In [53]:

```python
import pandas as pd
import matplotlib.pyplot as plt
import numpy as np
import scipy.stats
from scipy.stats import norm
import seaborn as sns
import math
```

In [54]:

```python
path = "heart.csv"
arquivo = pd.read_csv(path)
arquivo
```

Out[54]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	target
0	63	1	3	145	233	1	0	150	0	2.3	0	0	1	1
1	37	1	2	130	250	0	1	187	0	3.5	0	0	2	1
2	41	0	1	130	204	0	0	172	0	1.4	2	0	2	1
3	56	1	1	120	236	0	1	178	0	0.8	2	0	2	1
4	57	0	0	120	354	0	1	163	1	0.6	2	0	2	1
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
298	57	0	0	140	241	0	1	123	1	0.2	1	0	3	0
299	45	1	3	110	264	0	1	132	0	1.2	1	0	3	0
300	68	1	0	144	193	1	1	141	0	3.4	1	2	3	0
301	57	1	0	130	131	0	1	115	1	1.2	1	1	3	0
302	57	0	1	130	236	0	0	174	0	0.0	1	1	2	0

303 rows × 14 columns

In [55]:

```python
arquivo.isnull().sum()
```

Out[55]:

```
age         0
sex         0
cp          0
trestbps    0
chol        0
fbs         0
restecg     0
thalach     0
exang       0
oldpeak     0
slope       0
ca          0
thal        0
target      0
dtype: int64
```

In [56]:

```python
arquivo.describe()
```

Out[56]:

	age	sex	cp	trestbps	chol	fbs	restecg	thala
count	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303.0000
mean	54.366337	0.683168	0.966997	131.623762	246.264026	0.148515	0.528053	149.6468

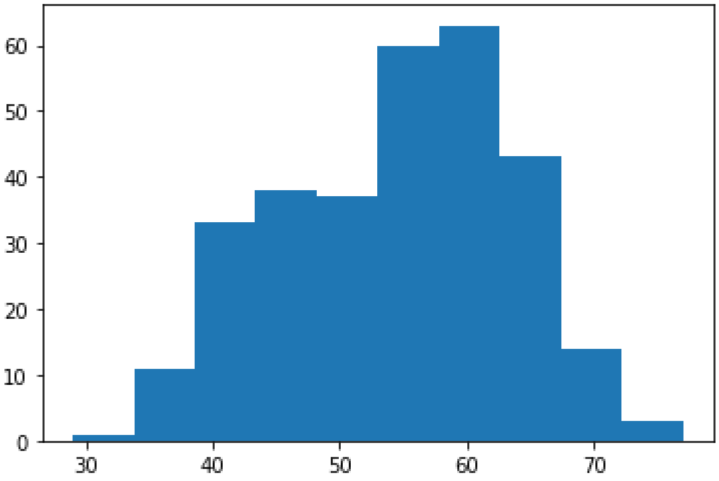
	age	sex	cp	trestbps	chol	fbs	restecg	thala
std	9.082101	0.466011	1.032052	17.538143	51.830751	0.356198	0.525860	22.9051
min	29.000000	0.000000	0.000000	94.000000	126.000000	0.000000	0.000000	71.0000
25%	47.500000	0.000000	0.000000	120.000000	211.000000	0.000000	0.000000	133.5000
50%	55.000000	1.000000	1.000000	130.000000	240.000000	0.000000	1.000000	153.0000
75%	61.000000	1.000000	2.000000	140.000000	274.500000	0.000000	1.000000	166.0000
max	77.000000	1.000000	3.000000	200.000000	564.000000	1.000000	2.000000	202.0000

In [57]:

```
#idades= arquivo['age'].unique()
#qtd_idades = arquivo['age'].value_counts()
#plt.bar(idades, qtd_idades)
plt.hist(arquivo['age'])
arquivo['age'].describe()
```

Out[57]:

```
count    303.000000
mean      54.366337
std        9.082101
min       29.000000
25%       47.500000
50%       55.000000
75%       61.000000
max       77.000000
Name: age, dtype: float64
```



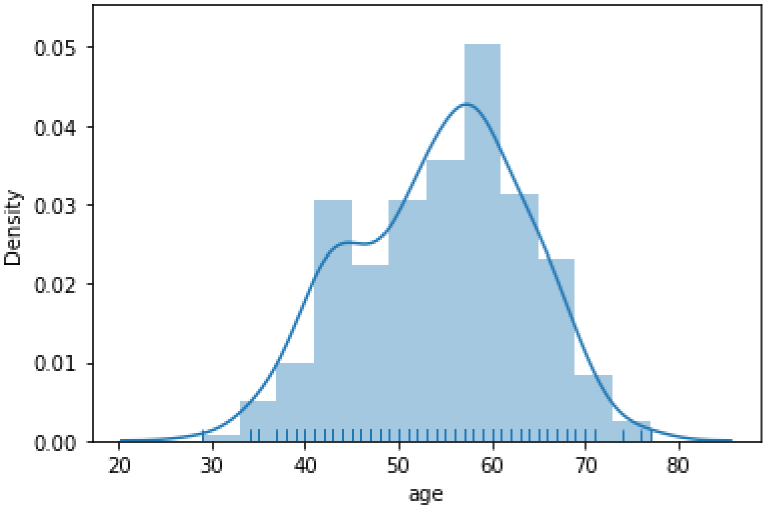
In [58]:

```
sns.distplot(arquivo['age'], hist=True, norm_hist=True, rug=True)
```

```
/home/gregorio/anaconda3/lib/python3.8/site-packages/seaborn/distributions.py:25
51: FutureWarning: `distplot` is a deprecated function and will be removed in a
future version. Please adapt your code to use either `displot` (a figure-level f
unction with similar flexibility) or `histplot` (an axes-level function for hist
ograms).
  warnings.warn(msg, FutureWarning)
/home/gregorio/anaconda3/lib/python3.8/site-packages/seaborn/distributions.py:20
55: FutureWarning: The `axis` variable is no longer used and will be removed. In
stead, assign variables directly to `x` or `y`.
  warnings.warn(msg, FutureWarning)
```

Out[58]:

```
<AxesSubplot:xlabel='age', ylabel='Density'>
```

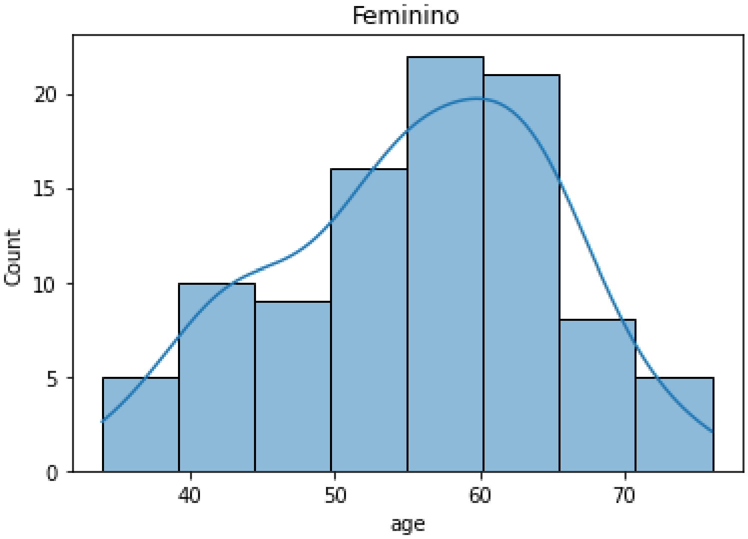


In [59]:

```
mulher= arquivo.query('sex ==0')
homem = arquivo.query('sex ==1')
sns.histplot(data=mulher['age'], kde="True")
plt.title("Feminino")
```

Out[59]:

```
Text(0.5, 1.0, 'Feminino')
```

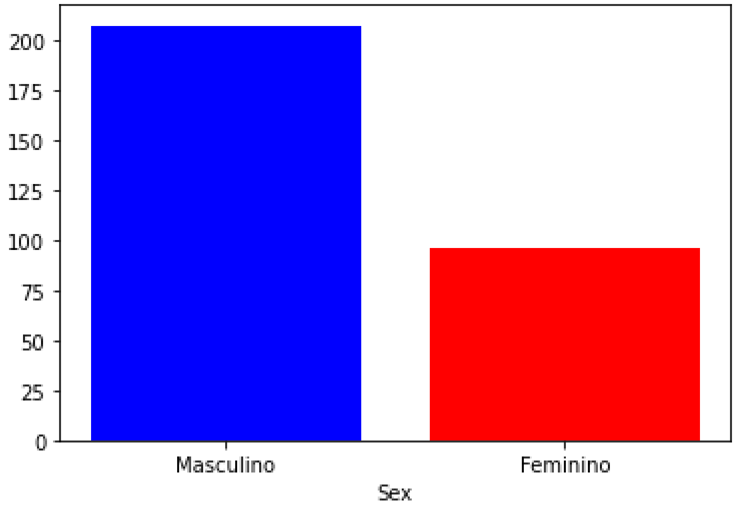


In [60]:

```
plt.bar([1,2], arquivo['sex'].value_counts(), color=['b', 'r'])
plt.xticks([1,2], ['Masculino', 'Feminino'])
plt.xlabel('Sex')
arquivo['sex'].value_counts()
```

Out[60]:

```
1    207
0     96
Name: sex, dtype: int64
```

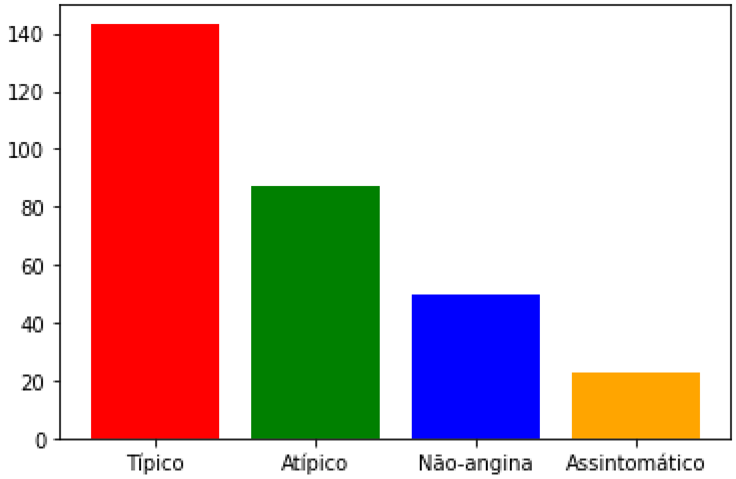


In [61]:

```
plt.bar([0,1,2,3], arquivo['cp'].value_counts(), color=['r', 'g', 'b', 'orange']
plt.xticks([0,1,2,3], ['Típico', 'Atípico', 'Não-angina', 'Assintomático'])
arquivo['cp'].value_counts()
```

Out[61]:

```
0    143
2     87
1     50
3     23
Name: cp, dtype: int64
```

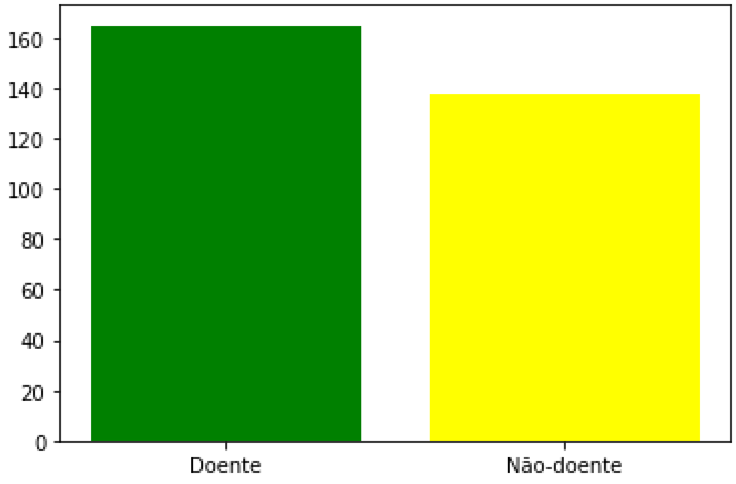


In [62]:

```
plt.bar([0,1], arquivo['target'].value_counts(), color=['green', 'yellow'])
plt.xticks([0,1], ['Doente', 'Não-doente'])
arquivo['target'].value_counts()
```

Out[62]:

```
1    165
0    138
Name: target, dtype: int64
```

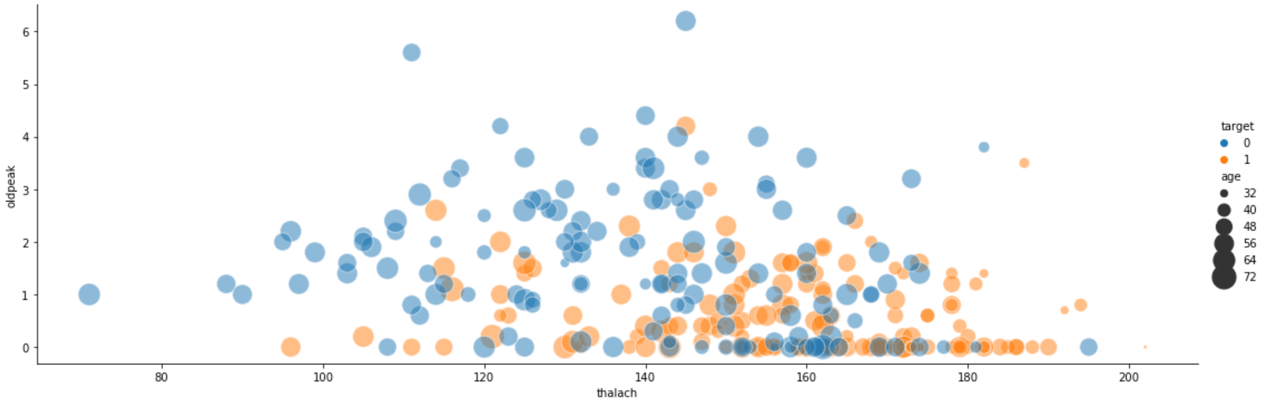


In [63]:

```
sns.relplot(data=arquivo, x='thalach', y='oldpeak', hue='target', size='age', si
```

Out[63]:

```
<seaborn.axisgrid.FacetGrid at 0x7fe2029b0880>
```



Teste 1

H0 : A amostra da pressão arterial é proveniente de uma distribuição normal

Rejeitar H0 se o p <= 0.05

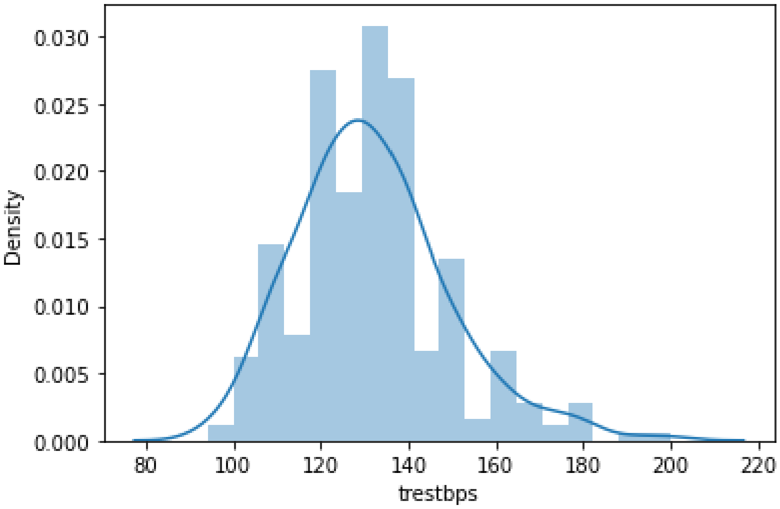
In [64]:

```
sns.distplot(arquivo['trestbps'])
```

```
/home/gregorio/anaconda3/lib/python3.8/site-packages/seaborn/distributions.py:25
51: FutureWarning: `distplot` is a deprecated function and will be removed in a
future version. Please adapt your code to use either `displot` (a figure-level f
unction with similar flexibility) or `histplot` (an axes-level function for hist
ograms).
  warnings.warn(msg, FutureWarning)
```

Out[64]:

```
<AxesSubplot:xlabel='trestbps', ylabel='Density'>
```



```
In [65]: stat1, pvalue1 =scipy.stats.normaltest(arquivo['trestbps'])
         pvalue1<=0.05
```

```
Out[65]: True
```

```
In [76]: pvalue1
```

```
Out[76]: 6.260708761946876e-07
```

Portanto, hipótese nula é rejeitada

Teste 2

H0: A amostra dos soro colesterol é proveniente de uma distribuição normal

Rejeitar H0 se o p<=0.05

```
In [66]: chol_400= arquivo.query('chol <400')
         chol_400
```

Out[66]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	target
0	63	1	3	145	233	1	0	150	0	2.3	0	0	1	1
1	37	1	2	130	250	0	1	187	0	3.5	0	0	2	1
2	41	0	1	130	204	0	0	172	0	1.4	2	0	2	1
3	56	1	1	120	236	0	1	178	0	0.8	2	0	2	1
4	57	0	0	120	354	0	1	163	1	0.6	2	0	2	1
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
298	57	0	0	140	241	0	1	123	1	0.2	1	0	3	0
299	45	1	3	110	264	0	1	132	0	1.2	1	0	3	0
300	68	1	0	144	193	1	1	141	0	3.4	1	2	3	0
301	57	1	0	130	131	0	1	115	1	1.2	1	1	3	0
302	57	0	1	130	236	0	0	174	0	0.0	1	1	2	0

299 rows × 14 columns

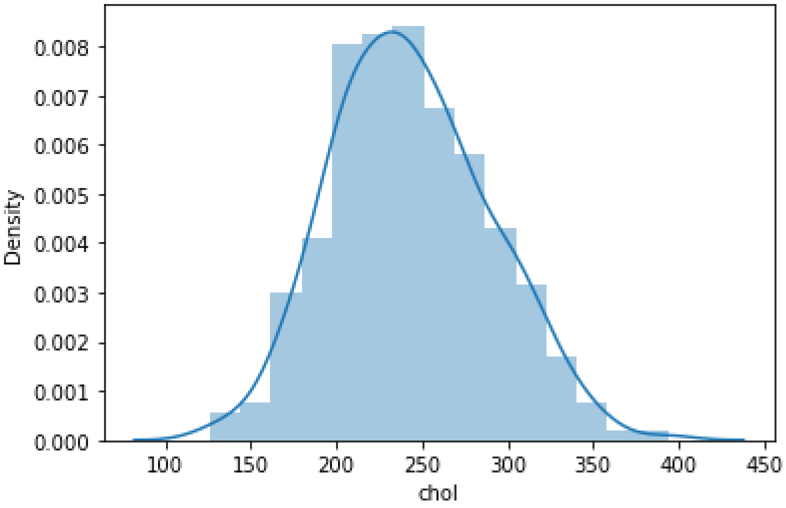
In [67]:

```
sns.distplot(chol_400['chol'])
```

```
/home/gregorio/anaconda3/lib/python3.8/site-packages/seaborn/distributions.py:25
51: FutureWarning: `distplot` is a deprecated function and will be removed in a
future version. Please adapt your code to use either `displot` (a figure-level f
unction with similar flexibility) or `histplot` (an axes-level function for hist
ograms).
  warnings.warn(msg, FutureWarning)
```

Out[67]:

```
<AxesSubplot:xlabel='chol', ylabel='Density'>
```



In [78]:

```
stat2, pvalue2 =scipy.stats.normaltest(chol_400['chol'])
pvalue2<=0.05
```

Out[78]:

```
False
```

In [77]:

```
pvalue2
```

Out[77]:

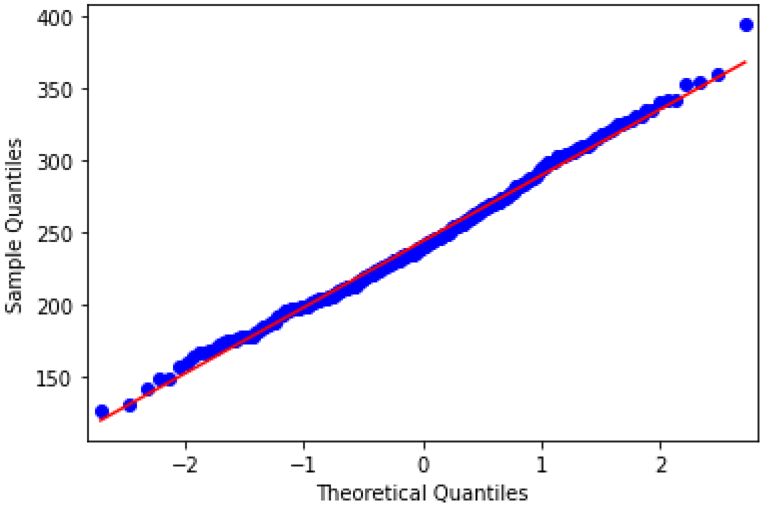
```
0.1748931592218597
```

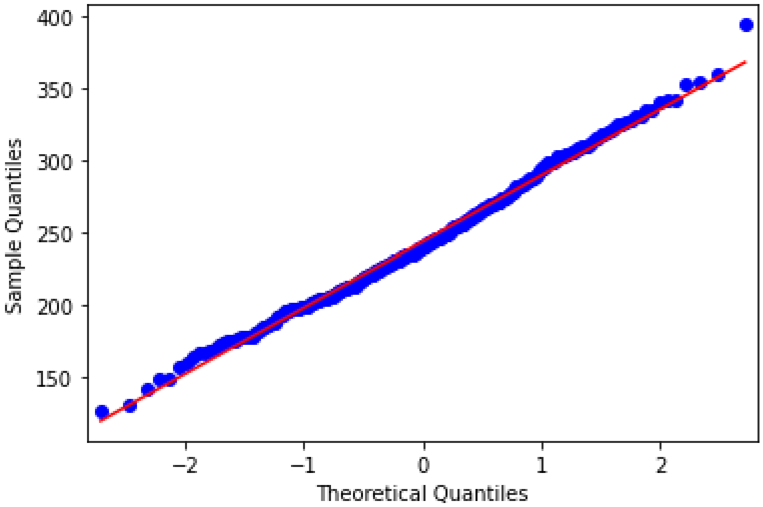
Portanto, a hipótese nula não é rejeitada

In [82]:

```
from statsmodels.graphics.gofplots import qqplot
qqplot(chol_400['chol'].values, line='s')
```

Out[82]:





Teste 3

H0: a distribuição do soro colesterol é normal com u = 162.5 mg/dl

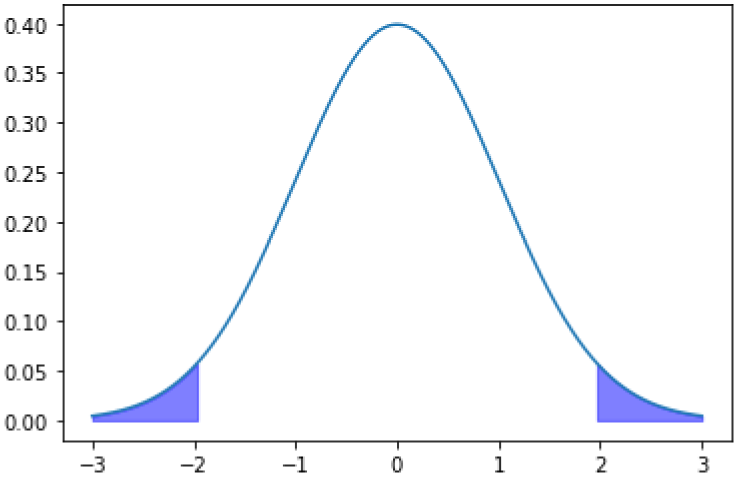
H1: a distribuição do soro colesterol é normal com u =! 162.5 mg/dl

```
In [69]: qt = scipy.stats.t(df=299).ppf(0.975) #alpha=5%
         qt
```

```
Out[69]: 1.9679296690653618
```

```
In [70]: x = np.arange(-3, 3, 0.001)
         y= norm.pdf(x,0,1)
         plt.plot(x,y )
         plt.fill_between(x[x>qt], y[x>qt], alpha=.5, color='blue')
         plt.fill_between(x[x<-qt], y[x<-qt], alpha=.5, color='blue')
```

```
Out[70]: <matplotlib.collections.PolyCollection at 0x7fe2027b7610>
```



```
In [71]: X = chol_400['chol'].mean()
         S =chol_400['chol'].std()
         T = (X - 162.5)*(math.sqrt(303))/S #estatistica t de Student
         T

Out[71]: 30.764859245475755
```

```
In [72]: 162.5 -(qt*S/(math.sqrt(303)))

Out[72]: 157.3155869448958
```

```
In [73]: 162.5 +(qt*S/(math.sqrt(303)))

Out[73]: 167.6844130551042
```

```
In [74]: X

Out[74]: 243.54849498327758
```

```
In [75]: T>qt

Out[75]: True
```

Portanto, a hipotese nula é rejeitada.

```
In [ ]:

In [ ]:

In [ ]:
```