

05122022_Cervical_Cancer_Classification

December 6, 2022

0.1 Cervical Cancer Prediction Using XG-Boost

Cervical cancer is a type of cancer that affects the cervix, which is the lower part of the uterus that connects to the vagina. It is typically caused by the human papillomavirus (HPV), which is a sexually transmitted infection. Other contributing factors to the development of cervical cancer can include a weakened immune system, smoking, and having multiple sexual partners. Regular screening tests, such as Pap tests, can help detect cervical cancer early, when it is most treatable. Treatment options may include surgery, radiation therapy, and chemotherapy. It is important to reduce the impact of this disease because it can have serious health consequences. Early detection and treatment are key, as well as reducing the risk of developing cervical cancer by practicing safe sex and getting vaccinated against HPV.

0.1.1 Import necessary libraries and dataset.

```
[ ]: import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt
import zipfile
import plotly.express as px

from jupyterthemes import jtplot
jtplot.style(theme='monokai', context='notebook', ticks=True, grid=False)
```

```
[ ]: cancer_df = pd.read_csv('cervical_cancer.csv')
```

0.1.2 Understand the structure, format, data types of the dataframe by using .info() and .describe()

```
[ ]: cancer_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	858 non-null	object

2	First sexual intercourse	858 non-null	object
3	Num of pregnancies	858 non-null	object
4	Smokes	858 non-null	object
5	Smokes (years)	858 non-null	object
6	Smokes (packs/year)	858 non-null	object
7	Hormonal Contraceptives	858 non-null	object
8	Hormonal Contraceptives (years)	858 non-null	object
9	IUD	858 non-null	object
10	IUD (years)	858 non-null	object
11	STDs	858 non-null	object
12	STDs (number)	858 non-null	object
13	STDs:condylomatosis	858 non-null	object
14	STDs:cervical condylomatosis	858 non-null	object
15	STDs:vaginal condylomatosis	858 non-null	object
16	STDs:vulvo-perineal condylomatosis	858 non-null	object
17	STDs:syphilis	858 non-null	object
18	STDs:pelvic inflammatory disease	858 non-null	object
19	STDs:genital herpes	858 non-null	object
20	STDs:molluscum contagiosum	858 non-null	object
21	STDs:AIDS	858 non-null	object
22	STDs:HIV	858 non-null	object
23	STDs:Hepatitis B	858 non-null	object
24	STDs:HPV	858 non-null	object
25	STDs: Number of diagnosis	858 non-null	int64
26	STDs: Time since first diagnosis	858 non-null	object
27	STDs: Time since last diagnosis	858 non-null	object
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: int64(10), object(26)

memory usage: 241.4+ KB

```
[ ]: cancer_df.describe()
```

```
[ ]:
      count      Age  STDs: Number of diagnosis  Dx:Cancer  Dx:CIN  \
count  858.000000      26.820513      858.000000  858.000000  858.000000
mean    26.820513      0.087413      0.020979   0.010490
std      8.497948      0.302545      0.143398   0.101939
min     13.000000      0.000000      0.000000   0.000000
25%     20.000000      0.000000      0.000000   0.000000
50%     25.000000      0.000000      0.000000   0.000000
75%     32.000000      0.000000      0.000000   0.000000
```

max	84.000000		3.000000	1.000000	1.000000	
	Dx:HPV	Dx	Hinselmann	Schiller	Citology	Biopsy
count	858.000000	858.000000	858.000000	858.000000	858.000000	858.000000
mean	0.020979	0.027972	0.040793	0.086247	0.051282	0.064103
std	0.143398	0.164989	0.197925	0.280892	0.220701	0.245078
min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
25%	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
50%	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
75%	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
max	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000

There are several values that are equal to '?' we need to replace these so that we can start to analyse our data more clearly

```
[ ]: cancer_df = cancer_df.replace('?', np.nan)
cancer_df
```

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

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

```
      Hormonal Contraceptives Hormonal Contraceptives (years) IUD ... \
0              0.0              0.0      0.0 ...
1              0.0              0.0      0.0 ...
```

2	0.0	0.0	0.0	...
3	1.0	3.0	0.0	...
4	1.0	15.0	0.0	...
..
853	0.0	0.0	0.0	...
854	1.0	8.0	0.0	...
855	1.0	0.08	0.0	...
856	1.0	0.08	0.0	...
857	1.0	0.5	0.0	...

	STDs: Time since first diagnosis	STDs: Time since last diagnosis	\
0	NaN	NaN	
1	NaN	NaN	
2	NaN	NaN	
3	NaN	NaN	
4	NaN	NaN	
..
853	NaN	NaN	
854	NaN	NaN	
855	NaN	NaN	
856	NaN	NaN	
857	NaN	NaN	

	Dx:Cancer	Dx:CIN	Dx:HPV	Dx Hinselmann	Schiller	Citology	Biopsy
0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0
3	1	0	1	0	0	0	0
4	0	0	0	0	0	0	0
..
853	0	0	0	0	0	0	0
854	0	0	0	0	0	0	0
855	0	0	0	0	0	1	0
856	0	0	0	0	0	0	0
857	0	0	0	0	0	0	0

[858 rows x 36 columns]

```
[ ]: cancer_df.isnull()
```

	Age	Number of sexual partners	First sexual intercourse	\
0	False	False	False	
1	False	False	False	
2	False	False	True	
3	False	False	False	
4	False	False	False	
..

853	False	False	False
854	False	False	False
855	False	False	False
856	False	False	False
857	False	False	False

	Num of pregnancies	Smokes	Smokes (years)	Smokes (packs/year)	\
0	False	False	False	False	
1	False	False	False	False	
2	False	False	False	False	
3	False	False	False	False	
4	False	False	False	False	
..	
853	False	False	False	False	
854	False	False	False	False	
855	False	False	False	False	
856	False	False	False	False	
857	False	False	False	False	

	Hormonal Contraceptives	Hormonal Contraceptives (years)	IUD	...	\
0	False	False	False	False	...
1	False	False	False	False	...
2	False	False	False	False	...
3	False	False	False	False	...
4	False	False	False	False	...
..
853	False	False	False	False	...
854	False	False	False	False	...
855	False	False	False	False	...
856	False	False	False	False	...
857	False	False	False	False	...

	STDs: Time since first diagnosis	STDs: Time since last diagnosis	\
0	True	True	
1	True	True	
2	True	True	
3	True	True	
4	True	True	
..	
853	True	True	
854	True	True	
855	True	True	
856	True	True	
857	True	True	

	Dx:Cancer	Dx:CIN	Dx:HPV	Dx	Hinselmann	Schiller	Citology	Biopsy
0	False	False	False	False	False	False	False	False

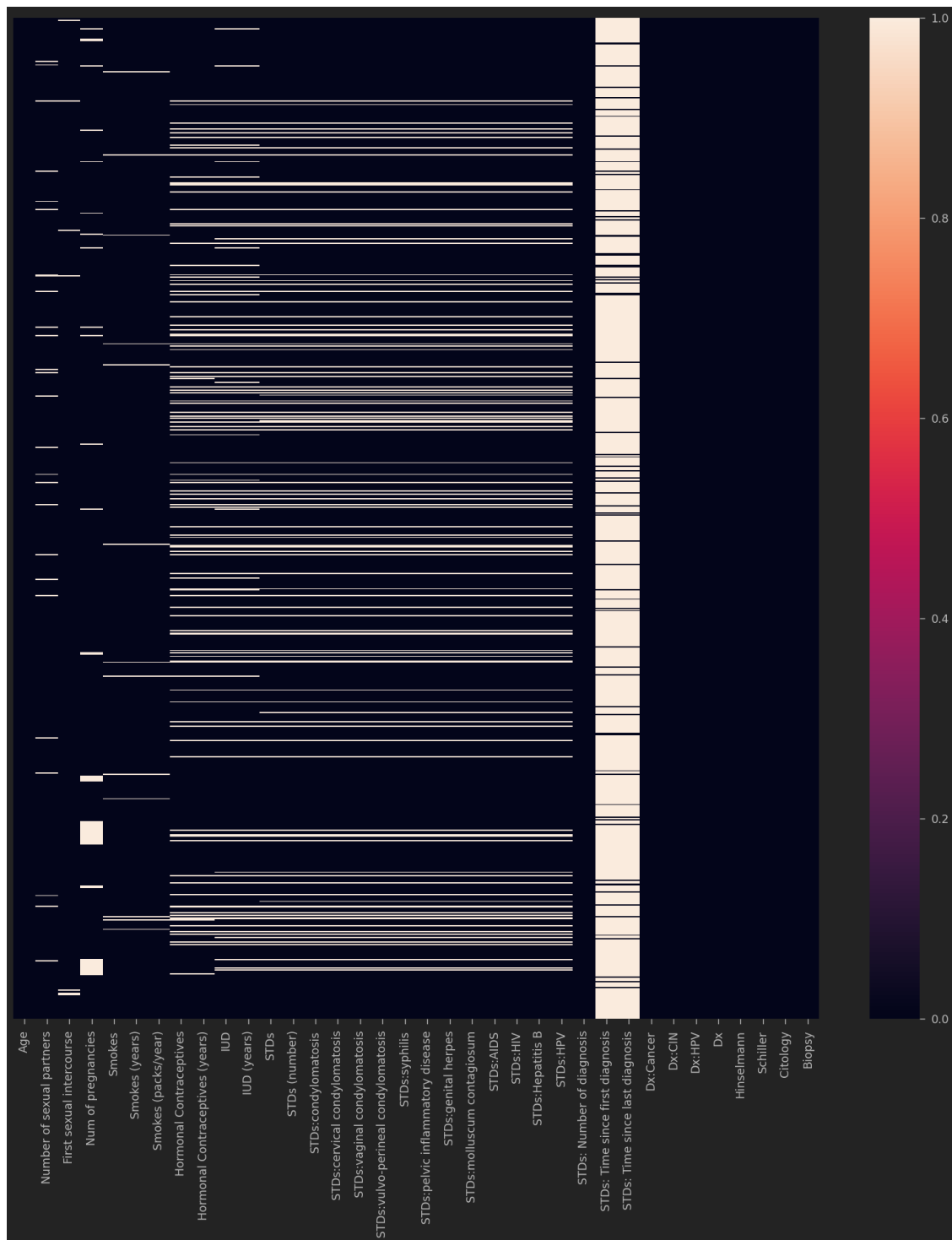
1	False	False	False	False	False	False	False	False
2	False	False	False	False	False	False	False	False
3	False	False	False	False	False	False	False	False
4	False	False	False	False	False	False	False	False
..
853	False	False	False	False	False	False	False	False
854	False	False	False	False	False	False	False	False
855	False	False	False	False	False	False	False	False
856	False	False	False	False	False	False	False	False
857	False	False	False	False	False	False	False	False

[858 rows x 36 columns]

Create a heatmap to represent how many null values are present in the dataset.

```
[ ]: plt.figure(figsize= (20, 20))
      sns.heatmap(cancer_df.isnull(), yticklabels=False)
```

```
[ ]: <AxesSubplot:>
```



It would be wise to drop the two columns with high amounts of null since we do not actually have a lot of data we can work with when we discount the null values.

```
[ ]: cancer_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	object
2	First sexual intercourse	851 non-null	object
3	Num of pregnancies	802 non-null	object
4	Smokes	845 non-null	object
5	Smokes (years)	845 non-null	object
6	Smokes (packs/year)	845 non-null	object
7	Hormonal Contraceptives	750 non-null	object
8	Hormonal Contraceptives (years)	750 non-null	object
9	IUD	741 non-null	object
10	IUD (years)	741 non-null	object
11	STDs	753 non-null	object
12	STDs (number)	753 non-null	object
13	STDs:condylomatosis	753 non-null	object
14	STDs:cervical condylomatosis	753 non-null	object
15	STDs:vaginal condylomatosis	753 non-null	object
16	STDs:vulvo-perineal condylomatosis	753 non-null	object
17	STDs:syphilis	753 non-null	object
18	STDs:pelvic inflammatory disease	753 non-null	object
19	STDs:genital herpes	753 non-null	object
20	STDs:molluscum contagiosum	753 non-null	object
21	STDs:AIDS	753 non-null	object
22	STDs:HIV	753 non-null	object
23	STDs:Hepatitis B	753 non-null	object
24	STDs:HPV	753 non-null	object
25	STDs: Number of diagnosis	858 non-null	int64
26	STDs: Time since first diagnosis	71 non-null	object
27	STDs: Time since last diagnosis	71 non-null	object
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: int64(10), object(26)
```

```
memory usage: 241.4+ KB
```

```
[ ]: cancer_df = cancer_df.drop(columns= ['STDs: Time since first diagnosis', 'STDs:
↳Time since last diagnosis'])
cancer_df
```



```

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

```

```

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

```

```

      Hormonal Contraceptives Hormonal Contraceptives (years) IUD ... \
0          0.0          0.0 0.0 ...
1          0.0          0.0 0.0 ...
2          0.0          0.0 0.0 ...
3          1.0          3.0 0.0 ...
4          1.0         15.0 0.0 ...
..      ...      ...      ...
853        0.0          0.0 0.0 ...
854        1.0          8.0 0.0 ...
855        1.0          0.08 0.0 ...
856        1.0          0.08 0.0 ...
857        1.0          0.5 0.0 ...

```

```

      STDs:HPV STDs: Number of diagnosis Dx:Cancer Dx:CIN Dx:HPV Dx Hinselmann \
0          0.0          0      0      0      0 0      0
1          0.0          0      0      0      0 0      0
2          0.0          0      0      0      0 0      0
3          0.0          0      1      0      1 0      0
4          0.0          0      0      0      0 0      0
..      ...      ...      ...      ... ..      ...
853        0.0          0      0      0      0 0      0

```

```

854      0.0      0      0      0      0 0      0
855      0.0      0      0      0      0 0      0
856      0.0      0      0      0      0 0      0
857      0.0      0      0      0      0 0      0

```

```

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

```

[858 rows x 34 columns]

We should also convert our object data types to a numeric type.

```
[ ]: cancer_df = cancer_df.apply(pd.to_numeric)
      cancer_df.info()
```

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

```
RangeIndex: 858 entries, 0 to 857
```

```
Data columns (total 34 columns):
```

#	Column	Non-Null Count	Dtype
0	Age	858 non-null	int64
1	Number of sexual partners	832 non-null	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	Dx:Cancer	858 non-null	int64
27	Dx:CIN	858 non-null	int64
28	Dx:HPV	858 non-null	int64
29	Dx	858 non-null	int64
30	Hinselmann	858 non-null	int64
31	Schiller	858 non-null	int64
32	Citology	858 non-null	int64
33	Biopsy	858 non-null	int64

dtypes: float64(24), int64(10)

memory usage: 228.0 KB

```
[ ]: cancer_df.describe()
```

```
[ ]:
```

	Age	Number of sexual partners	First sexual intercourse	\
count	858.000000	832.000000	851.000000	
mean	26.820513	2.527644	16.995300	
std	8.497948	1.667760	2.803355	
min	13.000000	1.000000	10.000000	
25%	20.000000	2.000000	15.000000	
50%	25.000000	2.000000	17.000000	
75%	32.000000	3.000000	18.000000	
max	84.000000	28.000000	32.000000	

	Num of pregnancies	Smokes	Smokes (years)	Smokes (packs/year)	\
count	802.000000	845.000000	845.000000	845.000000	
mean	2.275561	0.145562	1.219721	0.453144	
std	1.447414	0.352876	4.089017	2.226610	
min	0.000000	0.000000	0.000000	0.000000	
25%	1.000000	0.000000	0.000000	0.000000	
50%	2.000000	0.000000	0.000000	0.000000	
75%	3.000000	0.000000	0.000000	0.000000	
max	11.000000	1.000000	37.000000	37.000000	

	Hormonal Contraceptives	Hormonal Contraceptives (years)	IUD	\
count	750.000000	750.000000	741.000000	
mean	0.641333	2.256419	0.112011	
std	0.479929	3.764254	0.315593	
min	0.000000	0.000000	0.000000	
25%	0.000000	0.000000	0.000000	

50%	1.000000	0.500000	0.000000
75%	1.000000	3.000000	0.000000
max	1.000000	30.000000	1.000000

	...	STDs:HPV	STDs: Number of diagnosis	Dx:Cancer	Dx:CIN	\
count	...	753.000000	858.000000	858.000000	858.000000	
mean	...	0.002656	0.087413	0.020979	0.010490	
std	...	0.051503	0.302545	0.143398	0.101939	
min	...	0.000000	0.000000	0.000000	0.000000	
25%	...	0.000000	0.000000	0.000000	0.000000	
50%	...	0.000000	0.000000	0.000000	0.000000	
75%	...	0.000000	0.000000	0.000000	0.000000	
max	...	1.000000	3.000000	1.000000	1.000000	

	Dx:HPV	Dx	Hinselmann	Schiller	Citology	Biopsy
count	858.000000	858.000000	858.000000	858.000000	858.000000	858.000000
mean	0.020979	0.027972	0.040793	0.086247	0.051282	0.064103
std	0.143398	0.164989	0.197925	0.280892	0.220701	0.245078
min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
25%	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
50%	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
75%	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
max	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000

[8 rows x 34 columns]

We will now replace our null values in other columns with the average for that column. We can then use a heatmap to discover if we have any remaining null values.

```
[ ]: cancer_df.mean()
```

```
[ ]: Age                26.820513
      Number of sexual partners    2.527644
      First sexual intercourse    16.995300
      Num of pregnancies           2.275561
      Smokes                  0.145562
      Smokes (years)          1.219721
      Smokes (packs/year)      0.453144
      Hormonal Contraceptives    0.641333
      Hormonal Contraceptives (years)  2.256419
      IUD                    0.112011
      IUD (years)            0.514804
      STDs                   0.104914
      STDs (number)          0.176627
      STDs:condylomatosis     0.058433
      STDs:cervical condylomatosis  0.000000
      STDs:vaginal condylomatosis  0.005312
```

STDs:vulvo-perineal condylomatosis	0.057105
STDs:syphilis	0.023904
STDs:pelvic inflammatory disease	0.001328
STDs:genital herpes	0.001328
STDs:molluscum contagiosum	0.001328
STDs:AIDS	0.000000
STDs:HIV	0.023904
STDs:Hepatitis B	0.001328
STDs:HPV	0.002656
STDs: Number of diagnosis	0.087413
Dx:Cancer	0.020979
Dx:CIN	0.010490
Dx:HPV	0.020979
Dx	0.027972
Hinselmann	0.040793
Schiller	0.086247
Citology	0.051282
Biopsy	0.064103
dtype: float64	

```
[ ]: cancer_df = cancer_df.fillna(cancer_df.mean())
cancer_df
```

```
[ ]:
      Age  Number of sexual partners  First sexual intercourse \
0      18                        4.0                15.0000
1      15                        1.0                14.0000
2      34                        1.0                16.9953
3      52                        5.0                16.0000
4      46                        3.0                21.0000
..    ...
853    34                        3.0                18.0000
854    32                        2.0                19.0000
855    25                        2.0                17.0000
856    33                        2.0                24.0000
857    29                        2.0                20.0000

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

857	1.0	0.0	0.0	0.0
-----	-----	-----	-----	-----

	Hormonal Contraceptives	Hormonal Contraceptives (years)	IUD	...	\
0	0.0	0.00	0.0	...	
1	0.0	0.00	0.0	...	
2	0.0	0.00	0.0	...	
3	1.0	3.00	0.0	...	
4	1.0	15.00	0.0	...	
..	
853	0.0	0.00	0.0	...	
854	1.0	8.00	0.0	...	
855	1.0	0.08	0.0	...	
856	1.0	0.08	0.0	...	
857	1.0	0.50	0.0	...	

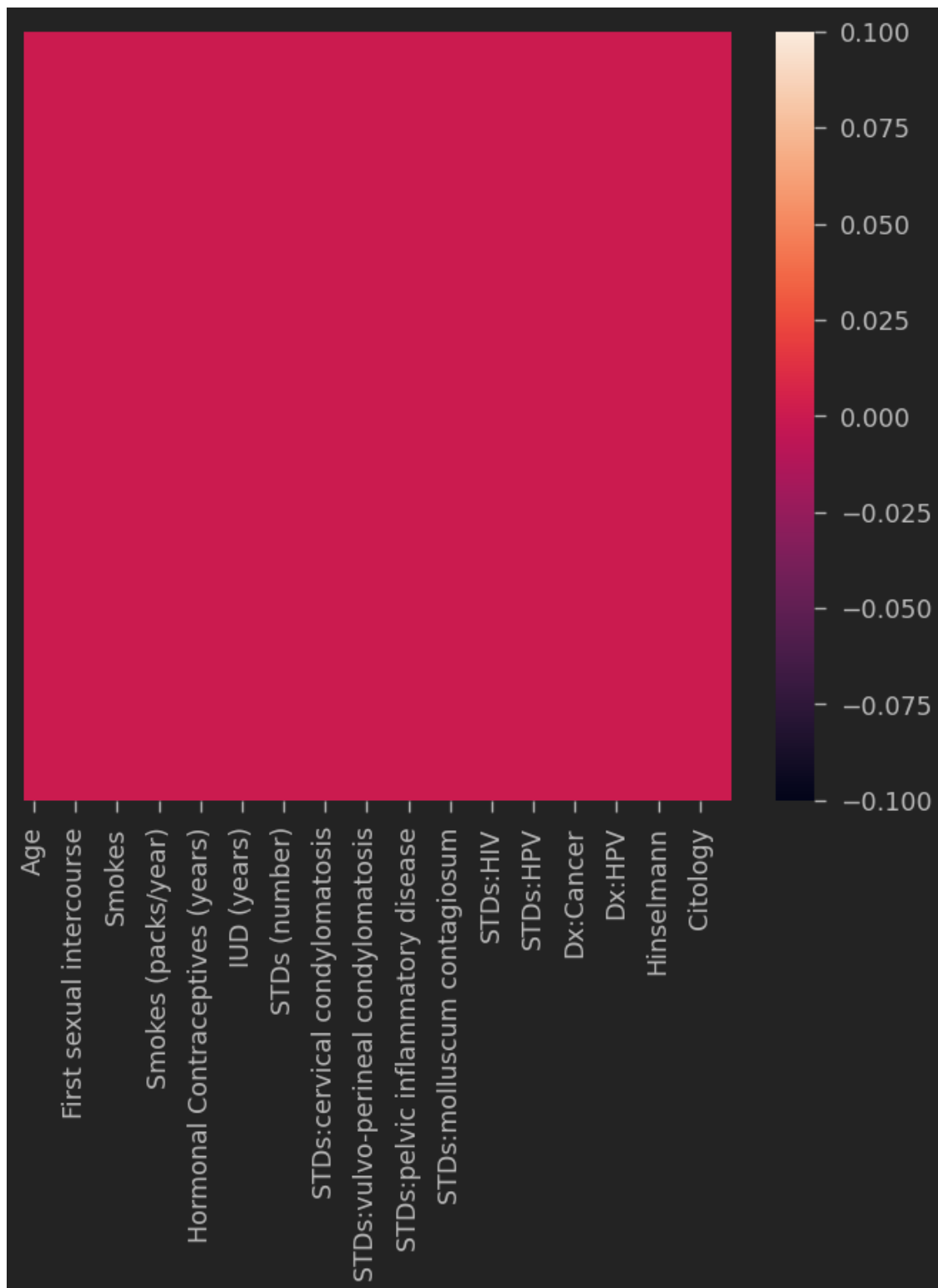
	STDs:HPV	STDs: Number of diagnosis	Dx:Cancer	Dx:CIN	Dx:HPV	Dx	\
0	0.0	0	0	0	0	0	
1	0.0	0	0	0	0	0	
2	0.0	0	0	0	0	0	
3	0.0	0	1	0	1	0	
4	0.0	0	0	0	0	0	
..	
853	0.0	0	0	0	0	0	
854	0.0	0	0	0	0	0	
855	0.0	0	0	0	0	0	
856	0.0	0	0	0	0	0	
857	0.0	0	0	0	0	0	

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

[858 rows x 34 columns]

```
[ ]: sns.heatmap(cancer_df.isnull(), yticklabels=False)
```

```
[ ]: <AxesSubplot:>
```



Since we have one color, this indicates that there are no null values remaining.

```
[ ]: min = cancer_df['Age'].min()
max = cancer_df['Age'].max()

def age_range(min, max):
    age_range = max - min
    return age_range

print(age_range(min, max))
```

71

```
[ ]: cancer_df[cancer_df['Age'] == 84]
```

```
[ ]:      Age  Number of sexual partners  First sexual intercourse \
668   84                             3.0                      20.0

      Num of pregnancies  Smokes  Smokes (years)  Smokes (packs/year) \
668                11.0      1.0             24.0             0.513202

      Hormonal Contraceptives  Hormonal Contraceptives (years)  IUD  ...  \
668                        0.0                                0.0  0.0  ...

      STDs:HPV  STDs: Number of diagnosis  Dx:Cancer  Dx:CIN  Dx:HPV  Dx  \
668          0.0                        0          0        0        0    0

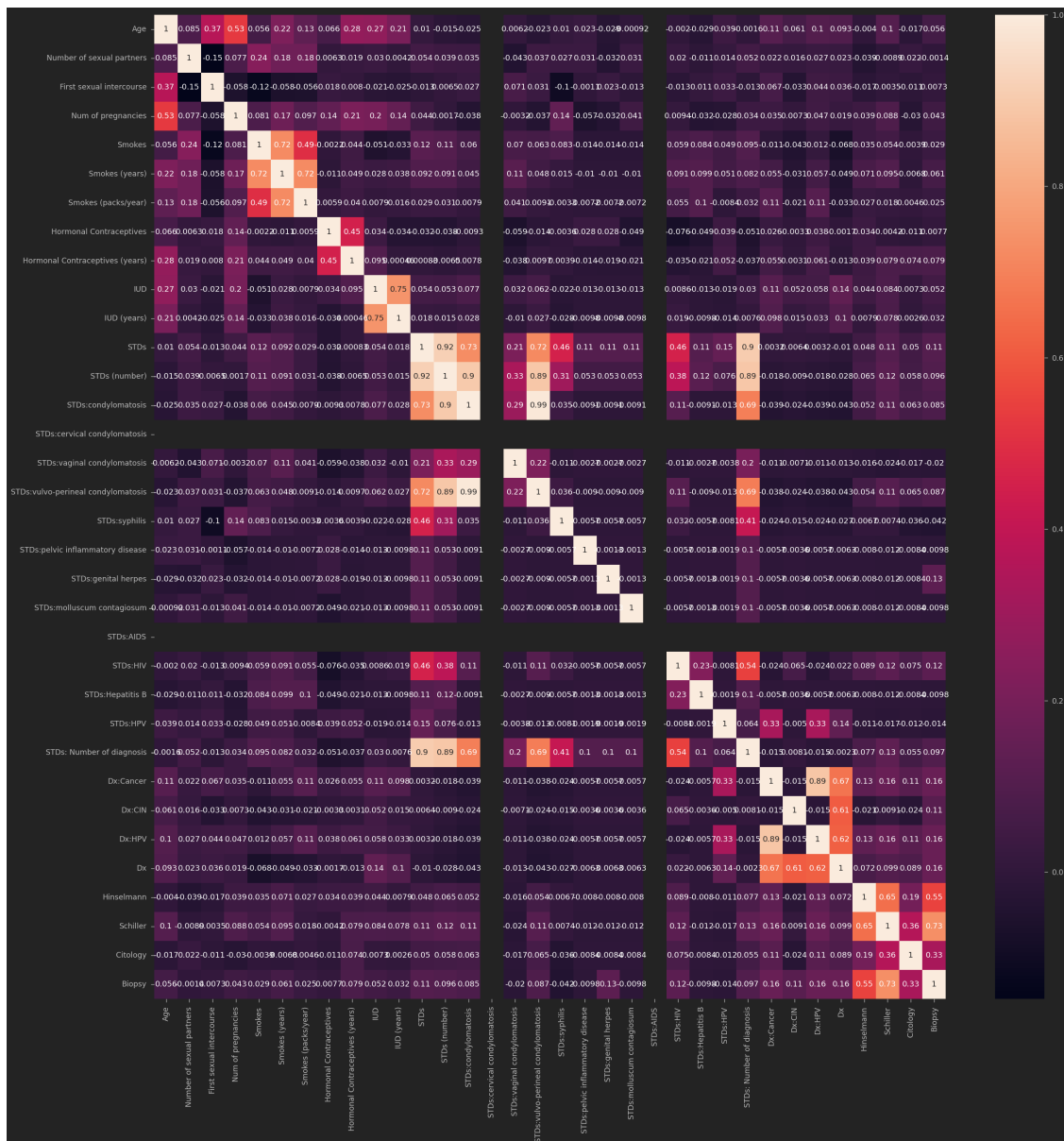
      Hinselmann  Schiller  Citology  Biopsy
668              0         1         0       0

[1 rows x 34 columns]
```

0.1.3 Data Visualisation

```
[ ]: corr = cancer_df.corr()

plt.figure(figsize = (30,30))
sns.heatmap(corr, annot=True)
plt.show()
```

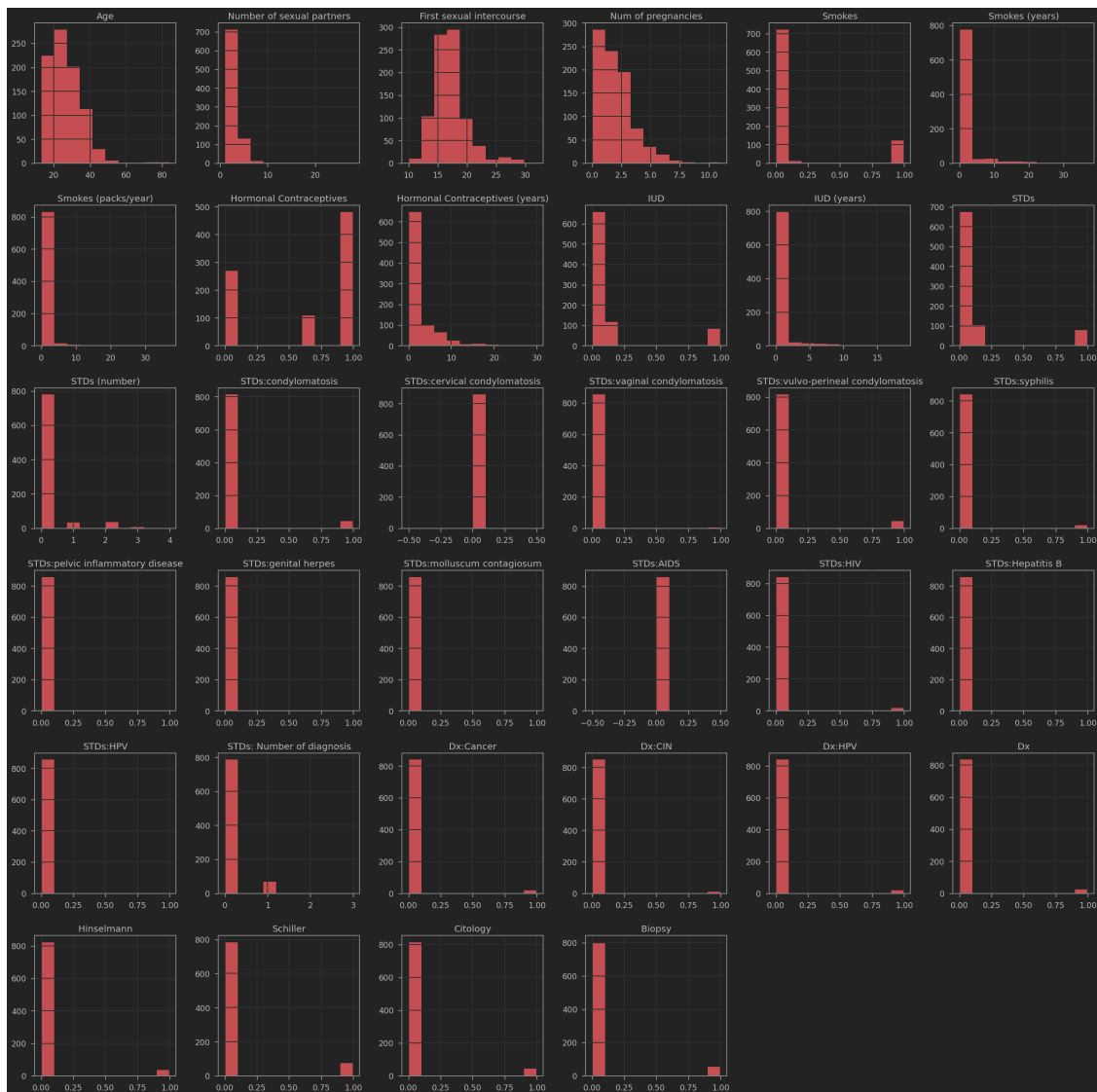
```
[ ]: cancer_df.hist(bins=10, figsize=(30, 30), color='r')
```

```
[ ]: array([[<AxesSubplot:title={'center': 'Age'}>,
<AxesSubplot:title={'center': 'Number of sexual partners'}>,
<AxesSubplot:title={'center': 'First sexual intercourse'}>,
<AxesSubplot:title={'center': 'Num of pregnancies'}>,
<AxesSubplot:title={'center': 'Smokes'}>,
<AxesSubplot:title={'center': 'Smokes (years)'}>],
[<AxesSubplot:title={'center': 'Smokes (packs/year)'}>,
<AxesSubplot:title={'center': 'Hormonal Contraceptives'}>,
<AxesSubplot:title={'center': 'Hormonal Contraceptives (years)'}>],
```

```

<AxesSubplot:title={'center':'IUD'}>,
<AxesSubplot:title={'center':'IUD (years)'}>,
<AxesSubplot:title={'center':'STDs'}>],
[<AxesSubplot:title={'center':'STDs (number)'}>,
<AxesSubplot:title={'center':'STDs:condylomatosis'}>,
<AxesSubplot:title={'center':'STDs:cervical condylomatosis'}>,
<AxesSubplot:title={'center':'STDs:vaginal condylomatosis'}>,
<AxesSubplot:title={'center':'STDs:vulvo-perineal condylomatosis'}>,
<AxesSubplot:title={'center':'STDs:syphilis'}>],
[<AxesSubplot:title={'center':'STDs:pelvic inflammatory disease'}>,
<AxesSubplot:title={'center':'STDs:genital herpes'}>,
<AxesSubplot:title={'center':'STDs:molluscum contagiosum'}>,
<AxesSubplot:title={'center':'STDs:AIDS'}>,
<AxesSubplot:title={'center':'STDs:HIV'}>,
<AxesSubplot:title={'center':'STDs:Hepatitis B'}>],
[<AxesSubplot:title={'center':'STDs:HPV'}>,
<AxesSubplot:title={'center':'STDs: Number of diagnosis'}>,
<AxesSubplot:title={'center':'Dx:Cancer'}>,
<AxesSubplot:title={'center':'Dx:CIN'}>,
<AxesSubplot:title={'center':'Dx:HPV'}>,
<AxesSubplot:title={'center':'Dx'}>],
[<AxesSubplot:title={'center':'Hinselmann'}>,
<AxesSubplot:title={'center':'Schiller'}>,
<AxesSubplot:title={'center':'Citology'}>,
<AxesSubplot:title={'center':'Biopsy'}>, <AxesSubplot:>,
<AxesSubplot:>]], dtype=object)

```



Since we have visualised our data, we will now prepare our data to be used in model training. This is where things get more fun.

```
[ ]: target_df = cancer_df['Biopsy']
input_df = cancer_df.drop(columns=['Biopsy'])
```

```
[ ]: X = np.array(input_df).astype('float32')
y = np.array(target_df).astype('float32')
```

```
[ ]: #we need to reshape the array but this version of python does it for us.
y.shape
```

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

```
[ ]: #applies a form of regularisation to our dataset.
from sklearn.preprocessing import StandardScaler, MinMaxScaler
scaler = StandardScaler()
X = scaler.fit_transform(X)
```

```
[ ]: #splitting the data in to test and train sets
from sklearn.model_selection import train_test_split

#assigning 40% of the data to testing
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=.4)
#assigning 50% of the 40% of data assigned to test to be assigned to validation
X_test, X_val, y_test, y_val = train_test_split(X_test, y_test, test_size=.5)
```

```
[ ]: #checking to see if I already have xgboost
# !pip install xgboost
```

```
[ ]: #import and training XGBoost model.
import xgboost as xgb

model = xgb.XGBClassifier(learning_rate=.1, max_depth=25, n_estimators=100)

model.fit(X_train, y_train)
```

```
[ ]: XGBClassifier(base_score=0.5, booster='gbtree', callbacks=None,
                  colsample_bylevel=1, colsample_bynode=1, colsample_bytree=1,
                  early_stopping_rounds=None, enable_categorical=False,
                  eval_metric=None, feature_types=None, gamma=0, gpu_id=-1,
                  grow_policy='depthwise', importance_type=None,
                  interaction_constraints='', learning_rate=0.1, max_bin=256,
                  max_cat_threshold=64, max_cat_to_onehot=4, max_delta_step=0,
                  max_depth=25, max_leaves=0, min_child_weight=1, missing=nan,
                  monotone_constraints='()', n_estimators=100, n_jobs=0,
                  num_parallel_tree=1, predictor='auto', random_state=0, ...)
```

```
[ ]: result_train = model.score(X_train, y_train)
result_train
```

```
[ ]: 0.9980544747081712
```

```
[ ]: result_test = model.score(X_test, y_test)
result_test
```

```
[ ]: 0.9476744186046512
```

```
[ ]: #make predictions on the test data
y_predict = model.predict(X_test)
```

```
[ ]: from sklearn.metrics import confusion_matrix, classification_report
print(classification_report(y_test, y_predict))
```

	precision	recall	f1-score	support
0.0	0.98	0.97	0.97	162
1.0	0.55	0.60	0.57	10
accuracy			0.95	172
macro avg	0.76	0.78	0.77	172
weighted avg	0.95	0.95	0.95	172

```
[ ]: cm = confusion_matrix(y_predict, y_test)
sns.heatmap(cm, annot=True)
```

```
[ ]: <AxesSubplot:>
```

