

De_Guzman_Hands_on_Activity_11_2_Classification_using_Logistic_Reg

April 28, 2024

1 Hands-on Activity 11.2 Classification using Logistic Regression

1.1 Objective(s):

- This activity aims to demonstrate how to apply simple linear regression analysis to solve regression problem

1.2 Intended Learning Outcomes (ILOs):

- Demonstrate how to solve classification problems using Logistic Regression
- Use the logistic regression model to perform classification

1.3 Resources:

- Jupyter Notebook

1.4 Dataset:

- <https://archive.ics.uci.edu/ml/datasets/Cervical+cancer+%28Risk+Factors%29>

1.5 Submission Requirements:

- PDF containing initial EDA and Data Wrangling
- PDF showing demonstration of simple linear regression.
- Submit a link to the colab file through the comment section.

1.6 Procedure:

1.6.1 Setup

```
[1]: import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
from scipy import stats

%matplotlib inline
```

```
[2]: import warnings
warnings.filterwarnings('ignore')
```

```
[3]: !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
```

```
[4]: from ucimlrepo import fetch_ucirepo

# fetch dataset
cervical_cancer_risk_factors = fetch_ucirepo(id=383)

# data (as pandas dataframes)
ccrf_df = cervical_cancer_risk_factors.data.features

# 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':
'https://archive.ics.uci.edu/dataset/383/cervical+cancer+risk+factors',
'data_url': 'https://archive.ics.uci.edu/static/public/383/data.csv',
'abstract': 'This dataset focuses 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_instances': 858,
'num_features': 36, 'feature_types': ['Integer', 'Real'], 'demographics':
['Age', 'Other'], 'target_col': None, 'index_col': None, 'has_missing_values':
'yes', 'missing_values_symbol': 'NaN', 'year_of_dataset_creation': 2017,
'last_updated': 'Sun Mar 10 2024', 'dataset_doi': '10.24432/C5Z310', 'creators':
['Kelwin Fernandes', 'Jaime Cardoso', 'Jessica Fernandes'], 'intro_paper':
{'title': 'Transfer Learning 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': 'https://www.semanticscholar.org/paper/Transfer-
Learning-with-Partial-Observability-to-Fernandes-
Cardoso/1c02438ba4dfa775399ba414508e9cd335b69012', 'doi': None},
'additional_info': {'summary': "The dataset was collected at 'Hospital
Universitario de Caracas' in Caracas, Venezuela. The dataset comprises
demographic information, habits, and historic medical records of 858 patients.
Several patients decided not to answer some of the questions because of privacy
concerns (missing values).", 'purpose': None, 'funded_by': None,
'instances_represent': None, 'recommended_data_splits': None, 'sensitive_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
(packs/year)\r\n(bool) Hormonal Contraceptives\r\n(int) Hormonal Contraceptives
(years)\r\n(bool) IUD\r\n(int) IUD (years)\r\n(bool) STDs\r\n(int) STDs
(number)\r\n(bool) STDs:condylomatosi\r\n(bool) STDs:cervical
condylomatosi\r\n(bool) STDs:vaginal condylomatosi\r\n(bool) STDs:vulvo-
perineal condylomatosi\r\n(bool) STDs:syphilis\r\n(bool) STDs:pelvic
inflammatory disease\r\n(bool) STDs:genital herpes\r\n(bool) STDs:molluscum
contagiosum\r\n(bool) STDs:AIDS\r\n(bool) STDs:HIV\r\n(bool) STDs:Hepatitis
B\r\n(bool) STDs:HPV\r\n(int) STDs: Number of diagnosis\r\n(int) STDs: Time
since first diagnosis\r\n(int) STDs: Time since last diagnosis\r\n(bool)
Dx:Cancer\r\n(bool) 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) Biopsy: 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:condylomatosi	Feature	Continuous	None
14	STDs:cervical condylomatosi	Feature	Continuous	None
15	STDs:vaginal condylomatosi	Feature	Continuous	None
16	STDs:vulvo-perineal condylomatosi	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

1.6.2 Data Wrangling and Cleaning

```
[5]: # Checking the shape of the dataset
ccrf_df.shape
```

```
[5]: (858, 36)
```

```
[6]: # Checking general information
ccrf_df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 858 entries, 0 to 857
Data columns (total 36 columns):
#   Column                                     Non-Null Count  Dtype
---  -
0   Age                                         858 non-null    int64
1   Number of sexual partners                 832 non-null    float64
2   First sexual intercourse                  851 non-null    float64
3   Num of pregnancies                        802 non-null    float64
4   Smokes                                     845 non-null    float64
5   Smokes (years)                           845 non-null    float64
6   Smokes (packs/year)                      845 non-null    float64
7   Hormonal Contraceptives                  750 non-null    float64
8   Hormonal Contraceptives (years)          750 non-null    float64
9   IUD                                        741 non-null    float64
10  IUD (years)                              741 non-null    float64
11  STDs                                       753 non-null    float64
12  STDs (number)                            753 non-null    float64
13  STDs:condylomatosis                      753 non-null    float64
14  STDs:cervical condylomatosis             753 non-null    float64
15  STDs:vaginal condylomatosis              753 non-null    float64
16  STDs:vulvo-perineal condylomatosis       753 non-null    float64
17  STDs:syphilis                            753 non-null    float64
18  STDs:pelvic inflammatory disease         753 non-null    float64
19  STDs:genital herpes                      753 non-null    float64
20  STDs:molluscum contagiosum               753 non-null    float64
21  STDs:AIDS                                753 non-null    float64
22  STDs:HIV                                  753 non-null    float64
23  STDs:Hepatitis B                         753 non-null    float64
24  STDs:HPV                                  753 non-null    float64
25  STDs: Number of diagnosis                 858 non-null    int64
26  STDs: Time since first diagnosis          71 non-null     float64
27  STDs: Time since last diagnosis           71 non-null     float64
28  Dx:Cancer                                858 non-null    int64
29  Dx:CIN                                    858 non-null    int64
30  Dx:HPV                                    858 non-null    int64
31  Dx                                         858 non-null    int64
32  Hinselmann                               858 non-null    int64
```

```

33 Schiller                        858 non-null    int64
34 Citology                       858 non-null    int64
35 Biopsy                         858 non-null    int64
dtypes: float64(26), int64(10)
memory usage: 241.4 KB

```

```

[7]: # Dropping unusable columns
ccrf_df.drop(columns=["STDs: Time since first diagnosis", "STDs: Time since last_
↳diagnosis"], inplace=True)

```

```

[8]: # Dropping Age records with only 1 row in the dataset
counts = ccrf_df['Age'].value_counts().sort_values()

for i in list(counts.index):
    if counts[i] < 2:
        ccrf_df.drop(ccrf_df[ccrf_df['Age'] == i].index, axis=0, inplace=True)

```

```

[9]: # Listing all NaN columns and filtering out the boolean-like datatypes
nan_cols = list(ccrf_df[ccrf_df.columns[ccrf_df.isna().any()]].columns)

for i in nan_cols:
    if len(list(ccrf_df[i].unique())) <= 3:
        print(i)
        print(list(ccrf_df[i].unique()))

```

```

Smokes
[0.0, 1.0, nan]
Hormonal Contraceptives
[0.0, 1.0, nan]
IUD
[0.0, 1.0, nan]
STDs
[0.0, 1.0, nan]
STDs:condylomatosis
[0.0, 1.0, nan]
STDs:cervical condylomatosis
[0.0, nan]
STDs:vaginal condylomatosis
[0.0, nan, 1.0]
STDs:vulvo-perineal condylomatosis
[0.0, 1.0, nan]
STDs:syphilis
[0.0, 1.0, nan]
STDs:pelvic inflammatory disease
[0.0, nan, 1.0]
STDs:genital herpes
[0.0, nan, 1.0]
STDs:molluscum contagiosum

```

```

[0.0, nan, 1.0]
STDs:AIDS
[0.0, nan]
STDs:HIV
[0.0, 1.0, nan]
STDs:Hepatitis B
[0.0, nan, 1.0]
STDs:HPV
[0.0, nan, 1.0]

```

```

[10]: # Dropping columns with only 0 and NaN values
ccrf_df.drop(['STDs:cervical condylomatosis', 'STDs:AIDS'], axis=1,
             inplace=True)

```

```

[11]: # Relisting all NaN columns and separating the boolean-like datatypes
nan_cols = list(ccrf_df[ccrf_df.columns[ccrf_df.isna().any()]].columns)

nan_mean = []

for i in nan_cols:
    if len(list(ccrf_df[i].unique())) <= 3:
        print(i)
        print(list(ccrf_df[i].unique()))
    else:
        nan_mean.append(i)

```

```

Smokes
[0.0, 1.0, nan]
Hormonal Contraceptives
[0.0, 1.0, nan]
IUD
[0.0, 1.0, nan]
STDs
[0.0, 1.0, nan]
STDs:condylomatosis
[0.0, 1.0, nan]
STDs:vaginal condylomatosis
[0.0, nan, 1.0]
STDs:vulvo-perineal condylomatosis
[0.0, 1.0, nan]
STDs:syphilis
[0.0, 1.0, nan]
STDs:pelvic inflammatory disease
[0.0, nan, 1.0]
STDs:genital herpes
[0.0, nan, 1.0]
STDs:molluscum contagiosum
[0.0, nan, 1.0]

```

```
STDs:HIV
[0.0, 1.0, nan]
STDs:Hepatitis B
[0.0, nan, 1.0]
STDs:HPV
[0.0, nan, 1.0]
```

```
[12]: # Checking the frequency of records for each non-boolean column
for i in nan_mean:
    print(ccrf_df[i].value_counts())
```

Number of sexual partners

```
2.0    268
3.0    206
1.0    205
4.0     78
5.0     44
6.0      9
7.0      7
8.0      4
15.0     1
10.0     1
28.0     1
9.0      1
```

Name: count, dtype: int64

First sexual intercourse

```
15.0    163
17.0    148
18.0    137
16.0    120
14.0     79
19.0     60
20.0     36
13.0     23
21.0     20
23.0      9
22.0      9
26.0      7
12.0      6
27.0      6
24.0      6
29.0      5
28.0      3
11.0      2
25.0      2
10.0      2
32.0      1
```

Name: count, dtype: int64


```

Num of pregnancies
1.0      270
2.0      240
3.0      138
4.0       74
5.0       34
6.0       17
0.0       15
7.0        5
8.0         2
10.0        1

```

```
Name: count, dtype: int64
```

```
Smokes (years)
```

```

0.000000      717
1.266973       15
5.000000        9
9.000000        9
1.000000        8
3.000000        7
2.000000        7
8.000000        6
7.000000        6
16.000000        6
11.000000        5
4.000000        5
10.000000        5
14.000000        4
15.000000        4
6.000000        4
13.000000        3
0.500000        3
19.000000        3
12.000000        3
22.000000        2
37.000000        1
21.000000        1
18.000000        1
32.000000        1
28.000000        1
20.000000        1
0.160000         1

```

```
Name: count, dtype: int64
```

```
Smokes (packs/year)
```

```

0.000000      717
0.513202       17
1.000000        6
3.000000        5
2.000000        4

```

```

...
37.000000      1
2.250000       1
0.003000       1
0.450000       1
0.300000       1
Name: count, Length: 61, dtype: int64
Hormonal Contraceptives (years)
0.000000      264
1.000000       77
0.250000       41
2.000000       40
3.000000       39
5.000000       33
0.080000       25
0.500000       25
6.000000       24
4.000000       22
7.000000       21
8.000000       18
0.160000       16
9.000000       12
10.000000      11
0.330000        9
0.420000        8
0.750000        7
15.000000        6
0.580000        6
0.660000        6
12.000000        4
20.000000        3
1.500000        3
0.670000        2
13.000000        2
11.000000        2
2.282201        2
14.000000        2
19.000000        2
16.000000        2
22.000000        1
2.500000        1
4.500000        1
6.500000        1
0.170000        1
3.500000        1
0.410000        1
30.000000        1
17.000000        1

```

Name: count, dtype: int64

IUD (years)

0.00	653
3.00	11
2.00	10
5.00	9
1.00	8
8.00	7
7.00	6
6.00	5
4.00	5
11.00	3
0.50	2
0.08	2
0.91	1
0.33	1
9.00	1
0.16	1
1.50	1
0.25	1
12.00	1
15.00	1
10.00	1
17.00	1
19.00	1
0.58	1
0.17	1

Name: count, dtype: int64

STDs (number)

0.0	667
2.0	37
1.0	34
3.0	7
4.0	1

Name: count, dtype: int64

```
[13]: # Since the distribution is more spread out between the high frequency records
# We will be using mean to fill the missing values
mean_cols = ['Number of sexual partners', 'First sexual intercourse', 'Num of_
↳pregnancies']

for i in mean_cols:
    nan_mean.remove(i)

for i in mean_cols:
    ave = ccrf_df[ccrf_df[i].isnull()]['Age'].apply(
        lambda x: ccrf_df[ccrf_df['Age'] == x][i].mean()
```

```
)
ccrf_df[i].fillna(ave, inplace=True)
ccrf_df[i] = ccrf_df[i].astype('int64')
nan_cols.remove(i)
```

```
[14]: # For the boolean-like values, we will be using mode instead
for i in nan_mean:
    mod = ccrf_df[ccrf_df[i].isnull()]['Age'].apply(
        lambda x: ccrf_df[ccrf_df['Age'] == x][i].mode()
    )
    ccrf_df[i].fillna(mod[0], inplace=True)
```

```
[15]: for i in nan_mean:
        nan_cols.remove(i)

for i in nan_cols:
    mod = ccrf_df[ccrf_df[i].isnull()]['Age'].apply(
        lambda x: ccrf_df[ccrf_df['Age'] == x][i].mode()
    )
    ccrf_df[i].fillna(mod[0], inplace=True)
```

```
[16]: # Rechecking the DataFrame
ccrf_df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
```

```
Index: 851 entries, 0 to 857
```

```
Data columns (total 32 columns):
```

#	Column	Non-Null Count	Dtype
0	Age	851 non-null	int64
1	Number of sexual partners	851 non-null	int64
2	First sexual intercourse	851 non-null	int64
3	Num of pregnancies	851 non-null	int64
4	Smokes	851 non-null	float64
5	Smokes (years)	851 non-null	float64
6	Smokes (packs/year)	851 non-null	float64
7	Hormonal Contraceptives	851 non-null	float64
8	Hormonal Contraceptives (years)	851 non-null	float64
9	IUD	851 non-null	float64
10	IUD (years)	851 non-null	float64
11	STDs	851 non-null	float64
12	STDs (number)	851 non-null	float64
13	STDs:condylomatosis	851 non-null	float64
14	STDs:vaginal condylomatosis	851 non-null	float64
15	STDs:vulvo-perineal condylomatosis	851 non-null	float64
16	STDs:syphilis	851 non-null	float64
17	STDs:pelvic inflammatory disease	851 non-null	float64

```

18 STDs:genital herpes          851 non-null    float64
19 STDs:molluscum contagiosum   851 non-null    float64
20 STDs:HIV                     851 non-null    float64
21 STDs:Hepatitis B            851 non-null    float64
22 STDs:HPV                    851 non-null    float64
23 STDs: Number of diagnosis    851 non-null    int64
24 Dx:Cancer                   851 non-null    int64
25 Dx:CIN                      851 non-null    int64
26 Dx:HPV                     851 non-null    int64
27 Dx                          851 non-null    int64
28 Hinselmann                  851 non-null    int64
29 Schiller                    851 non-null    int64
30 Citology                    851 non-null    int64
31 Biopsy                      851 non-null    int64
dtypes: float64(19), int64(13)
memory usage: 219.4 KB

```

```

[17]: # Converting the boolean-like columns to categorical
for i in ccrf_df.columns:
    if list(ccrf_df[i].unique()) == [0.0, 1.0]:
        ccrf_df[i] = ccrf_df[i].astype('category')

ccrf_df.info()

```

```
<class 'pandas.core.frame.DataFrame'>
```

```
Index: 851 entries, 0 to 857
```

```
Data columns (total 32 columns):
```

#	Column	Non-Null Count	Dtype
0	Age	851 non-null	int64
1	Number of sexual partners	851 non-null	int64
2	First sexual intercourse	851 non-null	int64
3	Num of pregnancies	851 non-null	int64
4	Smokes	851 non-null	category
5	Smokes (years)	851 non-null	float64
6	Smokes (packs/year)	851 non-null	float64
7	Hormonal Contraceptives	851 non-null	category
8	Hormonal Contraceptives (years)	851 non-null	float64
9	IUD	851 non-null	category
10	IUD (years)	851 non-null	float64
11	STDs	851 non-null	category
12	STDs (number)	851 non-null	float64
13	STDs:condylomatosis	851 non-null	category
14	STDs:vaginal condylomatosis	851 non-null	category
15	STDs:vulvo-perineal condylomatosis	851 non-null	category
16	STDs:syphilis	851 non-null	category
17	STDs:pelvic inflammatory disease	851 non-null	category
18	STDs:genital herpes	851 non-null	category

19	STDs:molluscum contagiosum	851 non-null	category
20	STDs:HIV	851 non-null	category
21	STDs:Hepatitis B	851 non-null	category
22	STDs:HPV	851 non-null	category
23	STDs: Number of diagnosis	851 non-null	int64
24	Dx:Cancer	851 non-null	category
25	Dx:CIN	851 non-null	category
26	Dx:HPV	851 non-null	category
27	Dx	851 non-null	category
28	Hinselmann	851 non-null	category
29	Schiller	851 non-null	category
30	Citology	851 non-null	category
31	Biopsy	851 non-null	category

dtypes: category(22), float64(5), int64(5)
memory usage: 94.1 KB

1.6.3 Exploratory Data Analysis

```
[18]: # Creating a list of columns that are categorical
cols = ccrf_df.columns

num_cols = ccrf_df._get_numeric_data().columns

cat_cols = list(set(cols)-set(num_cols))

cat_cols
```

```
[18]: ['STDs:molluscum contagiosum',
      'Dx:HPV',
      'Schiller',
      'STDs:HIV',
      'STDs:genital herpes',
      'Hormonal Contraceptives',
      'STDs:condylomatosis',
      'STDs:vaginal condylomatosis',
      'Smokes',
      'STDs:HPV',
      'STDs:vulvo-perineal condylomatosis',
      'Dx',
      'Dx:CIN',
      'STDs:Hepatitis B',
      'IUD',
      'Hinselmann',
      'STDs:syphilis',
      'STDs:pelvic inflammatory disease',
      'Dx:Cancer',
      'Biopsy',
```

```
'Citology',
'STDs']
```

```
[19]: ccrf_df.corr()
```

```
[19]:
```

	Age	Number of sexual partners \
Age	1.000000	0.096134
Number of sexual partners	0.096134	1.000000
First sexual intercourse	0.398508	-0.148443
Num of pregnancies	0.517323	0.087251
Smokes	0.039394	0.234972
Smokes (years)	0.173850	0.178917
Smokes (packs/year)	0.140875	0.172938
Hormonal Contraceptives	0.124810	0.018728
Hormonal Contraceptives (years)	0.329572	0.025183
IUD	0.294313	0.026920
IUD (years)	0.226458	0.002687
STDs	0.036554	0.052349
STDs (number)	0.007109	0.038665
STDs:condylomatosis	-0.008067	0.034708
STDs:vaginal condylomatosis	0.012258	-0.042824
STDs:vulvo-perineal condylomatosis	-0.005716	0.036804
STDs:syphilis	0.023119	0.027253
STDs:pelvic inflammatory disease	0.027830	0.030626
STDs:genital herpes	-0.028621	-0.031774
STDs:molluscum contagiosum	0.001776	0.030626
STDs:HIV	0.009678	0.017348
STDs:Hepatitis B	-0.028621	-0.010974
STDs:HPV	0.045525	0.013904
STDs: Number of diagnosis	0.006700	0.050313
Dx:Cancer	0.123406	0.022300
Dx:CIN	0.023543	0.020522
Dx:HPV	0.114101	0.027253
Dx	0.077433	0.025772
Hinselmann	-0.016784	-0.043440
Schiller	0.067803	-0.011495
Citology	-0.025413	0.023791
Biopsy	0.041659	-0.002841

	First sexual intercourse \
Age	0.398508
Number of sexual partners	-0.148443
First sexual intercourse	1.000000
Num of pregnancies	-0.061813
Smokes	-0.129191
Smokes (years)	-0.070663
Smokes (packs/year)	-0.057250

Hormonal Contraceptives	0.027286
Hormonal Contraceptives (years)	0.032884
IUD	0.003976
IUD (years)	-0.017582
STDs	-0.003167
STDs (number)	0.015584
STDs:condylomatosis	0.033990
STDs:vaginal condylomatosis	0.073726
STDs:vulvo-perineal condylomatosis	0.038207
STDs:syphilis	-0.096574
STDs:pelvic inflammatory disease	-0.000029
STDs:genital herpes	0.024522
STDs:molluscum contagiosum	-0.012304
STDs:HIV	-0.008892
STDs:Hepatitis B	0.012247
STDs:HPV	0.034700
STDs: Number of diagnosis	-0.014101
Dx:Cancer	0.067100
Dx:CIN	-0.017514
Dx:HPV	0.043718
Dx	0.046541
Hinselmann	-0.017350
Schiller	-0.001775
Citology	-0.011714
Biopsy	0.006744

	Num of pregnancies	Smokes \
Age	0.517323	0.039394
Number of sexual partners	0.087251	0.234972
First sexual intercourse	-0.061813	-0.129191
Num of pregnancies	1.000000	0.064492
Smokes	0.064492	1.000000
Smokes (years)	0.131540	0.731772
Smokes (packs/year)	0.107429	0.493729
Hormonal Contraceptives	0.174833	0.012862
Hormonal Contraceptives (years)	0.237313	0.049817
IUD	0.218666	-0.065794
IUD (years)	0.150820	-0.046597
STDs	0.063663	0.113248
STDs (number)	0.017135	0.101894
STDs:condylomatosis	-0.029894	0.056889
STDs:vaginal condylomatosis	0.001458	0.070408
STDs:vulvo-perineal condylomatosis	-0.029356	0.059695
STDs:syphilis	0.155067	0.080456
STDs:pelvic inflammatory disease	-0.055582	-0.013964
STDs:genital herpes	-0.030555	-0.013964
STDs:molluscum contagiosum	0.044525	-0.013964

STDs:HIV	0.023975	0.057072
STDs:Hepatitis B	-0.030555	0.084248
STDs:HPV	-0.025530	0.049727
STDs: Number of diagnosis	0.046418	0.092415
Dx:Cancer	0.041851	-0.013080
Dx:CIN	0.019837	-0.039661
Dx:HPV	0.053769	0.010304
Dx	0.031295	-0.067855
Hinselmann	0.037163	0.020027
Schiller	0.066088	0.035344
Citology	-0.021527	-0.001751
Biopsy	0.032965	0.020386

	Smokes (years)	Smokes (packs/year) \
Age	0.173850	0.140875
Number of sexual partners	0.178917	0.172938
First sexual intercourse	-0.070663	-0.057250
Num of pregnancies	0.131540	0.107429
Smokes	0.731772	0.493729
Smokes (years)	1.000000	0.756261
Smokes (packs/year)	0.756261	1.000000
Hormonal Contraceptives	0.022803	0.013656
Hormonal Contraceptives (years)	0.076611	0.050545
IUD	-0.000894	0.002299
IUD (years)	0.005594	0.010524
STDs	0.099750	0.029432
STDs (number)	0.098615	0.030416
STDs:condylomatosis	0.049766	0.007707
STDs:vaginal condylomatosis	0.122828	0.042018
STDs:vulvo-perineal condylomatosis	0.051908	0.008870
STDs:syphilis	0.016946	-0.003697
STDs:pelvic inflammatory disease	-0.010219	-0.006895
STDs:genital herpes	-0.010219	-0.006895
STDs:molluscum contagiosum	-0.010219	-0.006895
STDs:HIV	0.096700	0.054125
STDs:Hepatitis B	0.106008	0.101475
STDs:HPV	0.055122	-0.008004
STDs: Number of diagnosis	0.087610	0.030078
Dx:Cancer	0.058383	0.107425
Dx:CIN	-0.029023	-0.019582
Dx:HPV	0.061080	0.109316
Dx	-0.049654	-0.033502
Hinselmann	0.027587	0.018572
Schiller	0.045542	0.012742
Citology	-0.002630	0.005480
Biopsy	0.030026	0.019554

	Hormonal Contraceptives \
Age	0.124810
Number of sexual partners	0.018728
First sexual intercourse	0.027286
Num of pregnancies	0.174833
Smokes	0.012862
Smokes (years)	0.022803
Smokes (packs/year)	0.013656
Hormonal Contraceptives	1.000000
Hormonal Contraceptives (years)	0.396248
IUD	0.033442
IUD (years)	-0.036943
STDs	-0.028755
STDs (number)	-0.038108
STDs:condylomatosis	-0.013032
STDs:vaginal condylomatosis	-0.059996
STDs:vulvo-perineal condylomatosis	-0.017002
STDs:syphilis	0.001218
STDs:pelvic inflammatory disease	0.024468
STDs:genital herpes	0.024468
STDs:molluscum contagiosum	-0.048083
STDs:HIV	-0.067878
STDs:Hepatitis B	-0.048083
STDs:HPV	0.034623
STDs: Number of diagnosis	-0.046731
Dx:Cancer	0.018492
Dx:CIN	0.017978
Dx:HPV	0.035766
Dx	0.011599
Hinselmann	0.031303
Schiller	-0.009485
Citology	-0.039697
Biopsy	-0.001293

	Hormonal Contraceptives (years)	IUD \
Age	0.329572	0.294313
Number of sexual partners	0.025183	0.026920
First sexual intercourse	0.032884	0.003976
Num of pregnancies	0.237313	0.218666
Smokes	0.049817	-0.065794
Smokes (years)	0.076611	-0.000894
Smokes (packs/year)	0.050545	0.002299
Hormonal Contraceptives	0.396248	0.033442
Hormonal Contraceptives (years)	1.000000	0.164459
IUD	0.164459	1.000000
IUD (years)	0.019166	0.740203
STDs	0.004775	0.058620

STDs (number)	0.000246	0.059850
STDs:condylomatosis	0.014953	0.084224
STDs:vaginal condylomatosis	-0.033394	0.035316
STDs:vulvo-perineal condylomatosis	0.016604	0.068826
STDs:syphilis	0.002401	-0.020799
STDs:pelvic inflammatory disease	-0.011897	-0.011276
STDs:genital herpes	-0.016667	-0.011276
STDs:molluscum contagiosum	-0.019053	-0.011276
STDs:HIV	-0.036219	0.006728
STDs:Hepatitis B	-0.019053	-0.011276
STDs:HPV	0.054049	-0.015956
STDs: Number of diagnosis	-0.027758	0.035041
Dx:Cancer	0.064284	0.116834
Dx:CIN	0.010248	0.009019
Dx:HPV	0.083980	0.061781
Dx	0.010709	0.116183
Hinselmann	0.057177	0.034055
Schiller	0.084960	0.087015
Citology	0.057271	0.032660
Biopsy	0.076637	0.046396

	... STDs:HPV	STDs: Number of diagnosis \
Age	... 0.045525	0.006700
Number of sexual partners	... 0.013904	0.050313
First sexual intercourse	... 0.034700	-0.014101
Num of pregnancies	... -0.025530	0.046418
Smokes	... 0.049727	0.092415
Smokes (years)	... 0.055122	0.087610
Smokes (packs/year)	... -0.008004	0.030078
Hormonal Contraceptives	... 0.034623	-0.046731
Hormonal Contraceptives (years)	... 0.054049	-0.027758
IUD	... -0.015956	0.035041
IUD (years)	... -0.011811	0.013104
STDs	... 0.151725	0.907739
STDs (number)	... 0.077076	0.898375
STDs:condylomatosis	... -0.011333	0.701545
STDs:vaginal condylomatosis	... -0.003335	0.206469
STDs:vulvo-perineal condylomatosis	... -0.011197	0.693098
STDs:syphilis	... -0.007135	0.414744
STDs:pelvic inflammatory disease	... -0.001665	0.103052
STDs:genital herpes	... -0.001665	0.103052
STDs:molluscum contagiosum	... -0.001665	0.103052
STDs:HIV	... -0.007135	0.549282
STDs:Hepatitis B	... -0.001665	0.103052
STDs:HPV	... 1.000000	0.065865
STDs: Number of diagnosis	... 0.065865	1.000000
Dx:Cancer	... 0.330177	-0.015778

Dx:CIN	...	-0.004728	0.011834
Dx:HPV	...	0.330177	-0.015778
Dx	...	0.141562	-0.000645
Hinselmann	...	-0.009901	0.079145
Schiller	...	-0.014643	0.136406
Citology	...	-0.011197	0.056747
Biopsy	...	-0.012508	0.101398

	Dx:Cancer	Dx:CIN	Dx:HPV	Dx \
Age	0.123406	0.023543	0.114101	0.077433
Number of sexual partners	0.022300	0.020522	0.027253	0.025772
First sexual intercourse	0.067100	-0.017514	0.043718	0.046541
Num of pregnancies	0.041851	0.019837	0.053769	0.031295
Smokes	-0.013080	-0.039661	0.010304	-0.067855
Smokes (years)	0.058383	-0.029023	0.061080	-0.049654
Smokes (packs/year)	0.107425	-0.019582	0.109316	-0.033502
Hormonal Contraceptives	0.018492	0.017978	0.035766	0.011599
Hormonal Contraceptives (years)	0.064284	0.010248	0.083980	0.010709
IUD	0.116834	0.009019	0.061781	0.116183
IUD (years)	0.104382	0.010001	0.036566	0.103862
STDs	0.009259	0.010798	0.009259	-0.003374
STDs (number)	-0.012499	-0.005737	-0.012499	-0.021749
STDs:condylomatosis	-0.034324	-0.022747	-0.034324	-0.038917
STDs:vaginal condylomatosis	-0.010102	-0.006695	-0.010102	-0.011453
STDs:vulvo-perineal condylomatosis	-0.033911	-0.022473	-0.033911	-0.038448
STDs:syphilis	-0.021609	-0.014320	-0.021609	-0.024500
STDs:pelvic inflammatory disease	-0.005042	-0.003341	-0.005042	-0.005717
STDs:genital herpes	-0.005042	-0.003341	-0.005042	-0.005717
STDs:molluscum contagiosum	-0.005042	-0.003341	-0.005042	-0.005717
STDs:HIV	-0.021609	0.070308	-0.021609	0.025861
STDs:Hepatitis B	-0.005042	-0.003341	-0.005042	-0.005717
STDs:HPV	0.330177	-0.004728	0.330177	0.141562
STDs: Number of diagnosis	-0.015778	0.011834	-0.015778	-0.000645
Dx:Cancer	1.000000	-0.014320	0.886488	0.680550
Dx:CIN	-0.014320	1.000000	-0.014320	0.584497
Dx:HPV	0.886488	-0.014320	1.000000	0.630189
Dx	0.680550	0.584497	0.630189	1.000000
Hinselmann	0.136806	-0.019873	0.136806	0.077000
Schiller	0.162374	0.014644	0.162374	0.106942
Citology	0.115228	-0.022473	0.115228	0.093885
Biopsy	0.164877	0.126060	0.164877	0.166946

	Hinselmann	Schiller	Citology	Biopsy
Age	-0.016784	0.067803	-0.025413	0.041659
Number of sexual partners	-0.043440	-0.011495	0.023791	-0.002841
First sexual intercourse	-0.017350	-0.001775	-0.011714	0.006744
Num of pregnancies	0.037163	0.066088	-0.021527	0.032965

Smokes	0.020027	0.035344	-0.001751	0.020386
Smokes (years)	0.027587	0.045542	-0.002630	0.030026
Smokes (packs/year)	0.018572	0.012742	0.005480	0.019554
Hormonal Contraceptives	0.031303	-0.009485	-0.039697	-0.001293
Hormonal Contraceptives (years)	0.057177	0.084960	0.057271	0.076637
IUD	0.034055	0.087015	0.032660	0.046396
IUD (years)	-0.006759	0.076929	0.009205	0.023429
STDs	0.058795	0.123132	0.055613	0.118630
STDs (number)	0.075509	0.135198	0.063411	0.107235
STDs:condylomatosis	0.060753	0.121458	0.067276	0.093542
STDs:vaginal condylomatosis	-0.014019	-0.020733	-0.015853	-0.017710
STDs:vulvo-perineal condylomatosis	0.062511	0.124405	0.069249	0.095947
STDs:syphilis	0.011711	0.014714	-0.033911	-0.037884
STDs:pelvic inflammatory disease	-0.006997	-0.010348	-0.007913	-0.008839
STDs:genital herpes	-0.006997	-0.010348	-0.007913	0.133093
STDs:molluscum contagiosum	-0.006997	-0.010348	-0.007913	-0.008839
STDs:HIV	0.095108	0.132842	0.077943	0.131083
STDs:Hepatitis B	-0.006997	-0.010348	-0.007913	-0.008839
STDs:HPV	-0.009901	-0.014643	-0.011197	-0.012508
STDs: Number of diagnosis	0.079145	0.136406	0.056747	0.101398
Dx:Cancer	0.136806	0.162374	0.115228	0.164877
Dx:CIN	-0.019873	0.014644	-0.022473	0.126060
Dx:HPV	0.136806	0.162374	0.115228	0.164877
Dx	0.077000	0.106942	0.093885	0.166946
Hinselmann	1.000000	0.654458	0.199476	0.543296
Schiller	0.654458	1.000000	0.357211	0.731103
Citology	0.199476	0.357211	1.000000	0.317946
Biopsy	0.543296	0.731103	0.317946	1.000000

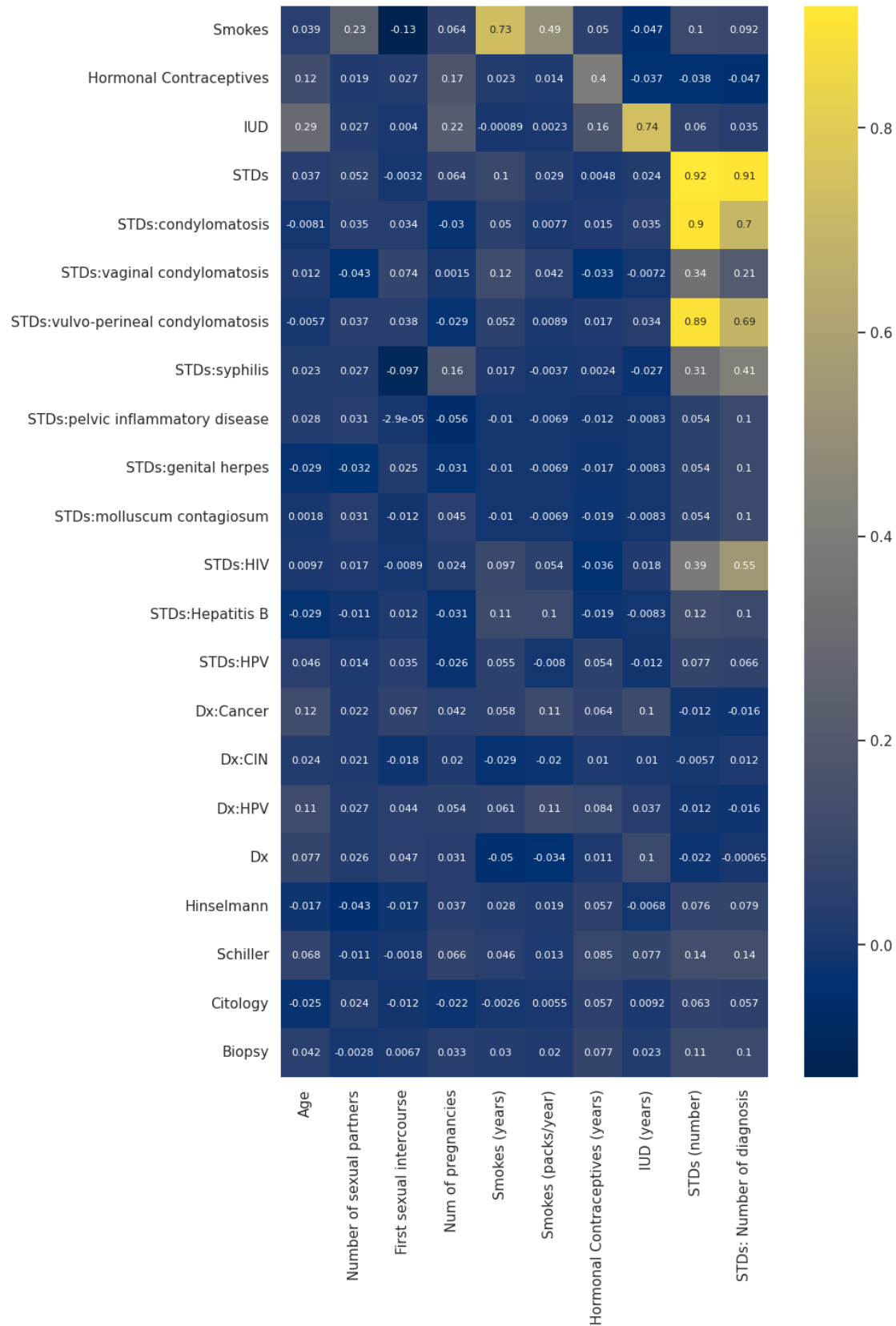
[32 rows x 32 columns]

```
[20]: x_corr = ccrf_df.corr().drop(num_cols, axis=0)
      cat_corr = x_corr.drop(cat_cols, axis=1)

      cat_corr

      sns.set(rc = {'figure.figsize':(10, 15)})
      sns.heatmap(cat_corr, annot=True, cmap='cividis',annot_kws={'size': 8},
                  square=True)
```

[20]: <Axes: >

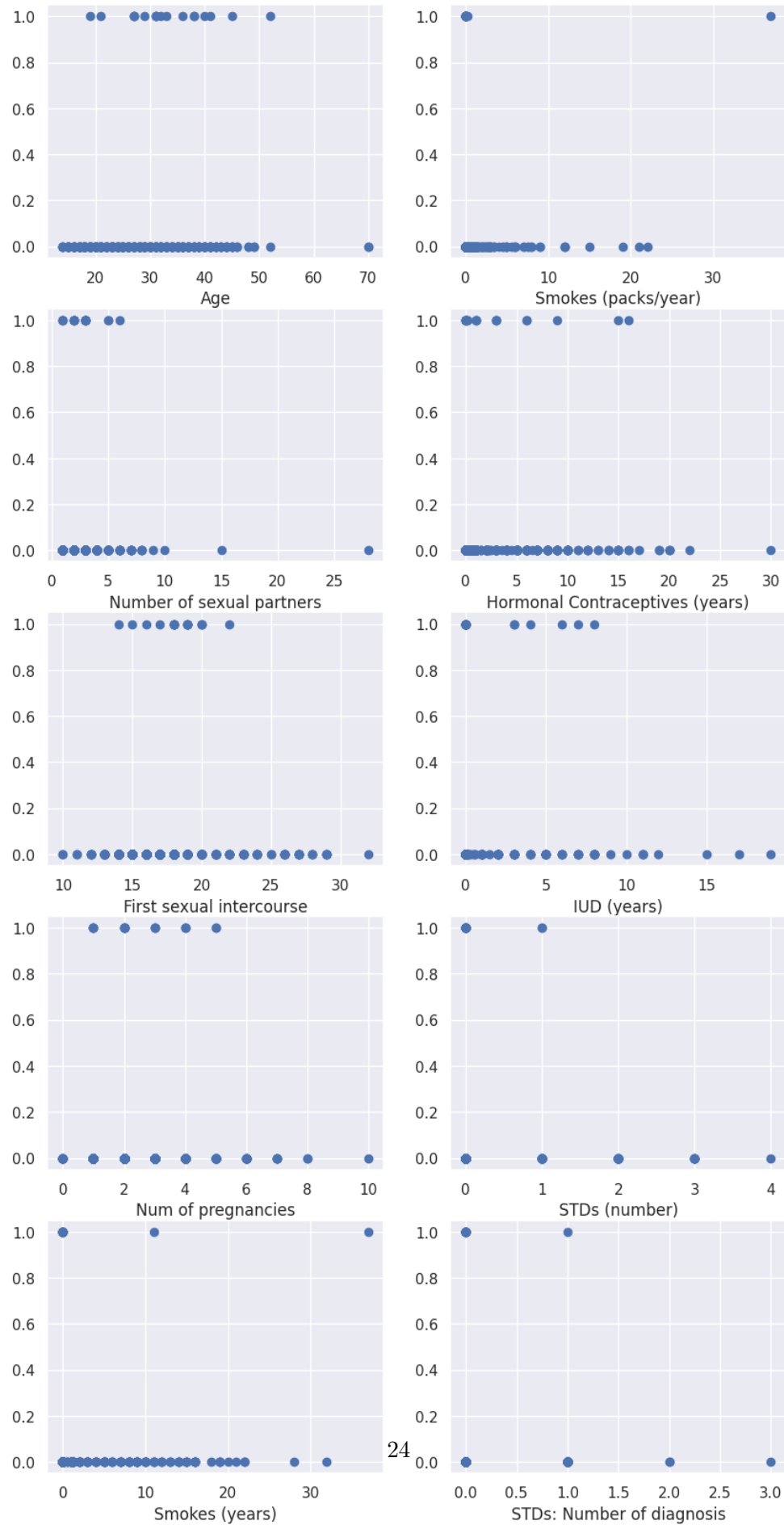


```
[21]: num1 = num_cols[:5]
num2 = num_cols[5:]

fig, ax = plt.subplots(nrows= 5, ncols=2, figsize=(10, 20))

ind = 0

for row in ax:
    row[0].scatter(ccrf_df[num1[ind]], ccrf_df['Dx:Cancer'])
    row[0].set_xlabel(num1[ind])
    row[1].scatter(ccrf_df[num2[ind]], ccrf_df['Dx:Cancer'])
    row[1].set_xlabel(num2[ind])
    ind += 1
```



1.6.4 Logistic Regression

Declare feature vector and target variable

```
[22]: X = ccrf_df.drop(cat_cols, axis=1)
      y = ccrf_df['Schiller']
```

Split data into separate training and test set

```
[23]: 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_state=0)
```

```
[24]: X_train.shape, X_test.shape
```

```
[24]: ((595, 10), (256, 10))
```

```
[25]: from sklearn.preprocessing import StandardScaler

      scaler = StandardScaler()

      X_train_scaled = scaler.fit_transform(X_train)

      X_test_scaled = scaler.transform(X_test)

      X_train_scaled
```

```
[25]: array([[ -8.19614616e-01, -1.04033386e+00, -7.14782754e-01, ...,
        -2.46062766e-01, -2.85220215e-01, -2.82879693e-01],
        [-4.44579474e-01, -3.53320935e-01,  3.64648055e-01, ...,
        -2.46062766e-01, -2.85220215e-01, -2.82879693e-01],
        [ 3.18076023e+00, -3.53320935e-01,  7.24458325e-01, ...,
        5.26966023e+00, -2.85220215e-01, -2.82879693e-01],
        ...,
        [-6.95443317e-02, -3.53320935e-01,  3.64648055e-01, ...,
        -2.46062766e-01, -2.85220215e-01, -2.82879693e-01],
        [ 1.43059624e+00, -1.04033386e+00,  2.52350967e+00, ...,
        -2.46062766e-01, -2.85220215e-01, -2.82879693e-01],
        [-6.95443317e-02, -3.53320935e-01,  4.83778514e-03, ...,
        -2.46062766e-01,  3.44458259e+00,  3.01738339e+00]])
```

```
[26]: X_test_scaled
```

```
[26]: array([[ 2.68071338,  1.02070492, -0.35497248, ...,  0.2553666 ,
            -0.28522021, -0.28287969],
            [ 0.30549081, -0.35332093,  0.36464805, ..., -0.24606277,
            -0.28522021, -0.28287969],
            [-1.31966147,  0.33369199, -1.07459302, ..., -0.24606277,
            -0.28522021, -0.28287969],
            ...,
            [-0.31956776, -0.35332093,  0.36464805, ..., -0.24606277,
            -0.28522021, -0.28287969],
            [ 1.18057281,  0.33369199,  1.08426859, ..., -0.24606277,
            1.57968119,  3.01738339],
            [ 0.55551424,  0.33369199,  0.36464805, ..., -0.24606277,
            -0.28522021, -0.28287969]])
```

```
[27]: from sklearn.linear_model import LogisticRegression

log_reg = LogisticRegression(random_state = 0).fit(X_train_scaled, y_train)
```

```
[28]: log_reg.score(X_train_scaled, y_train)
```

```
[28]: 0.9176470588235294
```

```
[29]: log_reg.score(X_test_scaled, y_test)
```

```
[29]: 0.9140625
```

```
[30]: log_reg1 = LogisticRegression(random_state = 0,
                                   C=0.01,
                                   fit_intercept= True,
                                   ).fit(X_train_scaled, y_train)
```

```
[31]: log_reg1.score(X_train_scaled,y_train)
```

```
[31]: 0.9176470588235294
```

```
[32]: log_reg1.score(X_test_scaled, y_test)
```

```
[32]: 0.9140625
```

1.6.5 Conclusion

From the activity, I was able to learn about Logistic Regression and see how it is very similar to Linear Regression. With Logistic Regression, the outcome that we are trying to predict is in boolean form, only representing values as 0 or 1, True or False. With this, we are able to use Logistic Regression to predict classification for our data being used to predict with the model. We are able to deal with categorical data instead of just continuous numerical data. It is important to learn Logistic Regression in order to predict and classify a given set of data