3. Diagnostic tumor size and post treatment

April 29, 2022

[1]:
```
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import numpy as np
import statsmodels.api as sm
%matplotlib inline
pd.set_option('display.max_rows', None)
import scipy.stats as stats
from scipy.stats import shapiro
import copy
import statsmodels.stats.api as sms
from scipy.stats import wilcoxon
sns.set(style="darkgrid")
import test_mod as mod
from scipy.stats import chi2_contingency
```

1 Descriptive analysis of attributes

1.1 Importing data

[2]:
```
df = pd.read_csv(r"C:\Users\gdbt0\OneDrive\GitHub\Projects\cancer␣
↪research\data\processed\research_variables.csv")
df.head()
```

[2]:

	id	tumour_stage	diagnos_tumor_size	after EBRT_tumor_size	\
0	101	2B	4		
1	102	2B	4	2	
2	103	3B	>4	>2	
3	104	2B	>4	>2	
4	105	3B	>4	2	

	before_brachy_categor	post_treatment_response
0	1	0
1	1	0
2	2	2
3	2	0
4	2	1

[3]:
```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 120 entries, 0 to 119
Data columns (total 6 columns):
 #   Column                  Non-Null Count  Dtype
---  ------                  --------------  -----
 0   id                      120 non-null    int64
 1   tumour_stage            120 non-null    object
 2   diagnos_tumor_size      120 non-null    object
 3   after EBRT_tumor_size   120 non-null    object
 4   before_brachy_categor   120 non-null    int64
 5   post_treatment_response  120 non-null    int64
dtypes: int64(3), object(3)
memory usage: 5.8+ KB
```

1.2 diagnos_tumor_size and post_treatment_response

[4]:
```
#Transforming data
primary_var_name = 'diagnos_tumor_size'
secondary_var_name = 'post_treatment_response'

primary_vs_secondary = df[[primary_var_name,secondary_var_name]].copy()
primary_vs_secondary.dropna(inplace=True)
primary_vs_secondary[primary_var_name] = primary_vs_secondary[primary_var_name].
 ↪astype('category')
```

1.2.1 Diagnostic tumor size

[5]:
```
# Declaration of the variable
primary_var = df[primary_var_name].copy()
primary_var.dropna(inplace=True)
primary_var_value_counts = primary_var.value_counts()
```

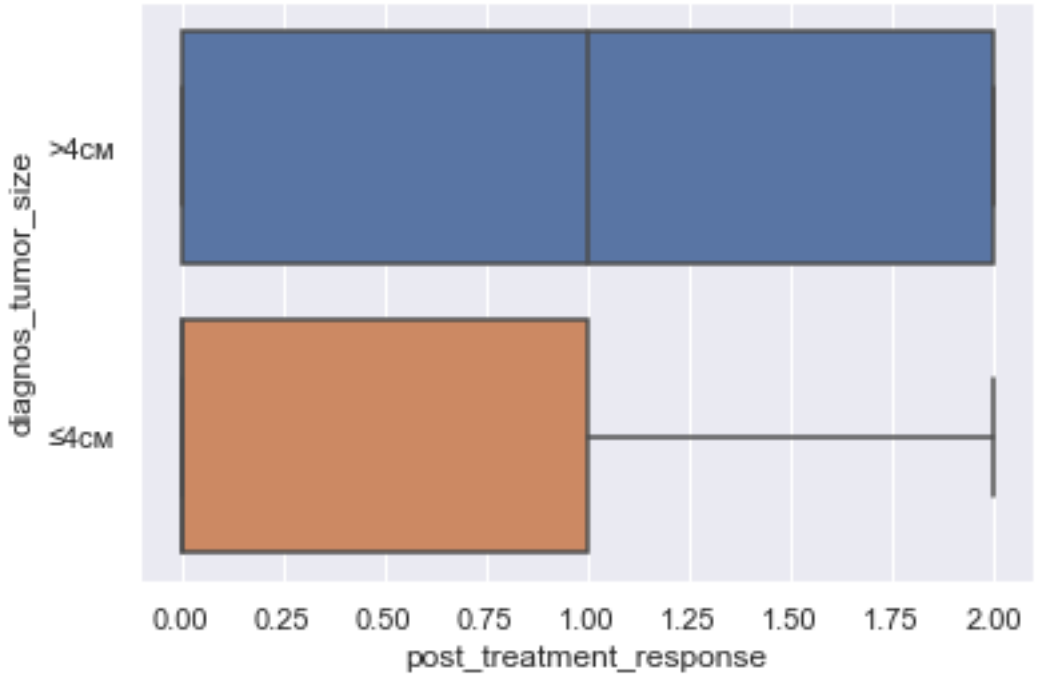
[6]:
```
## Finding the frequency distribution of categories in the variable
print("The frequency distribution of categories  in {}.".
 ↪format(primary_var_name))
print("In total, there are {} categories.".format(primary_var.value_counts().
 ↪count()))
primary_var.value_counts()
```

```
The frequency distribution of categories  in diagnos_tumor_size.
In total, there are 2 categories.
```

[6]:
```
>4     63
 4     57
Name: diagnos_tumor_size, dtype: int64
```

[7]:
```
# Boxplot for numberical valies
sns.boxplot(data=primary_vs_secondary,x=secondary_var_name, y=primary_var_name)
```

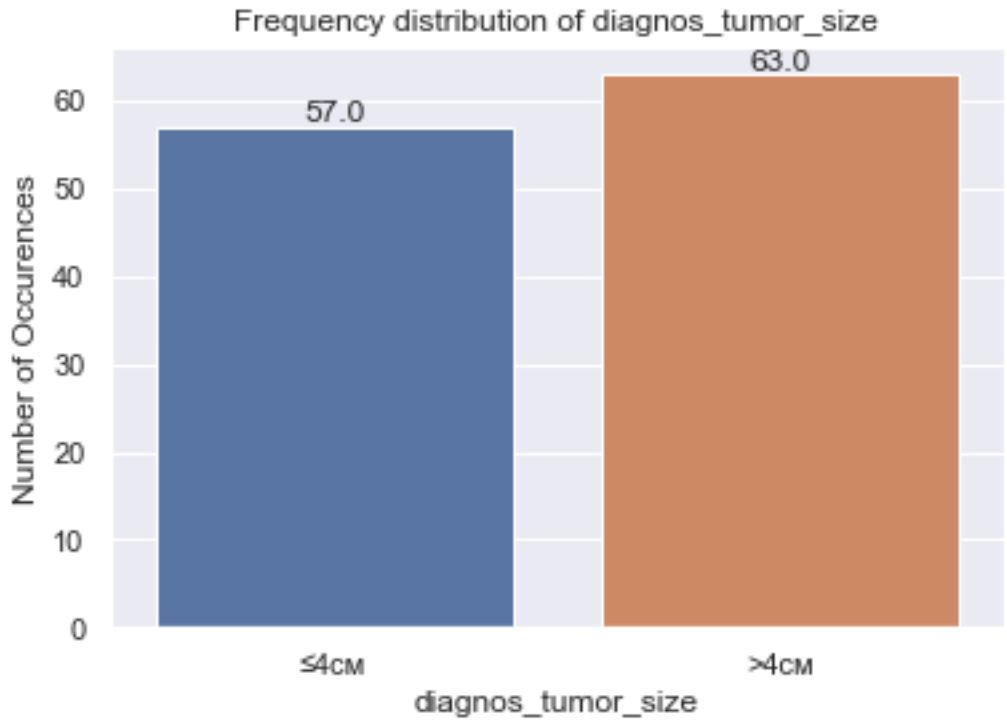
[7]: <AxesSubplot:xlabel='post_treatment_response', ylabel='diagnos_tumor_size'>



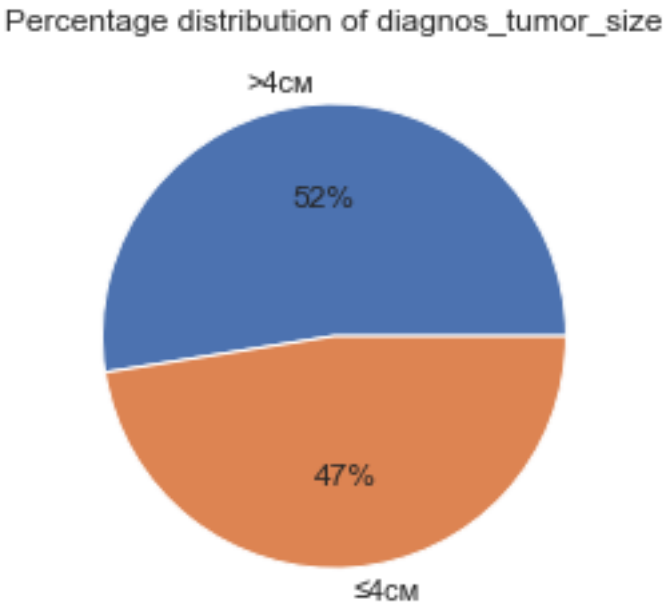
Let's graph the frequency distribution of the categorical features to a barplot.

[8]:
```
# Barplot
plot = sns.countplot(primary_var)
mod.show_values(plot)
plt.title("Frequency distribution of {}".format(primary_var_name))
plt.ylabel('Number of Occurences', fontsize=12)
plt.xlabel('{}'.format(primary_var_name),fontsize=12)
plt.show()
```

```
C:\Users\gdbt0\anaconda3\lib\site-packages\seaborn\_decorators.py:36:
FutureWarning: Pass the following variable as a keyword arg: x. From version
0.12, the only valid positional argument will be `data`, and passing other
arguments without an explicit keyword will result in an error or
misinterpretation.
  warnings.warn(
```



[9]:
```
#Making a pie chart
plt.title("Percentage distribution of {}".format(primary_var_name))
plt.pie(primary_var_value_counts, labels=primary_var_value_counts.index,␣
 ↪autopct='%.0f%%')
plt.show()
```



1.2.2 Post treatment response

[10]:
```
# Declaration of the variable
secondary_var = df[secondary_var_name].copy()
secondary_var.dropna(inplace=True)
secondary_var_value_counts = secondary_var.value_counts()
```

[11]:
```
## Finding the frequency distribution of categories in the variable
print("The frequency distribution of categories  in {}.".
 ↪format(secondary_var_name))
print("In total, there are {} categories.".format(secondary_var.value_counts().
 ↪count()))
secondary_var.value_counts()
```

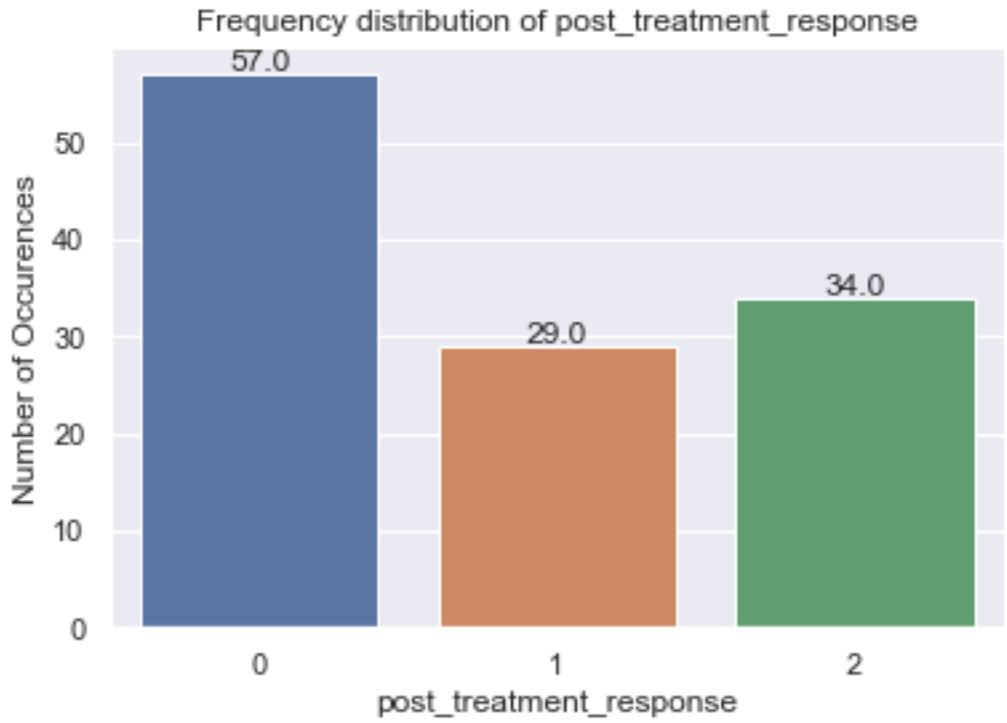
```
The frequency distribution of categories  in post_treatment_response.
In total, there are 3 categories.
```

[11]:
```
0    57
2    34
1    29
Name: post_treatment_response, dtype: int64
```

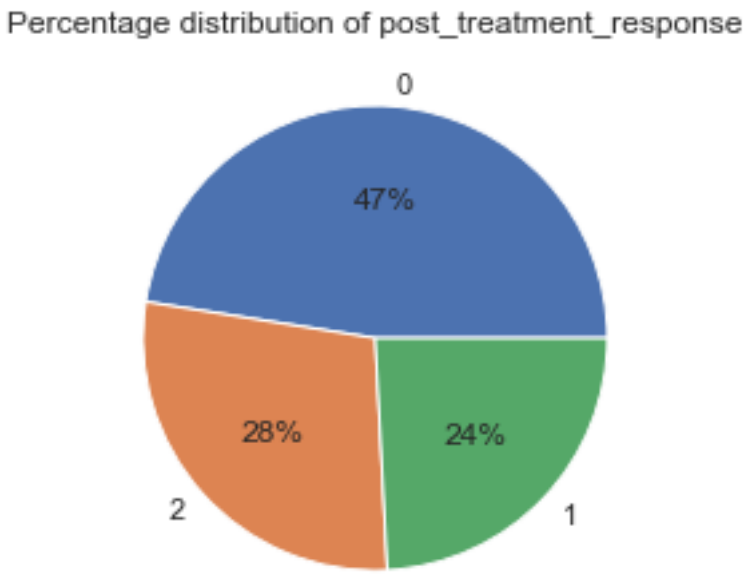
[12]:
```
# Barplot
plot = sns.countplot(secondary_var)
mod.show_values(plot)
plt.title("Frequency distribution of {}".format(secondary_var_name))
```

```
plt.ylabel('Number of Occurences', fontsize=12)
plt.xlabel('{}'.format(secondary_var_name),fontsize=12)
plt.show()
```

```
C:\Users\gdbt0\anaconda3\lib\site-packages\seaborn\_decorators.py:36:
FutureWarning: Pass the following variable as a keyword arg: x. From version
0.12, the only valid positional argument will be `data`, and passing other
arguments without an explicit keyword will result in an error or
misinterpretation.
  warnings.warn(
```



[13]:
```
#Pie chart
plt.title("Percentage distribution of {}".format(secondary_var_name))
plt.pie(secondary_var_value_counts, labels=secondary_var_value_counts.index,␣
 ↪autopct='%.0f%%')
plt.show()
```



1.2.3 Analysis of groups

Creates groups by tumour_stage

[14]:
```
firstGroup = primary_vs_secondary[primary_vs_secondary[primary_var_name] ==␣
 ↪" 4 "][secondary_var_name]
secondGroup = primary_vs_secondary[primary_vs_secondary[primary_var_name] ==␣
 ↪">4 "][secondary_var_name]
```

1.2.4 belowFour

The group where the initial tumor size is below 4cm

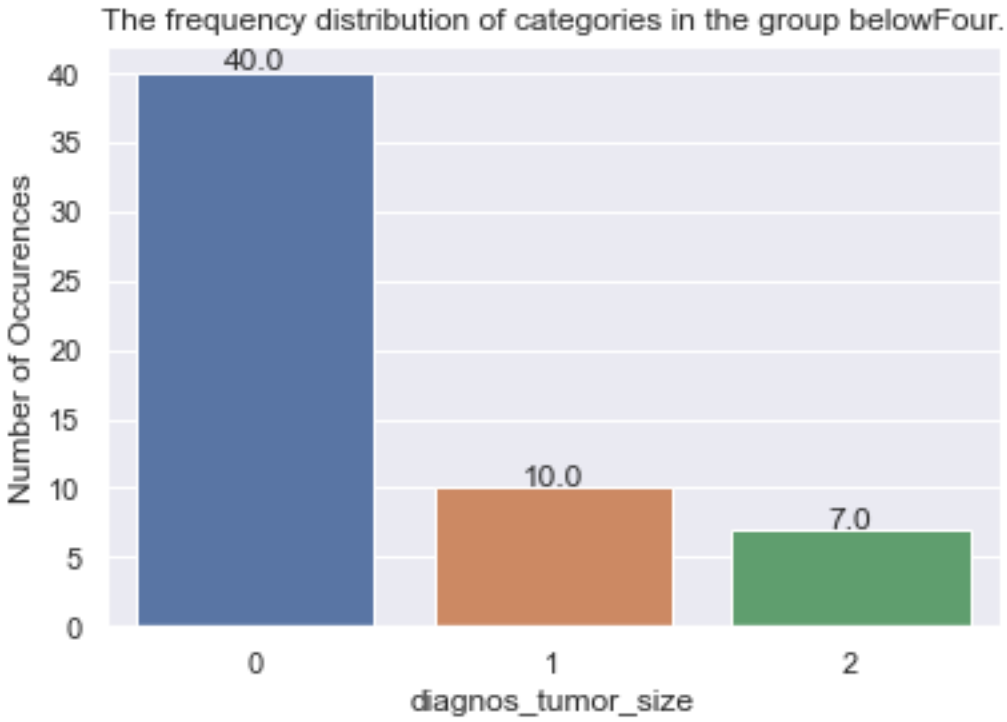
[15]:
```
## Finding the frequency distribution of categories in the variable
print("The frequency distribution of categories in the group 2B.")
print("In total, there are {} categories.".format(firstGroup.value_counts().
 ↪count()))
firstGroup.value_counts()
```

```
The frequency distribution of categories in the group 2B.
In total, there are 3 categories.
```

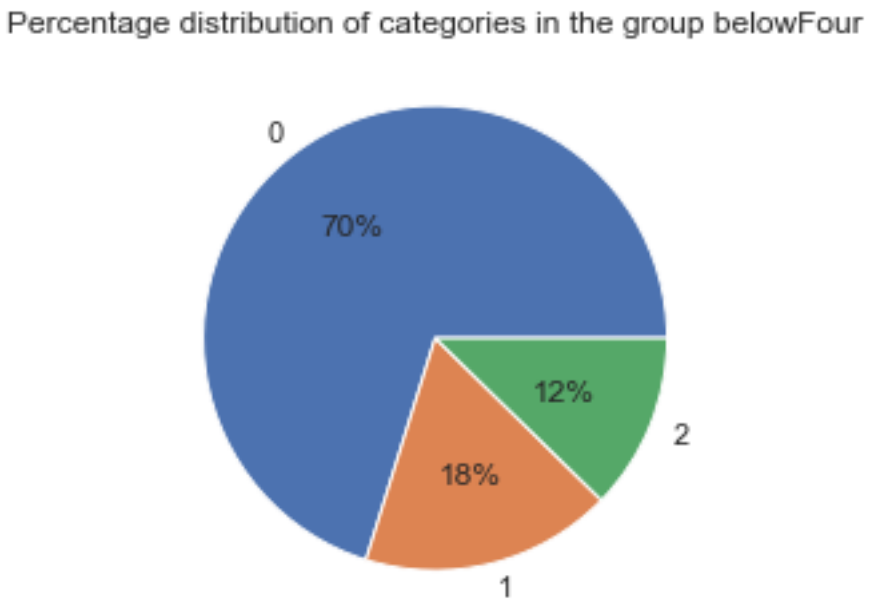
[15]:
```
0    40
1    10
2     7
Name: post_treatment_response, dtype: int64
```

[16]:
```
# Barplot
plot = sns.countplot(firstGroup)
mod.show_values(plot)
plt.title("The frequency distribution of categories in the group belowFour.")
plt.ylabel('Number of Occurences', fontsize=12)
plt.xlabel('{}'.format(primary_var_name),fontsize=12)
plt.show()
```

```
C:\Users\gdbt0\anaconda3\lib\site-packages\seaborn\_decorators.py:36:
FutureWarning: Pass the following variable as a keyword arg: x. From version
0.12, the only valid positional argument will be `data`, and passing other
arguments without an explicit keyword will result in an error or
misinterpretation.
  warnings.warn(
```



[17]:
```
#Pie chart
plt.title("Percentage distribution of categories in the group belowFour")
plt.pie(firstGroup.value_counts(), labels=firstGroup.value_counts().index,␣
 ↪autopct='%.0f%%')
plt.show()
```



1.2.5 aboveFour

The group where the initial tumor size is below 4cm

[18]:
```
## Finding the frequency distribution of categories in the variable
print("The frequency distribution of categories in the group aboveFour.")
print("In total, there are {} categories.".format(secondGroup.value_counts().
 ↪count()))
secondGroup.value_counts()
```

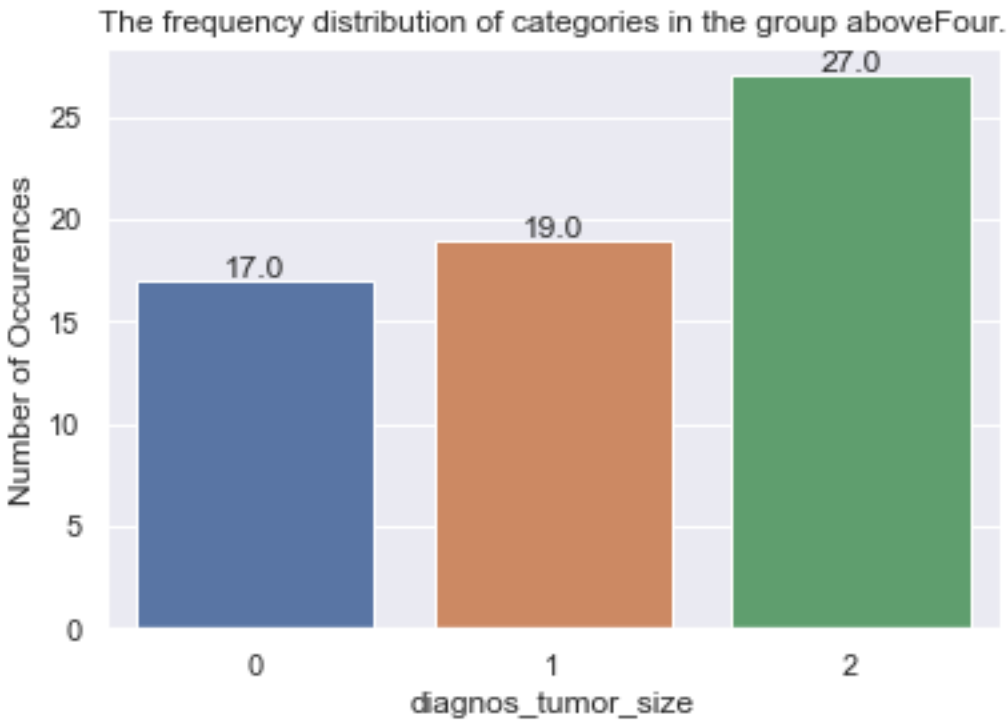
```
The frequency distribution of categories in the group aboveFour.
In total, there are 3 categories.
```

[18]:
```
2    27
1    19
0    17
Name: post_treatment_response, dtype: int64
```

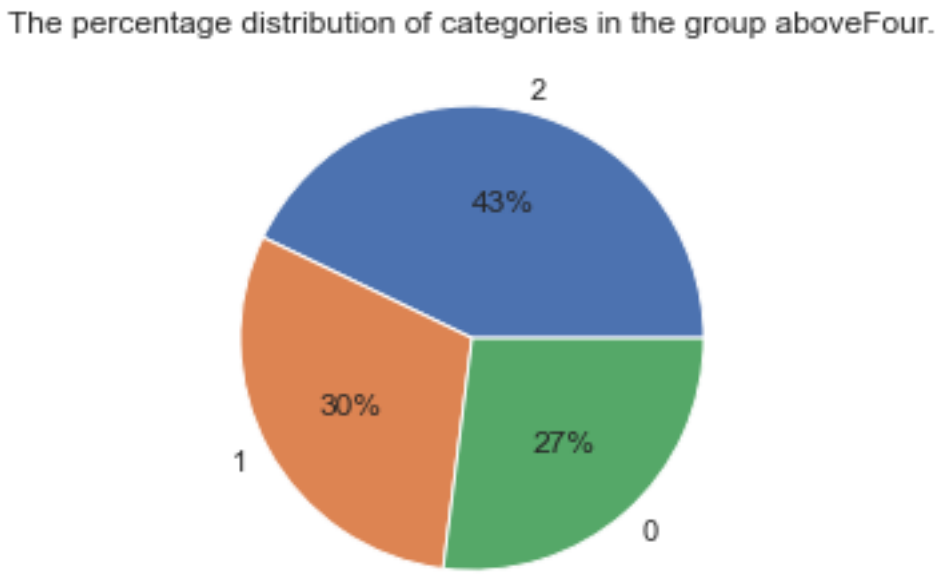
[19]:
```
# Barplot
plot = sns.countplot(secondGroup)
mod.show_values(plot)
plt.title("The frequency distribution of categories in the group aboveFour.")
plt.ylabel('Number of Occurences', fontsize=12)
plt.xlabel('{}'.format(primary_var_name),fontsize=12)
plt.show()
```

```
C:\Users\gdbt0\anaconda3\lib\site-packages\seaborn\_decorators.py:36:
```

```
FutureWarning: Pass the following variable as a keyword arg: x. From version
0.12, the only valid positional argument will be `data`, and passing other
arguments without an explicit keyword will result in an error or
misinterpretation.
  warnings.warn(
```



[20]:
```
#Pie chart
plt.title("The percentage distribution of categories in the group aboveFour.")
plt.pie(secondGroup.value_counts(), labels=secondGroup.value_counts().index,␣
 ↪autopct='%.0f%%')
plt.show()
```



1.2.6 Chi square test for Independence

Test that the categorical values of the two groups are different to each other.

Reference

[1] Chi-Bar-Squared. Retrieved March 9, 2022 from:

[2] Johns Hopkins.

[3] Kenney, J. F. and Keeping, E. S. Mathematics of Statistics, Pt. 2, 2nd ed. Princeton, NJ: Van Nostrand, 1951.

[4] https://www.statisticshowto.com/probability-and-statistics/chi-square/

[5] https://www.askpython.com/python/examples/chi-square-test

1.2.7 Uses the pandas crosstab() function to create a contingency table of the two selected variables

[21]:
```
chisqt = pd.crosstab(primary_var, secondary_var, margins=True)
print(chisqt)
```

```
post_treatment_response   0   1   2  All
diagnos_tumor_size
>4                       17  19  27   63
 4                       40  10   7   57
All                      57  29  34  120
```

[22]:
```
value = np.array([chisqt.iloc[0][0:5].values, chisqt.iloc[1][0:5].values])
print(value)
```

```
[[17 19 27 63]
 [40 10  7 57]]
```

[23]:
```
chi_stat = chi2_contingency(value)[0]
p_value = chi2_contingency(value)[1]
degrees_of_freedom = chi2_contingency(value)[2]
significance_level = 0.05
```

The null hypothesis: The grouping variables have no association or correlation amongst them. #### The alternate hypothesis The variables are associated with each other and happen to have a correlation between the variables.

[24]:
```
print("The p-value of the test is: {}".format(p_value) + "\nThe test statistic␣
 ↪is: {}".format(chi_stat) + "\nThe degrees of freedom is: {}".
 ↪format(degrees_of_freedom)
    )
```

```
The p-value of the test is: 3.031067690672718e-05
The test statistic is: 23.597504847132598
The degrees of freedom is: 3
```

[25]:
```
if p_value <= significance_level:
    print('Reject NULL HYPOTHESIS')
else:
    print('Accept NULL HYPOTHESIS')
```

```
Reject NULL HYPOTHESIS
```