

# breast\_cancer\_prediction

April 30, 2022

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## 0.1 Objective

Malignant tumors that occur in the glandular epithelium of the breast are called breast cancers, which are cancers that develop from breast tissue. Breast cancer has now become a relatively common tumor that threatens women's physical and mental health.

Although breast cancer is the most common gynecological cancer, most breast lumps are not cancer. In fact, more than 80 percent of breast lumps end up being benign. However, can we identify breast cancer from a breast lump?

I developed an analysis and prediction algorithm to predict breast cancer using data obtained from: <https://archive.ics.uci.edu/ml/datasets/Breast+Cancer+Wisconsin+%28Diagnostic%29>

Data can be viewed through Streamlit dashboard: [https://share.streamlit.io/liyiliang999/breast\\_cancer\\_prediction/main/app.py](https://share.streamlit.io/liyiliang999/breast_cancer_prediction/main/app.py)

I found out that some features can greatly help us distinguish malignant tumors.

## 0.2 Data Processing

First of all, data needs to be processed in order to further analyze. Let's take a look at our data.

```
[56]: #import packages
import warnings
warnings.filterwarnings("ignore")
```

```
[57]: import numpy as np
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
from sklearn.linear_model import LogisticRegression
```

```
[2]: #read data
data = pd.read_csv("data.csv")
```

```
[3]: data
```

```
[3]:      id diagnosis  radius_mean  texture_mean  perimeter_mean  area_mean  \
0    842302         M        17.99         10.38           122.80        1001.0
1    842517         M        20.57         17.77           132.90        1326.0
2    84300903        M        19.69         21.25           130.00        1203.0
```

3	84348301	M	11.42	20.38	77.58	386.1
4	84358402	M	20.29	14.34	135.10	1297.0
..	...	...	...	...	...	...
564	926424	M	21.56	22.39	142.00	1479.0
565	926682	M	20.13	28.25	131.20	1261.0
566	926954	M	16.60	28.08	108.30	858.1
567	927241	M	20.60	29.33	140.10	1265.0
568	92751	B	7.76	24.54	47.92	181.0

	smoothness_mean	compactness_mean	concavity_mean	concave points_mean	\
0	0.11840	0.27760	0.30010	0.14710	
1	0.08474	0.07864	0.08690	0.07017	
2	0.10960	0.15990	0.19740	0.12790	
3	0.14250	0.28390	0.24140	0.10520	
4	0.10030	0.13280	0.19800	0.10430	
..	...	...	...	...	
564	0.11100	0.11590	0.24390	0.13890	
565	0.09780	0.10340	0.14400	0.09791	
566	0.08455	0.10230	0.09251	0.05302	
567	0.11780	0.27700	0.35140	0.15200	
568	0.05263	0.04362	0.00000	0.00000	

	...	texture_worst	perimeter_worst	area_worst	smoothness_worst	\
0	...	17.33	184.60	2019.0	0.16220	
1	...	23.41	158.80	1956.0	0.12380	
2	...	25.53	152.50	1709.0	0.14440	
3	...	26.50	98.87	567.7	0.20980	
4	...	16.67	152.20	1575.0	0.13740	
..	...	...	...	...	...	
564	...	26.40	166.10	2027.0	0.14100	
565	...	38.25	155.00	1731.0	0.11660	
566	...	34.12	126.70	1124.0	0.11390	
567	...	39.42	184.60	1821.0	0.16500	
568	...	30.37	59.16	268.6	0.08996	

	compactness_worst	concavity_worst	concave points_worst	symmetry_worst	\
0	0.66560	0.7119	0.2654	0.4601	
1	0.18660	0.2416	0.1860	0.2750	
2	0.42450	0.4504	0.2430	0.3613	
3	0.86630	0.6869	0.2575	0.6638	
4	0.20500	0.4000	0.1625	0.2364	
..	...	...	...	...	
564	0.21130	0.4107	0.2216	0.2060	
565	0.19220	0.3215	0.1628	0.2572	
566	0.30940	0.3403	0.1418	0.2218	
567	0.86810	0.9387	0.2650	0.4087	
568	0.06444	0.0000	0.0000	0.2871	

	fractal_dimension_worst	Unnamed: 32
0	0.11890	NaN
1	0.08902	NaN
2	0.08758	NaN
3	0.17300	NaN
4	0.07678	NaN
..	...	...
564	0.07115	NaN
565	0.06637	NaN
566	0.07820	NaN
567	0.12400	NaN
568	0.07039	NaN

[569 rows x 33 columns]

I printed out our data, there are 569 rows and 33 columns in the data. I found out that the last column is meaningless, I decided to remove the last column.

```
[4]: data = data.iloc[:,0:-1] #removing the last column
```

```
[5]: data
```

```
[5]:
```

	id	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	\
0	842302	M	17.99	10.38	122.80	1001.0	
1	842517	M	20.57	17.77	132.90	1326.0	
2	84300903	M	19.69	21.25	130.00	1203.0	
3	84348301	M	11.42	20.38	77.58	386.1	
4	84358402	M	20.29	14.34	135.10	1297.0	
..	...	...	...	...	...	...	
564	926424	M	21.56	22.39	142.00	1479.0	
565	926682	M	20.13	28.25	131.20	1261.0	
566	926954	M	16.60	28.08	108.30	858.1	
567	927241	M	20.60	29.33	140.10	1265.0	
568	92751	B	7.76	24.54	47.92	181.0	

	smoothness_mean	compactness_mean	concavity_mean	concave points_mean	\
0	0.11840	0.27760	0.30010	0.14710	
1	0.08474	0.07864	0.08690	0.07017	
2	0.10960	0.15990	0.19740	0.12790	
3	0.14250	0.28390	0.24140	0.10520	
4	0.10030	0.13280	0.19800	0.10430	
..	...	...	...	...	
564	0.11100	0.11590	0.24390	0.13890	
565	0.09780	0.10340	0.14400	0.09791	
566	0.08455	0.10230	0.09251	0.05302	
567	0.11780	0.27700	0.35140	0.15200	
568	0.05263	0.04362	0.00000	0.00000	

	...	radius_worst	texture_worst	perimeter_worst	area_worst	\
0	...	25.380	17.33	184.60	2019.0	
1	...	24.990	23.41	158.80	1956.0	
2	...	23.570	25.53	152.50	1709.0	
3	...	14.910	26.50	98.87	567.7	
4	...	22.540	16.67	152.20	1575.0	
..	...	...	...	...	...	
564	...	25.450	26.40	166.10	2027.0	
565	...	23.690	38.25	155.00	1731.0	
566	...	18.980	34.12	126.70	1124.0	
567	...	25.740	39.42	184.60	1821.0	
568	...	9.456	30.37	59.16	268.6	

	smoothness_worst	compactness_worst	concavity_worst	\
0	0.16220	0.66560	0.7119	
1	0.12380	0.18660	0.2416	
2	0.14440	0.42450	0.4504	
3	0.20980	0.86630	0.6869	
4	0.13740	0.20500	0.4000	
..	...	...	...	
564	0.14100	0.21130	0.4107	
565	0.11660	0.19220	0.3215	
566	0.11390	0.30940	0.3403	
567	0.16500	0.86810	0.9387	
568	0.08996	0.06444	0.0000	

	concave	points_worst	symmetry_worst	fractal_dimension_worst
0		0.2654	0.4601	0.11890
1		0.1860	0.2750	0.08902
2		0.2430	0.3613	0.08758
3		0.2575	0.6638	0.17300
4		0.1625	0.2364	0.07678
..		...	...	...
564		0.2216	0.2060	0.07115
565		0.1628	0.2572	0.06637
566		0.1418	0.2218	0.07820
567		0.2650	0.4087	0.12400
568		0.0000	0.2871	0.07039

[569 rows x 32 columns]

Now the last column is gone.

**The first 5 rows of data**

[6]: data.head(5)

	id	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	\
0	842302	M	17.99	10.38	122.80	1001.0	
1	842517	M	20.57	17.77	132.90	1326.0	

2	84300903	M	19.69	21.25	130.00	1203.0
3	84348301	M	11.42	20.38	77.58	386.1
4	84358402	M	20.29	14.34	135.10	1297.0

	smoothness_mean	compactness_mean	concavity_mean	concave points_mean	\
0	0.11840	0.27760	0.3001	0.14710	
1	0.08474	0.07864	0.0869	0.07017	
2	0.10960	0.15990	0.1974	0.12790	
3	0.14250	0.28390	0.2414	0.10520	
4	0.10030	0.13280	0.1980	0.10430	

	... radius_worst	texture_worst	perimeter_worst	area_worst	\
0	... 25.38	17.33	184.60	2019.0	
1	... 24.99	23.41	158.80	1956.0	
2	... 23.57	25.53	152.50	1709.0	
3	... 14.91	26.50	98.87	567.7	
4	... 22.54	16.67	152.20	1575.0	

	smoothness_worst	compactness_worst	concavity_worst	concave points_worst	\
0	0.1622	0.6656	0.7119	0.2654	
1	0.1238	0.1866	0.2416	0.1860	
2	0.1444	0.4245	0.4504	0.2430	
3	0.2098	0.8663	0.6869	0.2575	
4	0.1374	0.2050	0.4000	0.1625	

	symmetry_worst	fractal_dimension_worst
0	0.4601	0.11890
1	0.2750	0.08902
2	0.3613	0.08758
3	0.6638	0.17300
4	0.2364	0.07678

[5 rows x 32 columns]

### The summary of data

[7]: data.describe()

	id	radius_mean	texture_mean	perimeter_mean	area_mean	\
count	5.690000e+02	569.000000	569.000000	569.000000	569.000000	
mean	3.037183e+07	14.127292	19.289649	91.969033	654.889104	
std	1.250206e+08	3.524049	4.301036	24.298981	351.914129	
min	8.670000e+03	6.981000	9.710000	43.790000	143.500000	
25%	8.692180e+05	11.700000	16.170000	75.170000	420.300000	
50%	9.060240e+05	13.370000	18.840000	86.240000	551.100000	
75%	8.813129e+06	15.780000	21.800000	104.100000	782.700000	
max	9.113205e+08	28.110000	39.280000	188.500000	2501.000000	

	smoothness_mean	compactness_mean	concavity_mean	concave points_mean	\
--	-----------------	------------------	----------------	---------------------	---

count	569.000000	569.000000	569.000000	569.000000
mean	0.096360	0.104341	0.088799	0.048919
std	0.014064	0.052813	0.079720	0.038803
min	0.052630	0.019380	0.000000	0.000000
25%	0.086370	0.064920	0.029560	0.020310
50%	0.095870	0.092630	0.061540	0.033500
75%	0.105300	0.130400	0.130700	0.074000
max	0.163400	0.345400	0.426800	0.201200

	symmetry_mean	...	radius_worst	texture_worst	perimeter_worst	\
count	569.000000	...	569.000000	569.000000	569.000000	
mean	0.181162	...	16.269190	25.677223	107.261213	
std	0.027414	...	4.833242	6.146258	33.602542	
min	0.106000	...	7.930000	12.020000	50.410000	
25%	0.161900	...	13.010000	21.080000	84.110000	
50%	0.179200	...	14.970000	25.410000	97.660000	
75%	0.195700	...	18.790000	29.720000	125.400000	
max	0.304000	...	36.040000	49.540000	251.200000	

	area_worst	smoothness_worst	compactness_worst	concavity_worst	\
count	569.000000	569.000000	569.000000	569.000000	
mean	880.583128	0.132369	0.254265	0.272188	
std	569.356993	0.022832	0.157336	0.208624	
min	185.200000	0.071170	0.027290	0.000000	
25%	515.300000	0.116600	0.147200	0.114500	
50%	686.500000	0.131300	0.211900	0.226700	
75%	1084.000000	0.146000	0.339100	0.382900	
max	4254.000000	0.222600	1.058000	1.252000	

	concave points_worst	symmetry_worst	fractal_dimension_worst
count	569.000000	569.000000	569.000000
mean	0.114606	0.290076	0.083946
std	0.065732	0.061867	0.018061
min	0.000000	0.156500	0.055040
25%	0.064930	0.250400	0.071460
50%	0.099930	0.282200	0.080040
75%	0.161400	0.317900	0.092080
max	0.291000	0.663800	0.207500

[8 rows x 31 columns]

Based on the output above, we can easily see the mean value, standard deviation, minimum, maximum and quantiles of each numeric features.

#### Data Info

```
[8]: data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 569 entries, 0 to 568
```

Data columns (total 32 columns):

#	Column	Non-Null Count	Dtype
0	id	569 non-null	int64
1	diagnosis	569 non-null	object
2	radius_mean	569 non-null	float64
3	texture_mean	569 non-null	float64
4	perimeter_mean	569 non-null	float64
5	area_mean	569 non-null	float64
6	smoothness_mean	569 non-null	float64
7	compactness_mean	569 non-null	float64
8	concavity_mean	569 non-null	float64
9	concave points_mean	569 non-null	float64
10	symmetry_mean	569 non-null	float64
11	fractal_dimension_mean	569 non-null	float64
12	radius_se	569 non-null	float64
13	texture_se	569 non-null	float64
14	perimeter_se	569 non-null	float64
15	area_se	569 non-null	float64
16	smoothness_se	569 non-null	float64
17	compactness_se	569 non-null	float64
18	concavity_se	569 non-null	float64
19	concave points_se	569 non-null	float64
20	symmetry_se	569 non-null	float64
21	fractal_dimension_se	569 non-null	float64
22	radius_worst	569 non-null	float64
23	texture_worst	569 non-null	float64
24	perimeter_worst	569 non-null	float64
25	area_worst	569 non-null	float64
26	smoothness_worst	569 non-null	float64
27	compactness_worst	569 non-null	float64
28	concavity_worst	569 non-null	float64
29	concave points_worst	569 non-null	float64
30	symmetry_worst	569 non-null	float64
31	fractal_dimension_worst	569 non-null	float64

dtypes: float64(30), int64(1), object(1)

memory usage: 142.4+ KB

Based on the information above, we can see that there are currently still 32 columns in the data.

'id' is integer. 'diagnosis' is 'B' or 'M' which means the tumor is benign or malignant. 'radius\_mean', 'texture\_mean', 'perimeter\_mean', 'area\_mean', 'smoothness\_mean', 'compactness\_mean', 'concavity\_mean', 'concave points\_mean', 'symmetry\_mean', 'fractal\_dimension\_mean', 'radius\_se', 'texture\_se', 'perimeter\_se', 'area\_se', 'smoothness\_se', 'compactness\_se', 'concavity\_se', 'concave points\_se', 'symmetry\_se', 'fractal\_dimension\_se', 'radius\_worst', 'texture\_worst', 'perimeter\_worst', 'area\_worst', 'smoothness\_worst', 'compactness\_worst', 'concavity\_worst', 'concave points\_worst', 'symmetry\_worst', 'fractal\_dimension\_worst' are features.

Ten real-valued features are computed for each cell nucleus:

- radius (mean of distances from center to points on the perimeter)
- texture (standard deviation of gray-scale values)
- perimeter
- area
- smoothness (local variation in radius lengths)
- compactness ( $\text{perimeter}^2 / \text{area} - 1.0$ )
- concavity (severity of concave portions of the contour)
- concave points (number of concave portions of the contour)
- symmetry
- fractal dimension ("coastline approximation" - 1)

The mean, standard error and "worst" or largest (mean of the three largest values) of these features were computed for each image.

### Check Missing Values

```
[9]: pd.isna(data)
```

```
[9]:      id  diagnosis  radius_mean  texture_mean  perimeter_mean  area_mean  \
0   False      False      False      False      False      False
1   False      False      False      False      False      False
2   False      False      False      False      False      False
3   False      False      False      False      False      False
4   False      False      False      False      False      False
..   ...      ...      ...      ...      ...      ...
564  False      False      False      False      False      False
565  False      False      False      False      False      False
566  False      False      False      False      False      False
567  False      False      False      False      False      False
568  False      False      False      False      False      False
```

```
      smoothness_mean  compactness_mean  concavity_mean  concave points_mean  \
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
..                ...                ...                ...                ...
564              False              False              False              False
565              False              False              False              False
566              False              False              False              False
567              False              False              False              False
568              False              False              False              False
```

```
      ...  radius_worst  texture_worst  perimeter_worst  area_worst  \
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
```



```

..      ...      ...      ...      ...      ...
564      ...      False      False      False      False
565      ...      False      False      False      False
566      ...      False      False      False      False
567      ...      False      False      False      False
568      ...      False      False      False      False

```

```

      smoothness_worst compactness_worst concavity_worst \
0      False      False      False
1      False      False      False
2      False      False      False
3      False      False      False
4      False      False      False
..      ...      ...      ...
564      False      False      False
565      False      False      False
566      False      False      False
567      False      False      False
568      False      False      False

```

```

      concave points_worst symmetry_worst fractal_dimension_worst
0      False      False      False
1      False      False      False
2      False      False      False
3      False      False      False
4      False      False      False
..      ...      ...      ...
564      False      False      False
565      False      False      False
566      False      False      False
567      False      False      False
568      False      False      False

```

[569 rows x 32 columns]

```
[10]: pd.isna(data).sum()
```

```

[10]: id      0
      diagnosis  0
      radius_mean  0
      texture_mean  0
      perimeter_mean  0
      area_mean  0
      smoothness_mean  0
      compactness_mean  0
      concavity_mean  0
      concave points_mean  0
      symmetry_mean  0

```

```

fractal_dimension_mean    0
radius_se                 0
texture_se                0
perimeter_se              0
area_se                   0
smoothness_se             0
compactness_se            0
concavity_se              0
concave points_se         0
symmetry_se               0
fractal_dimension_se      0
radius_worst              0
texture_worst              0
perimeter_worst           0
area_worst                0
smoothness_worst          0
compactness_worst         0
concavity_worst           0
concave points_worst      0
symmetry_worst            0
fractal_dimension_worst   0
dtype: int64

```

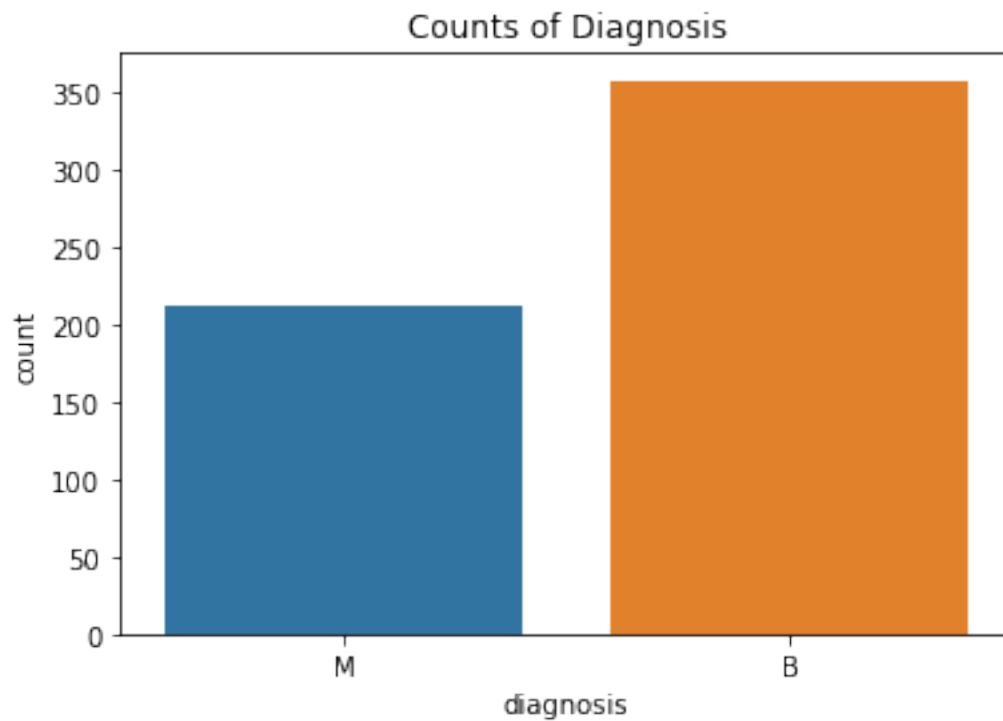
There are no missing values in this dataset.

### 0.3 Data Exploration

```
[11]: data2 = data.iloc[:,1:] #data2 dropped id
```

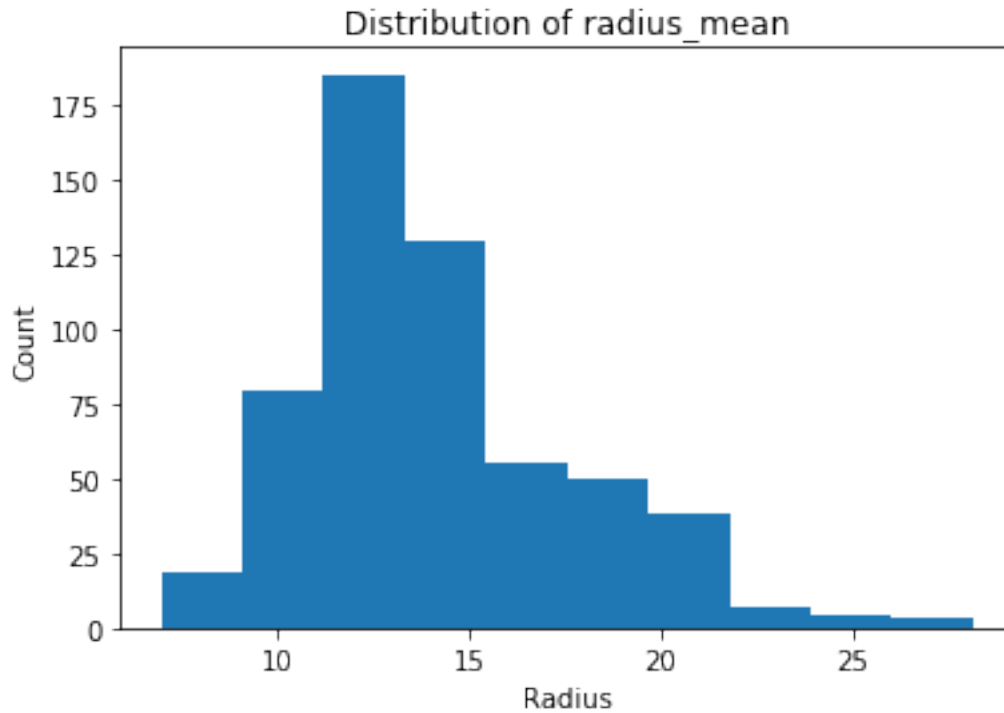
```
[12]: sns.countplot(x='diagnosis', data = data)
      plt.title( 'Counts of Diagnosis' )
```

```
[12]: Text(0.5, 1.0, 'Counts of Diagnosis')
```



Class distribution: 357 benign, 212 malignant.  
There are 357 benign cases and 212 malignant cases in the dataset.

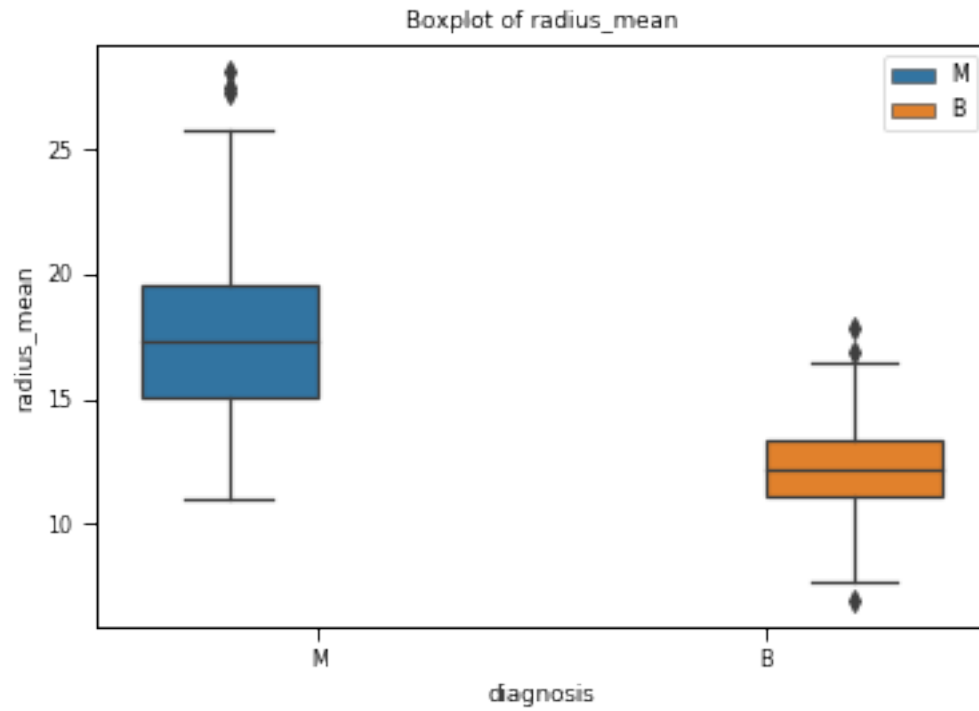
```
[13]: plt.hist( data['radius_mean'])  
      plt.xlabel('Radius')  
      plt.ylabel('Count')  
      plt.title( 'Distribution of radius_mean' )  
      plt.show()
```



radius\_mean is mostly distributed between 10-15.

```
[14]: sns.set_context('paper', font_scale=0.9)
sns.boxplot(x='diagnosis',y='radius_mean', data=data, hue='diagnosis')
plt.legend(loc=0)
plt.title( 'Boxplot of radius_mean' )
```

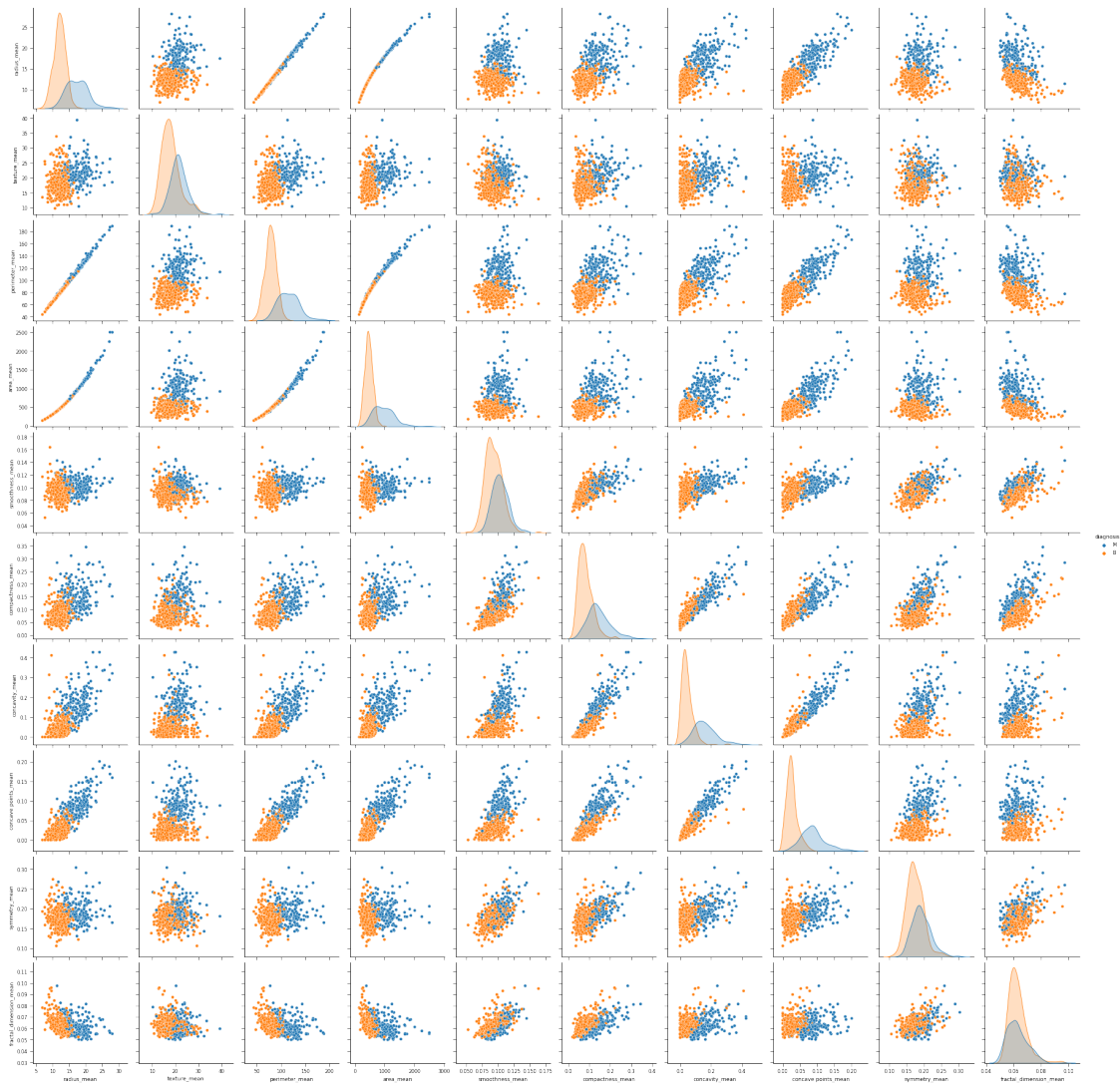
```
[14]: Text(0.5, 1.0, 'Boxplot of radius_mean')
```



From the boxplot above, we can easily tell that malignant tumors tend to have larger radius\_mean.

```
[15]: sns.pairplot(data2.iloc[:,0:11],hue='diagnosis')
```

```
[15]: <seaborn.axisgrid.PairGrid at 0x7f95e9107f60>
```



*From this pairplot, we can easily identify some patterns from the data.*

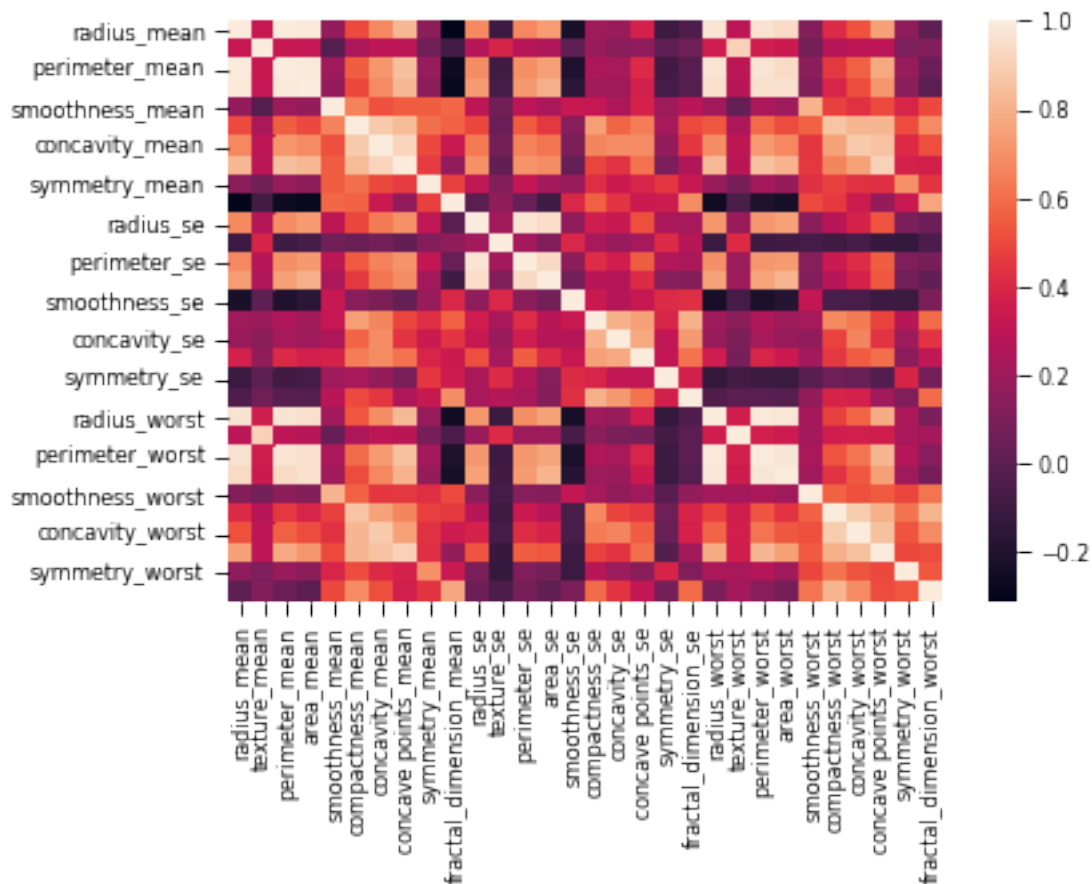
perimeter\_mean and radius\_mean are highly correlated. There is a strong positive linear relationship between them.

perimeter\_mean and area\_mean, perimeter\_mean and concavity\_mean, concavity\_mean and concave points\_mean are highly correlated too.

There is a huge difference between between benign cases and malignant cases in radius\_mean, perimeter\_mean, area\_mean, concavity\_mean, concave points\_mean. But not so much in fractal\_dimension\_mean. fractal\_dimension\_mean might be a bad indicator to distinguish benign cases and malignant cases.

```
[16]: sns.heatmap(data2.corr())
```

```
[16]: <matplotlib.axes._subplots.AxesSubplot at 0x7f95e90fef28>
```

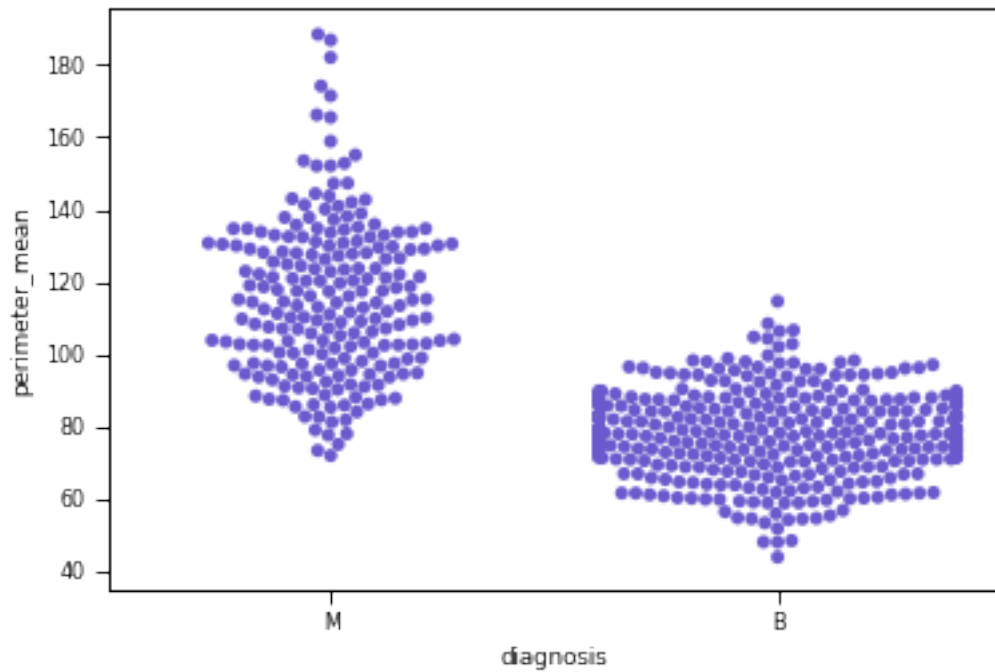


The lighter the color means the more the two features are correlated.

We can easily tell that features like `perimeter_mean` and `radius_mean` are highly correlated.

```
[17]: sns.swarmplot(x='diagnosis', y='perimeter_mean', data=data, color='slateblue')
```

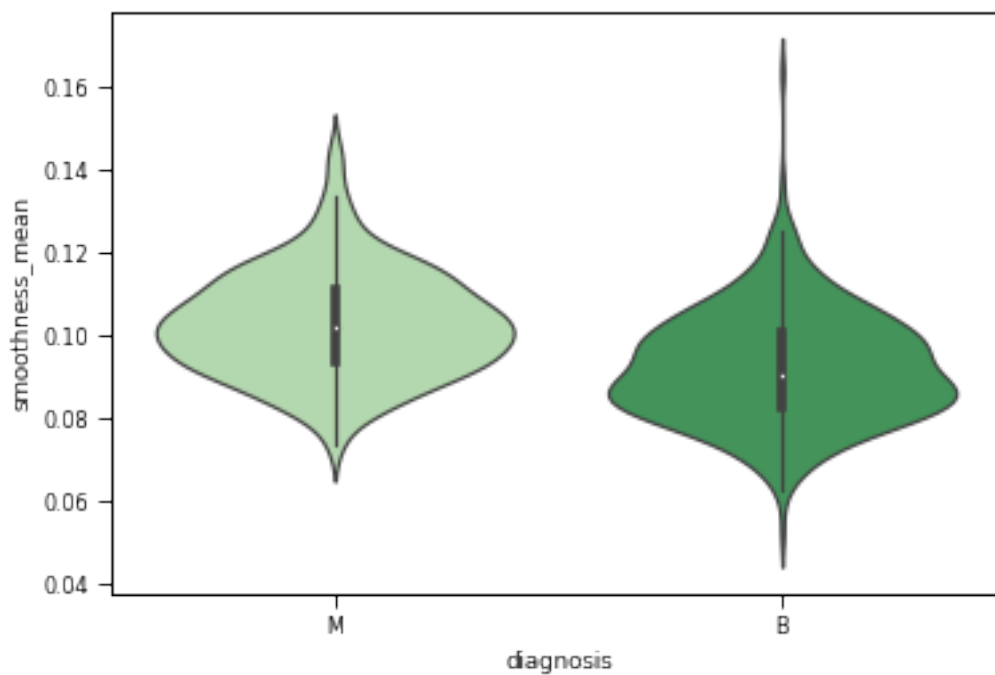
```
[17]: <matplotlib.axes._subplots.AxesSubplot at 0x7f95e9bc5668>
```



perimeter\_mean is higher in malignant tumors.

```
[18]: sns.violinplot(x='diagnosis', y='smoothness_mean', data=data, palette='Greens')
```

```
[18]: <matplotlib.axes._subplots.AxesSubplot at 0x7f95d93504e0>
```

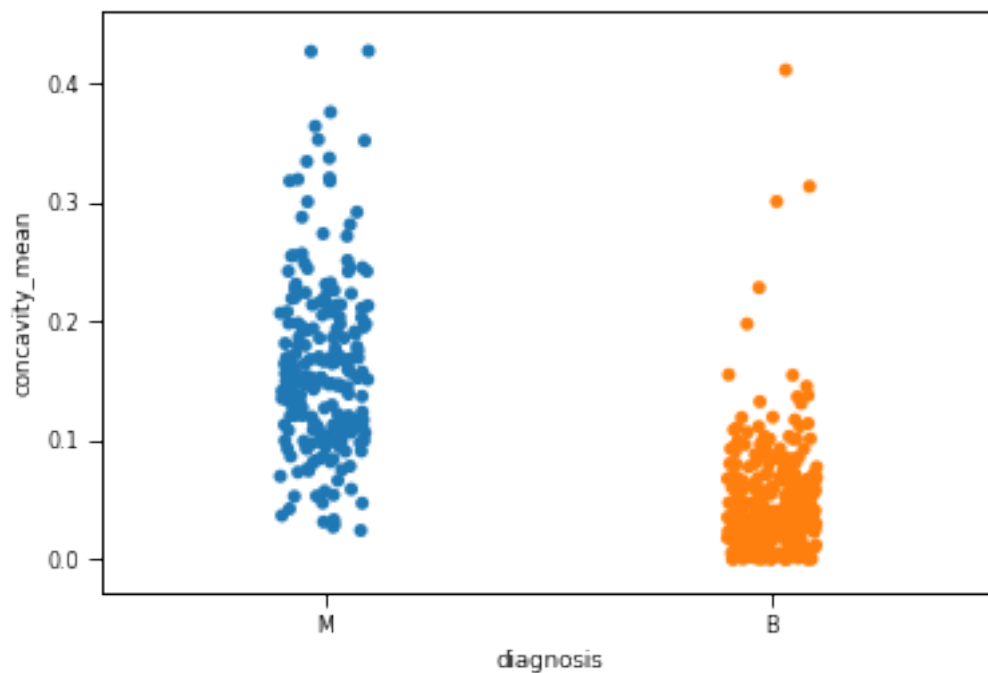




smoothness\_mean is higher in malignant tumors, but not by a huge margin compared to other features.

```
[19]: sns.stripplot(x='diagnosis', y='concavity_mean', data=data, jitter=True)
```

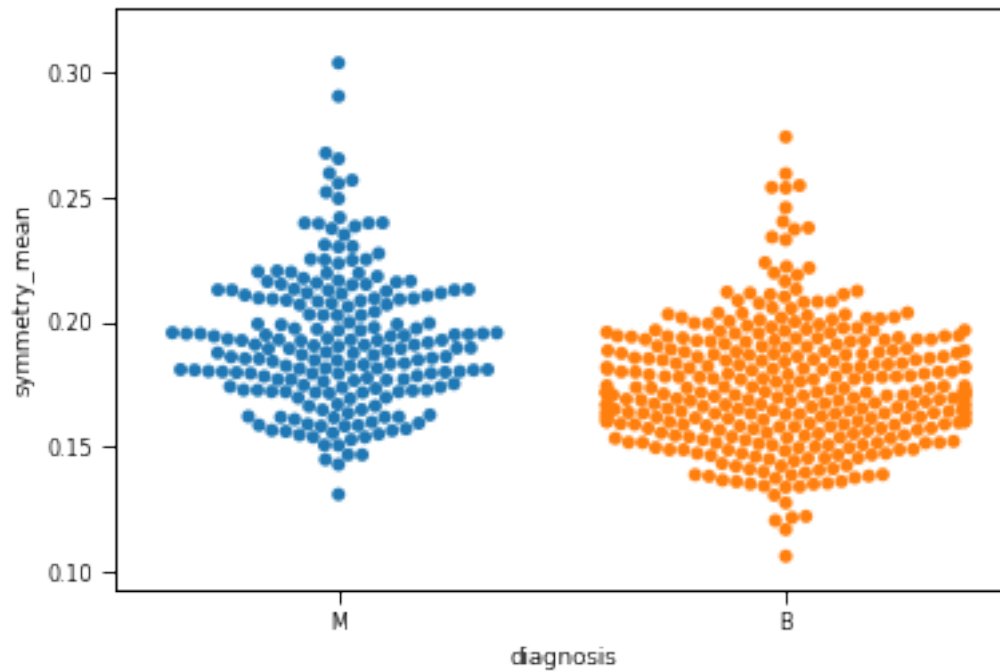
```
[19]: <matplotlib.axes._subplots.AxesSubplot at 0x7f95cbfc9390>
```



concavity\_mean is higher in malignant tumors.

```
[20]: sns.swarmplot(y='symmetry_mean', data=data, x='diagnosis')
```

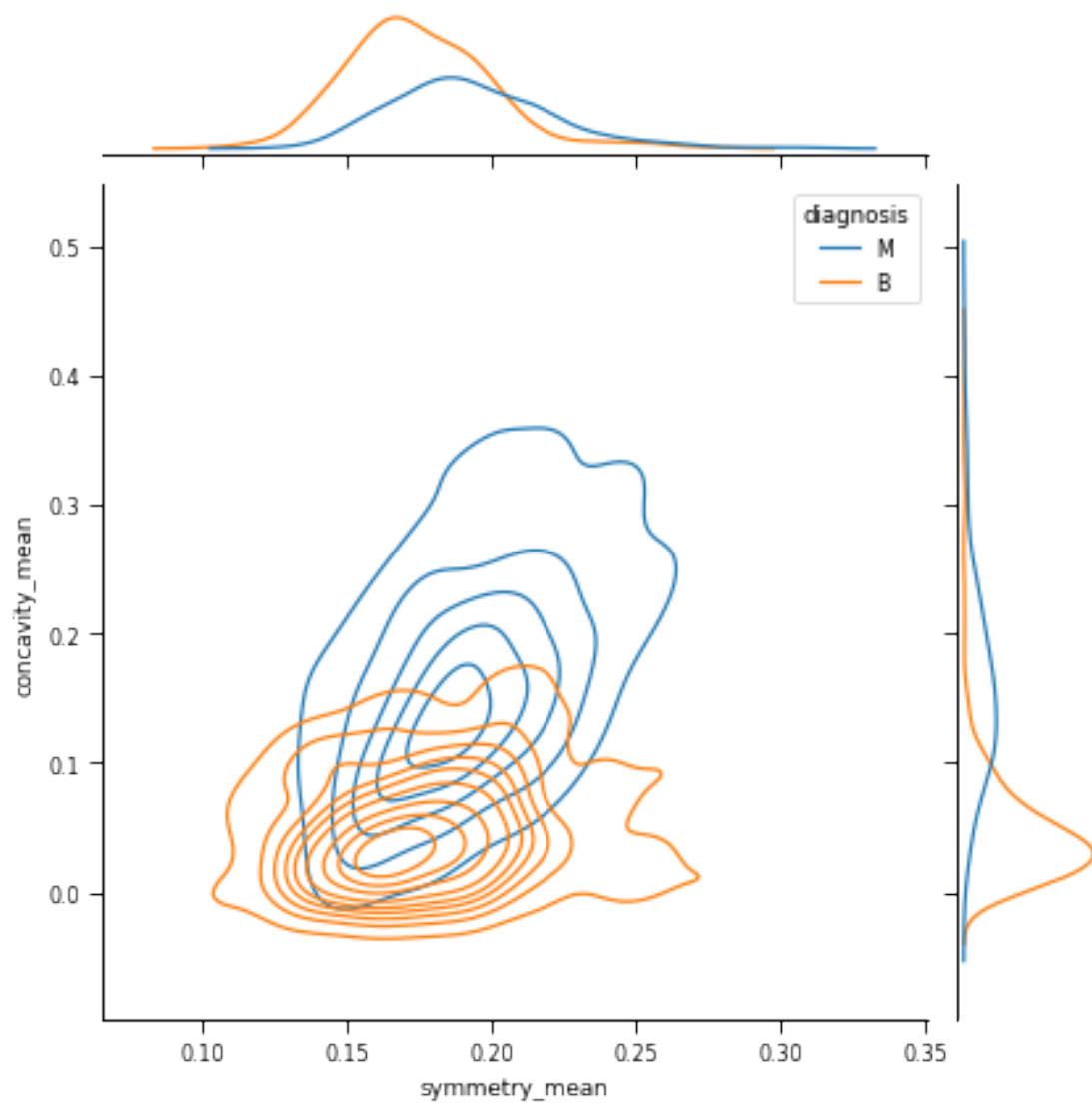
```
[20]: <matplotlib.axes._subplots.AxesSubplot at 0x7f95b8c062e8>
```



The difference in symmetry\_mean between benign and malignant tumors is not very huge, but malignant tumors tend to have higher symmetry\_mean.

```
[21]: sns.jointplot(x='symmetry_mean',y='concavity_mean', data=data,kind='kde',hue='diagnosis')
```

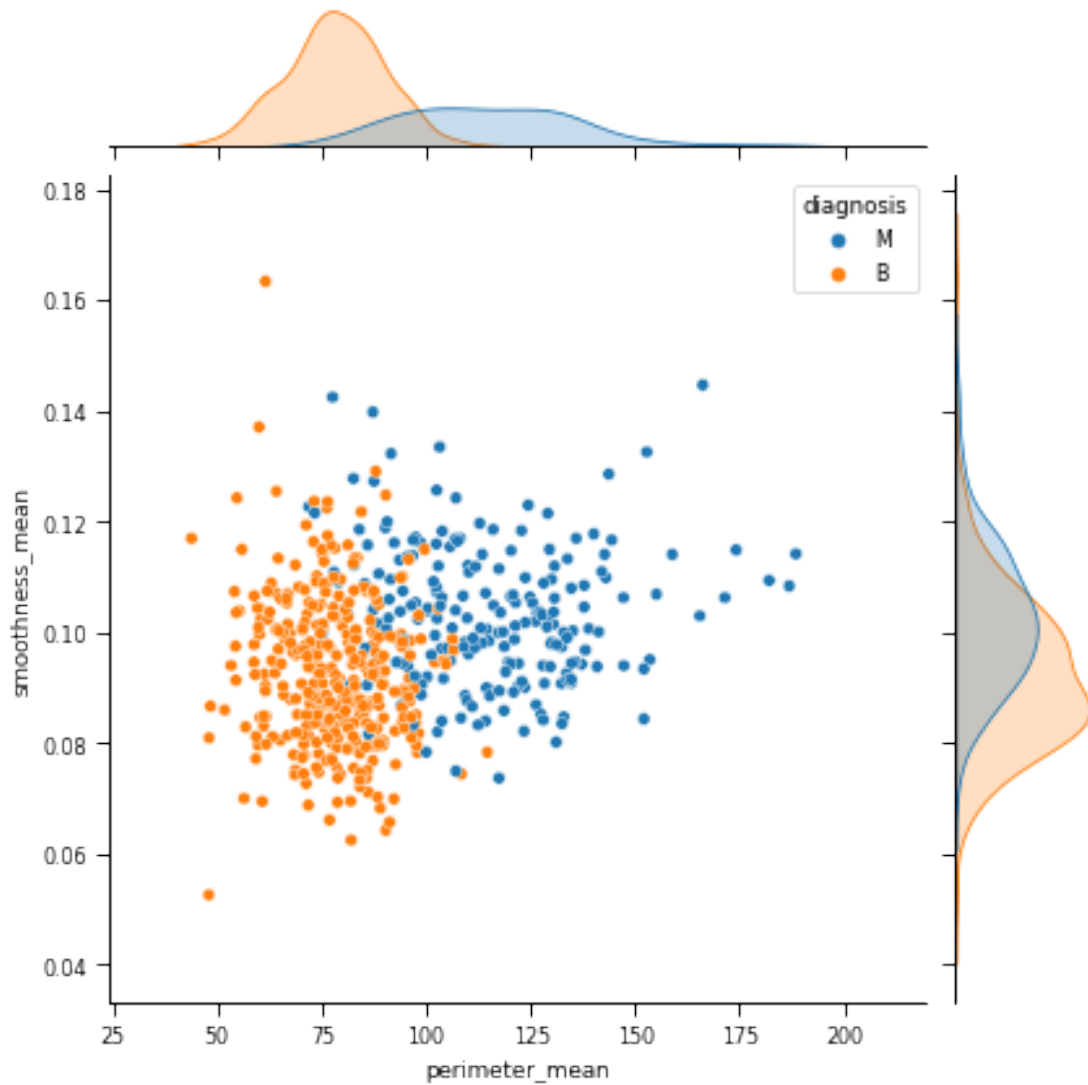
```
[21]: <seaborn.axisgrid.JointGrid at 0x7f95d9428198>
```



Malignant tumors seem to have higher symmetry\_mean and concavity\_mean.

```
[22]: sns.jointplot(x='perimeter_mean',y='smoothness_mean', data=data,hue='diagnosis')
```

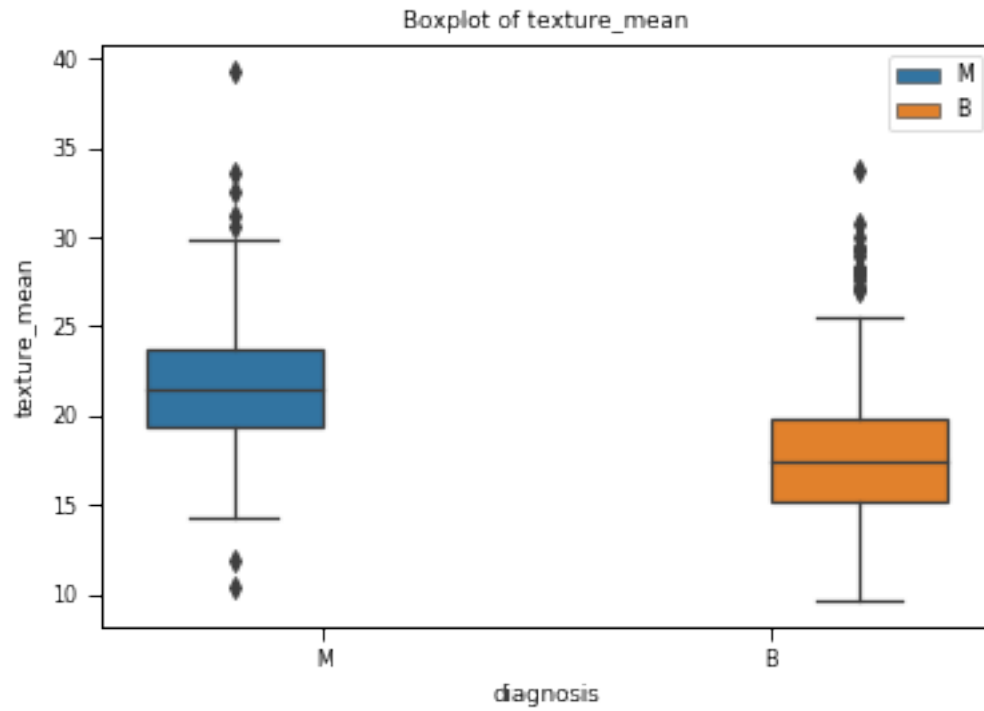
```
[22]: <seaborn.axisgrid.JointGrid at 0x7f95cc332c50>
```



Malignant tumors seem to have higher perimeter\_mean and smoothness\_mean. And they don't seem to be correlated.

```
[23]: sns.set_context('paper', font_scale=0.9)
sns.boxplot(x='diagnosis',y='texture_mean', data=data, hue='diagnosis')
plt.legend(loc=0)
plt.title( 'Boxplot of texture_mean' )
```

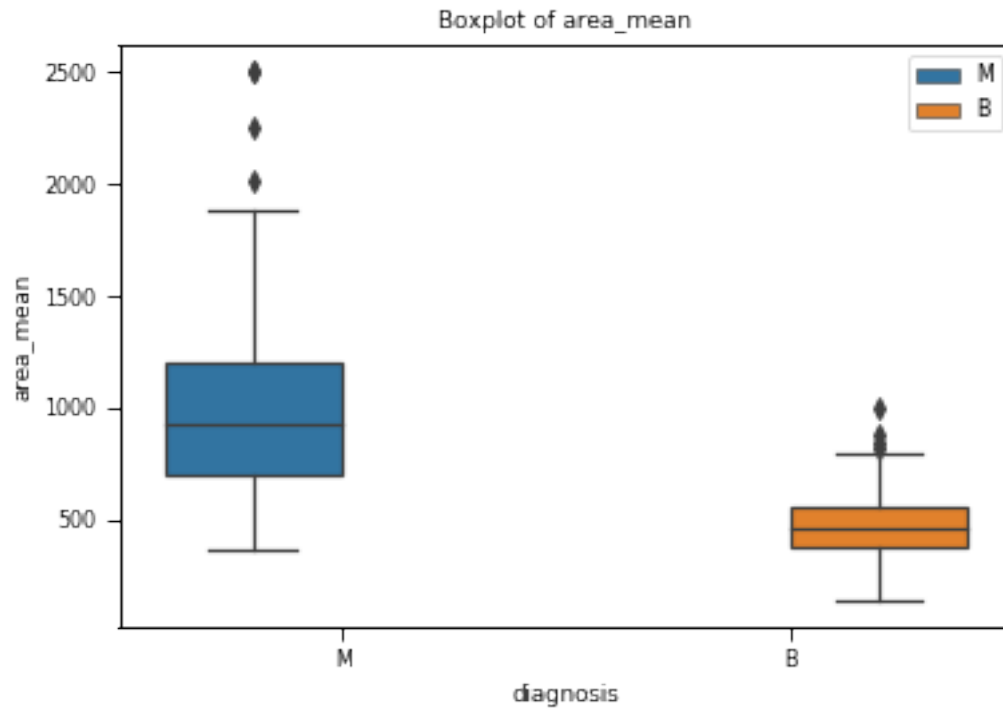
```
[23]: Text(0.5, 1.0, 'Boxplot of texture_mean')
```



Malignant tumors have higher texture\_mean.

```
[24]: sns.set_context('paper', font_scale=0.9)
sns.boxplot(x='diagnosis',y='area_mean', data=data, hue='diagnosis')
plt.legend(loc=0)
plt.title( 'Boxplot of area_mean' )
```

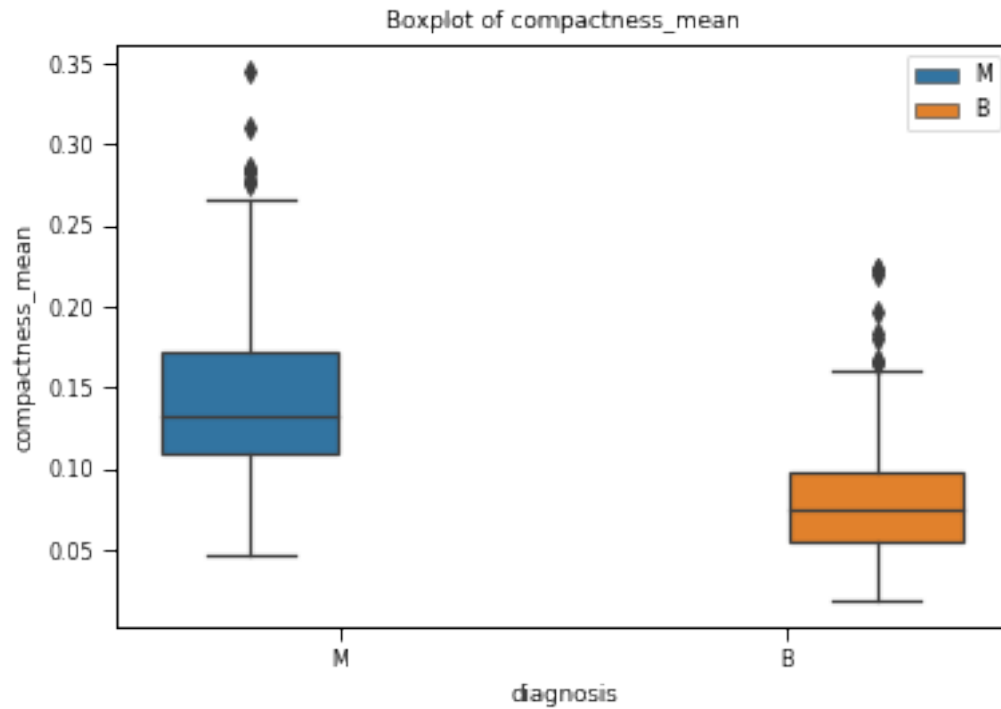
```
[24]: Text(0.5, 1.0, 'Boxplot of area_mean')
```



Malignant tumors have higher area\_mean.

```
[25]: sns.set_context('paper', font_scale=0.9)
sns.boxplot(x='diagnosis',y='compactness_mean', data=data, hue='diagnosis')
plt.legend(loc=0)
plt.title( 'Boxplot of compactness_mean' )
```

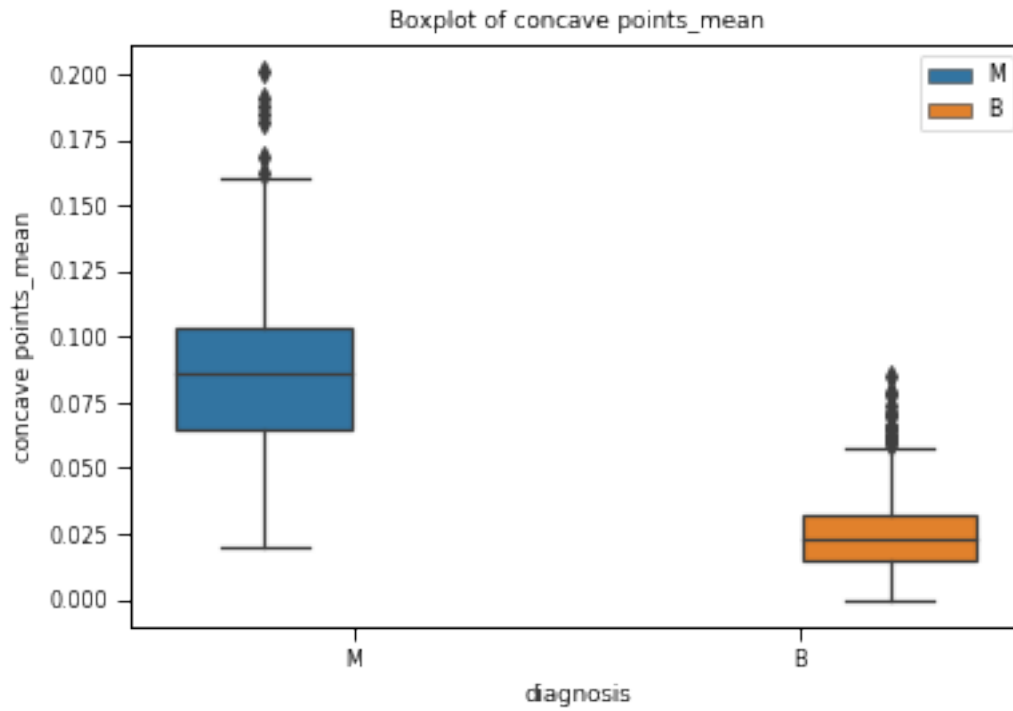
```
[25]: Text(0.5, 1.0, 'Boxplot of compactness_mean')
```



Malignant tumors have higher compactness\_mean.

```
[26]: sns.set_context('paper', font_scale=0.9)
sns.boxplot(x='diagnosis',y='concave points_mean', data=data, hue='diagnosis')
plt.legend(loc=0)
plt.title( 'Boxplot of concave points_mean' )
```

```
[26]: Text(0.5, 1.0, 'Boxplot of concave points_mean')
```

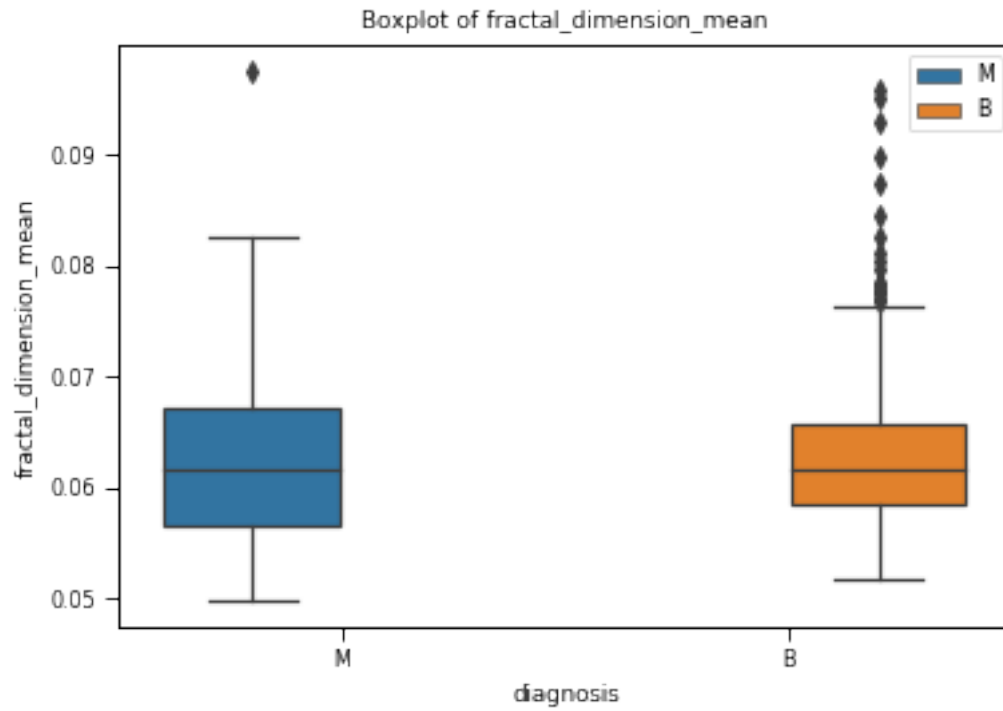


Malignant tumors have higher concave points\_mean.

```
[27]: sns.set_context('paper', font_scale=0.9)
sns.boxplot(x='diagnosis',y='fractal_dimension_mean', data=data,
            hue='diagnosis')
plt.legend(loc=0)
plt.title( 'Boxplot of fractal_dimension_mean' )
```

```
[27]: Text(0.5, 1.0, 'Boxplot of fractal_dimension_mean')
```

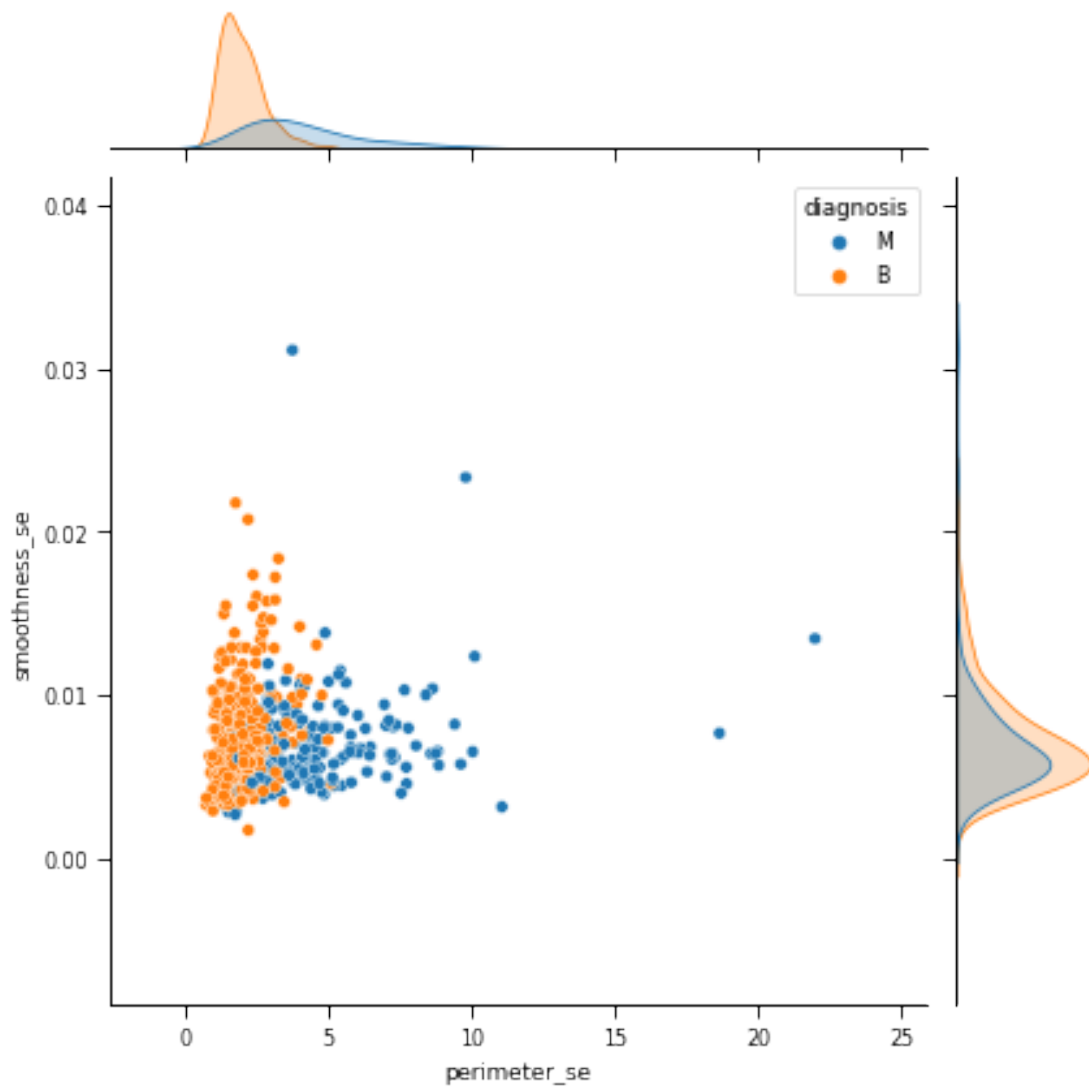




There is no noticeable difference in fractal\_dimension\_mean between benign and malignant tumors.

```
[28]: sns.jointplot(x='perimeter_se',y='smoothness_se', data=data,hue='diagnosis')
```

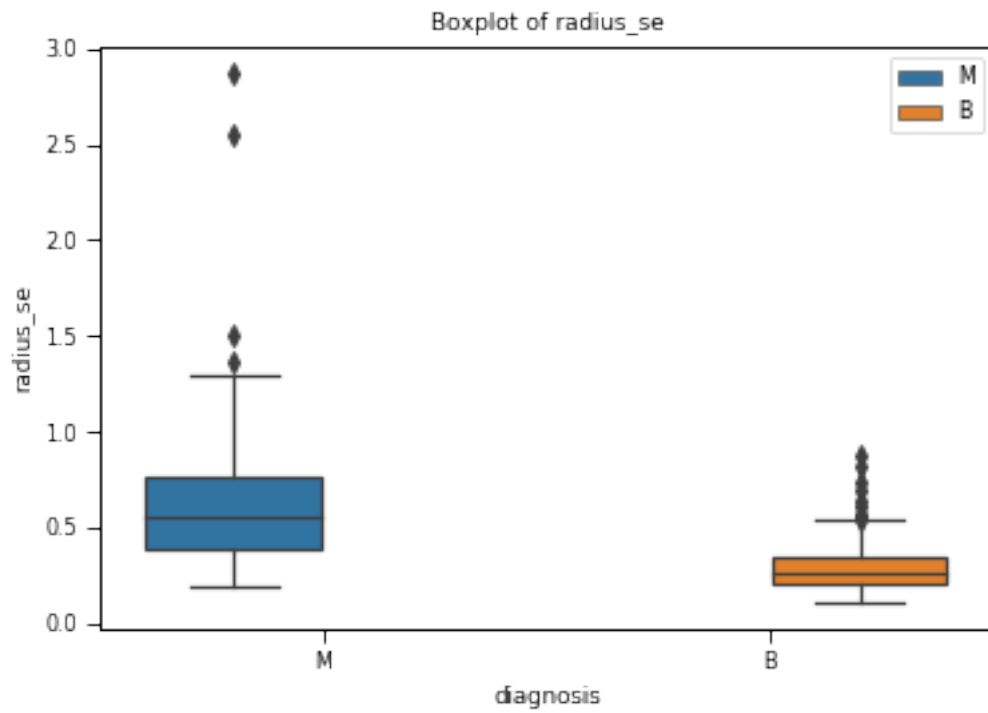
```
[28]: <seaborn.axisgrid.JointGrid at 0x7f95e9f43b70>
```



Malignant tumors tend to have higher `perimeter_se`, but no noticeable difference in `smoothness_se`.

```
[29]: sns.set_context('paper', font_scale=0.9)
sns.boxplot(x='diagnosis', y='radius_se', data=data, hue='diagnosis')
plt.legend(loc=0)
plt.title( 'Boxplot of radius_se' )
```

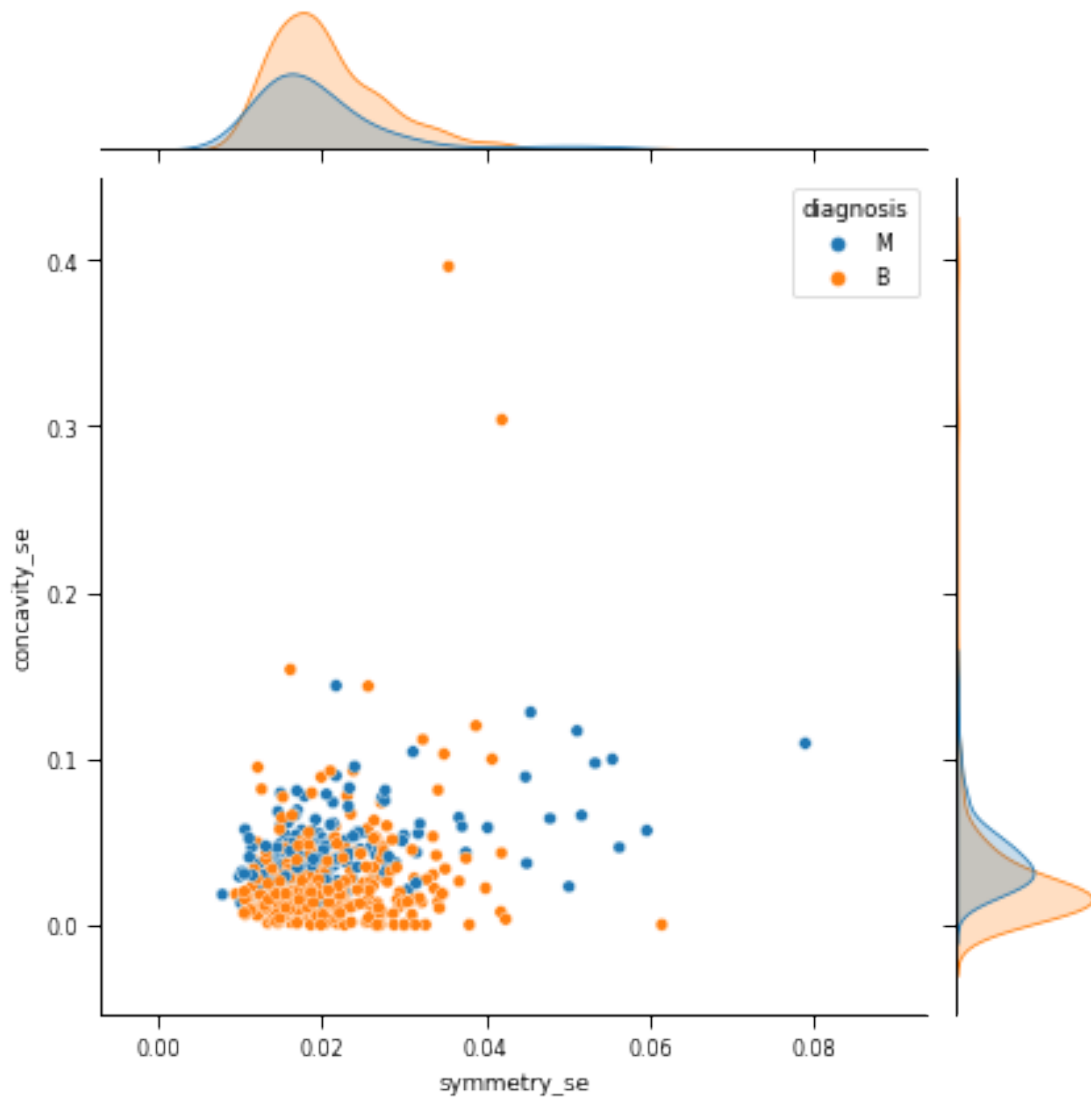
```
[29]: Text(0.5, 1.0, 'Boxplot of radius_se')
```



Malignant tumors have higher radius\_se.

```
[30]: sns.jointplot(x='symmetry_se',y='concavity_se', data=data,hue='diagnosis')
```

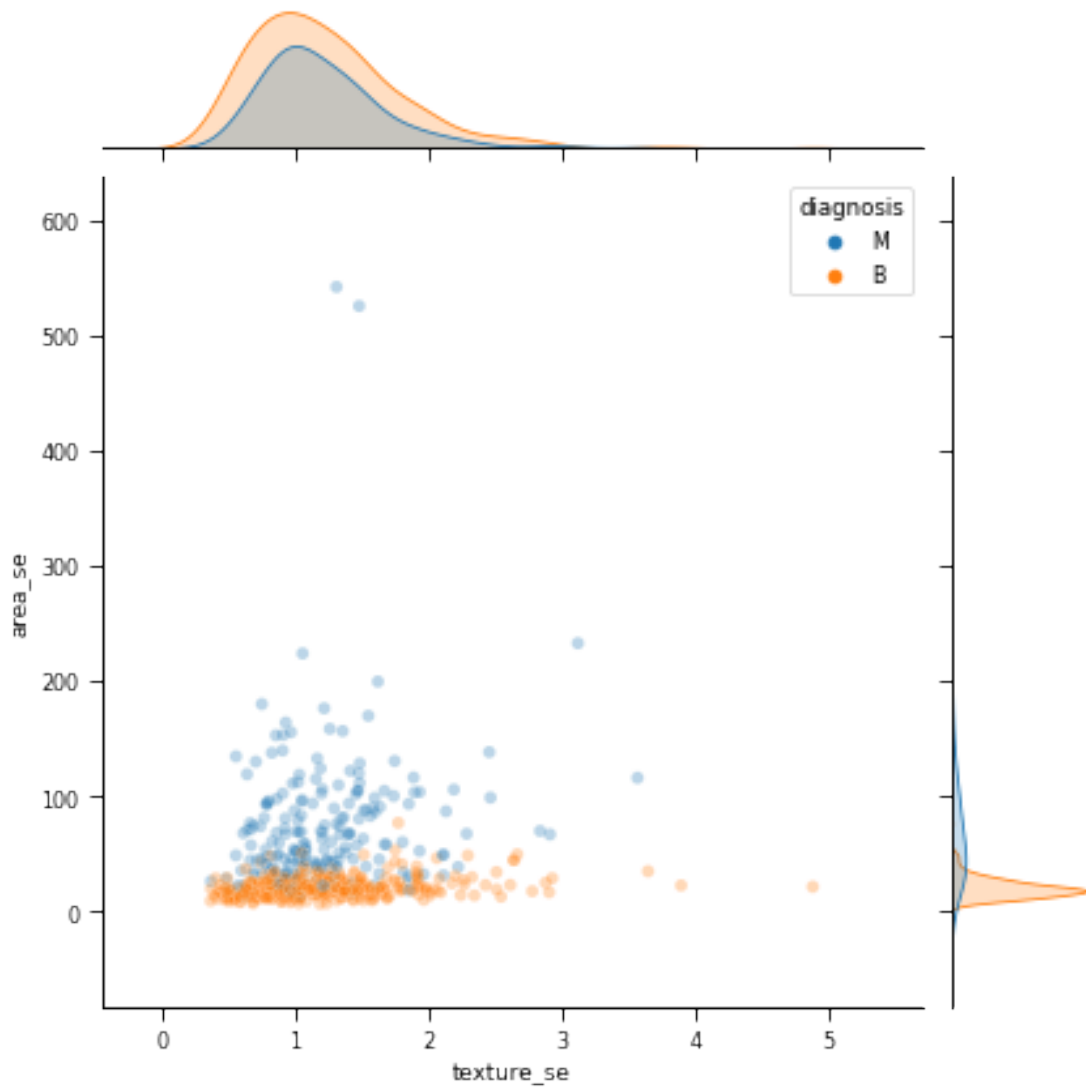
```
[30]: <seaborn.axisgrid.JointGrid at 0x7f95d99419e8>
```



There is no big difference between benign and malignant tumors in symmetry\_se. Malignant tumors may have higher concavity\_se.

```
[31]: sns.jointplot(x='texture_se',y='area_se', data=data, alpha=0.3,hue='diagnosis')
```

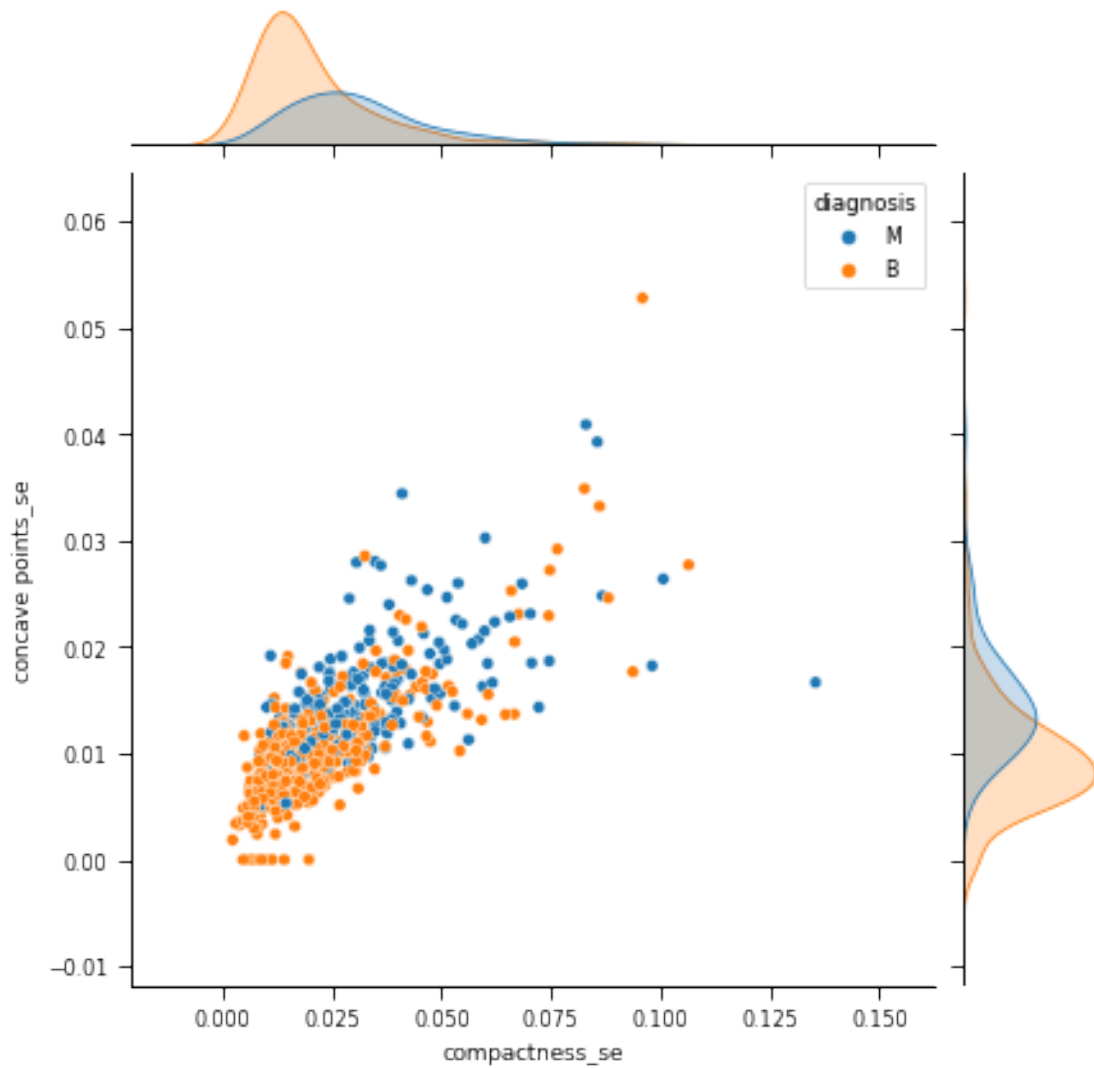
```
[31]: <seaborn.axisgrid.JointGrid at 0x7f95cc452eb8>
```



Malignant tumors have higher area\_se, but no noticeable texture\_se difference.

```
[32]: sns.jointplot(data=data, x="compactness_se", y="concave points_se",  
    ↪ hue='diagnosis')
```

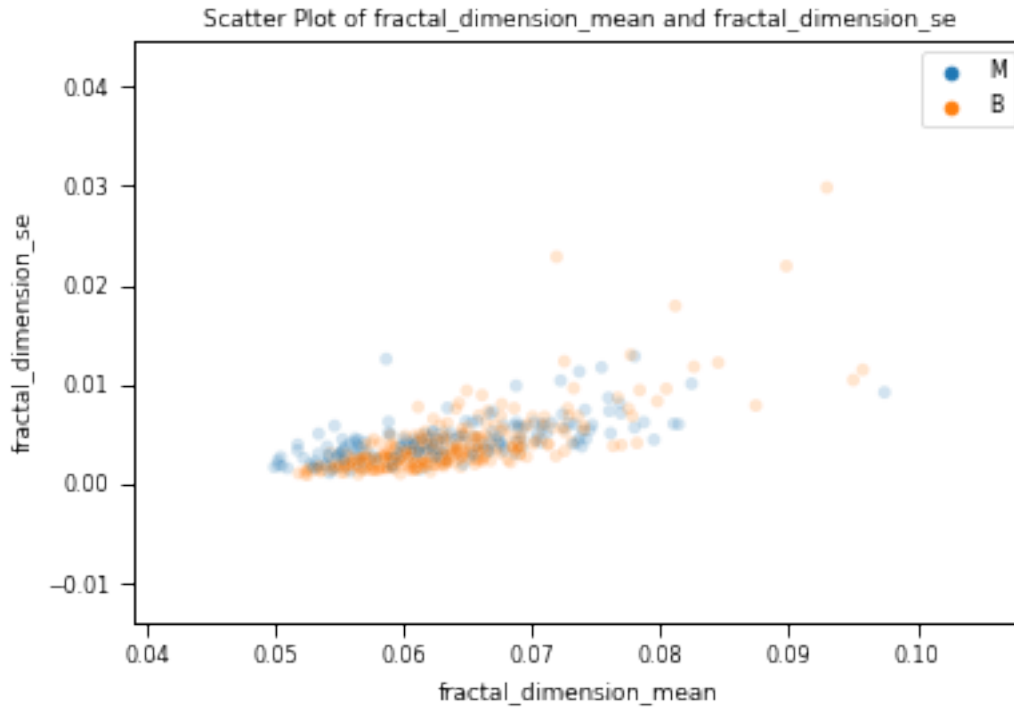
```
[32]: <seaborn.axisgrid.JointGrid at 0x7f95d9a8a7b8>
```



Malignant tumors have higher compactness\_se and concave points\_se. And these two features are highly correlated.

```
[33]: sns.set_context('paper', font_scale=0.9)
sns.scatterplot( x='fractal_dimension_mean',y='fractal_dimension_se',
↳data=data, hue='diagnosis', alpha=0.2)
plt.legend(loc=0)
plt.title( 'Scatter Plot of fractal_dimension_mean and fractal_dimension_se' )
```

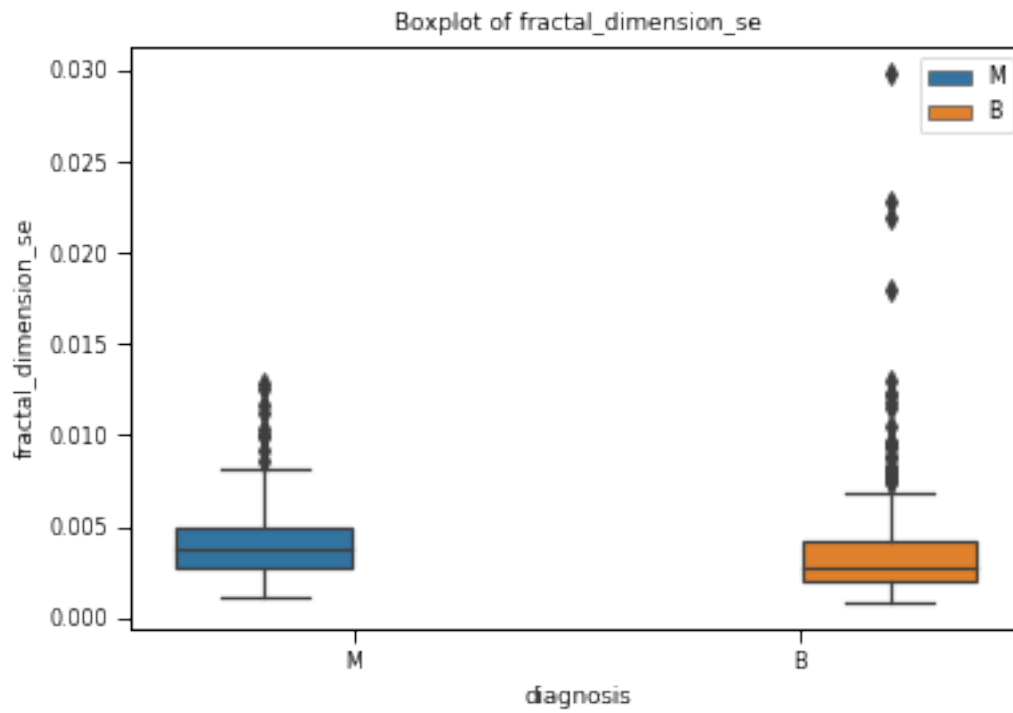
```
[33]: Text(0.5, 1.0, 'Scatter Plot of fractal_dimension_mean and
fractal_dimension_se')
```



fractal\_dimension\_mean and fractal\_dimension\_se are highly correlated. But there is no big fractal\_dimension\_mean or fractal\_dimension\_se difference between benign and malignant tumors.

```
[34]: sns.set_context('paper', font_scale=0.9)
sns.boxplot(x='diagnosis', y='fractal_dimension_se', data=data, hue='diagnosis')
plt.legend(loc=0)
plt.title( 'Boxplot of fractal_dimension_se' )
```

```
[34]: Text(0.5, 1.0, 'Boxplot of fractal_dimension_se')
```

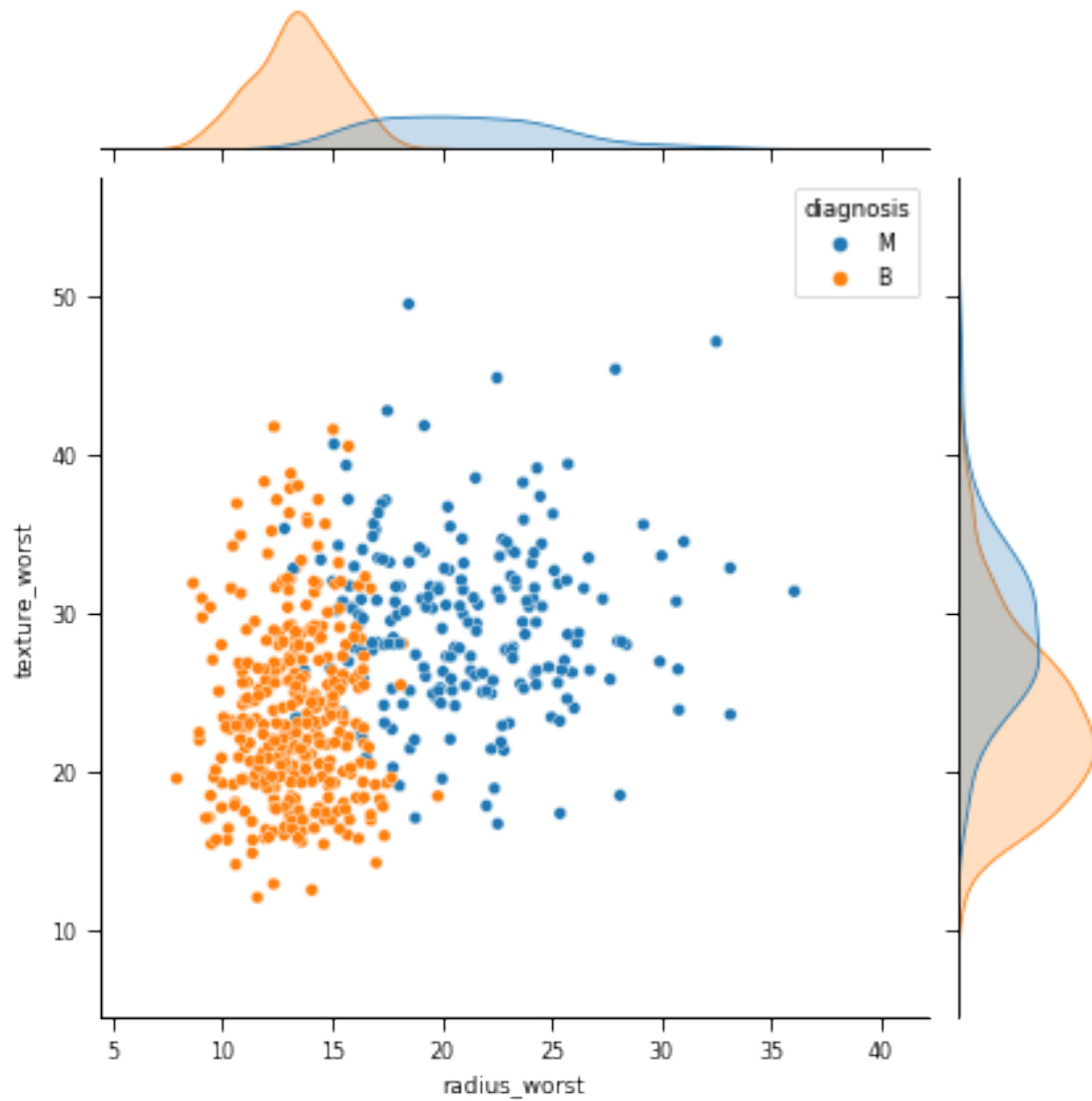


fractal\_dimension\_se doesn't vary much between benign tumors and malignant tumors.

```
[35]: sns.jointplot(x='radius_worst',y='texture_worst', data=data,hue='diagnosis')
```

```
[35]: <seaborn.axisgrid.JointGrid at 0x7f95b8eebeb8>
```

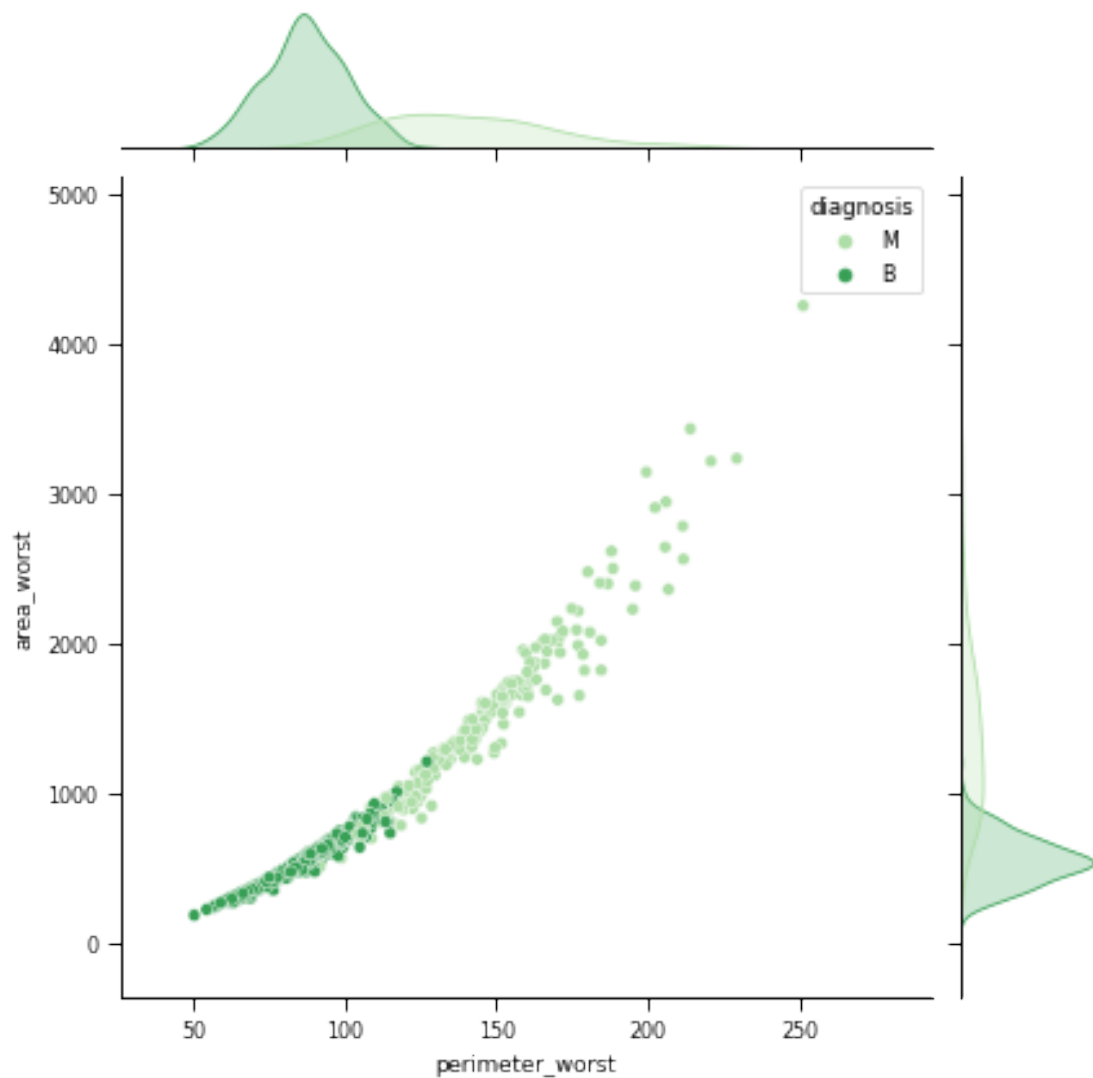




Malignant tumors have higher radius\_worst and texture\_worst.

```
[36]: sns.jointplot(x='perimeter_worst',y='area_worst',  
→data=data,hue='diagnosis',palette='Greens')
```

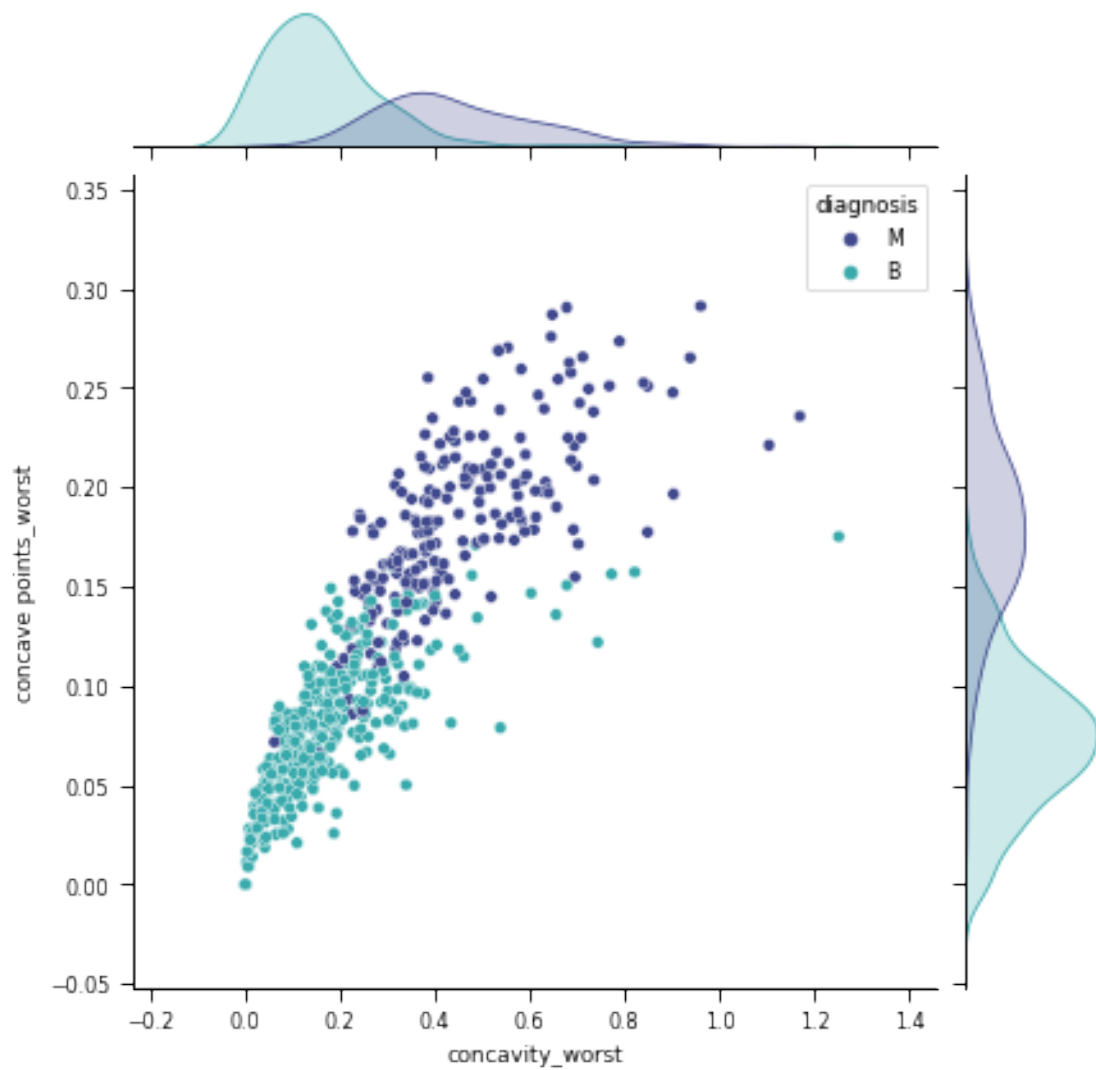
```
[36]: <seaborn.axisgrid.JointGrid at 0x7f95d9bc4e48>
```



Malignant tumors have higher perimeter\_worst and area\_worst. These two features are highly correlated.

```
[37]: sns.jointplot(x='concavity_worst',y='concave points_worst',  
→data=data,hue='diagnosis',palette='mako')
```

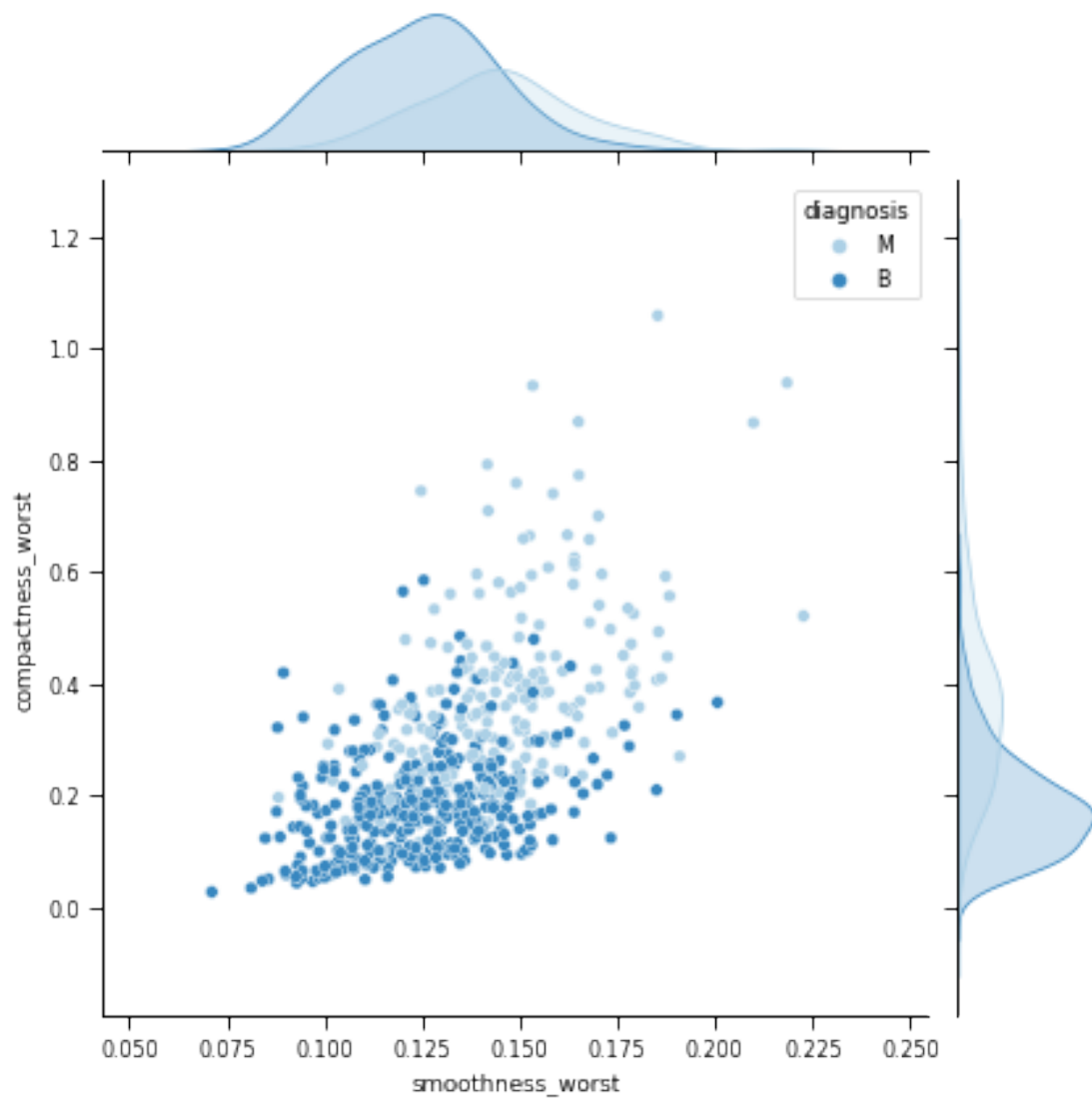
```
[37]: <seaborn.axisgrid.JointGrid at 0x7f95d9ddeb00>
```



Malignant tumors have higher concavity\_worst and concave points\_worst. These two features are highly correlated.

```
[38]: sns.jointplot(x='smoothness_worst',y='compactness_worst',  
→data=data,hue='diagnosis',palette='Blues')
```

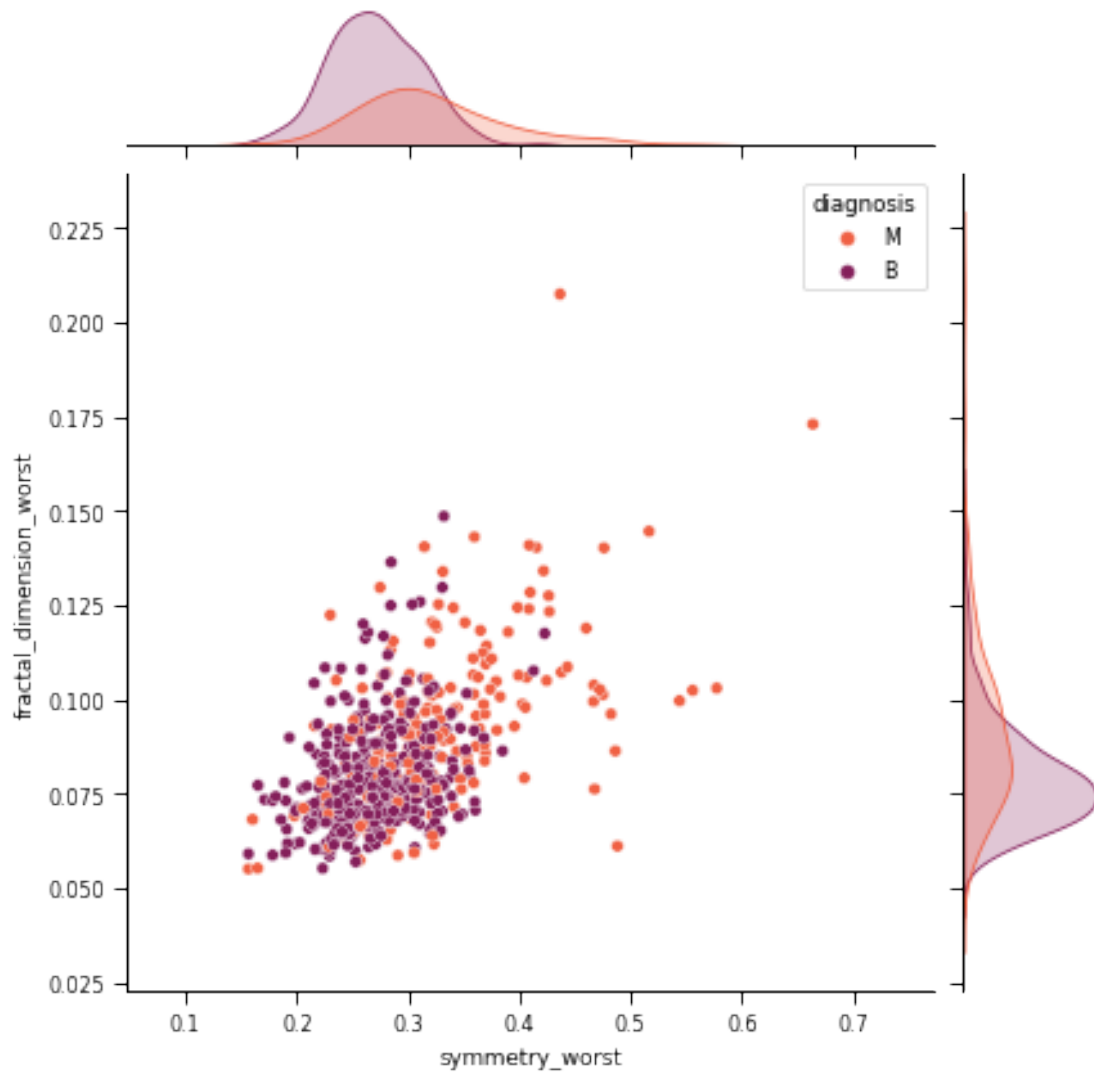
```
[38]: <seaborn.axisgrid.JointGrid at 0x7f95ea5d5a90>
```



Malignant tumors have higher smoothness\_worst and compactness\_worst. These two features are somewhat correlated.

```
[39]: sns.jointplot(x='symmetry_worst',y='fractal_dimension_worst',  
→data=data,hue='diagnosis',palette='rocket_r')
```

```
[39]: <seaborn.axisgrid.JointGrid at 0x7f95d9ce6978>
```



Malignant tumors have higher symmetry\_worst. Not much difference on fractal\_dimension\_worst.

## 0.4 Data Modelling

```
[58]: data = data2  
data.replace('M',1,inplace=True)
```

```
[59]: data.replace('B',0,inplace=True)
```

### 0.4.1 Training set and test set split

```
[60]: seed      = 0                                # pick a seed to keep it
      ↪consistent
df_train = data.sample( frac=0.7, random_state=seed ) # 0.7 means we used 70%
      ↪as the training set
df_test  = data.drop( df_train.index )              # "all the rows not in
      ↪df_train"
```

### 0.4.2 Logistic Regression

```
[61]: predictors = df_train.iloc[:,1:]
      response   = df_train['diagnosis']
```

```
[62]: # Import the module
      from sklearn.linear_model import LogisticRegression

      # Create a model and fit it to the data
      model = LogisticRegression()
      model.fit( predictors, response )
```

```
[62]: LogisticRegression(C=1.0, class_weight=None, dual=False, fit_intercept=True,
      intercept_scaling=1, l1_ratio=None, max_iter=100,
      multi_class='warn', n_jobs=None, penalty='l2',
      random_state=None, solver='warn', tol=0.0001, verbose=0,
      warm_start=False)
```

### 0.4.3 Test the model

```
[63]: predictors_test = df_test.iloc[:,1:]
      response_test    = df_test['diagnosis']
```

```
[64]: # Use the model to predict the output variable based on the input variables:
df_test['Prediction'] = model.predict( predictors_test )
# Check whether each prediction was correct or not, and show the results:
df_test['Correct'] = df_test['Prediction'] == response_test
df_test
```

```
[64]:
```

	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	\
0	1	17.99	10.38	122.80	1001.0	
3	1	11.42	20.38	77.58	386.1	
9	1	12.46	24.04	83.97	475.9	
11	1	15.78	17.89	103.60	781.0	
16	1	14.68	20.13	94.74	684.5	
...	...	...	...	...	...	
551	0	11.13	22.44	71.49	378.4	
556	0	10.16	19.59	64.73	311.7	
558	0	14.59	22.68	96.39	657.1	

559	0	11.51	23.93	74.52	403.5
568	0	7.76	24.54	47.92	181.0

	smoothness_mean	compactness_mean	concavity_mean	concave points_mean	\
0	0.11840	0.27760	0.300100	0.14710	
3	0.14250	0.28390	0.241400	0.10520	
9	0.11860	0.23960	0.227300	0.08543	
11	0.09710	0.12920	0.099540	0.06606	
16	0.09867	0.07200	0.073950	0.05259	
..	...	...	...	...	
551	0.09566	0.08194	0.048240	0.02257	
556	0.10030	0.07504	0.005025	0.01116	
558	0.08473	0.13300	0.102900	0.03736	
559	0.09261	0.10210	0.111200	0.04105	
568	0.05263	0.04362	0.000000	0.00000	

	symmetry_mean	...	perimeter_worst	area_worst	smoothness_worst	\
0	0.2419	...	184.60	2019.0	0.16220	
3	0.2597	...	98.87	567.7	0.20980	
9	0.2030	...	97.65	711.4	0.18530	
11	0.1842	...	136.50	1299.0	0.13960	
16	0.1586	...	123.40	1138.0	0.14640	
..	...	...	...	...	...	
551	0.2030	...	77.80	436.6	0.10870	
556	0.1791	...	67.88	347.3	0.12650	
558	0.1454	...	105.90	733.5	0.10260	
559	0.1388	...	82.28	474.2	0.12980	
568	0.1587	...	59.16	268.6	0.08996	

	compactness_worst	concavity_worst	concave points_worst	symmetry_worst	\
0	0.66560	0.71190	0.26540	0.4601	
3	0.86630	0.68690	0.25750	0.6638	
9	1.05800	1.10500	0.22100	0.4366	
11	0.56090	0.39650	0.18100	0.3792	
16	0.18710	0.29140	0.16090	0.3029	
..	...	...	...	...	
551	0.17820	0.15640	0.06413	0.3169	
556	0.12000	0.01005	0.02232	0.2262	
558	0.31710	0.36620	0.11050	0.2258	
559	0.25170	0.36300	0.09653	0.2112	
568	0.06444	0.00000	0.00000	0.2871	

	fractal_dimension_worst	Prediction	Correct
0	0.11890	1	True
3	0.17300	0	False
9	0.20750	1	True
11	0.10480	1	True

16	0.08216	1	True
..	...	...	...
551	0.08032	0	True
556	0.06742	0	True
558	0.08004	0	True
559	0.08732	0	True
568	0.07039	0	True

[171 rows x 33 columns]

```
[65]: df_test['Correct'].sum() / len(df_test)
```

```
[65]: 0.9649122807017544
```

The model reached 96.49% accuracy. Our model is pretty accurate.

```
[66]: # True positive means the answer and the prediction were positive.
```

```
TP = ( df_test['diagnosis'] & df_test['Prediction'] ).sum()
```

```
# Similarly for the other three.
```

```
TN = ( ~df_test['diagnosis'] & ~df_test['Prediction'] ).sum()
```

```
FP = ( ~df_test['diagnosis'] & df_test['Prediction'] ).sum()
```

```
FN = ( df_test['diagnosis'] & ~df_test['Prediction'] ).sum()
```

```
# Precision and recall are defined using the formulas above.
```

```
precision = TP / ( TP + FP )
```

```
recall = TP / ( TP + FN )
```

```
precision, recall
```

```
[66]: (0.9838709677419355, 0.9242424242424242)
```

The model has a precision as 98.39%, and recall as 92.42%.

## 0.5 Summary

In this report, I explored a breast cancer dataset with 30 features including 'radius\_mean', 'texture\_mean', 'perimeter\_mean', 'area\_mean', 'smoothness\_mean', 'compactness\_mean', 'concavity\_mean', 'concave points\_mean', 'symmetry\_mean', 'fractal\_dimension\_mean', 'radius\_se', 'texture\_se', 'perimeter\_se', 'area\_se', 'smoothness\_se', 'compactness\_se', 'concavity\_se', 'concave points\_se', 'symmetry\_se', 'fractal\_dimension\_se', 'radius\_worst', 'texture\_worst', 'perimeter\_worst', 'area\_worst', 'smoothness\_worst', 'compactness\_worst', 'concavity\_worst', 'concave points\_worst', 'symmetry\_worst', 'fractal\_dimension\_worst'.

They are computed for each cell nucleus:

- radius (mean of distances from center to points on the perimeter)
- texture (standard deviation of gray-scale values)
- perimeter
- area
- smoothness (local variation in radius lengths)
- compactness ( $\text{perimeter}^2 / \text{area} - 1.0$ )
- concavity (severity of concave portions of the contour)



- concave points (number of concave portions of the contour)
- symmetry
- fractal dimension (“coastline approximation” - 1)

The mean, standard error and “worst” or largest (mean of the three largest values) of these features were computed for each image.

Malignant tumors tend to have higher ‘radius\_mean’, ‘texture\_mean’, ‘perimeter\_mean’, ‘area\_mean’, ‘smoothness\_mean’, ‘compactness\_mean’, ‘concavity\_mean’, ‘concave points\_mean’, ‘symmetry\_mean’, ‘radius\_se’, ‘perimeter\_se’, ‘area\_se’, ‘compactness\_se’, ‘concavity\_se’, ‘concave points\_se’, ‘radius\_worst’, ‘texture\_worst’, ‘perimeter\_worst’, ‘area\_worst’, ‘smoothness\_worst’, ‘compactness\_worst’, ‘concavity\_worst’, ‘concave points\_worst’, ‘symmetry\_worst’. But malignant tumors and benign tumors tend to have similar ‘fractal\_dimension\_mean’, ‘fractal\_dimension\_se’, ‘fractal\_dimension\_worst’, ‘smoothness\_se’, ‘symmetry\_se’, ‘texture\_se’.

Based on our study, these features can help us identify malignant tumors and alert patients.

In the last part of my research, I developed a logistic regression model that reached 96.49% accuracy. We can use this model to predict if someone has breast cancer according to these features of her tumor and further assist modern medicine.