In [1]:
```
# importing the required libraries for the project
import numpy as np
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
from scipy import stats
import warnings
warnings.filterwarnings("ignore")
from scipy import stats
from sklearn.model_selection import train_test_split
from sklearn.linear_model import LogisticRegression
from sklearn.model_selection import KFold
from sklearn import metrics
from sklearn.linear_model import LogisticRegression
from sklearn.model_selection import train_test_split
```

In [2]:
```
# read file
df=pd.read_csv('breast-cancer.csv')
```

In [3]:
```
df.head()
```

Out[3]:

	id	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean	compactness_mean	concavity_
0	842302	M	17.99	10.38	122.80	1001.0	0.11840	0.27760	0
1	842517	M	20.57	17.77	132.90	1326.0	0.08474	0.07864	0
2	84300903	M	19.69	21.25	130.00	1203.0	0.10960	0.15990	0
3	84348301	M	11.42	20.38	77.58	386.1	0.14250	0.28390	0
4	84358402	M	20.29	14.34	135.10	1297.0	0.10030	0.13280	0

5 rows × 32 columns

In [4]:
```
df.shape
```

Out[4]:
```
(569, 32)
```

In [5]:
```
df.tail()
```

Out[5]:
```
         id  diagnosis  radius_mean  texture_mean  perimeter_mean  area_mean  smoothness_mean  compactness_mean  concavity_
564  926424          M        21.56         22.39          142.00     1479.0          0.11100           0.11590        0.2
565  926682          M        20.13         28.25          131.20     1261.0          0.09780           0.10340        0.1
566  926954          M        16.60         28.08          108.30      858.1          0.08455           0.10230        0.0
567  927241          M        20.60         29.33          140.10     1265.0          0.11780           0.27700        0.3
568   92751          B         7.76         24.54           47.92      181.0          0.05263           0.04362        0.0

5 rows × 32 columns
```

In [6]:
```
df.dtypes
```

Out[6]:
```
id                           int64
diagnosis                   object
radius_mean                float64
texture_mean               float64
perimeter_mean             float64
area_mean                  float64
smoothness_mean            float64
compactness_mean           float64
concavity_mean             float64
concave points_mean        float64
symmetry_mean              float64
fractal_dimension_mean     float64
radius_se                  float64
texture_se                 float64
perimeter_se               float64
area_se                    float64
smoothness_se              float64
compactness_se             float64
concavity_se               float64
concave points_se          float64
symmetry_se                float64
fractal_dimension_se       float64
radius_worst               float64
texture_worst              float64
perimeter_worst            float64
area_worst                 float64
smoothness_worst           float64
compactness_worst          float64
concavity_worst            float64
concave points_worst       float64
symmetry_worst             float64
fractal_dimension_worst    float64
dtype: object
```

Data cleaning

In [7]:
```
# check for missing values
df.isna().sum()
```

Out[7]:
```
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
```

```
No data is missing
```

In [8]:
```
# check for duplicates
df.duplicated().sum()
```

Out[8]:
```
0
```

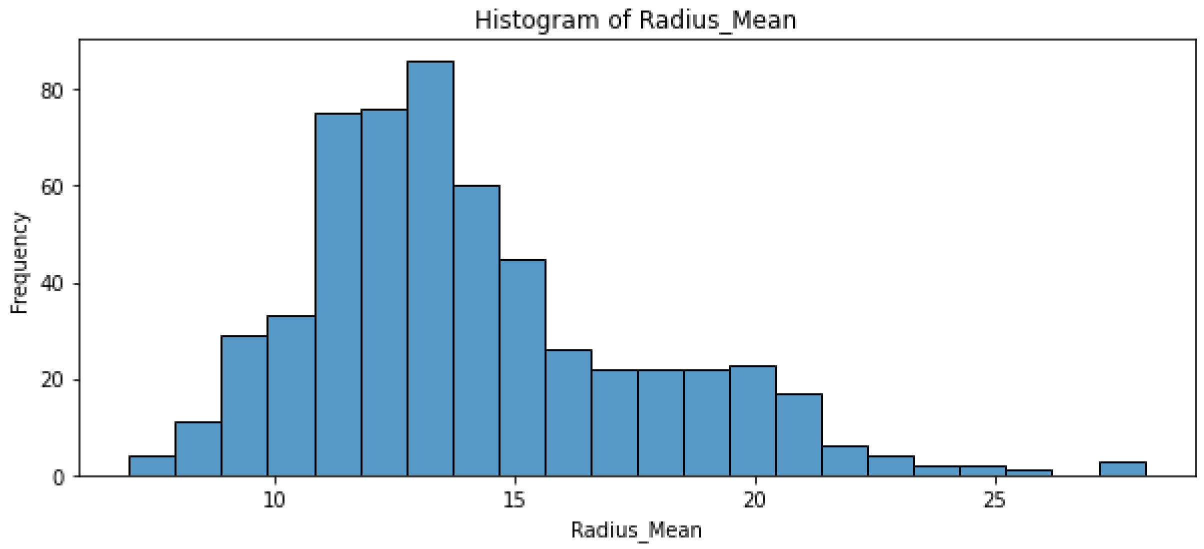
```
No duplicates found
```

EDA

Plotting Histograms

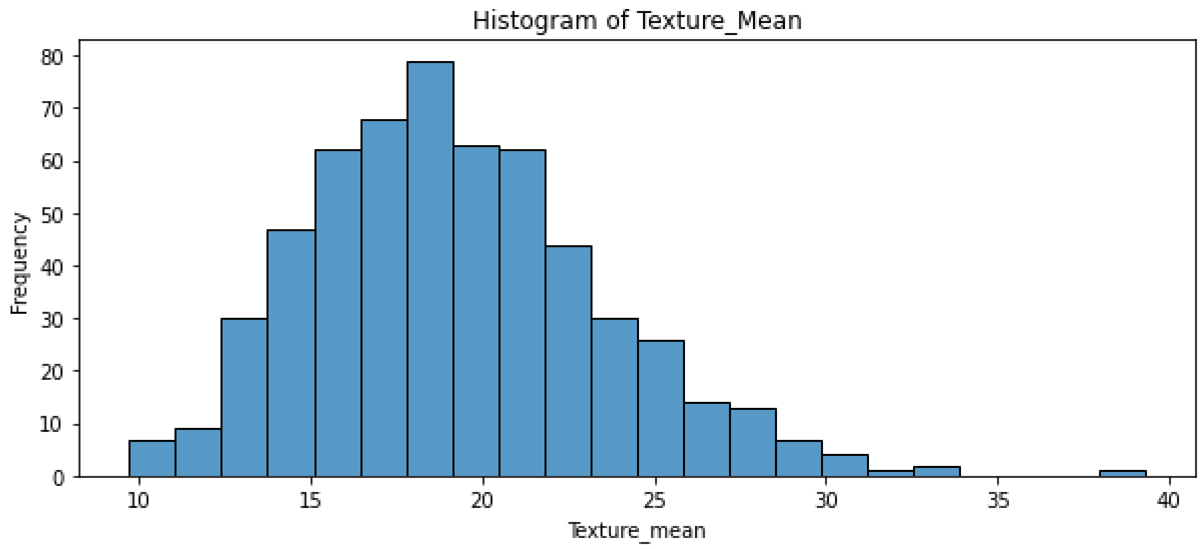
In [9]:
```
plt.figure(figsize=(10,4))
plt.xlabel("Radius_Mean")
plt.ylabel("Frequency")
plt.title("Histogram of Radius_Mean")
sns.histplot(df['radius_mean'])
```

Out[9]:
```
<AxesSubplot:title={'center':'Histogram of Radius_Mean'}, xlabel='Radius_Mean', ylabel='Frequency'>
```



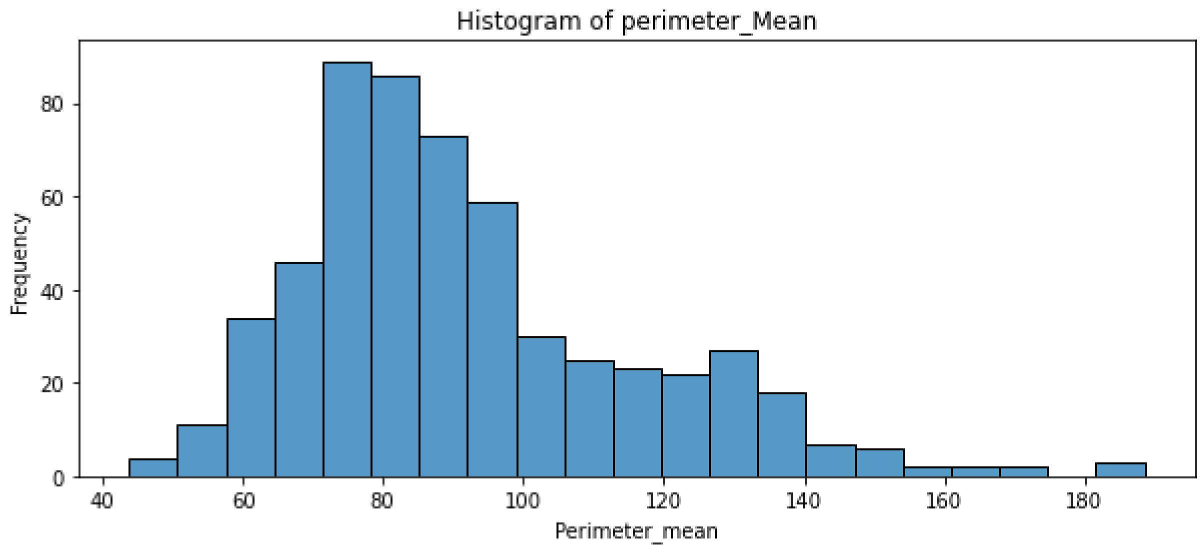
In [10]:
```
plt.figure(figsize=(10,4))
plt.xlabel("Texture_mean")
plt.ylabel("Frequency")
plt.title("Histogram of Texture_Mean")
sns.histplot(df['texture_mean'])
```

Out[10]:
```
<AxesSubplot:title={'center':'Histogram of Texture_Mean'}, xlabel='Texture_mean', ylabel='Frequency'>
```



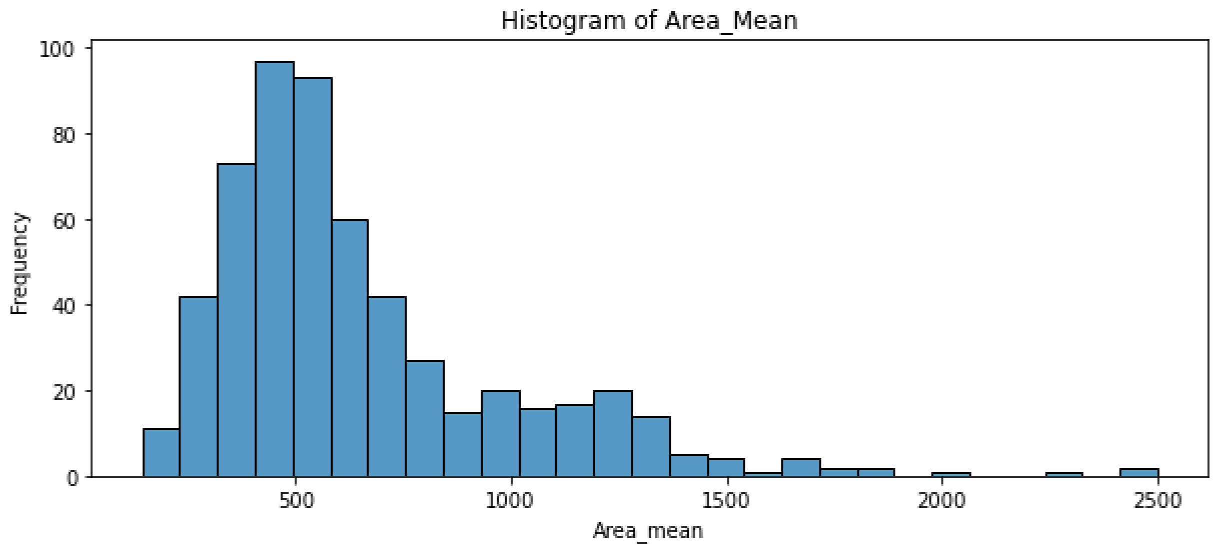
In [11]:
```
plt.figure(figsize=(10,4))
plt.xlabel("Perimeter_mean")
plt.ylabel("Frequency")
plt.title("Histogram of perimeter_Mean")
sns.histplot(df['perimeter_mean'])
```

Out[11]:
```
<AxesSubplot:title={'center':'Histogram of perimeter_Mean'}, xlabel='Perimeter_mean', ylabel='Frequency'>
```



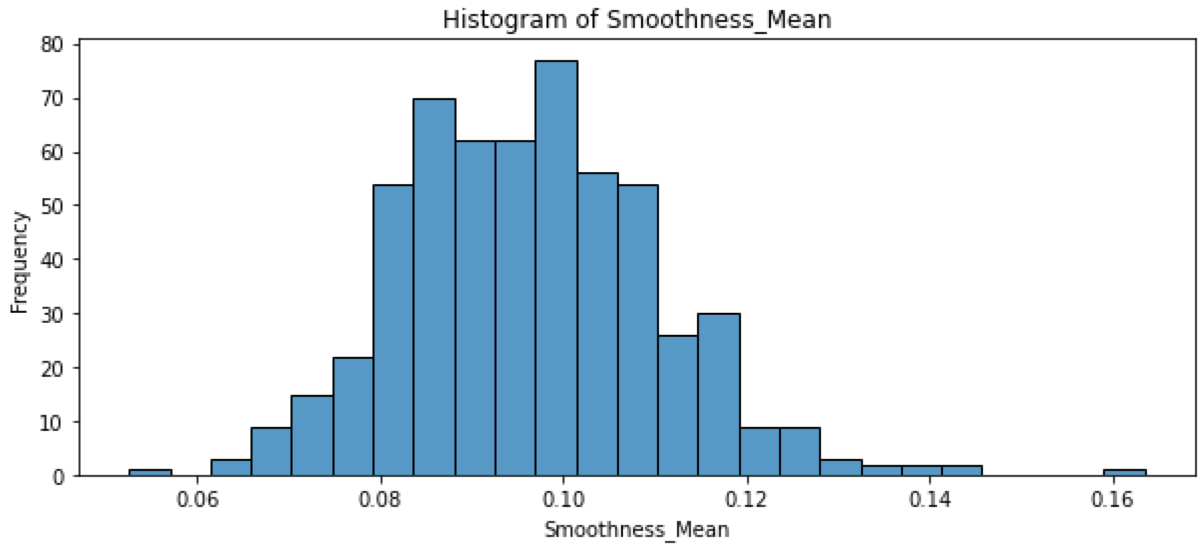
In [12]:
```
plt.figure(figsize=(10,4))
plt.xlabel("Area_mean")
plt.ylabel("Frequency")
plt.title("Histogram of Area_Mean")
sns.histplot(df['area_mean'])
```

Out[12]:
```
<AxesSubplot:title={'center':'Histogram of Area_Mean'}, xlabel='Area_mean', ylabel='Frequency'>
```



In [13]:
```
plt.figure(figsize=(10,4))
plt.xlabel("Smoothness_Mean")
plt.ylabel("Frequency")
plt.title("Histogram of Smoothness_Mean")
sns.histplot(df['smoothness_mean'])
```

Out[13]:
```
<AxesSubplot:title={'center':'Histogram of Smoothness_Mean'}, xlabel='Smoothness_Mean', ylabel='Frequency'>
```



```
Conclusion: From the above plots, i can conclude that the values are higher for malignant than benign. So the
size of malignant tumors are higher than the benign tumors.
```

Counting the benign and malignant tumors

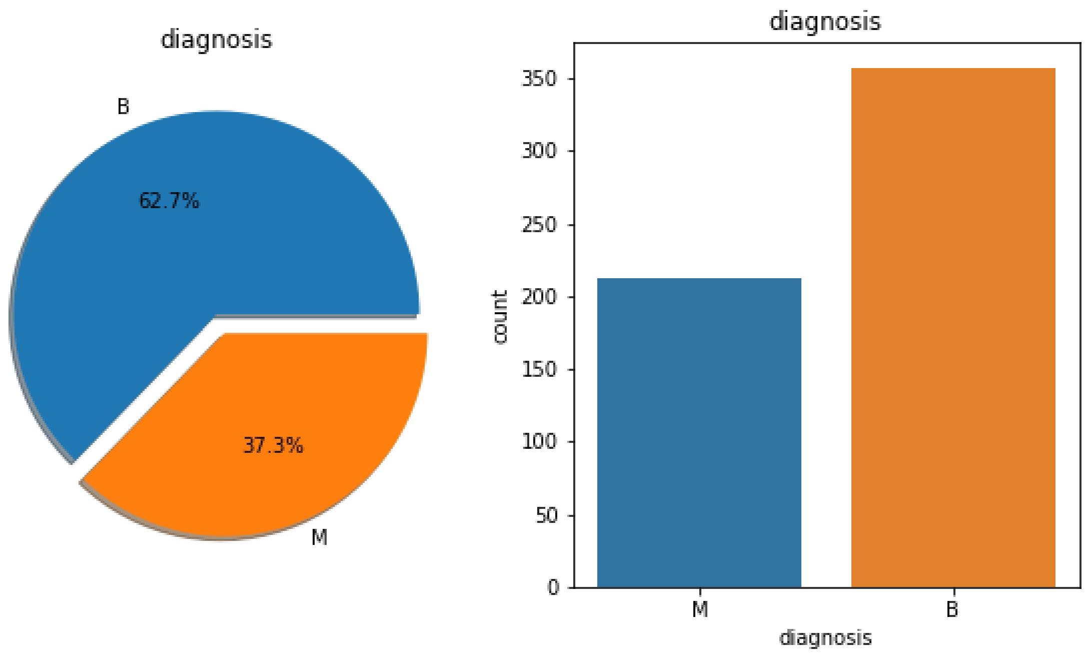
In [14]:
```
df.diagnosis.value_counts()
```

Out[14]:
```
B    357
M    212
Name: diagnosis, dtype: int64
```

```
Here,
Diagnosis (M = malignant, B = benign).
we observed there are 569 patient. 357 patients are benign that means they are not cancer affected and 212
patients are cancer.
```

In [15]:

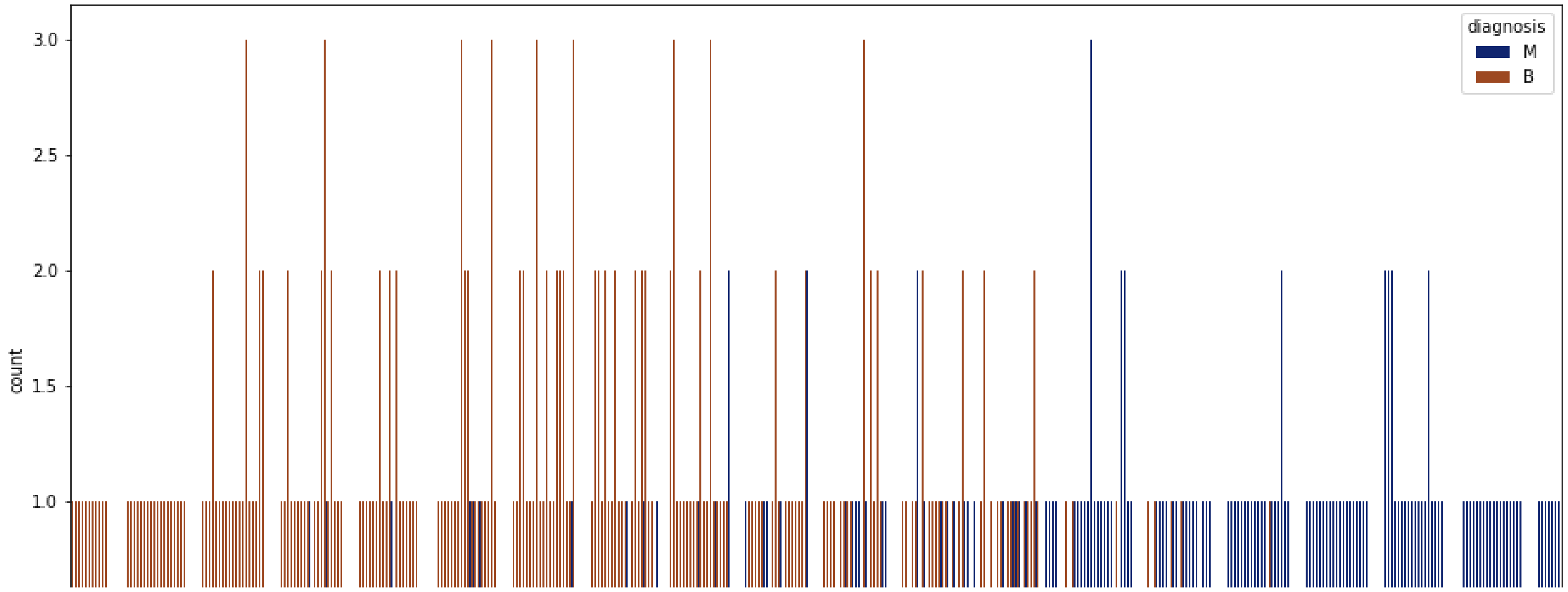
```
f,ax=plt.subplots(1,2,figsize=(10,5))
df['diagnosis'].value_counts().plot.pie(explode=[0,0.1],autopct='%1.1f%%',ax=ax[0],shadow=True)
ax[0].set_title('diagnosis')
ax[0].set_ylabel('')
sns.countplot('diagnosis',data=df,ax=ax[1])
ax[1].set_title('diagnosis')
plt.show()
```



```
It is evident that there are more patients who are not affected by cancer disease.
Here, 62.7% patients are not affected by cancer and 37.3% patients are affected by cancer.
```

In [16]:
```
plt.figure(figsize=(16,8))
sns.countplot(df['radius_mean'],hue=df['diagnosis'],palette='dark')
```

Out[16]:
```
<AxesSubplot:xlabel='radius_mean', ylabel='count'>
```

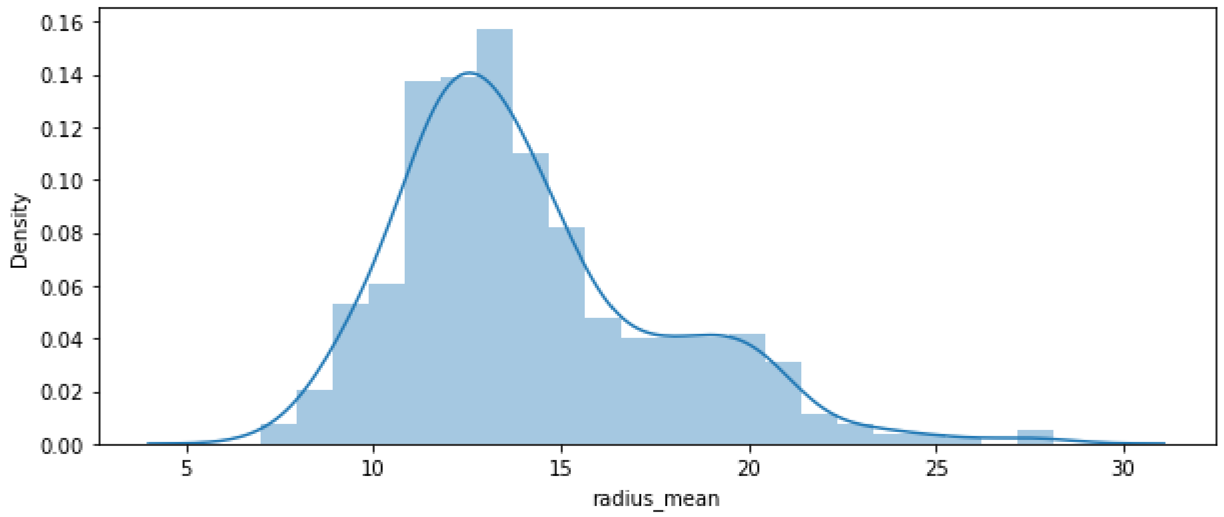


Most of the tumors are beningn and have low mean_radius.

calculating Tumors size

In [17]:
```
plt.figure(figsize=(10,4))
sns.distplot(df['radius_mean'])
print(df['radius_mean'].skew())
print(df['radius_mean'].kurt())
```

```
0.9423795716730992
0.8455216229065377
```



```
Most of the tumors lies in size range of (12,15)
```

Calculating outliers

While looking at the above histograms, I can see there are some rare values in benign and malignant distributions. These values can be errors or rare events. These errors and rare events can be called outliers. Calculating outliers: first we need to calculate first quartile (Q1-25%) and third quartile (Q3- 75%) then find IQR(inter quartile range) = Q3-Q1 finally compute Q1 - 1.5IQR and Q3 + 1.5IQR Anything outside this range is an outlier The code for finding outliers for different features is written below. The identified outliers can be removed or can be replaced with some other suitable value.

In [18]:

```
# Outliers in radius mean
df_benign = df[df["diagnosis"] == "B"]
df_malignant = df[df["diagnosis"] == "M"]
desc = df_benign.radius_mean.describe()
desc1 = df_malignant.radius_mean.describe()
Q1 = desc[4]
Q3 = desc[6]
IQR = Q3-Q1
lower_bound = Q1 - 1.5*IQR
upper_bound = Q3 + 1.5*IQR
print("Anything outside this range is Benign outlier: (", lower_bound ,",", upper_bound,")")
df_benign[df_benign.radius_mean < lower_bound].radius_mean
print("Radius_Mean benign Outliers: ",df_benign[(df_benign.radius_mean < lower_bound) | (df_benign.radius_me

Q1 = desc1[4]
Q3 = desc1[6]
IQR = Q3-Q1
lower_bound = Q1 - 1.5*IQR
upper_bound = Q3 + 1.5*IQR
print("Anything outside this range is Malignant outlier: (", lower_bound ,",", upper_bound,")")
df_malignant[df_malignant.radius_mean < lower_bound].radius_mean
print("Radius_Mean Malignant Outliers: ",df_malignant[(df_malignant.radius_mean < lower_bound) | (df_maligna
```

```
Anything outside this range is Benign outlier: ( 7.645000000000001 , 16.805 )
Radius_Mean benign Outliers:  [ 6.981 16.84  17.85 ]
Anything outside this range is Malignant outlier: ( 8.302499999999998 , 26.3625 )
Radius_Mean Malignant Outliers:  [27.22 28.11 27.42]
```

In [19]:
```
# Outliers in texture mean
df_benign = df[df["diagnosis"] == "B"]
df_malignant = df[df["diagnosis"] == "M"]
desc = df_benign.texture_mean.describe()
desc1 = df_malignant.texture_mean.describe()
Q1 = desc[4]
Q3 = desc[6]
IQR = Q3-Q1
lower_bound = Q1 - 1.5*IQR
upper_bound = Q3 + 1.5*IQR
print("Anything outside this range is benign outlier: (", lower_bound ,",", upper_bound,")")
df_benign[df_benign.texture_mean < lower_bound].texture_mean
print("Texture_Mean Benign Outliers: ",df_benign[(df_benign.texture_mean < lower_bound) | (df_benign.texture

Q1 = desc1[4]
Q3 = desc1[6]
IQR = Q3-Q1
lower_bound = Q1 - 1.5*IQR
upper_bound = Q3 + 1.5*IQR
print("Anything outside this range is Malignant outlier: (", lower_bound ,",", upper_bound,")")
df_malignant[df_malignant.texture_mean < lower_bound].texture_mean
print("Texture_Mean Malignant Outliers: ",df_malignant[(df_malignant.texture_mean < lower_bound) | (df_malig
```

```
Anything outside this range is benign outlier: ( 8.235 , 26.675000000000004 )
Texture_Mean Benign Outliers:  [27.08 33.81 27.85 28.21 28.23 30.72 29.29 28.2  26.99 28.14 29.97 28.06
 29.43 28.92 27.61 27.88 27.15 29.37]
Anything outside this range is Malignant outlier: ( 12.67125 , 30.42125 )
Texture_Mean Malignant Outliers:  [10.38 11.89 32.47 39.28 33.56 31.12 30.62]
```

In [20]:

```
# Outliers in perimeter mean
df_benign = df[df["diagnosis"] == "B"]
df_malignant = df[df["diagnosis"] == "M"]
desc = df_benign.perimeter_mean.describe()
desc1 = df_malignant.perimeter_mean.describe()
Q1 = desc[4]
Q3 = desc[6]
IQR = Q3-Q1
lower_bound = Q1 - 1.5*IQR
upper_bound = Q3 + 1.5*IQR
print("Anything outside this range is benign outlier: (", lower_bound ,",", upper_bound,")")
df_benign[df_benign.perimeter_mean < lower_bound].perimeter_mean
print("Perimeter_Mean Benign Outliers: ",df_benign[(df_benign.perimeter_mean < lower_bound) | (df_benign.per

Q1 = desc1[4]
Q3 = desc1[6]
IQR = Q3-Q1
lower_bound = Q1 - 1.5*IQR
upper_bound = Q3 + 1.5*IQR
print("Anything outside this range is Malignant outlier: (", lower_bound ,",", upper_bound,")")
df_malignant[df_malignant.perimeter_mean < lower_bound].perimeter_mean
print("Perimeter_Mean Malignant Outliers: ",df_malignant[(df_malignant.perimeter_mean < lower_bound) | (df_m
```

```
Anything outside this range is benign outlier: ( 48.02500000000002 , 108.94499999999998 )
Perimeter_Mean Benign Outliers:  [ 43.79 114.6   47.98  47.92]
Anything outside this range is Malignant outlier: ( 51.974999999999994 , 176.69500000000002 )
Perimeter_Mean Malignant Outliers:  [182.1 188.5 186.9]
```

In [21]:
```
# Outliers in area mean
df_benign = df[df["diagnosis"] == "B"]
df_malignant = df[df["diagnosis"] == "M"]
desc = df_benign.area_mean.describe()
desc1 = df_malignant.area_mean.describe()
Q1 = desc[4]
Q3 = desc[6]
IQR = Q3-Q1
lower_bound = Q1 - 1.5*IQR
upper_bound = Q3 + 1.5*IQR
print("Anything outside this range is benign outlier: (", lower_bound ,",", upper_bound,")")
df_benign[df_benign.area_mean < lower_bound].area_mean
print("area_mean Benign Outliers: ",df_benign[(df_benign.area_mean < lower_bound) | (df_benign.area_mean > u

Q1 = desc1[4]
Q3 = desc1[6]
IQR = Q3-Q1
lower_bound = Q1 - 1.5*IQR
upper_bound = Q3 + 1.5*IQR
print("Anything outside this range is Malignant outlier: (", lower_bound ,",", upper_bound,")")
df_malignant[df_malignant.area_mean < lower_bound].area_mean
print("area_mean Malignant Outliers: ",df_malignant[(df_malignant.area_mean < lower_bound) | (df_malignant.a
```

```
Anything outside this range is benign outlier: ( 118.84999999999997 , 810.45 )
area_mean Benign Outliers:  [880.2 838.1 992.1 819.8]
Anything outside this range is Malignant outlier: ( -42.375000000000114 , 1951.4250000000002 )
area_mean Malignant Outliers:  [2250. 2499. 2010. 2501.]
```

In [22]:
```
# Outliers in smoothness mean
df_benign = df[df["diagnosis"] == "B"]
df_malignant = df[df["diagnosis"] == "M"]
desc = df_benign.smoothness_mean.describe()
desc1 = df_malignant.smoothness_mean.describe()
Q1 = desc[4]
Q3 = desc[6]
IQR = Q3-Q1
lower_bound = Q1 - 1.5*IQR
upper_bound = Q3 + 1.5*IQR
print("Anything outside this range is benign outlier: (", lower_bound ,",", upper_bound,")")
df_benign[df_benign.smoothness_mean < lower_bound].smoothness_mean
print("smoothness_mean Benign Outliers: ",df_benign[(df_benign.smoothness_mean < lower_bound) | (df_benign.s

Q1 = desc1[4]
Q3 = desc1[6]
IQR = Q3-Q1
lower_bound = Q1 - 1.5*IQR
upper_bound = Q3 + 1.5*IQR
print("Anything outside this range is Malignant outlier: (", lower_bound ,",", upper_bound,")")
df_malignant[df_malignant.smoothness_mean < lower_bound].smoothness_mean
print("smoothness_mean Malignant Outliers: ",df_malignant[(df_malignant.smoothness_mean < lower_bound) | (df
```

```
Anything outside this range is benign outlier: ( 0.05659999999999999 , 0.12716 )
smoothness_mean Benign Outliers:  [0.1291  0.1634  0.1371  0.05263]
Anything outside this range is Malignant outlier: ( 0.06863749999999999 , 0.1362975 )
smoothness_mean Malignant Outliers:  [0.1425 0.1398 0.1447]
```

Mean, Mode, Spread, and Tails

In [23]:
```
# calculating Mean of all the 5 features
print("Radius Mean of Benign Tumor : ",df_benign.radius_mean.mean())
print("Radius Mean of Malignant Tumor : ",df_malignant.radius_mean.mean())
print("Texture Mean of Benign Tumor : ",df_benign.texture_mean.mean())
print("Texture Mean of Malignant Tumor : ",df_malignant.texture_mean.mean())
print("Perimeter Mean of Benign Tumor : ",df_benign.perimeter_mean.mean())
print("Perimeter Mean of Malignant Tumor : ",df_malignant.perimeter_mean.mean())
print("Area Mean of Benign Tumor : ",df_benign.area_mean.mean())
print("Area Mean of Malignant Tumor : ",df_malignant.area_mean.mean())
print("Smoothness Mean of Benign Tumor : ",df_benign.smoothness_mean.mean())
print("Smoothness Mean of Malignant Tumor : ",df_malignant.smoothness_mean.mean())
```

```
Radius Mean of Benign Tumor :  12.14652380952381
Radius Mean of Malignant Tumor :  17.46283018867925
Texture Mean of Benign Tumor :  17.914761904761892
Texture Mean of Malignant Tumor :  21.60490566037735
Perimeter Mean of Benign Tumor :  78.07540616246497
Perimeter Mean of Malignant Tumor :  115.36537735849062
Area Mean of Benign Tumor :  462.79019607843145
Area Mean of Malignant Tumor :  978.3764150943397
Smoothness Mean of Benign Tumor :  0.09247764705882354
Smoothness Mean of Malignant Tumor :  0.10289849056603775
```

In [24]:

```
# calculating Mode of all the 5 features
print("Radius Mode of Benign Tumor : ",df_benign.radius_mean.mode())
print("Radius Mode of Malignant Tumor : ",df_malignant.radius_mean.mode())
print("Texture Mode of Benign Tumor : ",df_benign.texture_mean.mode())
print("Texture Mode of Malignant Tumor : ",df_malignant.texture_mean.mode())
print("Perimeter Mode of Benign Tumor : ",df_benign.perimeter_mean.mode())
print("Perimeter Mode of Malignant Tumor : ",df_malignant.perimeter_mean.mode())
print("Area Mode of Benign Tumor : ",df_benign.area_mean.mode())
print("Area Mode of Malignant Tumor : ",df_malignant.area_mean.mode())
print("Smoothness Mode of Benign Tumor : ",df_benign.smoothness_mean.mode())
print("Smoothness Mode of Malignant Tumor : ",df_malignant.smoothness_mean.mode())
```

```
Radius Mode of Benign Tumor :  0    10.26
1    11.06
2    11.60
3    11.71
4    11.89
5    12.18
6    12.34
7    12.89
8    13.05
9    13.85
dtype: float64
Radius Mode of Malignant Tumor :  0    15.46
dtype: float64
Texture Mode of Benign Tumor :  0    14.93
1    16.84
2    18.22
dtype: float64
Texture Mode of Malignant Tumor :  0     18.70
1     19.83
2     19.98
3     20.20
4     20.25
5     20.26
6     20.52
7     21.46
8     21.59
9     22.15
10    23.21
11    23.29
12    23.95
dtype: float64
```

```
Perimeter Mode of Benign Tumor :  0    82.61
dtype: float64
Perimeter Mode of Malignant Tumor :  0    134.7
dtype: float64
Area Mode of Benign Tumor :  0    512.2
dtype: float64
Area Mode of Malignant Tumor :  0     716.6
1     758.6
2    1075.0
3    1076.0
4    1138.0
5    1214.0
6    1264.0
dtype: float64
Smoothness Mode of Benign Tumor :  0    0.08511
1    0.09462
2    0.10070
3    0.10750
4    0.11500
dtype: float64
Smoothness Mode of Malignant Tumor :  0    0.1063
1    0.1141
dtype: float64
```

In [25]:

```
# calculating spread or varience of all the 5 features
print("Radius variance of Benign Tumor : ",df_benign.radius_mean.var())
print("Radius variance of Malignant Tumor : ",df_malignant.radius_mean.var())
print("Texture variance of Benign Tumor : ",df_benign.texture_mean.var())
print("Texture variance of Malignant Tumor : ",df_malignant.texture_mean.var())
print("Perimeter variance of Benign Tumor : ",df_benign.perimeter_mean.var())
print("Perimeter variance of Malignant Tumor : ",df_malignant.perimeter_mean.var())
print("Area variance of Benign Tumor : ",df_benign.area_mean.var())
print("Area variance of Malignant Tumor : ",df_malignant.area_mean.var())
print("Smoothness variance of Benign Tumor : ",df_benign.smoothness_mean.var())
print("Smoothness variance of Malignant Tumor : ",df_malignant.smoothness_mean.var())
```

```
Radius variance of Benign Tumor :  3.170221722043872
Radius variance of Malignant Tumor :  10.265430814629346
Texture variance of Benign Tumor :  15.961020518994113
Texture variance of Malignant Tumor :  14.284392882053117
Perimeter variance of Benign Tumor :  139.41558220816412
Perimeter variance of Malignant Tumor :  477.6258704730394
Area variance of Benign Tumor :  18033.030100242337
Area variance of Malignant Tumor :  135378.35536528655
Smoothness variance of Benign Tumor :  0.00018079699557171176
Smoothness variance of Malignant Tumor :  0.00015896760245014748
```

In [26]:

```
# calculating tails of all the features
print("Radius tails of Benign Tumor : ",df_benign.radius_mean.tail())
print("Radius tails of Malignant Tumor : ",df_malignant.radius_mean.tail())
print("Texture tails of Benign Tumor : ",df_benign.texture_mean.tail())
print("Texture tails of Malignant Tumor : ",df_malignant.texture_mean.tail())
print("Perimeter tails of Benign Tumor : ",df_benign.perimeter_mean.tail())
print("Perimeter tails of Malignant Tumor : ",df_malignant.perimeter_mean.tail())
print("Area tails of Benign Tumor : ",df_benign.area_mean.tail())
print("Area tails of Malignant Tumor : ",df_malignant.area_mean.tail())
print("Smoothness tails of Benign Tumor : ",df_benign.smoothness_mean.tail())
print("Smoothness tails of Malignant Tumor : ",df_malignant.smoothness_mean.tail())
```

```
Radius tails of Benign Tumor :  558    14.59
559    11.51
560    14.05
561    11.20
568     7.76
Name: radius_mean, dtype: float64
Radius tails of Malignant Tumor :  563    20.92
564    21.56
565    20.13
566    16.60
567    20.60
Name: radius_mean, dtype: float64
Texture tails of Benign Tumor :  558    22.68
559    23.93
560    27.15
561    29.37
568    24.54
Name: texture_mean, dtype: float64
Texture tails of Malignant Tumor :  563    25.09
564    22.39
565    28.25
566    28.08
567    29.33
Name: texture_mean, dtype: float64
Perimeter tails of Benign Tumor :  558    96.39
559    74.52
560    91.38
561    70.67
568    47.92
Name: perimeter_mean, dtype: float64
Perimeter tails of Malignant Tumor :  563    143.0
```

```
564    142.0
565    131.2
566    108.3
567    140.1
Name: perimeter_mean, dtype: float64
Area tails of Benign Tumor :  558    657.1
559    403.5
560    600.4
561    386.0
568    181.0
Name: area_mean, dtype: float64
Area tails of Malignant Tumor :  563    1347.0
564    1479.0
565    1261.0
566     858.1
567    1265.0
Name: area_mean, dtype: float64
Smoothness tails of Benign Tumor :  558    0.08473
559    0.09261
560    0.09929
561    0.07449
568    0.05263
Name: smoothness_mean, dtype: float64
Smoothness tails of Malignant Tumor :  563    0.10990
564    0.11100
565    0.09780
566    0.08455
567    0.11780
Name: smoothness_mean, dtype: float64
```

In [27]:
```
df.radius_mean.describe()
```

Out[27]:
```
count    569.000000
mean      14.127292
std        3.524049
min        6.981000
25%       11.700000
50%       13.370000
75%       15.780000
max       28.110000
Name: radius_mean, dtype: float64
```

In [28]:
```
df.texture_mean.describe()
```

Out[28]:
```
count    569.000000
mean      19.289649
std        4.301036
min        9.710000
25%       16.170000
50%       18.840000
75%       21.800000
max       39.280000
Name: texture_mean, dtype: float64
```

In [29]:
```
df.perimeter_mean.describe()
```

Out[29]:
```
count    569.000000
mean      91.969033
std       24.298981
min       43.790000
25%       75.170000
50%       86.240000
75%      104.100000
max      188.500000
Name: perimeter_mean, dtype: float64
```

In [30]:
```
df.area_mean.describe()
```

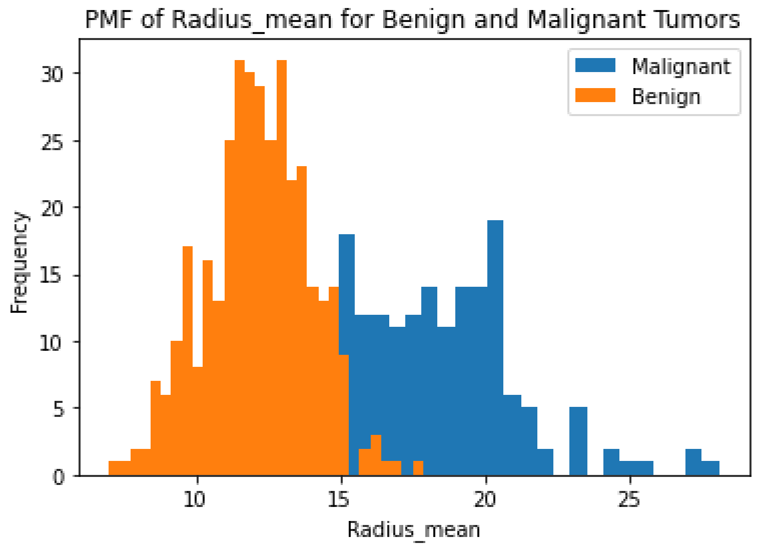
Out[30]:
```
count     569.000000
mean      654.889104
std       351.914129
min       143.500000
25%       420.300000
50%       551.100000
75%       782.700000
max      2501.000000
Name: area_mean, dtype: float64
```

In [31]:
```
df.smoothness_mean.describe()
```

Out[31]:
```
count    569.000000
mean       0.096360
std        0.014064
min        0.052630
25%        0.086370
50%        0.095870
75%        0.105300
max        0.163400
Name: smoothness_mean, dtype: float64
```

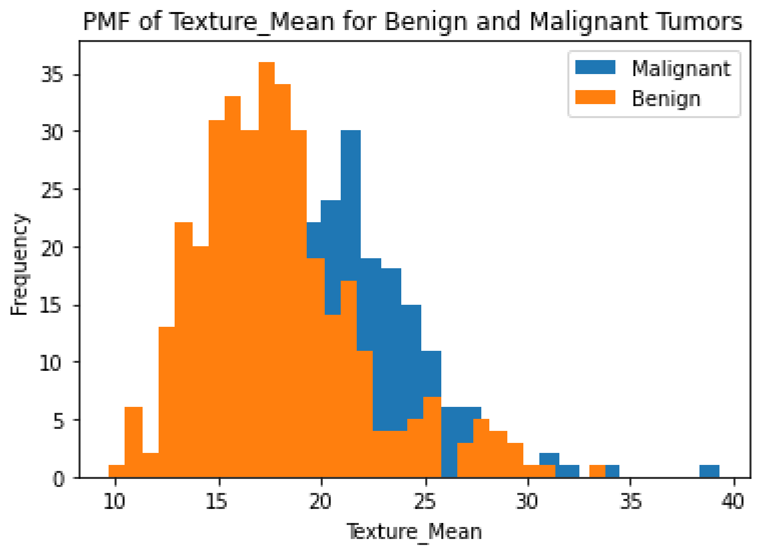
Probability Mass Function

In [32]:
```
#PMF of Radius_mean for Benign and Malignant Tumors
m = plt.hist(df[df["diagnosis"] == "M"].radius_mean,bins=30,label = "Malignant")
b = plt.hist(df[df["diagnosis"] == "B"].radius_mean,bins=30,label = "Benign")
plt.legend()
plt.xlabel("Radius_mean")
plt.ylabel("Frequency")
plt.title("PMF of Radius_mean for Benign and Malignant Tumors")
plt.show()
frequent_malignant_radius_mean = m[0].max()
index_frequent_malignant_radius_mean = list(m[0]).index(frequent_malignant_radius_mean)
most_frequent_malignant_radius_mean = m[1][index_frequent_malignant_radius_mean]
print("Most frequent malignant radius mean is: ",most_frequent_malignant_radius_mean)
```



```
Most frequent malignant radius mean is:  20.101999999999997
```

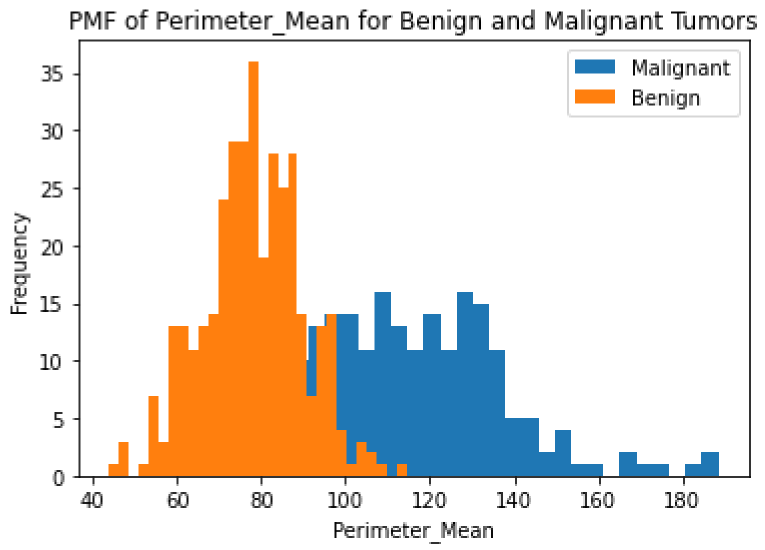
In [33]:
```
#PMF of Texture_Mean for Benign and Malignant Tumors
m1 = plt.hist(df[df["diagnosis"] == "M"].texture_mean,bins=30,label = "Malignant")
b1 = plt.hist(df[df["diagnosis"] == "B"].texture_mean,bins=30,label = "Benign")
plt.legend()
plt.xlabel("Texture_Mean")
plt.ylabel("Frequency")
plt.title("PMF of Texture_Mean for Benign and Malignant Tumors")
plt.show()
frequent_malignant_texture_mean = m1[0].max()
index_frequent_malignant_texture_mean = list(m1[0]).index(frequent_malignant_texture_mean)
most_frequent_malignant_texture_mean = m1[1][index_frequent_malignant_texture_mean]
print("Most frequent malignant texture mean is: ",most_frequent_malignant_texture_mean)
```



```
Most frequent malignant texture mean is:  20.976666666666667
```

In [34]:

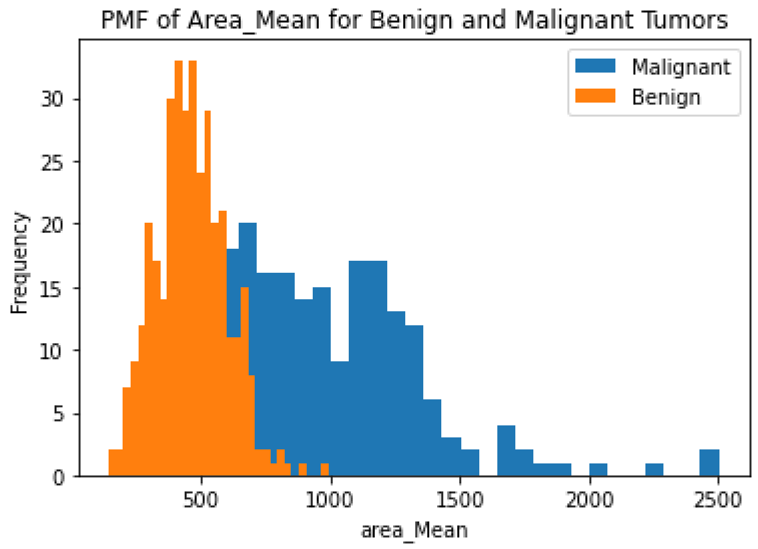
```
# PMF of Perimeter_Mean for Benign and Malignant Tumors
m2 = plt.hist(df[df["diagnosis"] == "M"].perimeter_mean,bins=30,label = "Malignant")
b2 = plt.hist(df[df["diagnosis"] == "B"].perimeter_mean,bins=30,label = "Benign")
plt.legend()
plt.xlabel("Perimeter_Mean")
plt.ylabel("Frequency")
plt.title("PMF of Perimeter_Mean for Benign and Malignant Tumors")
plt.show()
frequent_malignant_perimeter_mean = m2[0].max()
index_frequent_malignant_perimeter_mean = list(m2[0]).index(frequent_malignant_perimeter_mean)
most_frequent_malignant_perimeter_mean = m2[1][index_frequent_malignant_perimeter_mean]
print("Most frequent malignant perimeter mean is: ",most_frequent_malignant_perimeter_mean)
```



```
Most frequent malignant perimeter mean is:  106.88
```

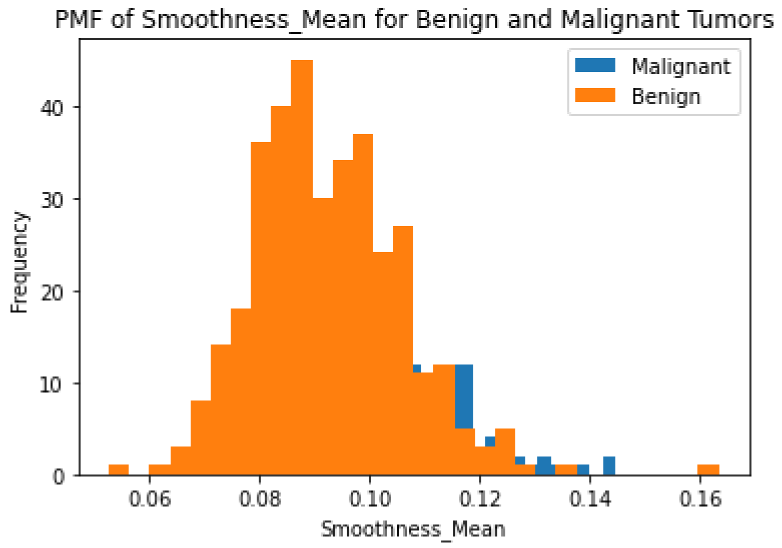
In [35]:

```
#PMF of Area_Mean for Benign and Malignant Tumors
m3 = plt.hist(df[df["diagnosis"] == "M"].area_mean,bins=30,label = "Malignant")
b3 = plt.hist(df[df["diagnosis"] == "B"].area_mean,bins=30,label = "Benign")
plt.legend()
plt.xlabel("area_Mean")
plt.ylabel("Frequency")
plt.title("PMF of Area_Mean for Benign and Malignant Tumors")
plt.show()
frequent_malignant_area_mean = m3[0].max()
index_frequent_malignant_area_mean = list(m3[0]).index(frequent_malignant_area_mean)
most_frequent_malignant_area_mean = m3[1][index_frequent_malignant_area_mean]
print("Most frequent malignant Area_Mean is: ",most_frequent_malignant_area_mean)
```



```
Most frequent malignant Area_Mean is:  646.8533333333334
```

In [36]:
```
#PMF of Smoothness_Mean for Benign and Malignant Tumors
m4 = plt.hist(df[df["diagnosis"] == "M"].smoothness_mean,bins=30,label = "Malignant")
b4 = plt.hist(df[df["diagnosis"] == "B"].smoothness_mean,bins=30,label = "Benign")
plt.legend()
plt.xlabel("Smoothness_Mean")
plt.ylabel("Frequency")
plt.title("PMF of Smoothness_Mean for Benign and Malignant Tumors")
plt.show()
frequent_malignant_smoothness_mean = m4[0].max()
index_frequent_malignant_smoothness_mean = list(m4[0]).index(frequent_malignant_smoothness_mean)
most_frequent_malignant_smoothness_mean = m4[1][index_frequent_malignant_smoothness_mean]
print("Most frequent malignant Smoothness mean is: ",most_frequent_malignant_smoothness_mean)
```



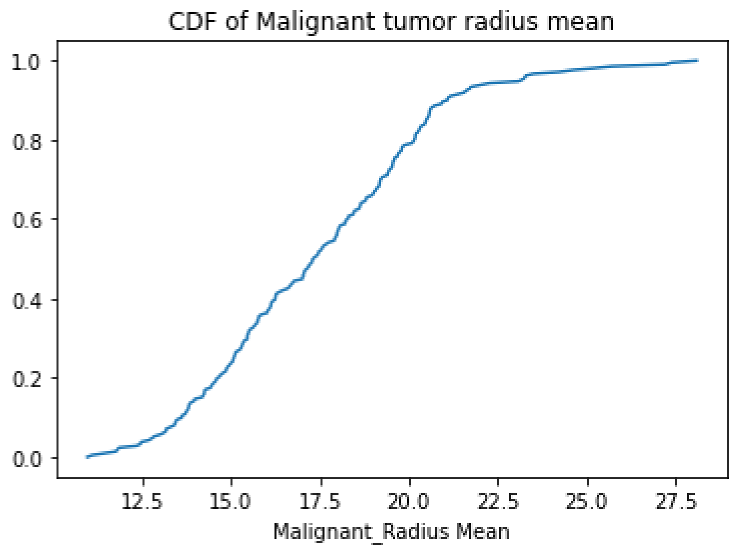
```
Most frequent malignant Smoothness mean is:  0.09737333333333333
```

Cumulative Distribution Functions

```
In [37]: data =df_malignant.radius_mean
         # sort the data in ascending order
         x = np.sort(data)
         # get the cdf values of y
         y = np.arange(len(x))/float(len(x)-1)

         # plotting
         plt.xlabel('Malignant_Radius Mean')
         plt.title('CDF of Malignant tumor radius mean')
         plt.plot(x, y)
```

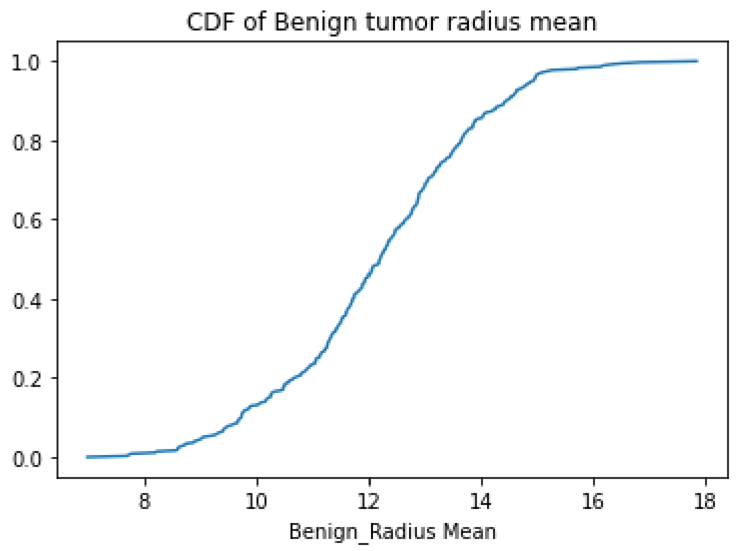
```
Out[37]: [<matplotlib.lines.Line2D at 0x22b352551c0>]
```



In [38]:
```
data =df_benign.radius_mean
# sort the data in ascending order
x = np.sort(data)
# get the cdf values of y
y = np.arange(len(x))/float(len(x)-1)

# plotting
plt.xlabel('Benign_Radius Mean')
plt.title('CDF of Benign tumor radius mean')
plt.plot(x, y)
```

Out[38]:
```
[<matplotlib.lines.Line2D at 0x22b352bd1f0>]
```



```
From the above CDF graphs, as the radius mean of the tumor increases the chance of turning benign cancer cell
to malignant cell is increasing.
```

Normal Distribution

```
Also called bell shaped and gaussian distributions
Here the average radius is 12.146524 and standard deviation is 1.780512
There are few people who are malignant  and their radius is higher than 12. It can be 16-20.
Also there are few people who are benign and their radius is lower than 12. It can be 6-8.
Mean and standart deviation are parameters of normal distribution.
```

In [39]:

```python
# parameters of normal distribution
mean= 12.146524
std =  1.780512
s = np.random.normal(mean, std, 10000)
print("mean: ", np.mean(s))
print("standard deviation: ", np.std(s))
# visualize with histogram
plt.figure(figsize = (5,5))
plt.hist(s, 100)
plt.ylabel("frequency")
plt.xlabel("Radius_mean")
plt.title("Normal Distribution of Radius_Mean")
plt.show()
```

```
mean:  12.133158802183178
standard deviation:  1.7893799785931963
```

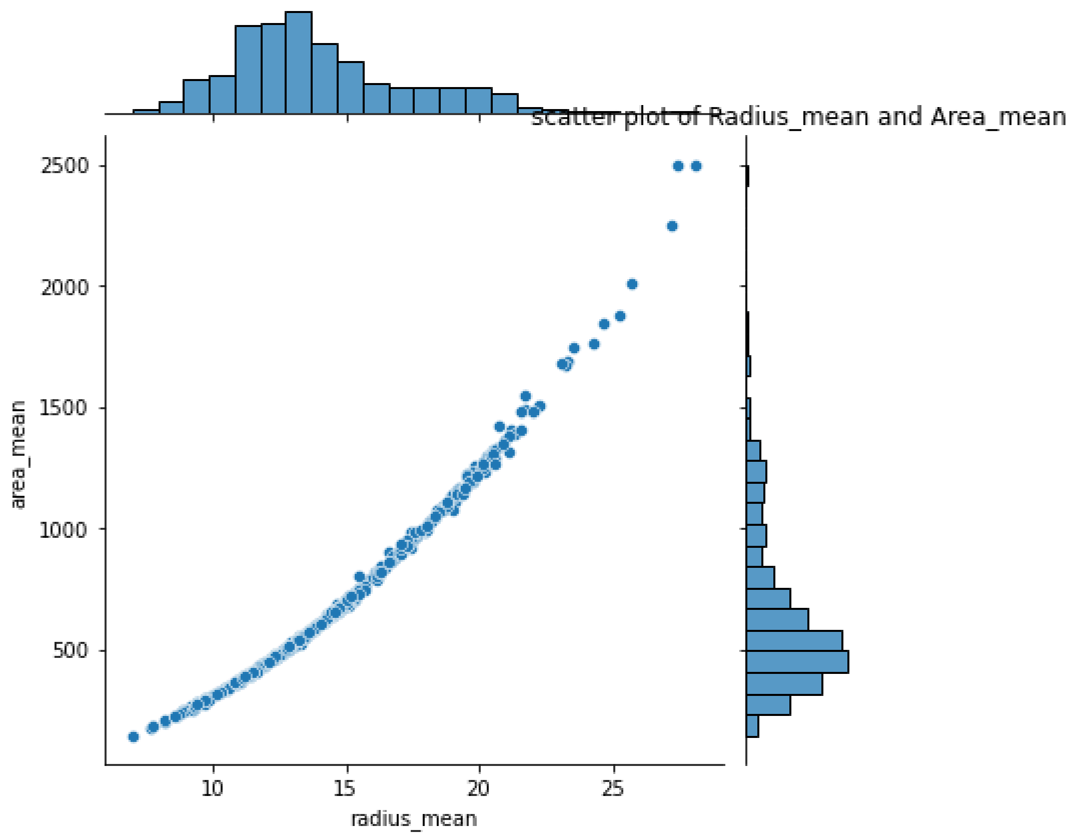
```
As it can be seen from above plot most of the people are cumulated near to 12 that is mean of our normal
distribution. Malignant tumors are distributed more towards right side and the benign tumors distributed on the
left side of the graph.
```

Scatter Plots- Relationship between the variables

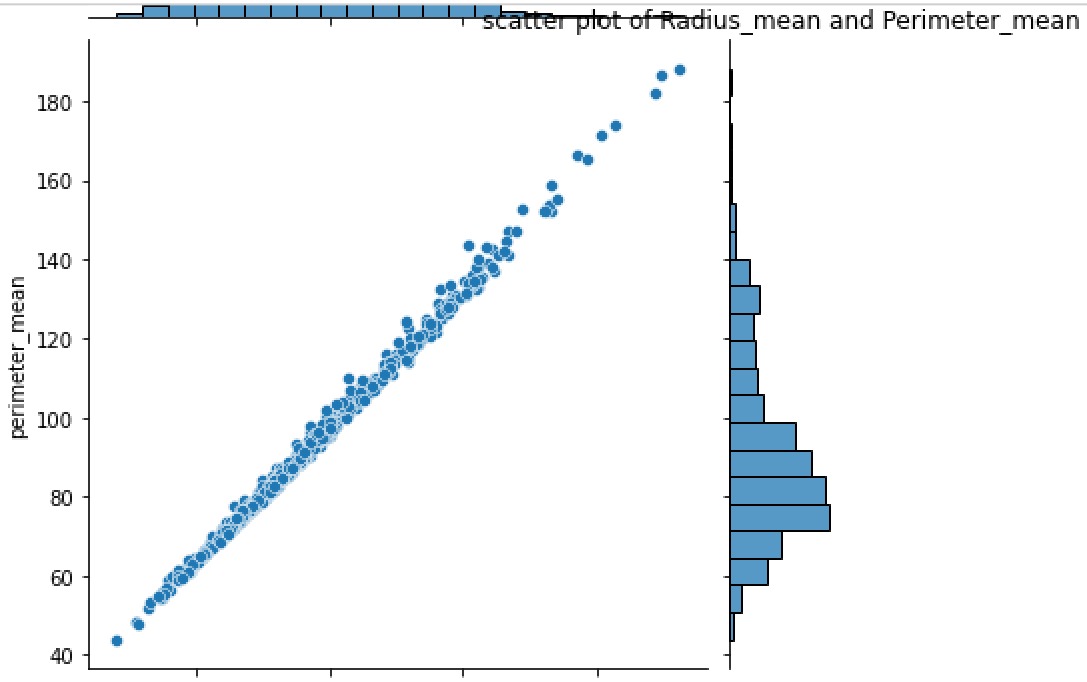
```
We can say that two variables are related with each other, if one of them gives information about others
Scatter Plot: Simplest way to check relationship between two variables
Lets look at relationship between the two different variables.
```

In [40]:
```
plt.figure(figsize = (10,5))
sns.jointplot(df.radius_mean,df.area_mean,kind="scatter")
plt.title("scatter plot of Radius_mean and Area_mean")
plt.show()
```

```
<Figure size 720x360 with 0 Axes>
```



In [41]:
```
plt.figure(figsize = (10,5))
sns.jointplot(df.radius_mean,df.perimeter_mean,kind="scatter")
plt.title("scatter plot of Radius_mean and Perimeter_mean")
plt.show()
```

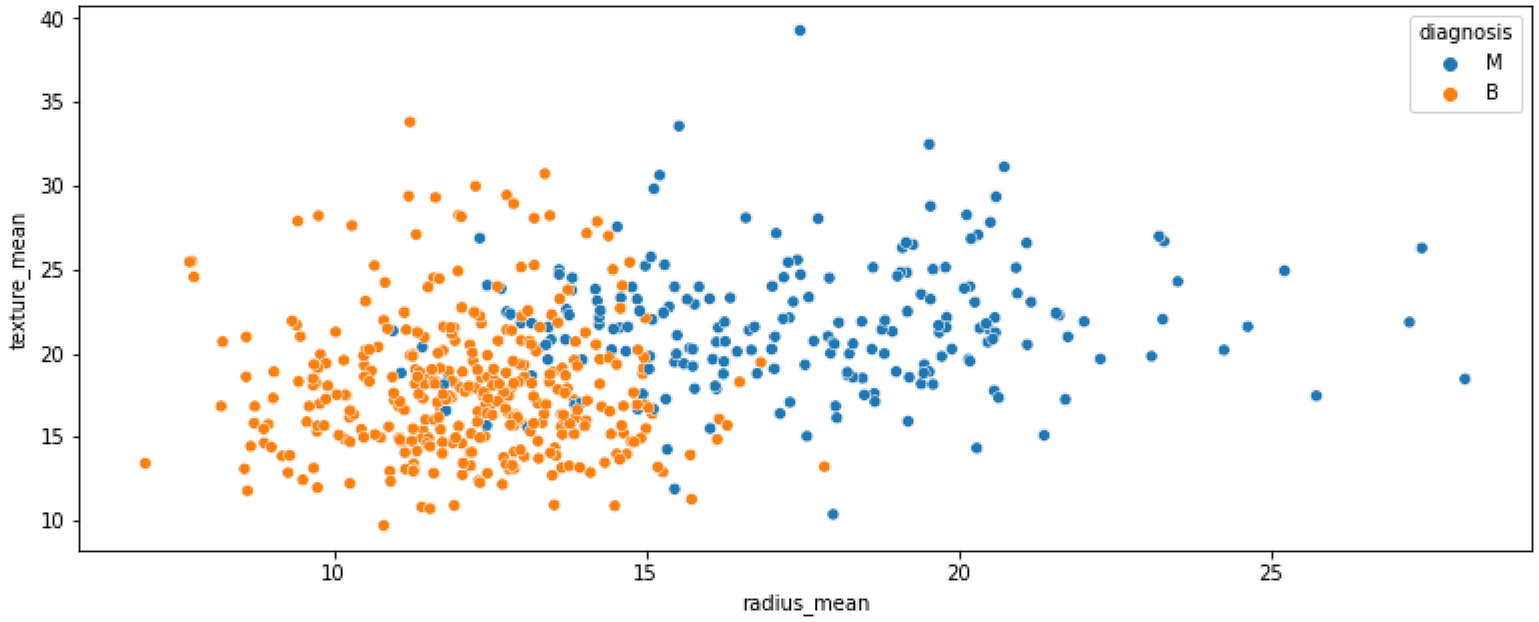


```
From the above scatter plots, we can observe that
when radius mean increases, area mean also increases. Therefore, they are positively correlated with each other
and area_mean is caused by radius_mean.
when radius mean increases, perimeter mean also increases. Therefore, they are positively correlated with each
other and perimeter_mean is caused by radius_mean.
```

Tumor statistics

In [42]:
```
plt.figure(figsize=(13,5))
sns.scatterplot(df['radius_mean'],df['texture_mean'],hue=df['diagnosis'])
```

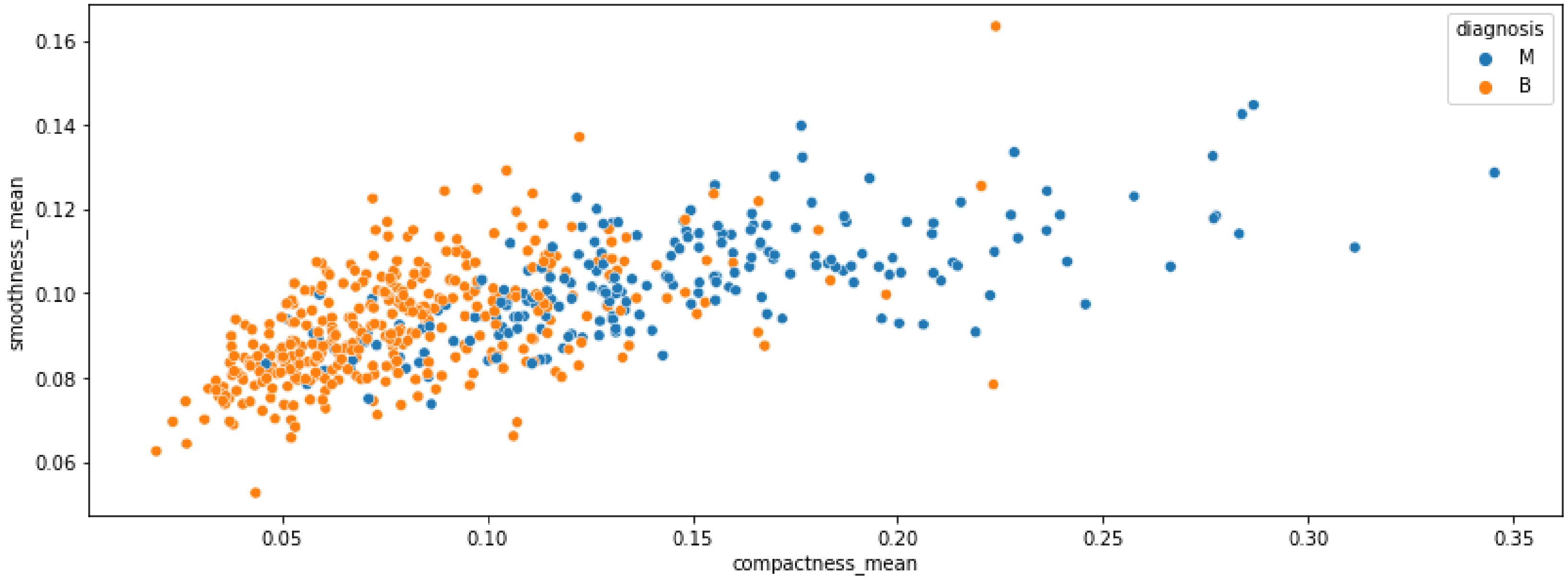
Out[42]:
```
<AxesSubplot:xlabel='radius_mean', ylabel='texture_mean'>
```



```
Radius_mean and texture mean for malignant tumor is higher than for beningn tumor
```

In [43]:
```
plt.figure(figsize=(14,5),)
sns.scatterplot(df['compactness_mean'],df['smoothness_mean'],hue=df['diagnosis'])
```

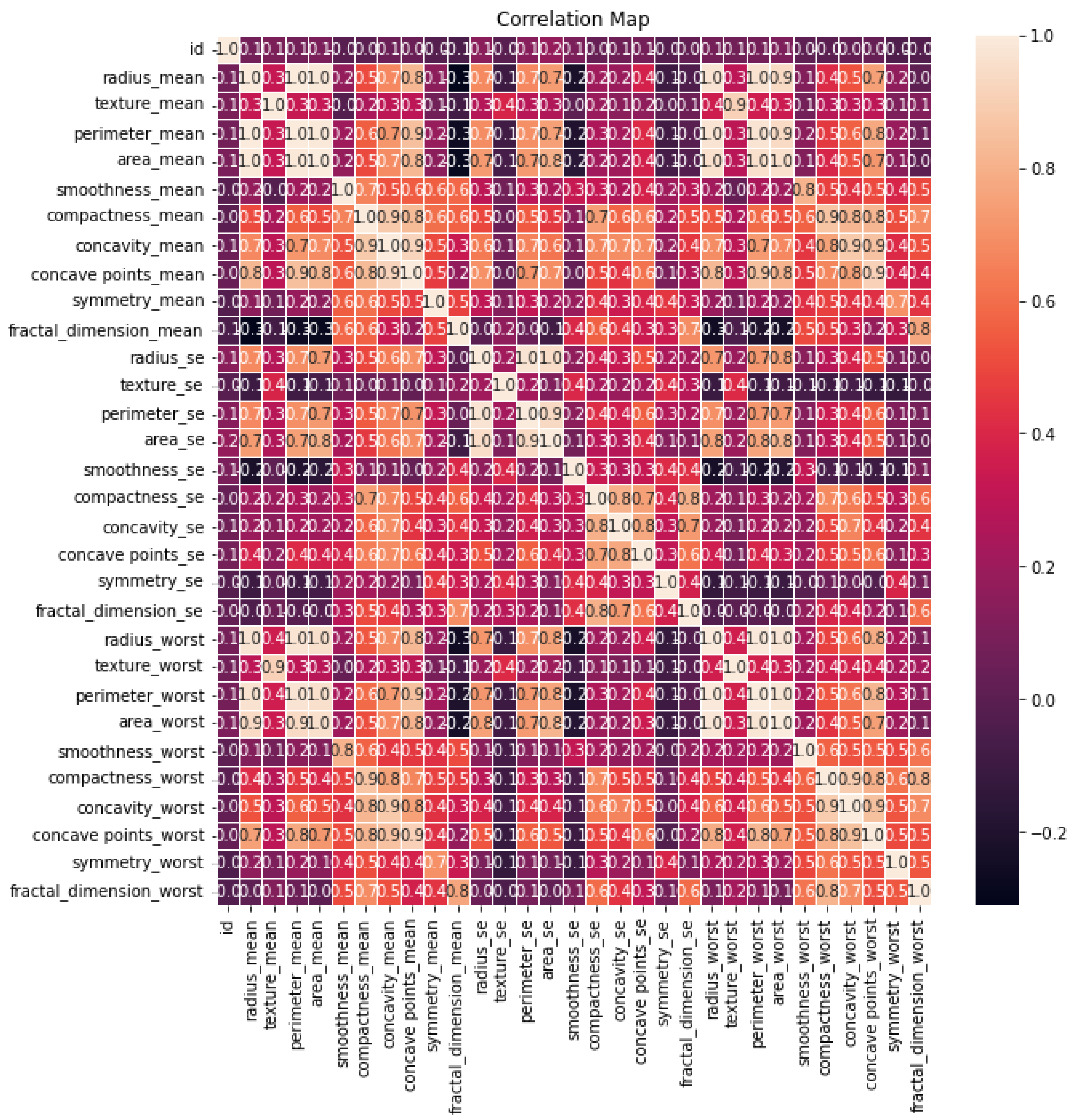
Out[43]:
```
<AxesSubplot:xlabel='compactness_mean', ylabel='smoothness_mean'>
```



```
compactness_mean and smoothness_mean both are higher for Beningn tumor.
```

Correlation

In [44]:
```
f,ax=plt.subplots(figsize = (10,10))
sns.heatmap(df.corr(),annot= True,linewidths=0.5,fmt = ".1f",ax=ax)
plt.xticks(rotation=90)
plt.yticks(rotation=0)
plt.title('Correlation Map')
plt.savefig('CorrelationMap.png')
plt.show()
```


Correlation Map
id
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
1.0
0.8
0.6
0.4
0.2
0.0
−0.2

```
As it can be seen in map heat figure radius_mean, perimeter_mean and area_mean are correlated with each other
Compactness_mean, concavity_mean and concave points_mean are correlated with each other. Apart from these,
radius_se, perimeter_se and area_se are correlated. radius_worst, perimeter_worst and area_worst are correlated
Compactness_worst, concavity_worst and concave points_worst are correlated. Compactness_se, concavity_se and
concave points_se are correlated. texture_mean and texture_worst are correlated. area_worst and area_mean are
correlated.
```

Covariance

In [45]:

```
np.cov(df.radius_mean,df.area_mean)
print("Covariance between radius mean and area mean: ",df.radius_mean.cov(df.area_mean))
```

```
Covariance between radius mean and area mean:  1224.483409346457
```

In [46]:

```
np.cov(df.radius_mean,df.perimeter_mean)
print("Covariance between radius mean and perimeter mean: ",df.radius_mean.cov(df.perimeter_mean))
```

```
Covariance between radius mean and perimeter mean:  85.44714165573404
```

Pearson’s correlation

In [47]:

```
# finding pearson's correlation between radius_mean and area_mean
p1 = df.loc[:,["area_mean","radius_mean"]].corr(method= "pearson")
p2 = df.radius_mean.cov(df.area_mean)/(df.radius_mean.std()*df.area_mean.std())
print('Pearson correlation: ')
print(p1)
print('Pearson correlation: ',p2)
```

```
Pearson correlation: 
             area_mean  radius_mean
area_mean     1.000000     0.987357
radius_mean   0.987357     1.000000
Pearson correlation:  0.9873571700566132
```

In [48]:
```
# finding pearson's correlation between radius_mean and perimeter_mean
p1 = df.loc[:,["perimeter_mean","radius_mean"]].corr(method= "pearson")
p2 = df.radius_mean.cov(df.perimeter_mean)/(df.radius_mean.std()*df.perimeter_mean.std())
print('Pearson correlation: ')
print(p1)
print('Pearson correlation: ',p2)
```

```
Pearson correlation: 
                perimeter_mean  radius_mean
perimeter_mean        1.000000     0.997855
radius_mean           0.997855     1.000000
Pearson correlation:  0.9978552814938109
```

Non-Linear Relationships

```
If relationship between distributions are non linear, spearman's correlation tends to better estimate the
strength of relationship
```

In [49]:
```
ranked_data = df.rank()
spearman_corr = ranked_data.loc[:,["area_mean","radius_mean"]].corr(method= "pearson")
print("Spearman's correlation: ")
print(spearman_corr)
```

```
Spearman's correlation: 
             area_mean  radius_mean
area_mean     1.000000     0.999602
radius_mean   0.999602     1.000000
```

```
Spearman's correlation is little higher than pearson correlation
```

Classical Hypothesis Testing

In [50]:
```
statistic, p_value = stats.ttest_rel(df.radius_mean,df.area_mean)
print('p-value: ',p_value)
```

```
p-value:  1.5253492492559045e-184
```

```
P values is almost zero so we can reject null hypothesis.
```

Regression model

```
Based on the observations in the histogram plots, we can reasonably hypothesize that the cancer diagnosis
depends on the mean cell radius, mean perimeter, mean area, mean texture, mean smoothness points. We can then
perform a logistic regression analysis using those features as follows:
```

In [52]:

```
#Breaking data in to labels and Features
Labls= df.diagnosis
Features= df.loc[:, ('radius_mean', 'texture_mean', 'perimeter_mean', 'area_mean', 'smoothness_mean')]
Features.head()
Features.shape
Xtrain, Xtest, Ytrain, Ytest= train_test_split(Features, Labls, test_size=0.3, shuffle=True)
Log_Reg=LogisticRegression()
#Training Model
Log_Reg.fit(Xtrain, Ytrain)
#Prediction
Log_Reg.score(Xtrain, Ytrain)
```

Out[52]:

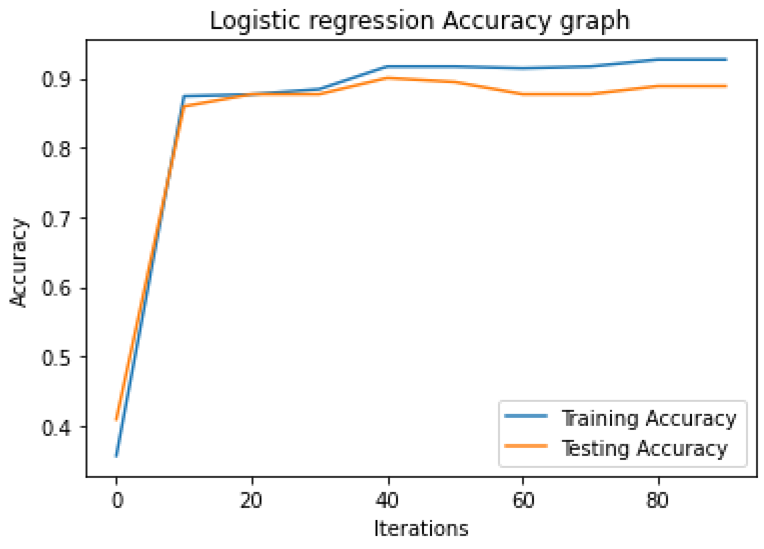
```
0.9271356783919598
```

In [53]:
```
#Loop for taking average result (More accurate)
Array= 10*(np.arange(10))
Test_Score=[]
Train_Score=[]

for i in Array:
    Log_Reg= LogisticRegression(max_iter=i)
    Log_Reg.fit(Xtrain, Ytrain)
    Test_Score.append(Log_Reg.score(Xtest, Ytest))
    Train_Score.append(Log_Reg.score(Xtrain, Ytrain))

plt.xlabel("Iterations")
plt.ylabel("Accuracy")
plt.title("Logistic regression Accuracy graph")
plt.plot(Array, Train_Score, label= 'Training Accuracy')
plt.plot(Array, Test_Score, label= 'Testing Accuracy')
plt.legend()
```

Out[53]:
```
<matplotlib.legend.Legend at 0x22b352d4220>
```



```
The model accuracy is 97%
```