Unit 2 Homework

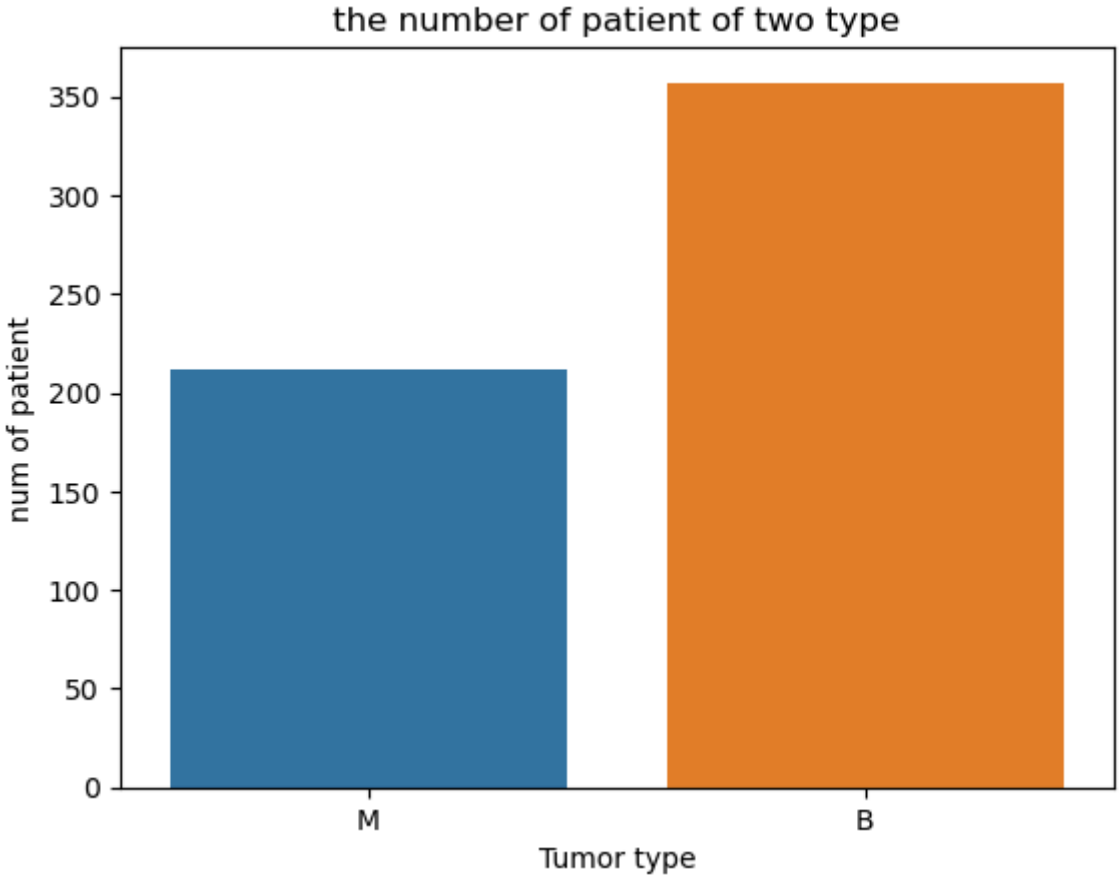
In [2]:
```
#七件套
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import scipy.stats as stats
import seaborn as sns
import statsmodels.api as sm
import statistics as sta

data = pd.read_csv("C:/Users/25167\Desktop\data.csv")
```

1 可视化

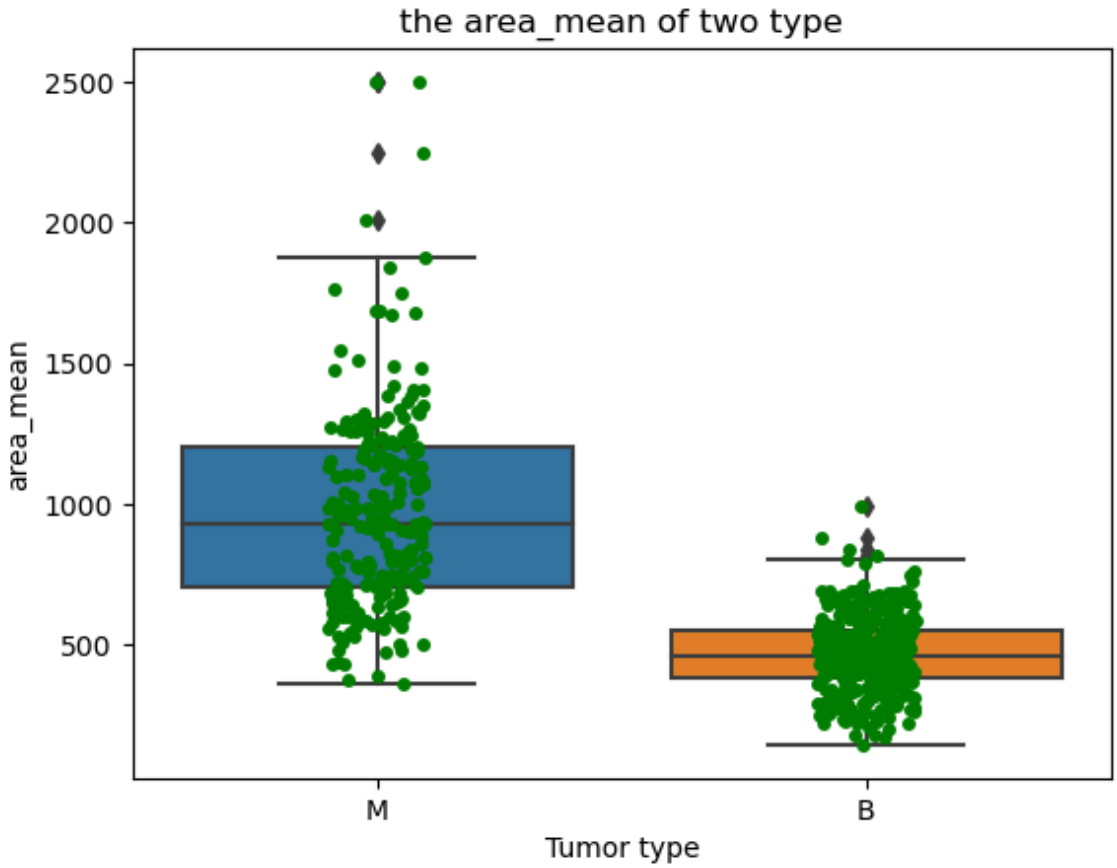
1.1 画出B，M组的病人数的直方图

In [3]:
```
sns.countplot(x="diagnosis", data=data)      #用数数图画
plt.xlabel("Tumor type")
plt.ylabel("num of patient")
plt.title("the number of patient of two type")
plt.show()
```



1.2 同一个图中画出B,M组area_mean的箱体图+stripplot

In [4]:
```
sns.boxplot(y="area_mean", data=data, x="diagnosis")              #先画箱体图
sns.stripplot(y="area_mean", data=data, color="g", x="diagnosis")  #再加上散点
plt.xlabel("Tumor type")
plt.ylabel("area_mean")
plt.title("the area_mean of two type")
plt.show()
```



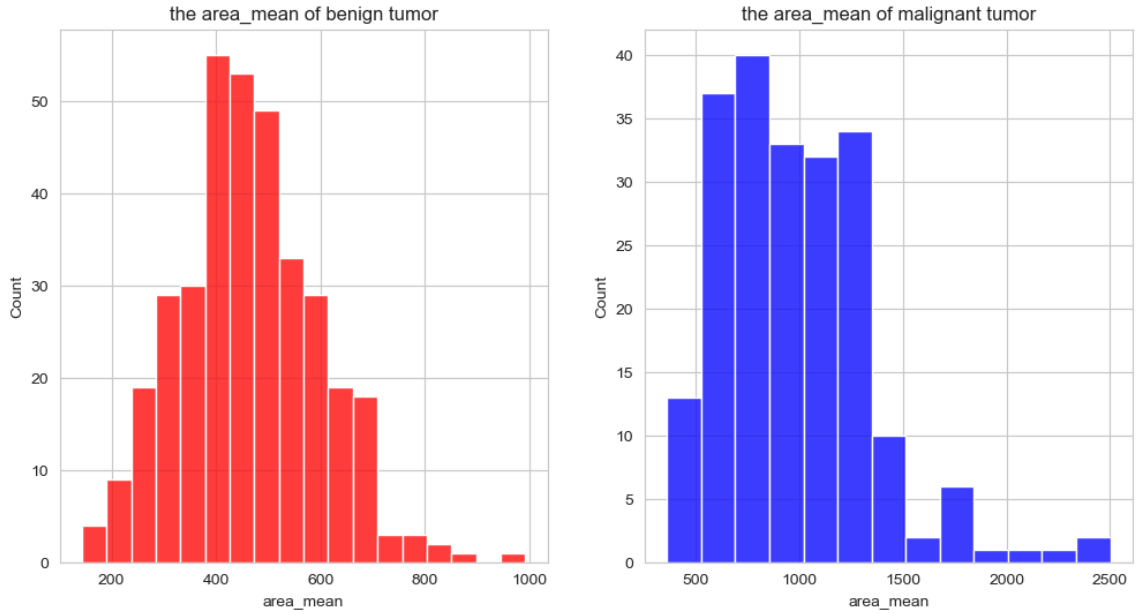
1.3 分别画出B,M组的area_mean直方图

In [5]:
```
df = pd.DataFrame(data)
sns.set_style("whitegrid") #设置风格

fig, ax = plt.subplots(1, 2, figsize=(12,6))                    #设置子图，下面画图
sns.histplot(data=df[df["diagnosis"]=="B"], x="area_mean", color="r", ax=ax[0]) #筛
ax[0].set_title("the area_mean of benign tumor")

sns.histplot(data=df[df["diagnosis"]=="M"], x="area_mean", color="b", ax=ax[1]) #筛
ax[1].set_title("the area_mean of malignant tumor")

plt.show()
```

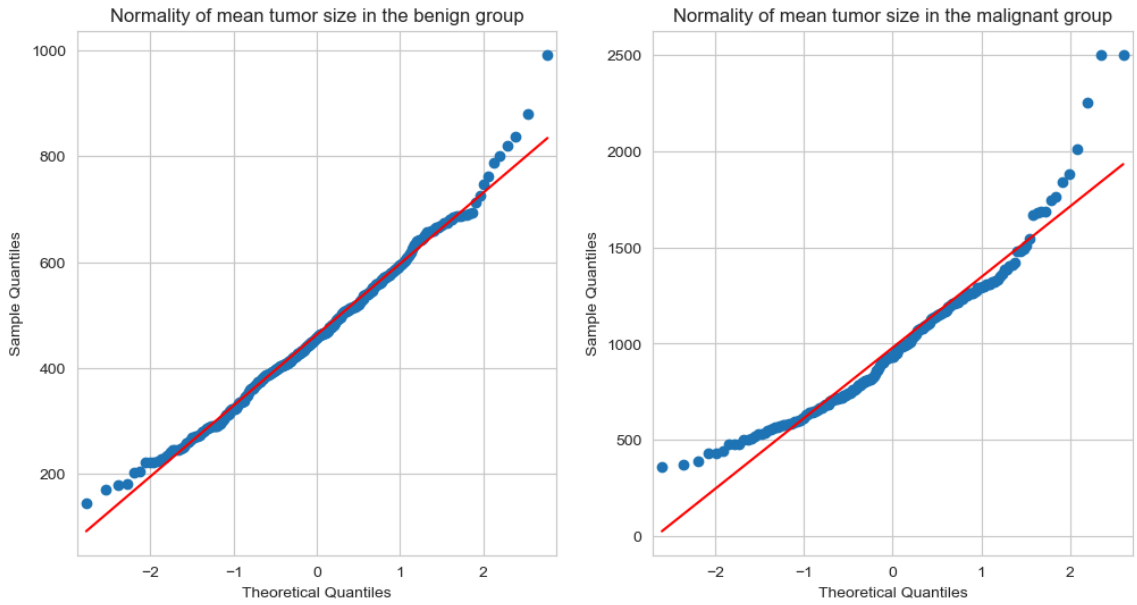


1.4 通过sm.qqplot, 评价B,M组的area_mean的正态性

In [6]:
```
fig, ax = plt.subplots(1, 2, figsize=(12,6))            #设置子图
sm.qqplot(df[df["diagnosis"]=="B"]["area_mean"], stats.norm, line="s", ax=ax[0])  #
ax[0].set_title("Normality of mean tumor size in the benign group")

sm.qqplot(df[df["diagnosis"]=="M"]["area_mean"], stats.norm, line="s", ax=ax[1])  #
ax[1].set_title("Normality of mean tumor size in the malignant group")

plt.show()
```



2 计算B,M组的样本各种值

In [7]:
```
df_use = df.loc[:,["area_mean","diagnosis"]]
df_use1 = df_use.groupby("diagnosis") #去掉表头，不知道为什么表头的str一直报错
```

In [8]:
```
#样本均值
sample_mean = df_use1.mean()
print(sample_mean)
```

```
           area_mean
diagnosis
B         462.790196
M         978.376415
```

In [9]:
```
#样本方差
sample_variance = df_use1.var(ddof=1) #自由度为n-1，为样本方差
print(sample_variance)
```

```
              area_mean
diagnosis
B          18033.030100
M         135378.355365
```

In [10]:
```
#样本标准差,直接开根号即可
sample_standard_variance = sample_variance**0.5
print(sample_standard_variance)
```

```
             area_mean
diagnosis
B          134.287118
M          367.937978
```

In [11]:
```
#样本变异系数，直接除就可以得到，最后是百分数值
sample_CoV = sample_standard_variance / sample_mean * 100
print(sample_CoV)
```

```
           area_mean
diagnosis
B          29.016846
M          37.606996
```

In [12]:
```
#样本偏度
sample_skew = df_use1.skew()
print(sample_skew)
```

```
           area_mean
diagnosis
B           0.342265
M           1.117668
```

In [13]:
```
#样本峰度
sample_kurtosis = df_use1.apply(lambda x: x.kurt())   #groupby之后没有原生的kurt函数
print(sample_kurtosis)
```

```
           area_mean
diagnosis
B           0.309498
M           2.306042
```

In [14]:
```
#样本IQR
q3 = df_use1.quantile(q=0.75)
q1 = df_use1.quantile(q=0.25)
IQR = q3 - q1
print(IQR)
```

```
           area_mean
diagnosis
B             172.90
M             498.45
```