

* LinearRegression
LinearRegression()

Logistic Regression

model.predict(X_test)

model.score(X_train, y_train)

0.9384885764499121

model.score(X_test, y_test)

0.9346938775510204