

```
from google.colab import files
uploaded = files.upload()
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```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
%matplotlib inline
```

```
from sklearn.datasets import load_breast_cancer
cancer = load_breast_cancer()
```

```
df_cancer = pd.DataFrame(np.c_[cancer['data'], cancer['target']], columns = np.append(cancer['feature_names'], ['target']))
df_cancer.head()
```

	mean radius	mean texture	mean perimeter	mean area	mean smoothness	mean compactness	mean concavity	mean concave points	sy
0	17.99	10.38	122.80	1001.0	0.11840	0.27760	0.3001	0.14710	
1	20.57	17.77	132.90	1326.0	0.08474	0.07864	0.0869	0.07017	
2	19.69	21.25	130.00	1203.0	0.10960	0.15990	0.1974	0.12790	
3	11.42	20.38	77.58	386.1	0.14250	0.28390	0.2414	0.10520	
4	20.29	14.34	135.10	1297.0	0.10030	0.13280	0.1980	0.10430	

5 rows × 31 columns

```
df_cancer.shape
```

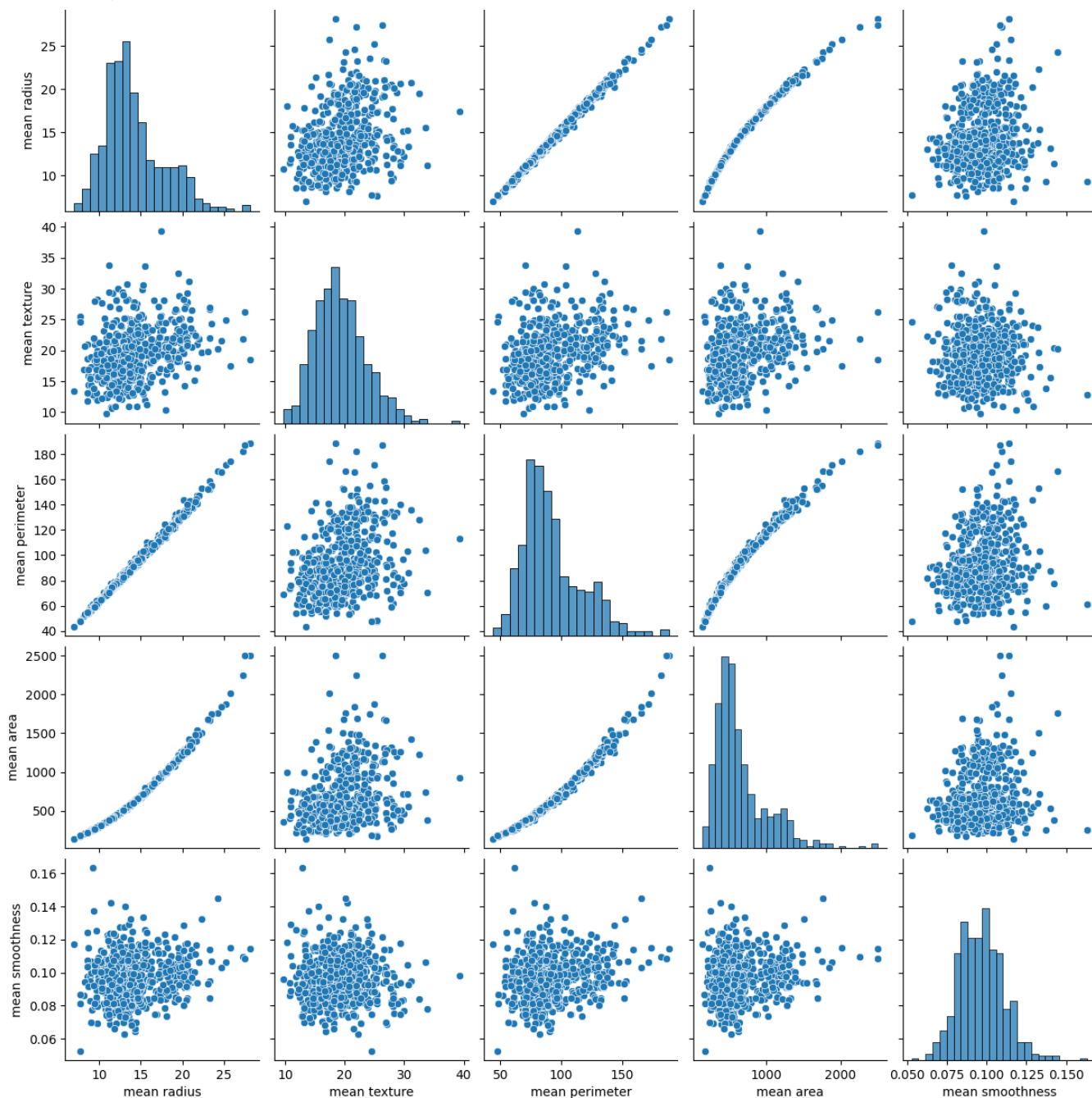
(569, 31)

```
df_cancer.columns
```

```
Index(['mean radius', 'mean texture', 'mean perimeter', 'mean area',
      'mean smoothness', 'mean compactness', 'mean concavity',
      'mean concave points', 'mean symmetry', 'mean fractal dimension',
      'radius error', 'texture error', 'perimeter error', 'area error',
      'smoothness error', 'compactness error', 'concavity error',
      'concave points error', 'symmetry error', 'fractal dimension error',
      'worst radius', 'worst texture', 'worst perimeter', 'worst area',
      'worst smoothness', 'worst compactness', 'worst concavity',
      'worst concave points', 'worst symmetry', 'worst fractal dimension',
      'target'],
      dtype='object')
```

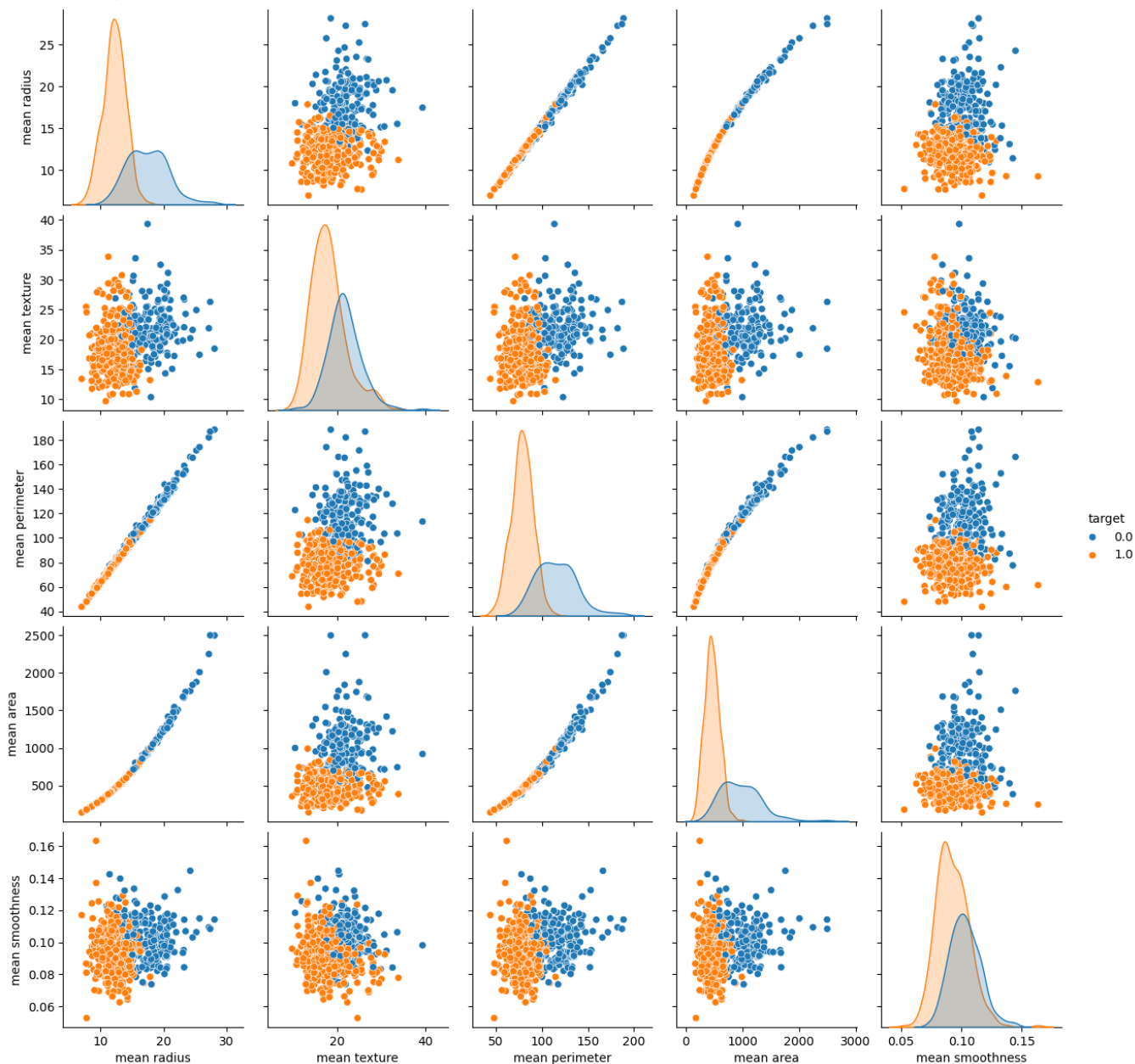
```
sns.pairplot(df_cancer, vars = ['mean radius', 'mean texture', 'mean perimeter', 'mean area',
                                'mean smoothness'] )
```

<seaborn.axisgrid.PairGrid at 0x7e9e52403670>



```
sns.pairplot(df_cancer, hue = 'target', vars = ['mean radius', 'mean texture',  
                                                'mean perimeter', 'mean area', 'mean smoothness'] )
```

 <seaborn.axisgrid.PairGrid at 0x7e9e4f15f2e0>

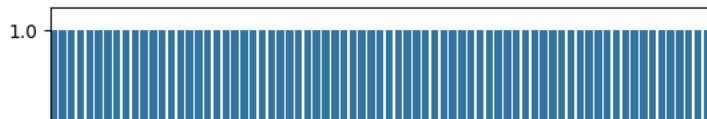


```
df_cancer['target'].value_counts()
```

```
1.0    357
0.0    212
Name: target, dtype: int64
```

```
sns.countplot(df_cancer['target'], label = "Count")
```

<Axes: ylabel='count'>



```
X = df_cancer.drop(['target'], axis = 1)
X.head()
```

	mean radius	mean texture	mean perimeter	mean area	mean smoothness	mean compactness	mean concavity	mean concave points	mean symmetry	mean fractal dimension	...	worst radius	worst texture	wor perimet
0	17.99	10.38	122.80	1001.0	0.11840	0.27760	0.3001	0.14710	0.2419	0.07871	...	25.38	17.33	184
1	20.57	17.77	132.90	1326.0	0.08474	0.07864	0.0869	0.07017	0.1812	0.05667	...	24.99	23.41	158
2	19.69	21.25	130.00	1203.0	0.10960	0.15990	0.1974	0.12790	0.2069	0.05999	...	23.57	25.53	152
3	11.42	20.38	77.58	386.1	0.14250	0.28390	0.2414	0.10520	0.2597	0.09744	...	14.91	26.50	98
4	20.29	14.34	135.10	1297.0	0.10030	0.13280	0.1980	0.10430	0.1809	0.05883	...	22.54	16.67	152

5 rows × 30 columns

```
y = df_cancer['target']
y.head()
```

```
0    0.0
1    0.0
2    0.0
3    0.0
4    0.0
Name: target, dtype: float64
```

```
from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(X, y, train_size = 0.8, random_state = 20)
```

```
from sklearn.svm import SVC
```

```
svc = SVC(kernel="poly", C = 100)
svc.fit(X_train, y_train)
y_predict = svc.predict(X_test)
```

```
from sklearn.metrics import classification_report, confusion_matrix
cm = np.array(confusion_matrix(y_test, y_predict, labels=[1,0]))
confusion = pd.DataFrame(cm, index=['is_cancer', 'is_healthy'],
                        columns=['predicted_cancer', 'predicted_healthy'])
confusion
```

	predicted_cancer	predicted_healthy
is_cancer	65	1
is_healthy	5	43

```
sns.heatmap(confusion, annot=True)
```

<Axes: >

