We have a product called Drug 390 for breast cancer treatment and our team is interested in understanding how long patients are on treatment when they are taking our product compared to the generic. For additional context, breast cancer patients can fall into four categories based on their HER2 status (0 or 1) or their Hormone Receptor (HR) status (0 or 1) so we are also interested in understanding how the cancer category might impact length of treatment as well.

In [364]:
```
#libraries

import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
import datetime as dt
import time

from sklearn.model_selection import train_test_split
from sklearn.model_selection import cross_val_score
from sklearn.neighbors import KNeighborsClassifier
from sklearn.linear_model import LogisticRegression
from sklearn.svm import LinearSVC
from sklearn.naive_bayes import GaussianNB
from sklearn.naive_bayes import BernoulliNB
```

In [365]:
```
# dataframes

# Contains Flags and Receptor Markers - 37 Rows 5 Columns
d390 = pd.read_csv('drug390.csv')
# Contains Treatment Dates for each Patient ID - 339 Rows 4 Columns
adm_main = pd.read_csv('pat_drug_admin_date.csv')
```

In [366]:
```
#create copies of dataframes to work with
admin_date = adm_main.copy()
markers_390 = d390.copy()
```

In [367]:
```
admin_date.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 339 entries, 0 to 338
Data columns (total 2 columns):
 #   Column           Non-Null Count  Dtype 
---  ------           --------------  ----- 
 0   Patient_ID       339 non-null    int64 
 1   Drug_admin_date  339 non-null    object
dtypes: int64(1), object(1)
memory usage: 5.4+ KB
```

In [368]:
```
markers_390.head(5)
```

	Patient_ID	drug_390_admin_flag	ER_positive	PR_positive	HER2_positive
0	2038	1	1	1	0
1	2120	0	1	0	1
2	2175	0	0	0	0
3	2407	0	0	1	0
4	2425	1	0	0	0

In [369]:
```
markers_390.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 37 entries, 0 to 36
Data columns (total 5 columns):
 #   Column               Non-Null Count  Dtype
---  ------               --------------  -----
 0   Patient_ID           37 non-null     int64
 1   drug_390_admin_flag  37 non-null     int64
 2   ER_positive          37 non-null     int64
 3   PR_positive          37 non-null     int64
 4   HER2_positive        37 non-null     int64
dtypes: int64(5)
memory usage: 1.6 KB
```

a. Describe how you would compute the length of treatment for each patient --

The length of treatment is obtained by aggregating each Patient_ID to filter out just for uniques and then take the resulting data structure and subtract the min date (start of treatment) from the max date (current treatment date).
The data must be prepared however as the date column is actually a

In [370]:
```
# sort the dates by most recent to oldest and replaces back to original da
taframe
admin_date.sort_values(by=['Patient_ID', 'Drug_admin_date'], inplace=True)

# converts the string object type of the Drug_admin_date column and conver
ts it into a datetime object with a placeholder value for the year of 1900
across the dataset
admin_date['Date'] =  pd.to_datetime(admin_date['Drug_admin_date'], format
='%d-%b')
admin_date.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 339 entries, 1 to 324
Data columns (total 3 columns):
 #   Column           Non-Null Count  Dtype
---  ------           --------------  -----
 0   Patient_ID       339 non-null    int64
 1   Drug_admin_date  339 non-null    object
 2   Date             339 non-null    datetime64[ns]
dtypes: datetime64[ns](1), int64(1), object(1)
memory usage: 10.6+ KB
```

In [371]:
```
# Option 1 of Calculating Treatment Length
start_q1o1 = time.time()
def trx_length(x):
    """
    This function will iterate over each row in the dataframe and verify t
he ID in the list pat_id is the one being reviewed and then take the diffe
rence between these values.
    """
    pat_id = list(admin_date['Patient_ID'].unique())
    for item in pat_id:
        max_date = admin_date[admin_date['Patient_ID'] == item]['Date'].ma
x()
        min_date = admin_date[admin_date['Patient_ID'] == item]['Date'].mi
n()
        trx_length = max_date - min_date
        if x == item:
            return trx_length

admin_date['Trx_Length'] = admin_date['Patient_ID'].apply(lambda x: trx_le
ngth(x))
end_q1o1 = time.time()

# Option 2 of Calculating Treatment Length
start_q1o2 = time.time()
"""
The data is grouped by the Patient_Id and then the max and min are subtrac
ted to leave a series object which we have to reset the index on and then
 do a merge with the original dataframe using the
Patient_ID column as the 'primary key'
"""
calc_dates = (admin_date.groupby('Patient_ID')['Date'].max() - admin_date.
groupby('Patient_ID')['Date'].min()).reset_index()
# merge this new group by on the index to the main dataframe
admin_date = admin_date.merge(calc_dates, left_on='Patient_ID',right_on='P
atient_ID', suffixes=('','_Goupby'))
end_q1o2 = time.time()

# Option 3 - create two columns identifying the start and end date for eac
h Patient_ID and then do series arthmetic assigning to a new column called
'Date_Difference'
start_q1o3 = time.time()
def trx_end(x):
    pat_id = list(admin_date['Patient_ID'].unique())
    for item in pat_id:
        max_date = admin_date[admin_date['Patient_ID'] == item]['Date'].ma
x()
        if x == item:
            return max_date

def trx_start(x):
    pat_id = list(admin_date['Patient_ID'].unique())
    for item in pat_id:
        min_date = admin_date[admin_date['Patient_ID'] == item]['Date'].mi
n()
        if x == item:
            return min_date

admin_date['Trx_End'] = admin_date['Patient_ID'].apply(lambda x:trx_end(x
))
```

```
admin_date['Trx_Start'] = admin_date['Patient_ID'].apply(lambda x:trx_star
t(x))

# series arithmetic to create new column
admin_date['Date_Difference'] = admin_date['Trx_End'] - admin_date['Trx_St
art']
end_q1o3 = time.time()

print('Option 1 Run Time: ', end_q1o1 - start_q1o1)
print('Option 2 Run Time: ', end_q1o2 - start_q1o2)
print('Option 3 Run Time: ', end_q1o3 - start_q1o3)
```

```
Option 1 Run Time:  10.100568771362305
Option 2 Run Time:  0.005798816680908203
Option 3 Run Time:  10.88792896270752
```

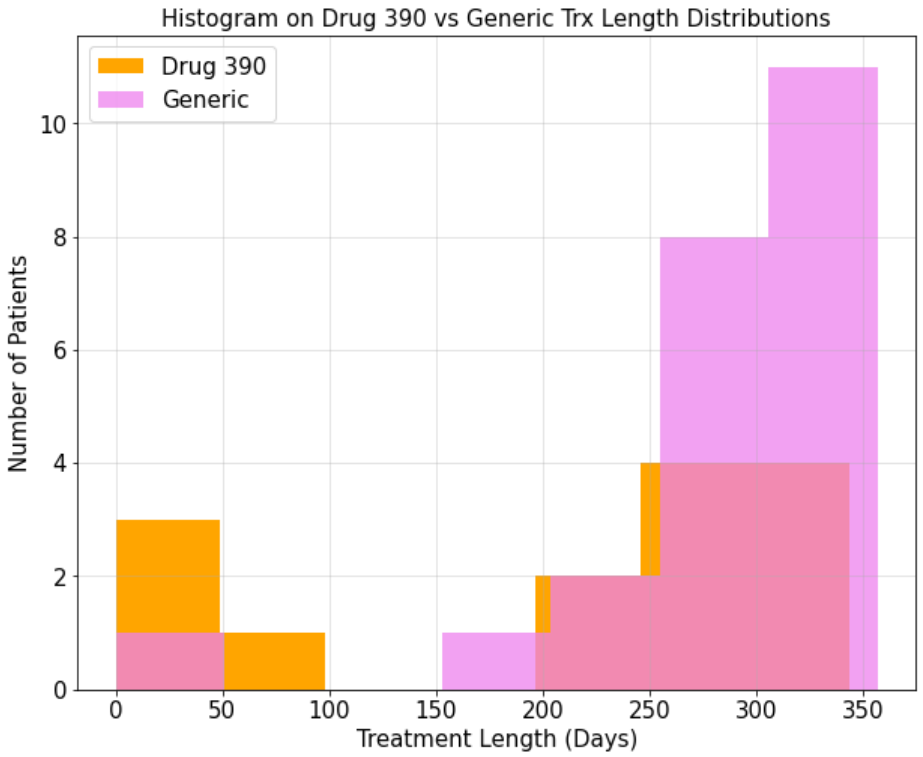
b. Describe or show how you might go about comparing the length of treatment by drug 390 vs. the generic (i.e. through a visualization, descriptive analytics, statistical tests, or machine learning)

In [372]:
```
unique_patientid = admin_date.drop_duplicates(subset='Patient_ID').sort_va
lues(by='Trx_Length',ascending=False)[['Patient_ID', 'Trx_Length']]
unique_patientid['Trx_Length'] = unique_patientid['Trx_Length'].dt.days
```

In [373]:
```
markers_dates = markers_390.merge(unique_patientid, left_on='Patient_ID',
right_on='Patient_ID').sort_values(by='Trx_Length', ascending=False)
generic = markers_dates[markers_390['drug_390_admin_flag']==0]
on_390 = markers_dates[markers_390['drug_390_admin_flag']==1]
```

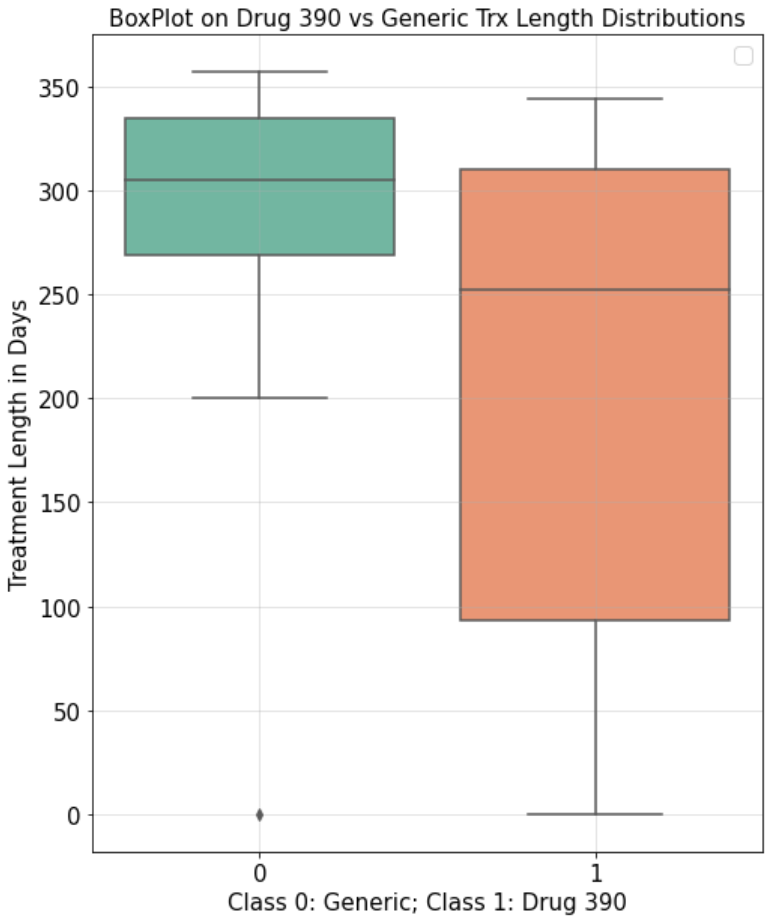
```
/Users/oldvasegreenbird/miniconda3/lib/python3.7/site-packages/ipykern
el_launcher.py:2: UserWarning: Boolean Series key will be reindexed to
match DataFrame index.

/Users/oldvasegreenbird/miniconda3/lib/python3.7/site-packages/ipykern
el_launcher.py:3: UserWarning: Boolean Series key will be reindexed to
match DataFrame index.
  This is separate from the ipykernel package so we can avoid doing im
ports until
```

In [374]:
```
plt.figure(figsize=(10,8))
plt.tick_params(labelsize=15)


plt.hist(on_390['Trx_Length'], bins=7, color='orange', label='Drug 390')
plt.hist(generic['Trx_Length'], bins=7, color='violet', alpha=0.75, label=
'Generic')
plt.xlabel('Treatment Length (Days)', fontsize=15)
plt.title('Histogram on Drug 390 vs Generic Trx Length Distributions', fon
tsize=15)

plt.ylabel('Number of Patients', fontsize=15)
plt.legend(fontsize=15)
plt.grid(True, alpha=.4)
```



In [375]:
```
plt.figure(figsize=(8,10))
plt.tick_params(labelsize=15)


sns.boxplot(x='drug_390_admin_flag',y='Trx_Length',data=markers_dates, pal
ette='Set2')
plt.xlabel('Class 0: Generic; Class 1: Drug 390', fontsize=15)
plt.title('BoxPlot on Drug 390 vs Generic Trx Length Distributions', fonts
ize=15)

plt.ylabel('Treatment Length in Days', fontsize=15)
plt.legend(fontsize=15)
plt.grid(True, alpha=.4)
```

```
No handles with labels found to put in legend.
```



The histogram shows us that the data is not normally distrubuted for both drug datasets. This shows an assymetric pattern in the data which would make it difficult to calculate confidence intervals and see how representative these numbers are of an actual population's results with our two drugs. From the sample mean and standard deviation we collect we can create random sampling simulations with different sample sizes to see how accurate our estimation can be.

Upon first glance you notice there is an outlier in the 0 label, 'not on drug 390', for column drug_390_admin_flag. Looking at the boxplot we see we have zeros as well in marker 1, 'on drug 390', and these are affecting the data. These must also be corrected for.

When running a minimum statistic for our data it shows 0 as a value which is actually an outlier and can be dropped if the dataset was larger. We could say this patient never received treatment and is not valid in the sample. However, since samples are limited on our dataset we can fill this specific instance with the median. The median is used as there is quite a variance in our values.

```
In [ ]:
```

In [376]:
```
def stats_comparison_95_confident(dataframe):
    # p_values for t test with a 95% confidence interval
    ninetyfive_confidence_pvals = {1:12.71, 2:4.303, 3:3.182, 4:2.776, 5:
2.571, 6:2.447, 7:2.365, 8:2.306, 9:2.262, 10:2.228, 11:2.201, 12:2.179, 1
3:2.16, 14:2.145, 15:2.131,
                                   16:2.12, 17:2.11, 18:2.101, 19:2.093, 2
0:2.086, 21:2.086, 22:2.086, 23:2.086, 24:2.086, 25:2.086, 26:2.086, 27:2.
086, 28:2.086, 29:2.086}
    # remove 0 treatment day patients
    def replace_zeros(y):
        if y == 0:
            return np.median(dataframe['Trx_Length'])
        else:
            return y
    dataframe['Trx_Length'] = dataframe['Trx_Length'].apply(lambda y: repl
ace_zeros(y))
    # sample
    sample_mean = dataframe['Trx_Length'].mean()
    sample_std = dataframe['Trx_Length'].std()
    sample_size = dataframe['Trx_Length'].shape[0]
    t_top = sample_mean + (ninetyfive_confidence_pvals[sample_size-1] * (s
ample_std/(np.sqrt(sample_size))))
    t_bottom = sample_mean - (ninetyfive_confidence_pvals[sample_size-1] *
(sample_std/(np.sqrt(sample_size))))
    # sample sizes
    a_sizes = [10000, 100000, 1000000]
    # create random sampling
    np.random.seed(42)
    for a in a_sizes:
        sim1 = np.random.normal(sample_mean, sample_std, a)
        # calculate 95% confidence interval
        z_score_95_bottom = sim1.mean() - 1.960 * (sim1.std() / (np.sqrt(a
)))
        z_score_95_top = sim1.mean() + 1.960 * (sim1.std() / (np.sqrt(a)))
        z_95 = (z_score_95_bottom, z_score_95_top)


        print('Simulation of {aa} size mean:'.format(aa=a), sim1.mean())
        print('95% Confidence Interval of {ab} Sample Size'.format(ab=z_95
))
        print('\n')
    print('Sample Mean:', sample_mean, 'Sample Std:', sample_std, 'Sample
 Size:', sample_size, 'Degrees of Freedom:', sample_size-1)
    print('95% Confidence Less Than 30 Samples Using t-score:', t_bottom,
t_top )

    return dataframe
```

In [377]:
```
generic_only = stats_comparison_95_confident(generic)
```

```
/Users/oldvasegreenbird/miniconda3/lib/python3.7/site-packages/ipykern
el_launcher.py:11: SettingWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: https://pandas.pydata.org/pandas
-docs/stable/user_guide/indexing.html#returning-a-view-versus-a-copy
  # This is added back by InteractiveShellApp.init_path()


Simulation of 10000 size mean: 300.2538767872502
95% Confidence Interval of (299.38884686270467, 301.1189067117957) Sam
ple Size


Simulation of 100000 size mean: 300.4495270709093
95% Confidence Interval of (300.1769043161912, 300.7221498256274) Samp
le Size


Simulation of 1000000 size mean: 300.2722575048093
95% Confidence Interval of (300.1859777996804, 300.3585372099382) Samp
le Size


Sample Mean: 300.3478260869565 Sample Std: 43.98409701828417 Sample Si
ze: 23 Degrees of Freedom: 22
95% Confidence Less Than 30 Samples Using t-score: 281.21645628504905
319.47919588886396
```

In [378]:
```
on_drug_390 = stats_comparison_95_confident(on_390)
```

```
Simulation of 10000 size mean: 241.9391750848481
95% Confidence Interval of (240.06379042714826, 243.81455974254794) Sa
mple Size


Simulation of 100000 size mean: 242.3633448503526
95% Confidence Interval of (241.77229878705393, 242.95439091365128) Sa
mple Size


Simulation of 1000000 size mean: 241.97902447586867
95% Confidence Interval of (241.79197009696426, 242.16607885477308) Sa
mple Size


Sample Mean: 242.14285714285714 Sample Std: 95.35751121466492 Sample S
ize: 14 Degrees of Freedom: 13
95% Confidence Less Than 30 Samples Using t-score: 187.09446469737307
297.1912495883412


/Users/oldvasegreenbird/miniconda3/lib/python3.7/site-packages/ipykern
el_launcher.py:11: SettingWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: https://pandas.pydata.org/pandas
-docs/stable/user_guide/indexing.html#returning-a-view-versus-a-copy
  # This is added back by InteractiveShellApp.init_path()
```

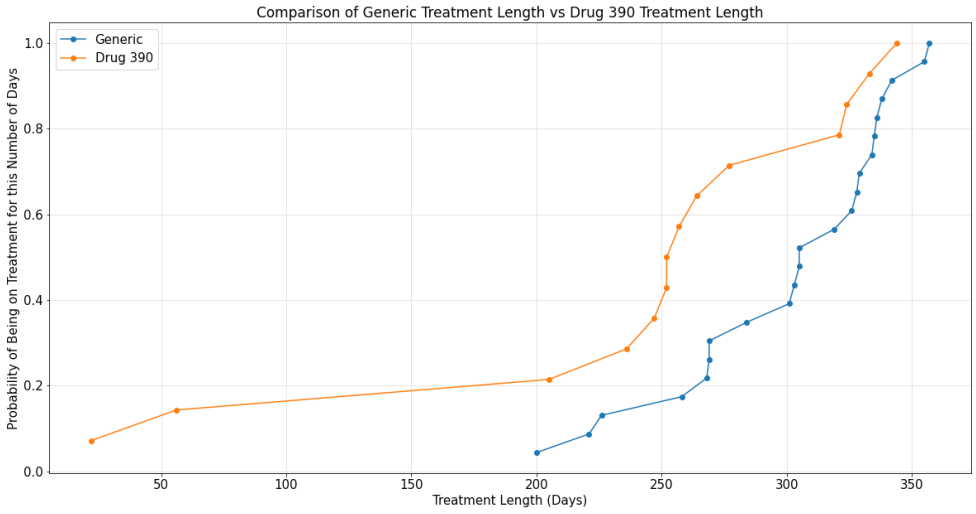
Simulations were run which ranged from 10K samples to 1M samples based on our sample means and standard deviations for both markers.

Using t-scores due to low number of samples we can be 95% confident our sample means are representative of the population means for each drug marker group, on 390 or not. To verify three simulations were run using our specific sample means and standard deviations. Each subsequent simulation was also confidence tested and provided confirmation the mean was representative of the true population with 95% confidence.

From this we can continue working with our values for the 'Trx_Length' columns as they are close representations of the true values observed if given to larger groups.

In [379]:
```
def ecdf(data):
    """Compute ECDF for a one-dimensional array of measurements."""
    # Number of data points: n
    n = len(data)

    # x-data for the ECDF: x
    x = np.sort(data)

    # y-data for the ECDF: y
    y = np.arange(1, n+1) / n

    return x, y
```

In [380]:
```
x_gen, y_gen = ecdf(generic['Trx_Length'])
x_390, y_390 = ecdf(on_drug_390['Trx_Length'])

plt.figure(figsize=(20,10))
plt.tick_params(labelsize=15)

gen_plot = plt.plot(x_gen,y_gen, marker='o', label='Generic')
plot_390 = plt.plot(x_390, y_390, marker='o', label='Drug 390')
m_gen, b_gen = np.polyfit(x_gen, y_gen, 1)
m_390, b_390 = np.polyfit(x_390, y_390, 1)
plt.title('Comparison of Generic Treatment Length vs Drug 390 Treatment Le
ngth',fontsize=17)

# gen_reg_line = plt.plot(x_gen, m_gen*x_gen + b_gen, label='Generic')
# reg_line_390 = plt.plot(x_390, m_390*x_390 + b_390, label='Drug 390')

plt.xlabel('Treatment Length (Days)', fontsize=15)
plt.ylabel('Probability of Being on Treatment for this Number of Days', fo
ntsize=15)
plt.legend(fontsize=15)
plt.grid(True, alpha=.4)
```



The data shows that a patient on the generic has a higher probability, based on the ECDF scale, to be on treatment for longer than if they were on our 'drug 390.'

Using this chart one could estimate a new patient with similar health conditions as these used in the sample would demonstrate similar behaviors. This can be backed up by our confidence interval calculations further up on the document.

In [381]:
```
# creates new column for Hormone Receptor Status with Generics
generic['HR_status'] = 0
generic.loc[(generic['ER_positive'] ==1) | (generic['PR_positive'] ==1),
'HR_status'] = 1

# creates new column for Hormone Receptor Status with D390
on_390['HR_status'] = 0
on_390.loc[(on_390['ER_positive'] ==1) | (on_390['PR_positive'] ==1), 'HR_
status'] = 1

# merges generic and 390 and then creates class labels for the four types
 of tumor categories
hr_status_set = generic.append(on_390, ignore_index=True)
hr_status_set['class_category'] = 0

# HER2_positive

# Generic HR
hr_status_set.loc[(hr_status_set['drug_390_admin_flag'] ==0) & (hr_status_
set['HER2_positive'] ==1) & (hr_status_set['HR_status'] ==1), 'class_categ
ory'] = 0
hr_status_set.loc[(hr_status_set['drug_390_admin_flag'] ==0) & (hr_status_
set['HER2_positive'] ==1) & (hr_status_set['HR_status'] ==1), 'class_name'
] = 'Generic HER2+/HR+'
hr_status_set.loc[(hr_status_set['drug_390_admin_flag'] ==0) & (hr_status_
set['HER2_positive'] ==1) & (hr_status_set['HR_status'] ==0), 'class_categ
ory'] = 1
hr_status_set.loc[(hr_status_set['drug_390_admin_flag'] ==0) & (hr_status_
set['HER2_positive'] ==1) & (hr_status_set['HR_status'] ==0), 'class_name'
] = 'Generic HER2+/HR-'
hr_status_set.loc[(hr_status_set['drug_390_admin_flag'] ==0) & (hr_status_
set['HER2_positive'] ==0) & (hr_status_set['HR_status'] ==1), 'class_categ
ory'] = 2
hr_status_set.loc[(hr_status_set['drug_390_admin_flag'] ==0) & (hr_status_
set['HER2_positive'] ==0) & (hr_status_set['HR_status'] ==1), 'class_name'
] = 'Generic HER2-/HR+'
hr_status_set.loc[(hr_status_set['drug_390_admin_flag'] ==0) & (hr_status_
set['HER2_positive'] ==0) & (hr_status_set['HR_status'] ==0), 'class_categ
ory'] = 3
hr_status_set.loc[(hr_status_set['drug_390_admin_flag'] ==0) & (hr_status_
set['HER2_positive'] ==0) & (hr_status_set['HR_status'] ==0), 'class_name'
] = 'Generic HER2-/HR-'

# Drug 390
hr_status_set.loc[(hr_status_set['drug_390_admin_flag'] ==1) & (hr_status_
set['HER2_positive'] ==1) & (hr_status_set['HR_status'] ==1), 'class_categ
ory'] = 4
hr_status_set.loc[(hr_status_set['drug_390_admin_flag'] ==1) & (hr_status_
set['HER2_positive'] ==1) & (hr_status_set['HR_status'] ==1), 'class_name'
] = 'D390 HER2+/HR+'
hr_status_set.loc[(hr_status_set['drug_390_admin_flag'] ==1) & (hr_status_
set['HER2_positive'] ==1) & (hr_status_set['HR_status'] ==0), 'class_categ
ory'] = 5
hr_status_set.loc[(hr_status_set['drug_390_admin_flag'] ==1) & (hr_status_
set['HER2_positive'] ==1) & (hr_status_set['HR_status'] ==0), 'class_name'
] = 'D390 HER2+/HR-'
hr_status_set.loc[(hr_status_set['drug_390_admin_flag'] ==1) & (hr_status_
set['HER2_positive'] ==0) & (hr_status_set['HR_status'] ==1), 'class_categ
ory'] = 6
```

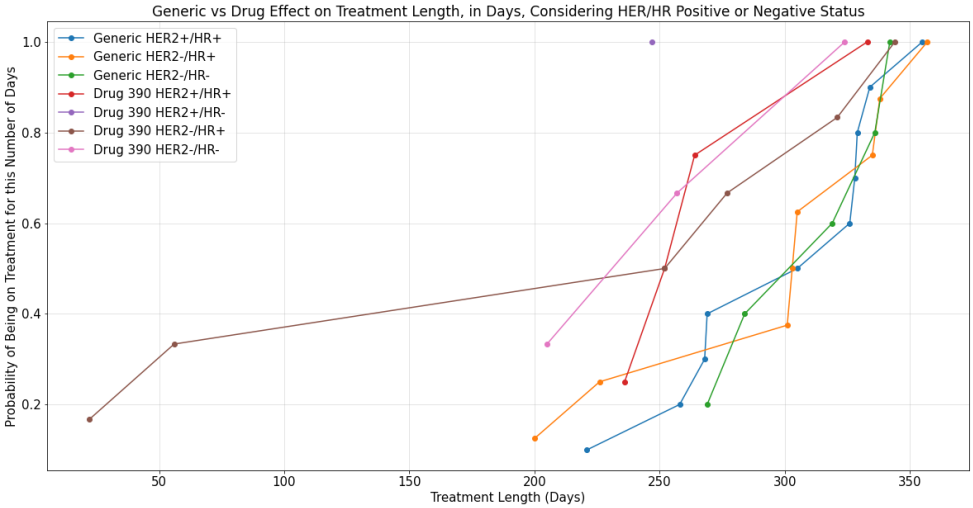
```
hr_status_set.loc[(hr_status_set['drug_390_admin_flag'] ==1) & (hr_status_
set['HER2_positive'] ==0) & (hr_status_set['HR_status'] ==1), 'class_name'
] = 'D390 HER2-/HR+'
hr_status_set.loc[(hr_status_set['drug_390_admin_flag'] ==1) & (hr_status_
set['HER2_positive'] ==0) & (hr_status_set['HR_status'] ==0), 'class_categ
ory'] = 7
hr_status_set.loc[(hr_status_set['drug_390_admin_flag'] ==1) & (hr_status_
set['HER2_positive'] ==0) & (hr_status_set['HR_status'] ==0), 'class_name'
] = 'D390 HER2-/HR-'
```

```
/Users/oldvasegreenbird/miniconda3/lib/python3.7/site-packages/ipykern
el_launcher.py:2: SettingWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: https://pandas.pydata.org/pandas
-docs/stable/user_guide/indexing.html#returning-a-view-versus-a-copy

/Users/oldvasegreenbird/miniconda3/lib/python3.7/site-packages/pandas/
core/indexing.py:966: SettingWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: https://pandas.pydata.org/pandas
-docs/stable/user_guide/indexing.html#returning-a-view-versus-a-copy
  self.obj[item] = s
/Users/oldvasegreenbird/miniconda3/lib/python3.7/site-packages/ipykern
el_launcher.py:6: SettingWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: https://pandas.pydata.org/pandas
-docs/stable/user_guide/indexing.html#returning-a-view-versus-a-copy
```

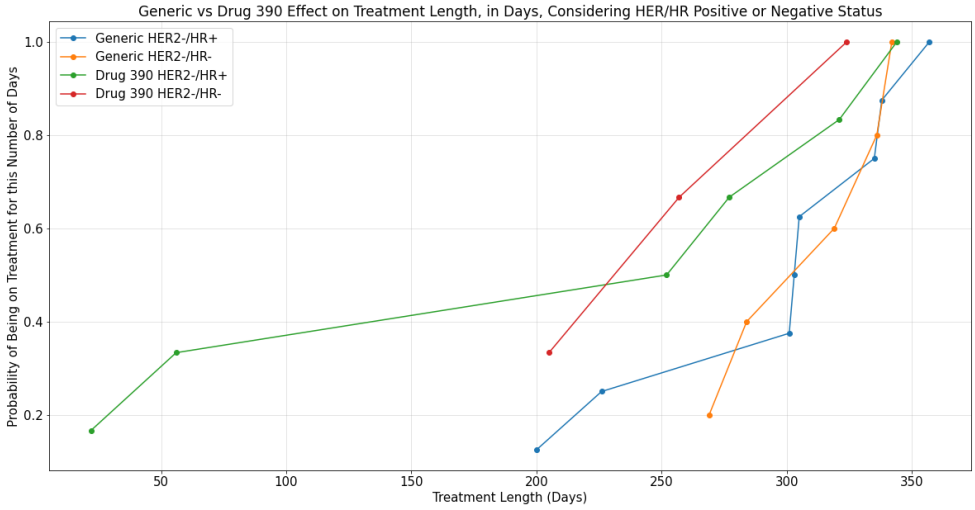
In [382]:
```
hr_status_set['class_name'].value_counts()
```

```
Generic HER2+/HR+    10
Generic HER2-/HR+     8
D390 HER2-/HR+        6
Generic HER2-/HR-     5
D390 HER2+/HR+        4
D390 HER2-/HR-        3
D390 HER2+/HR-        1
Name: class_name, dtype: int64
```

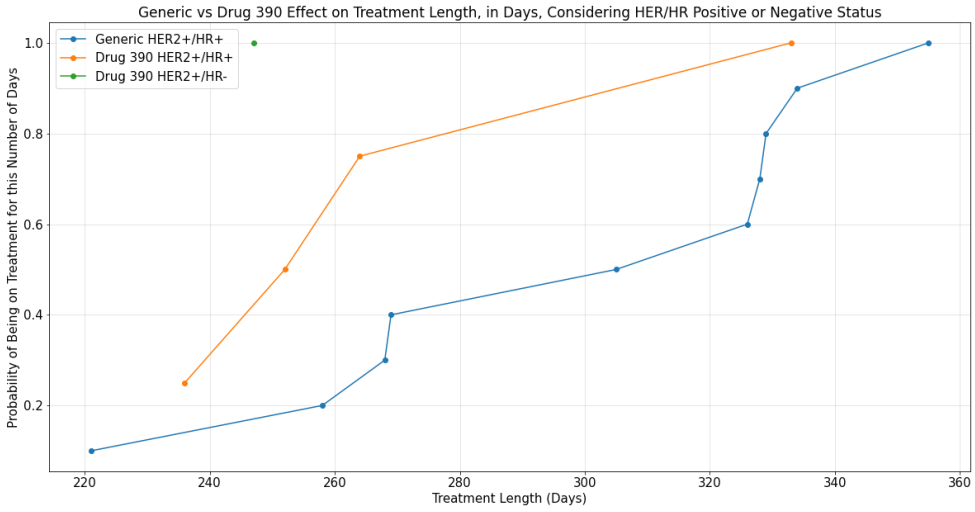
In [383]:
```
plt.figure(figsize=(20,10))
plt.tick_params(labelsize=15)
# Generic and HER2+/HR+
x0,y0 = ecdf(hr_status_set[hr_status_set['class_category'] == 0]['Trx_Leng
th'])
cat0_plot = plt.plot(x0,y0, marker='o', label='Generic HER2+/HR+')
# Generic HER2+ HR - 0 values
# x1,y1 = ecdf(hr_status_set[hr_status_set['class_category'] == 1]['Trx_Le
ngth'])
# cat1_plot = plt.plot(x1,y1, marker='o', label='Generic HER2+/HR-')
# Generic and HER2-/HR+
x2,y2 = ecdf(hr_status_set[hr_status_set['class_category'] == 2]['Trx_Leng
th'])
cat2_plot = plt.plot(x2,y2, marker='o', label='Generic HER2-/HR+')
# Generic and HER2-/HR-
x3,y3 = ecdf(hr_status_set[hr_status_set['class_category'] == 3]['Trx_Leng
th'])
cat3_plot = plt.plot(x3,y3, marker='o', label='Generic HER2-/HR-')
# D390 and HER2+/HR+
x4,y4 = ecdf(hr_status_set[hr_status_set['class_category'] == 4]['Trx_Leng
th'])
cat4_plot = plt.plot(x4,y4, marker='o', label='Drug 390 HER2+/HR+')
# D390 and HER2+/HR-
x5,y5 = ecdf(hr_status_set[hr_status_set['class_category'] == 5]['Trx_Leng
th'])
cat5_plot = plt.plot(x5,y5, marker='o', label='Drug 390 HER2+/HR-')
# D390 and HER2-/HR+
x6,y6 = ecdf(hr_status_set[hr_status_set['class_category'] == 6]['Trx_Leng
th'])
cat6_plot = plt.plot(x6,y6, marker='o', label='Drug 390 HER2-/HR+')
# D390 and HER2-/HR-
x7,y7 = ecdf(hr_status_set[hr_status_set['class_category'] == 7]['Trx_Leng
th'])
cat7_plot = plt.plot(x7,y7, marker='o', label='Drug 390 HER2-/HR-')


plt.title('Generic vs Drug Effect on Treatment Length, in Days, Considerin
g HER/HR Positive or Negative Status',fontsize=17)
plt.xlabel('Treatment Length (Days)', fontsize=15)
plt.ylabel('Probability of Being on Treatment for this Number of Days', fo
ntsize=15)
plt.legend(fontsize=15)
plt.grid(True, alpha=.4)
plt.show()
```


Generic vs Drug Effect on Treatment Length, in Days, Considering HER/HR Positive or Negative Status
Generic HER2+/HR+
Generic HER2-/HR+
Generic HER2-/HR-
Drug 390 HER2+/HR+
Drug 390 HER2+/HR-
Drug 390 HER2-/HR+
Drug 390 HER2-/HR-
Probability of Being on Treatment for this Number of Days
Treatment Length (Days)
1.0
0.8
0.6
0.4
0.2
50
100
150
200
250
300
350

In [384]:
```
plt.figure(figsize=(20,10))
plt.tick_params(labelsize=15)

# Generic and HER2-/HR+
x2,y2 = ecdf(hr_status_set[hr_status_set['class_category'] == 2]['Trx_Length'])
cat2_plot = plt.plot(x2,y2, marker='o', label='Generic HER2-/HR+')
# Generic and HER2-/HR-
x3,y3 = ecdf(hr_status_set[hr_status_set['class_category'] == 3]['Trx_Length'])
cat3_plot = plt.plot(x3,y3, marker='o', label='Generic HER2-/HR-')

# D390 and HER2-/HR+
x6,y6 = ecdf(hr_status_set[hr_status_set['class_category'] == 6]['Trx_Length'])
cat6_plot = plt.plot(x6,y6, marker='o', label='Drug 390 HER2-/HR+')
# D390 and HER2-/HR-
x7,y7 = ecdf(hr_status_set[hr_status_set['class_category'] == 7]['Trx_Length'])
cat7_plot = plt.plot(x7,y7, marker='o', label='Drug 390 HER2-/HR-')


plt.title('Generic vs Drug 390 Effect on Treatment Length, in Days, Considering HER/HR Positive or Negative Status',fontsize=17)
plt.xlabel('Treatment Length (Days)', fontsize=15)
plt.ylabel('Probability of Being on Treatment for this Number of Days', fontsize=15)
plt.legend(fontsize=15)
plt.grid(True, alpha=.4)
plt.show()
```



In [385]:
```
plt.figure(figsize=(20,10))
plt.tick_params(labelsize=15)
# Generic and HER2+/HR+
x0,y0 = ecdf(hr_status_set[hr_status_set['class_category'] == 0]['Trx_Length'])
cat0_plot = plt.plot(x0,y0, marker='o', label='Generic HER2+/HR+')
# # Generic HER2+ HR -
# x1,y1 = ecdf(hr_status_set[hr_status_set['class_category'] == 1]['Trx_Length'])
# cat1_plot = plt.plot(x1,y1, marker='o', label='Generic HER2+/HR-')

# D390 and HER2+/HR+
x4,y4 = ecdf(hr_status_set[hr_status_set['class_category'] == 4]['Trx_Length'])
cat4_plot = plt.plot(x4,y4, marker='o', label='Drug 390 HER2+/HR+')
# D390 and HER2+/HR-
x5,y5 = ecdf(hr_status_set[hr_status_set['class_category'] == 5]['Trx_Length'])
cat5_plot = plt.plot(x5,y5, marker='o', label='Drug 390 HER2+/HR-')



plt.title('Generic vs Drug 390 Effect on Treatment Length, in Days, Considering HER/HR Positive or Negative Status',fontsize=17)
plt.xlabel('Treatment Length (Days)', fontsize=15)
plt.ylabel('Probability of Being on Treatment for this Number of Days', fontsize=15)
plt.legend(fontsize=15)
plt.grid(True, alpha=.4)
plt.show()
```



In [386]:
```
def knn_classifier( X, y):
    startf = time.time()

    neighbors_vals = [2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16]
    knn_train_scores = []
    knn_test_scores = []
    cv_scores_means = []
    for i in neighbors_vals:
        X_train, X_test, y_train, y_test = train_test_split(X, y, test_siz
e = 0.2, random_state=42, stratify=y)
        knn = KNeighborsClassifier(n_neighbors=i).fit(X_train, y_train)

#       knn.fit(X_train, y_train)

        train_score = knn.score(X_train, y_train)
        knn_train_scores.append(train_score)

        test_score = knn.score(X_test,y_test)
        knn_test_scores.append(test_score)

        cv_results = cross_val_score(knn, X, y, cv=5)
        cv_means = cv_results.mean()
        cv_scores_means.append(cv_means)

    plt.figure(figsize=(20,10))
    plt.tick_params(labelsize=15)
    plt.plot(neighbors_vals, knn_train_scores, marker='o',markersize=15, l
abel='Train Scores')
    plt.plot(neighbors_vals, knn_test_scores, marker='h',markersize=15, la
bel='Test Scores')
    plt.plot(neighbors_vals, cv_scores_means, marker='v',markersize=15, la
bel='Cross Validation Mean', alpha=0.5)
    plt.title('KNN Classifier Accuracy Scores & 5-Fold Validation Scores C
lassifying: On Drug 390 vs Generic', fontsize=18)
    plt.xlabel('Neighbors Parameter', fontsize=15)
    plt.ylabel('Test Score', fontsize=15)
    plt.legend(fontsize=17)
    plt.grid(True, alpha=.4)
    plt.show()
    endf = time.time()
    print('Comp Time:', round(endf - startf, 3))

def log_classifier(X, y):
    startf = time.time()
    alphas_log = [0.01, 0.1, 1, 10, 20, 30, 40, 50]
    log_test_list = []
    cv_scores_means = []

    for al in alphas_log:
        logreg = LogisticRegression(C=al).fit(X, y)
        log_test_score = logreg.score(X, y)
        log_test_list.append(log_test_score)


    plt.figure(figsize=(20,10))
    plt.tick_params(labelsize=15)
    plt.plot(alphas_log, log_test_list, marker='h', label='Scores', marker
size=15)
    plt.title('Logistic Regressor Classifying Accuracy Scores on Drug 390
```

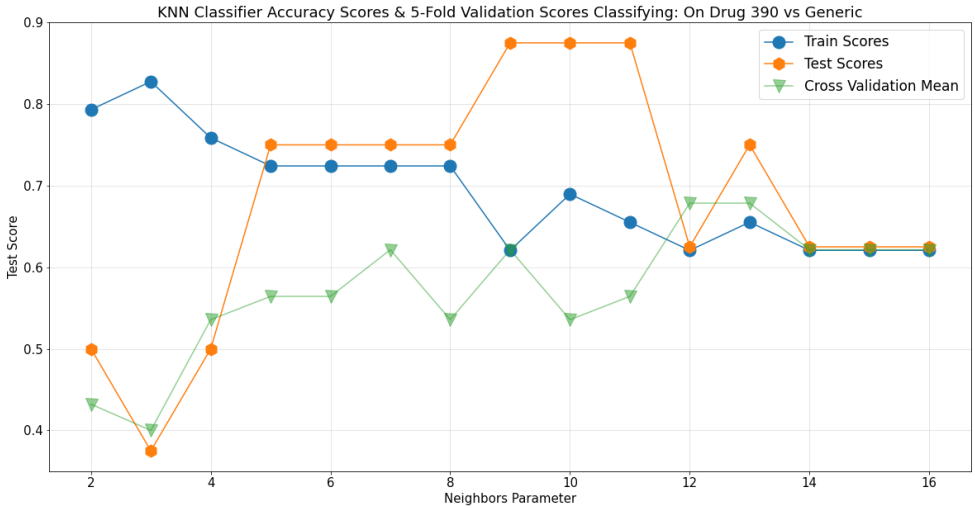
```
 v Generic', fontsize=18)
    plt.xlabel('Variable C(alpha) Parameter Range: 0.01 to 50', fontsize=1
5)
    plt.ylabel('Test Score', fontsize=15)
    plt.legend(fontsize=17)
    plt.grid(True, alpha=.4)
    plt.show()
    endf = time.time()
    print('Comp Time:', round(endf - startf, 3))


# attempts to cut a divider across a 3-dimensional space however our data
 does not do well with this model since data is sparse and heavily categor
ical
def linear_svc_classifier(X, y):
    startf = time.time()

    alphas_log = [0.01, 0.1, 1, 10, 20, 30, 40, 50, 100, 200, 300, 400, 50
0, 600]
    cv_scores_means = []

    linear_SVC_train_list = []
    linear_SVC_test_list = []
    for al in alphas_log:
        linear_SVC = LinearSVC(C=al).fit(X, y)
        linear_SVC_score = linear_SVC.score(X, y)
        linear_SVC = linear_SVC.score(X, y)


    plt.figure(figsize=(20,10))
    plt.title(' LinearSVC Classifying Accuracy Score on Drug 390 v Generi
c', fontsize=18)
    plt.xlabel('Alpha Parameter', fontsize=15)
    plt.ylabel('Test Score', fontsize=15)
    plt.plot(alphas_log, alphas_log, marker='h',markersize=15, label='Scor
es')
    plt.legend(fontsize=17)
    plt.grid(True, alpha=.4)
    plt.show()
    endf = time.time()
    print('Comp Time:', round(endf - startf, 3))


def gaussian_naive_bayes(X, y):
    gnb_train_scores = []
    gnb_test_scores = []
    cv_scores_means = []
    startf = time.time()
    sizer = [0.1, 0.2, 0.3, 0.4, 0.5, 0.6]
    for sz in sizer:
        X_train, X_test, y_train, y_test = train_test_split(X, y, test_siz
e = sz, random_state=42, stratify=y)
        gnb = GaussianNB()
        gnb.fit(X_train, y_train)

        train_score = gnb.score(X_train, y_train)
        gnb_train_scores.append(train_score)

        test_score = gnb.score(X_test,y_test)
```

```
        gnb_test_scores.append(test_score)

        cv_results = cross_val_score(gnb, X, y, cv=5)
        cv_means = cv_results.mean()
        cv_scores_means.append(cv_means)

    plt.figure(figsize=(20,10))
    plt.tick_params(labelsize=15)
    plt.plot(sizer, gnb_train_scores, marker='o',markersize=15, label='Tra
in Scores')
    plt.plot(sizer, gnb_test_scores, marker='h',markersize=15, label='Test
Scores')
    plt.plot(sizer, cv_scores_means, marker='v',markersize=15, label='Cros
s Validation Mean', alpha=0.5)
    plt.title('Gaussian Naive Bayes Classifier Accuracy Score Values Based
on Test Sizes from \'TTS\'', fontsize=18)
    plt.xlabel('Test Size Parameter from \'TTS\'', fontsize=15)
    plt.ylabel('Score', fontsize=15)
    plt.legend(fontsize=17)
    plt.grid(True, alpha=.4)
    plt.show()
    endf = time.time()
    print('Comp Time:', round(endf - startf, 3))

def bernoulli_naive_bayes(X, y):
    bern_train_scores = []
    bern_test_scores = []
    cv_scores_means = []
    startf = time.time()
    sizer = [0.1, 0.2, 0.3, 0.4, 0.5, 0.6]
    for sz in sizer:
        X_train, X_test, y_train, y_test = train_test_split(X, y, test_siz
e = sz, random_state=42, stratify=y)
        bern = BernoulliNB()
        bern.fit(X_train, y_train)

        train_score = bern.score(X_train, y_train)
        bern_train_scores.append(train_score)

        test_score = bern.score(X_test,y_test)
        bern_test_scores.append(test_score)

        cv_results = cross_val_score(bern, X, y, cv=5)
        cv_means = cv_results.mean()
        cv_scores_means.append(cv_means)

    plt.figure(figsize=(20,10))
    plt.tick_params(labelsize=15)
    plt.plot(sizer, bern_train_scores, marker='o',markersize=15, label='Tr
ain Scores')
    plt.plot(sizer, bern_test_scores, marker='h',markersize=15, label='Tes
t Scores')
    plt.plot(sizer, cv_scores_means, marker='v',markersize=15, label='Cros
s Validation Mean', alpha=0.5)
    plt.title('Bernoulli Naive Bayes Classifier Accuracy Score Values Base
d on Test Sizes from \'TTS\'', fontsize=18)
    plt.xlabel('Test Size Parameter from \'TTS\'', fontsize=15)
    plt.ylabel('Score', fontsize=15)
    plt.legend(fontsize=17)
```

```
    plt.grid(True, alpha=.4)
    plt.show()
    endf = time.time()
    print('Comp Time:', round(endf - startf, 3))
```

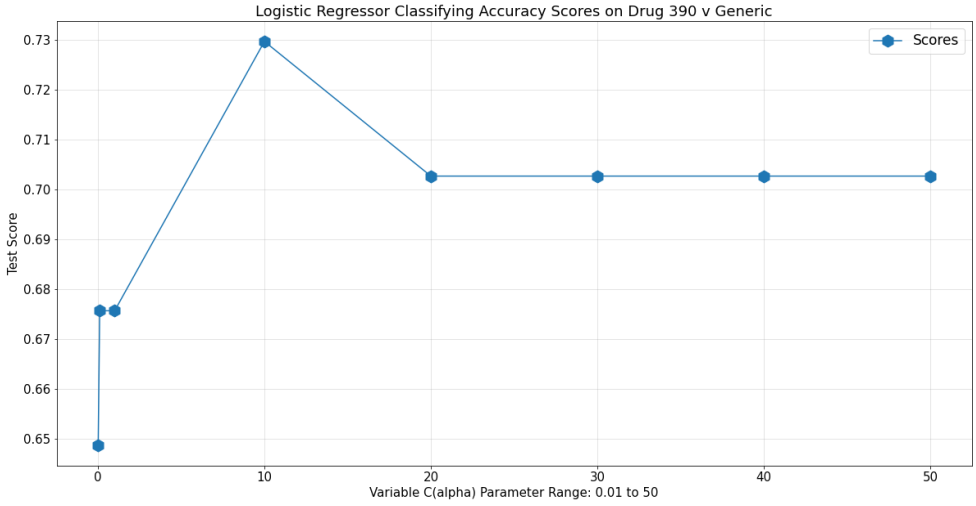
In [387]:
```
features = hr_status_set[['ER_positive', 'PR_positive', 'HER2_positive',
'Trx_Length', 'HR_status']]
target_col = hr_status_set['drug_390_admin_flag']
```

In [388]:
```
knn_modeler = knn_classifier(features, target_col)
```



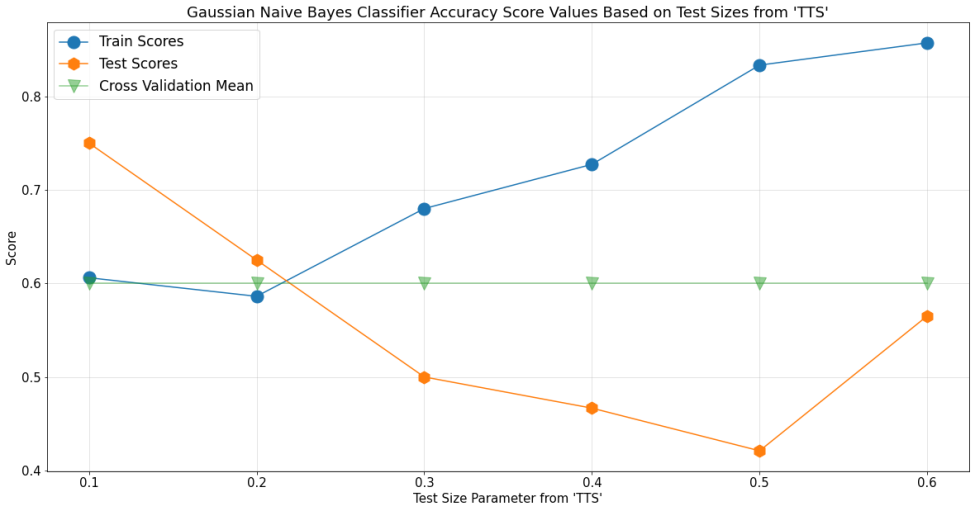

```
Comp Time: 0.648
```

In [389]:
```
logreg_modeler = log_classifier(features, target_col)
```



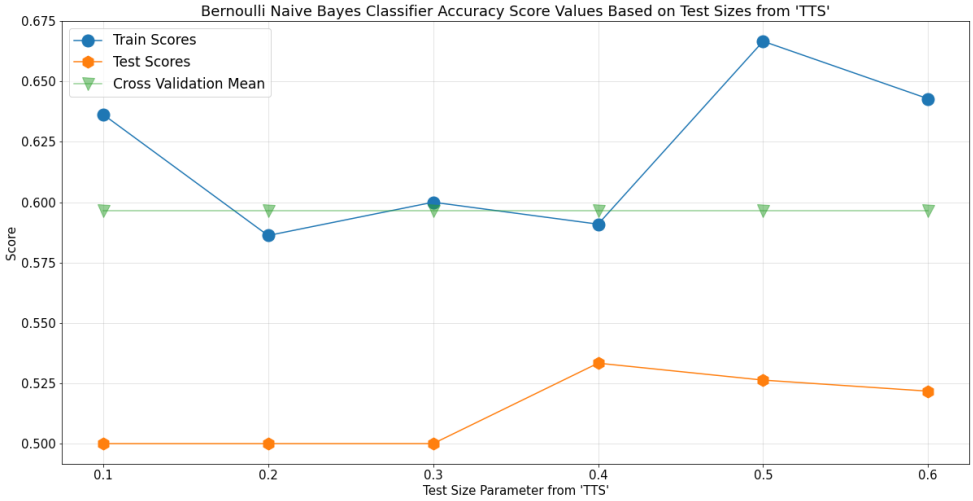

```
Comp Time: 0.357
```

In [390]:
```
gnb_modeler = gaussian_naive_bayes(features, target_col)
```




```
Comp Time: 0.383
```

In [391]:
```
bernoulli_naive_bayes(features, target_col)
```




```
Comp Time: 0.4
```

In [392]:
```
hr_status_set.to_csv('hormone_receptor_status_corrected.csv')
```