Exploratory Data Analysis-BreakHis Dataset

March 24,2019

[1] About Data

The dataset which we are going to use is BreakHis dataset caontainin 7909 histopathical breast cancer sample images from 82 patients respectively.
REPRESENTATION OF DATASET IN PROJECT IS AS FOLLOWS-

1. Cancer Class
1.1. Benign
This Class is represented by Integer-1
1.2. Malignant
This Class is represented by Integer-2

2. Cancer Type
2.1 Benign-A
Benign-A represents Adenosis.This Class is represented by Integer-11
2.2 Benign-FA
Benign-FA represents Fibro Adenoma.This Class is represented by Integer-12
2.3 Benign-TA
Benign-TA represents Tubulor Adenoma.This Class is represented by Integer-13
2.4 Benign-PT
Benign-PT represents Phyllodes Tumor.This Class is represented by Integer-14
2.5. Malignant-DC
Malignant-DC represents Ductol Carinoma.This Class is represented by Integer-21
2.6. Malignant-LC
Malignant-LC represents Lobular Carinoma.This Class is represented by Integer-22
2.7. Malignant-MC
Malignant-Mc represents Mucious Carinoma.This Class is represented by Integer-23
2.8. Malignant-PC
Malignant-PC represents Pappillary Carinoma.This Class is represented by Integer-24

3. Magnification
3.1. 40X - 40
3.2. 100X - 100
3.3. 200X - 200
3.4. 400X - 400

Note -

After Each visualization some counts are represented for elaborations of plots which are used for distribution.

Pre-Exploratory Data Analysis

Import Library

In [1]:

```
import pandas as pd
import numpy as np
import seaborn as sb
sb.set(style="darkgrid")
import matplotlib.pyplot as plt
```

Loading Numpy Array

In [2]:

```
# Train Arrays
data_cancerclass_train=np.load("train/data_cancerclass_train.npy")
data_cancertype_train=np.load("train/data_cancertype_train.npy")
data_mag_train=np.load("train/data_mag_train.npy")
# Test Arrays
data_cancerclass_test=np.load("test/data_cancerclass_test.npy")
data_cancertype_test=np.load("test/data_cancertype_test.npy")
data_mag_test=np.load("test/data_mag_test.npy")
```

[2] Train Arrays Visualization

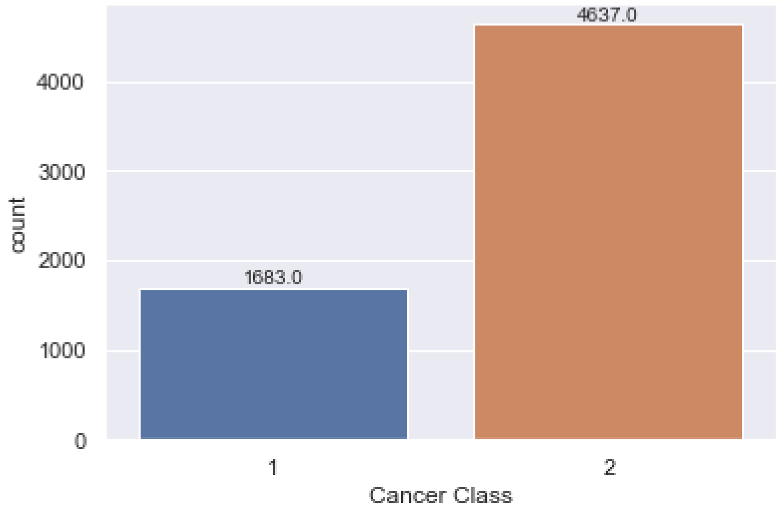
In [3]:

```
train_df=pd.DataFrame({'Cancer Class':data_cancerclass_train,
                      'Cancer Type':data_cancertype_train,
                      'Magnification':data_mag_train})
```

[2.1] Cancer Class

In [4]:

```
ax = sb.countplot(x="Cancer Class", data=train_df)
fig=ax.get_figure()
fig.savefig("Train Cancer Class.png")
for p in ax.patches:
    x=p.get_bbox().get_points()[:,0]
    y=p.get_bbox().get_points()[1,1]
    ax.annotate(y,(x.mean(), y),ha='center', va='bottom')
```



In [5]:

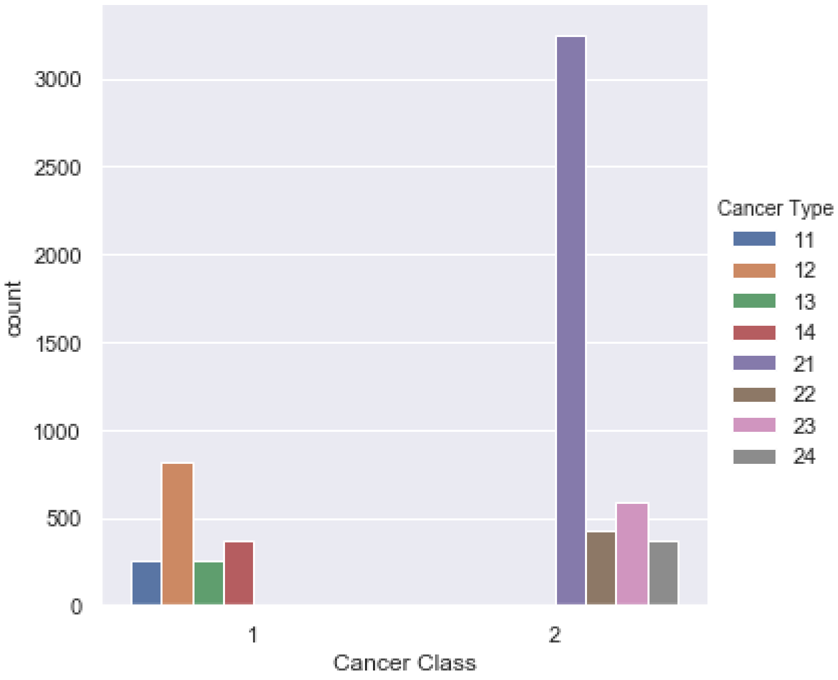
```
print(train_df.groupby("Cancer Class").count())
```

```
              Cancer Type  Magnification
Cancer Class                            
1                    1683           1683
2                    4637           4637
```

[2.3] Cancer Type

In [6]:

```
ax = sb.catplot(x="Cancer Class",hue="Cancer Type", data=train_df,kind="count")
ax.savefig("Train Cancer Class with cancer type.png")
```



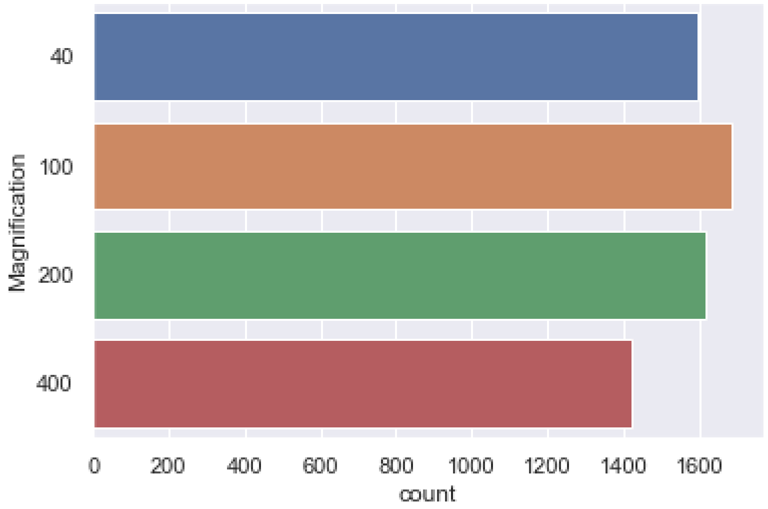
In [7]:

```
print(train_df.groupby("Cancer Type").count())
```

```
             Cancer Class  Magnification
Cancer Type
11                    252            252
12                    813            813
13                    251            251
14                    367            367
21                   3250           3250
22                    425            425
23                    591            591
24                    371            371
```

[2.3] Magnification

In [8]:
```
ax=sb.countplot(y="Magnification", data=train_df)
fig=ax.get_figure()
fig.savefig("Train Magnification.png")
```

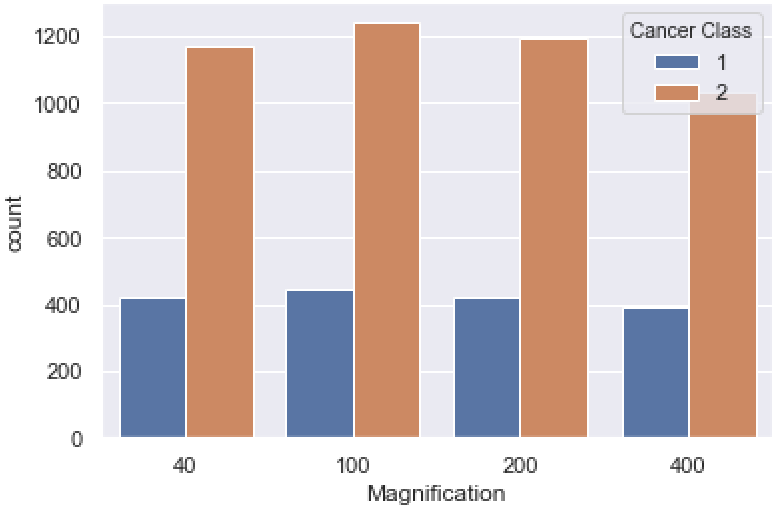


In [9]:
```
print(train_df.groupby("Magnification").count())
```

```
               Cancer Class  Cancer Type
Magnification
40                     1596         1596
100                    1687         1687
200                    1617         1617
400                    1420         1420
```

[2.4] Cancer Class Data Distribution

```
In [10]: ax=sb.countplot(x="Magnification",hue="Cancer Class", data=train_df)
         fig=ax.get_figure()
         fig.savefig("Train Magnification in Train Numpy.png")
```



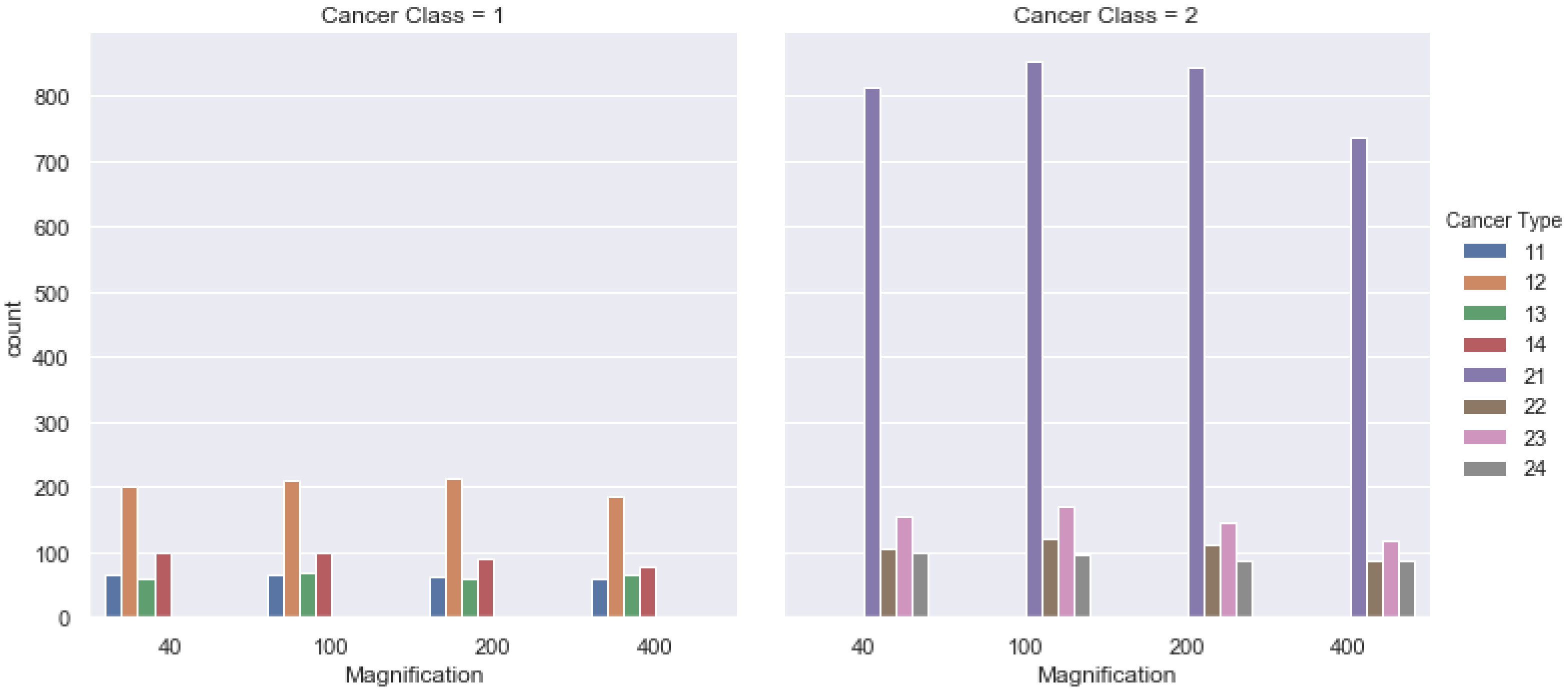
```
In [11]: print(train_df.groupby(["Cancer Class","Magnification"]).count())
```

```
                            Cancer Type
Cancer Class Magnification             
1            40                     424
             100                    446
             200                    424
             400                    389
2            40                    1172
             100                   1241
             200                   1193
             400                   1031
```

[2.5] Train Data Distribution

In [12]:

```
ax= sb.catplot(x="Magnification", hue="Cancer Type", col="Cancer Class",data=train_df, kind="count")
ax.savefig("Train Cancer Type with Magnification using Cancer Class.png")
```



In [13]:
```
print(train_df.groupby(["Cancer Type","Magnification"]).count())
```

```
                           Cancer Class
Cancer Type Magnification
11          40                       64
            100                      66
            200                      63
            400                      59
12          40                      202
            100                     210
            200                     214
            400                     187
13          40                       59
            100                      70
            200                      58
            400                      64
14          40                       99
            100                     100
            200                      89
            400                      79
21          40                      813
            100                     853
            200                     846
            400                     738
22          40                      106
            100                     120
            200                     113
            400                      86
23          40                      155
            100                     171
            200                     146
            400                     119
24          40                       98
            100                      97
            200                      88
            400                      88
```

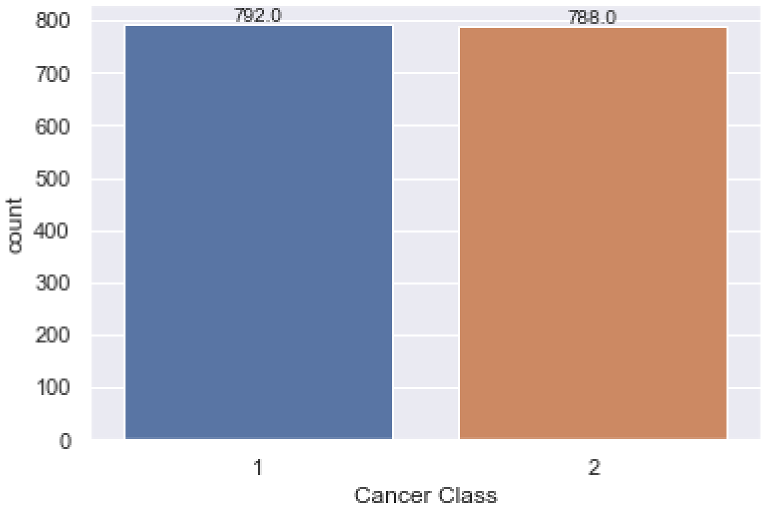
[3] Test Arrays Visualization

In [14]:
```
test_df=pd.DataFrame({'Cancer Class':data_cancerclass_test,
                      'Cancer Type':data_cancertype_test,
                      'Magnification':data_mag_test})
```

[3.1] Cancer Class

In [15]:

```
ax = sb.countplot(x="Cancer Class", data=test_df)
fig=ax.get_figure()
fig.savefig("Test Cancer Class.png")
for p in ax.patches:
    x=p.get_bbox().get_points()[:,0]
    y=p.get_bbox().get_points()[1,1]
    ax.annotate(y,(x.mean(), y),ha='center', va='bottom')
```



In [16]:

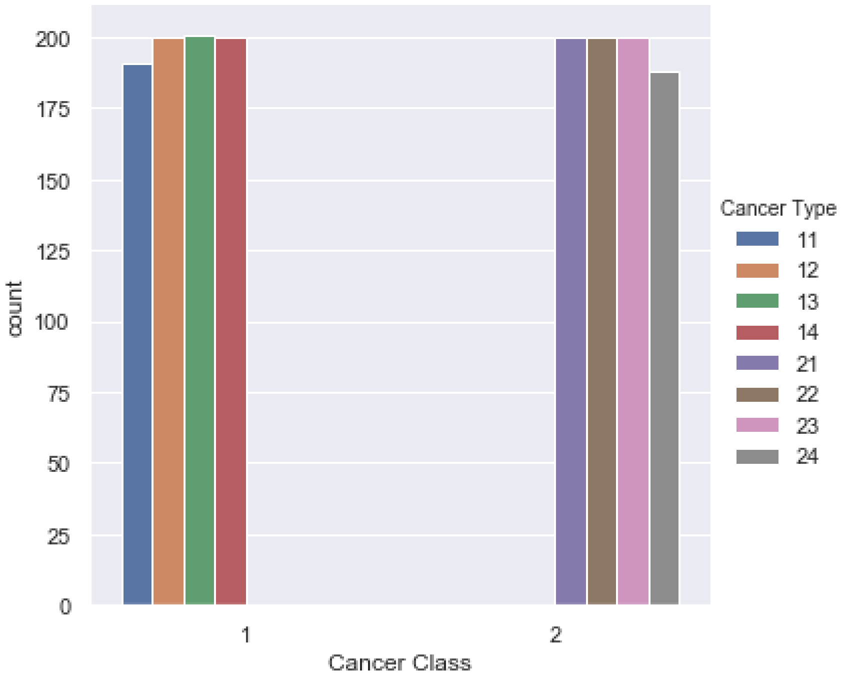
```
print(test_df.groupby("Cancer Class").count())
```

```
              Cancer Type  Magnification
Cancer Class
1                     792            792
2                     788            788
```

[3.2] Cancer Type

In [17]:

```python
ax = sb.catplot(x="Cancer Class",hue="Cancer Type", data=test_df,kind="count")
ax.savefig("Test Cancer Class with cancer type.png")
```



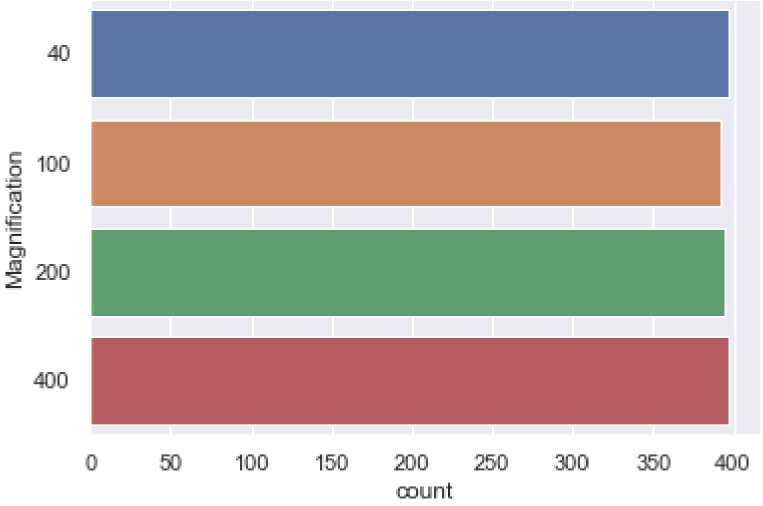
In [18]:

```python
print(test_df.groupby("Cancer Type").count())
```

```
             Cancer Class  Magnification
Cancer Type                             
11                    191            191
12                    200            200
13                    201            201
14                    200            200
21                    200            200
22                    200            200
23                    200            200
24                    188            188
```

[3.3] Cancer Class Maginification

```
In [19]: ax=sb.countplot(y="Magnification", data=test_df)
         fig=ax.get_figure()
         fig.savefig("Test Magnification.png")
```



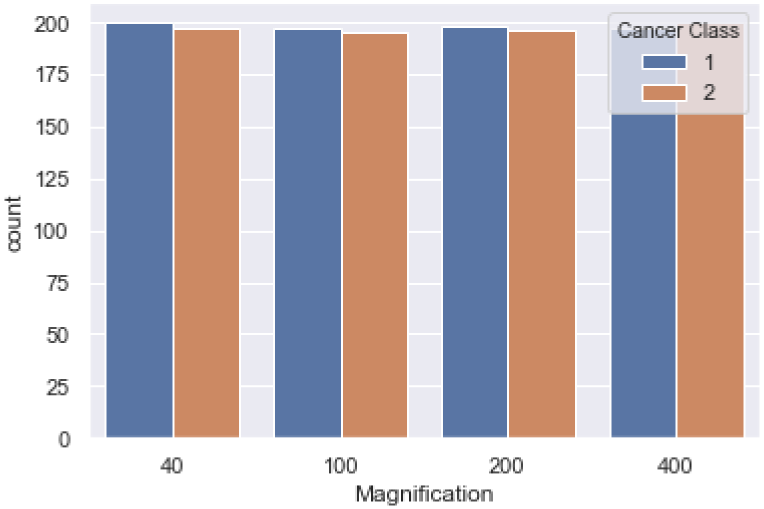
```
In [20]: print(test_df.groupby("Magnification").count())
```

```
               Cancer Class  Cancer Type
Magnification
40                      397          397
100                     392          392
200                     394          394
400                     397          397
```

[3.4] Cancer Class Data Distribution

In [21]:

```
ax=sb.countplot(x="Magnification",hue="Cancer Class", data=test_df)
fig=ax.get_figure()
fig.savefig("Test Magnification in Test Numpy.png")
```



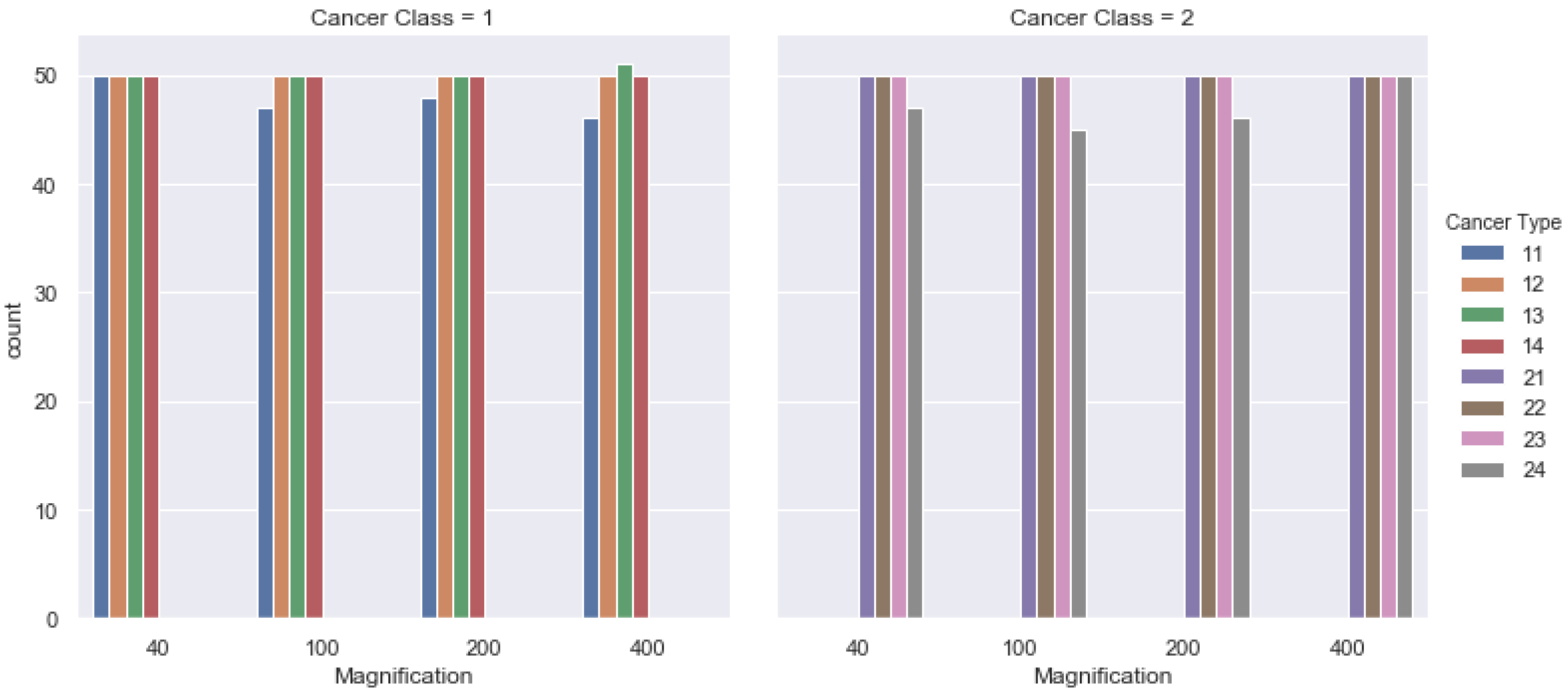
In [22]:

```
print(test_df.groupby(["Cancer Class","Magnification"]).count())
```

```
                          Cancer Type
Cancer Class Magnification
1            40                   200
             100                  197
             200                  198
             400                  197
2            40                   197
             100                  195
             200                  196
             400                  200
```

[3.5] Test Data Distribution

```
In [23]: ax= sb.catplot(x="Magnification", hue="Cancer Type", col="Cancer Class",
         ...                    data=test_df, kind="count");
         ax.savefig("Test Cancer Type with Magnification using Cancer Class.png")
```



```
In [24]: print(test_df.groupby(["Cancer Type","Magnification"]).count())
```

```
                           Cancer Class
Cancer Type Magnification              
11          40                       50
            100                      47
            200                      48
            400                      46
12          40                       50
            100                      50
            200                      50
            400                      50
13          40                       50
            100                      50
            200                      50
            400                      51
14          40                       50
            100                      50
            200                      50
            400                      50
21          40                       50
            100                      50
            200                      50
            400                      50
22          40                       50
            100                      50
            200                      50
            400                      50
23          40                       50
            100                      50
            200                      50
            400                      50
24          40                       47
            100                      45
            200                      46
            400                      50
```

Post-Exploratory Data Analysis

After the dataset is retrived, it was passed through some Deep-Learning Algorithms for feature Extraction.The Algorithms are known as Deep Convolution Neural Networks.

The Used CNN's are as follows

1. **VGG16**
2. **VGG19**
3. **Xception**
4. **ResNet50**
5. **InceptionV3**
6. **InceptionResNetV2**

The Dataset was distributed as 5000 Train Samples,2900 Test Samples and Randomly 9 Images were removed for the checking of model.