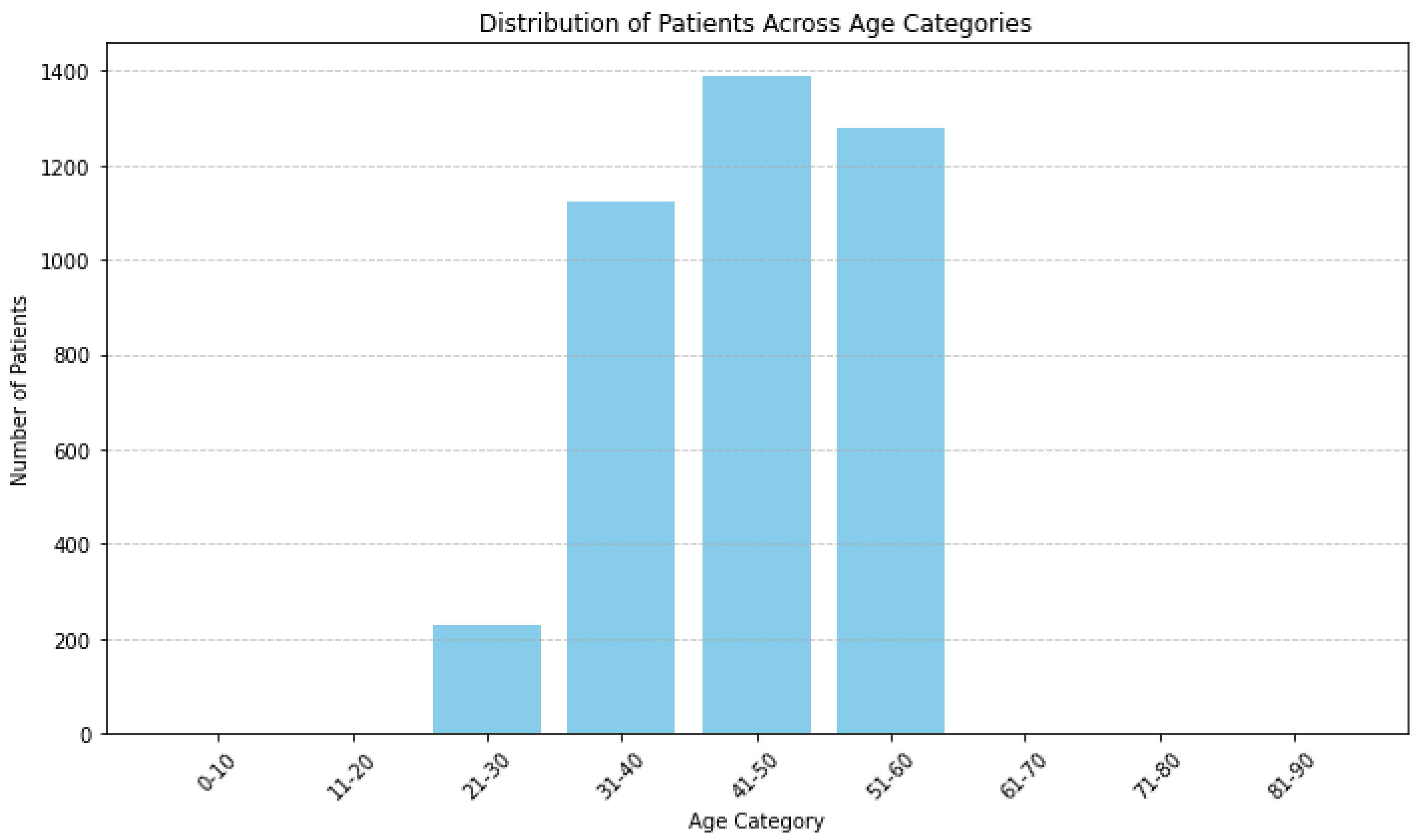
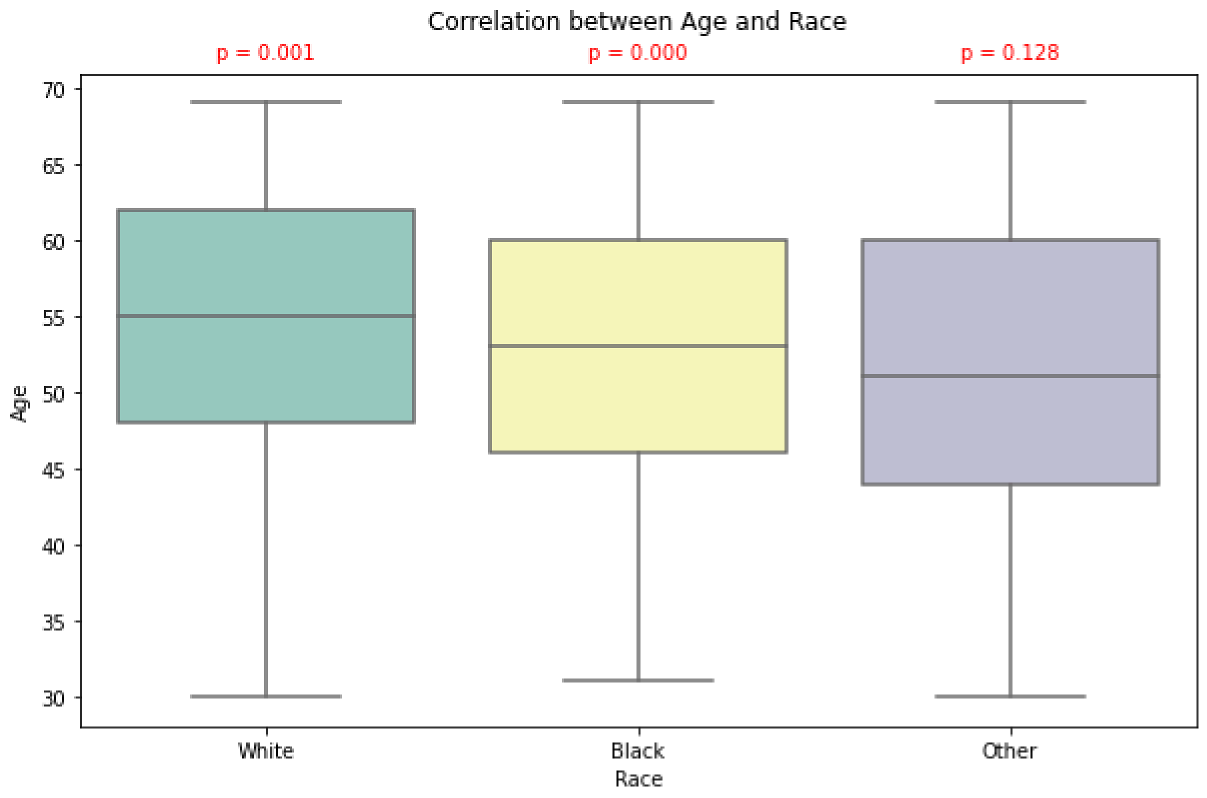
In [ ]:
```
#This project is accessible on GitHub via the following link:

https://github.com/moshtaqtsr/ADA_course_2024
```

In [117]:
```
# plot the Distribution of Patients Across Age Categories
## Import necessary libraries
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
from scipy import stats
from scipy.stats import kruskal
from scipy.stats import ttest_ind
from scipy.stats import f_oneway

## Define the folder path for saving figures
fig_folder="../plots//"

## Load the dataset

df = pd.read_csv('../data/Breast_Cancer.csv')

## Categorize patients based on Age

Age_bins = [0, 20, 30, 40, 50, 60, 70, 80, 90, 100]
Age_labels = ['0-10', '11-20', '21-30', '31-40', '41-50', '51-60', '61-70', '71-80', '81-90']


df['Age_Category'] = pd.cut(df['Age'], bins=Age_bins, labels=Age_labels, right=False)

## Count the number of patients in each age category
age_counts = df['Age_Category'].value_counts().sort_index()

## Plot the bar chart showing the distribution of patients across age categories
plt.figure(figsize=(10, 6))
plt.bar(age_counts.index, age_counts.values, color='skyblue')
plt.title('Distribution of Patients Across Age Categories')
plt.xlabel('Age Category')
plt.ylabel('Number of Patients')
plt.xticks(rotation=45)
plt.grid(axis='y', linestyle='--', alpha=0.7)
plt.tight_layout()
##save the plot
plt.savefig(fig_folder + "age_cat.png")

## Display the plot
```

```
plt.show()
```


Distribution of Patients Across Age Categories
Number of Patients
0
200
400
600
800
1000
1200
1400
0-10
11-20
21-30
31-40
41-50
51-60
61-70
71-80
81-90
Age Category

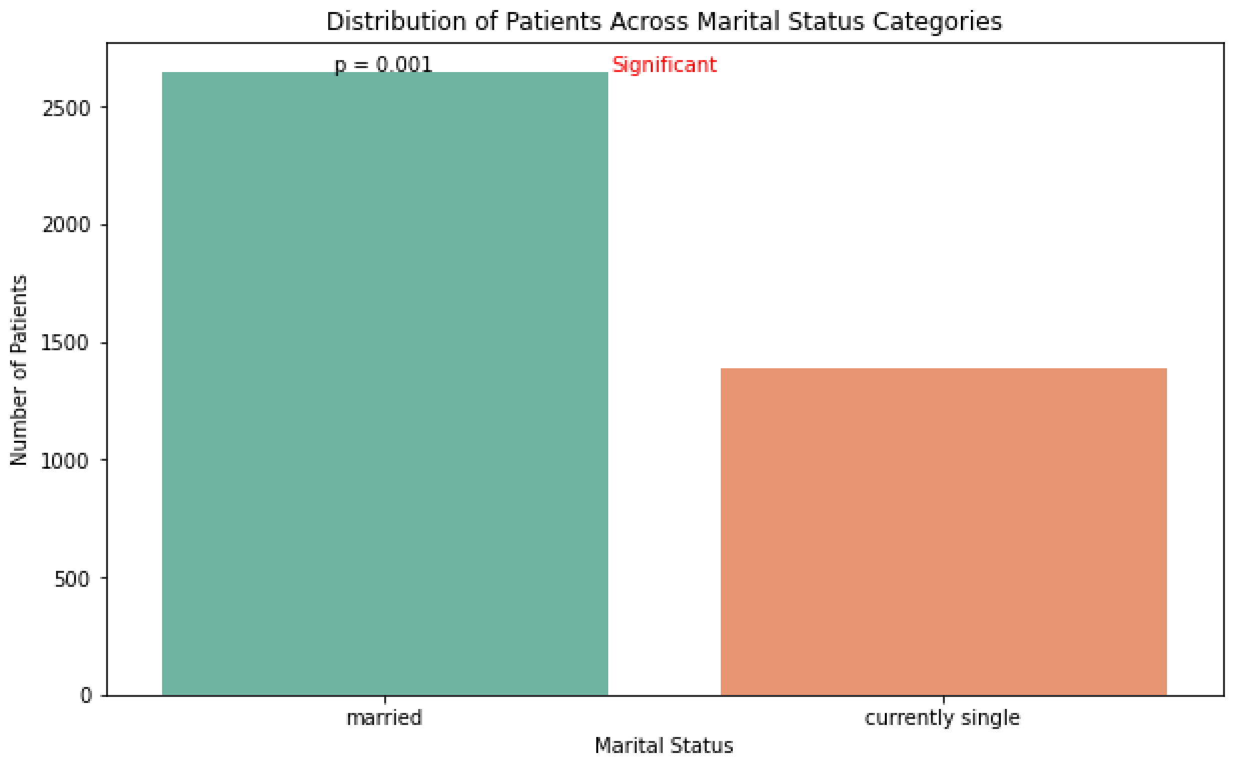
In [118]:
```
# Plot the correlation between age and race using a box plot
plt.figure(figsize=(10, 6))
sns.boxplot(x='Race', y='Age', data=df, palette='Set3')
plt.title('Correlation between Age and Race', y=1.05)

## Perform t-tests for pairwise comparisons
white_age = df[df['Race'] == 'White']['Age']
black_age = df[df['Race'] == 'Black']['Age']
other_age = df[df['Race'] == 'Other']['Age']

white_black_pval = stats.ttest_ind(white_age, black_age).pvalue
white_other_pval = stats.ttest_ind(white_age, other_age).pvalue
black_other_pval = stats.ttest_ind(black_age, other_age).pvalue

## Annotate with p-values and significance levels
plt.text(0, white_age.max() + 3, f'p = {white_black_pval:.3f}', ha='center', color='red')
plt.text(1, black_age.max() + 3, f'p = {white_other_pval:.3f}', ha='center', color='red')
plt.text(2, other_age.max() + 3, f'p = {black_other_pval:.3f}', ha='center', color='red')

plt.xlabel('Race')
plt.ylabel('Age')

##save the plot
plt.savefig(fig_folder + "age_race.png")
## Display the plot
plt.show()
```


Correlation between Age and Race
p = 0.001
p = 0.000
p = 0.128
70
65
60
55
50
45
40
35
30
Age
White
Black
Other
Race

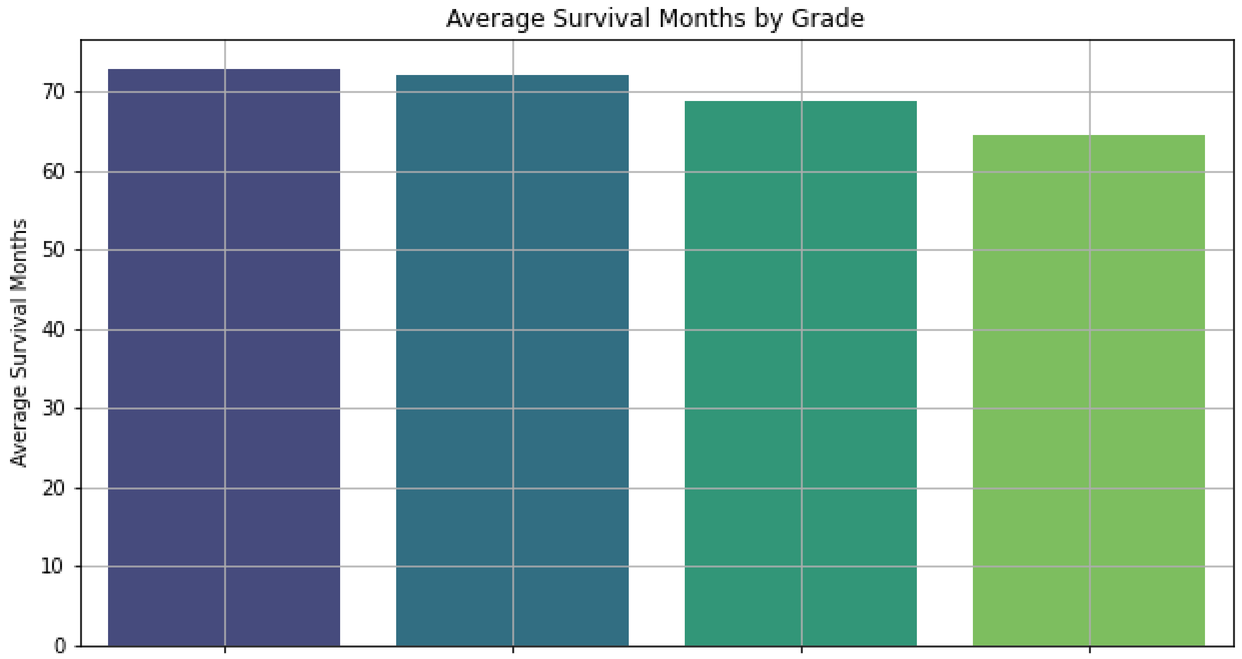
In [119]:
```
#t-test

## Separate age data for each race group
white_age = df[df['Race'] == 'White']['Age']
black_age = df[df['Race'] == 'Black']['Age']
other_age = df[df['Race'] == 'Other']['Age']

## Perform t-tests for pairwise comparisons
white_black_pval = stats.ttest_ind(white_age, black_age).pvalue
white_other_pval = stats.ttest_ind(white_age, other_age).pvalue
black_other_pval = stats.ttest_ind(black_age, other_age).pvalue

## Print p-values
print("White vs. Black p-value:", white_black_pval)
print("White vs. Other p-value:", white_other_pval)
print("Black vs. Other p-value:", black_other_pval)
```

```
White vs. Black p-value: 0.0012555792765483553
White vs. Other p-value: 2.8678317568481284e-08
Black vs. Other p-value: 0.12798007526770538
```

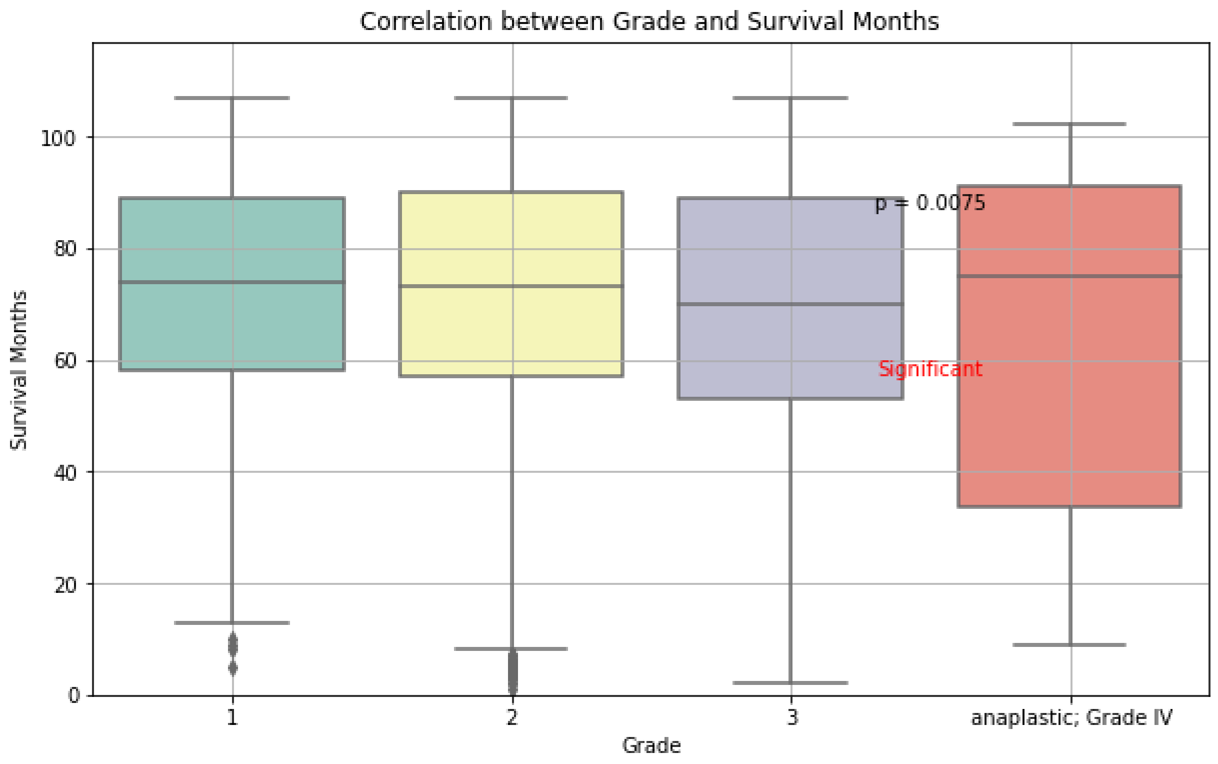
In [120]:
```
# Distribution of Patients Across Marital Status Categories
## Categorize marital status into 'married' and 'currently single'
df['Marital_Status_Category'] = df['Marital Status'].apply(lambda x: 'married' if x == 'Married' else 'currer

## Plot the distribution of patient data across marital status categories
plt.figure(figsize=(10, 6))
sns.countplot(x='Marital_Status_Category', data=df, palette='Set2')
plt.title('Distribution of Patients Across Marital Status Categories')
plt.xlabel('Marital Status')
plt.ylabel('Number of Patients')

## Perform the T-test for significance
married_age = df[df['Marital_Status_Category'] == 'married']['Age']
single_age = df[df['Marital_Status_Category'] == 'currently single']['Age']
p_val = stats.ttest_ind(married_age, single_age).pvalue

## Annotate with p-value and significance level
plt.text(0, married_age.count() + 2, f'p = {p_val:.3f}', ha='center')
plt.text(1, single_age.count() + 2, '', ha='center')  # No p-value for single group

## Determine significance based on p-value
if p_val < 0.05:
    plt.text(0.5, married_age.count() + 10, 'Significant', ha='center', color='red')
else:
    plt.text(0.5, married_age.count() + 10, 'Not Significant', ha='center', color='green')
##save the plot
plt.savefig(fig_folder + "marital_Status.png")
##Display the plot
plt.show()
```


Distribution of Patients Across Marital Status Categories
p = 0.001
Significant
Number of Patients
2500
2000
1500
1000
500
0
married
currently single
Marital Status

In [121]:
```
#ploting the Average Survival Months by Grade

## Convert Grade to numeric values
grade_mapping = {'1': 'One', '2': 'Two', '3': 'Three', ' anaplastic; Grade IV': 'Four'}
df['Grade'] = df['Grade'].map(grade_mapping)

## Define the order for the Grade column
grade_order = ['One', 'Two', 'Three', 'Four']
## Group the data by Grade and calculate the average Survival Months
average_survival = df.groupby('Grade')['Survival Months'].mean().reset_index()

## Convert 'Grade' column to categorical type with the specified order
average_survival['Grade'] = pd.Categorical(average_survival['Grade'], categories=grade_order)

## Plot the grouped bar plot
plt.figure(figsize=(10, 6))
sns.barplot(x='Grade', y='Survival Months', data=average_survival, palette='viridis')
plt.title('Average Survival Months by Grade')
plt.xlabel('Grade')
plt.ylabel('Average Survival Months')
plt.xticks(rotation=45)  # Rotate the x-axis labels for better readability
plt.subplots_adjust(left=0.1, right=0.9, top=0.9, bottom=0.2)
plt.grid(True)
##save the plot
plt.savefig(fig_folder + "Grade_survival_bar.png")
## Display the plot
plt.show()
```


Average Survival Months by Grade
Average Survival Months
0
10
20
30
40
50
60
70

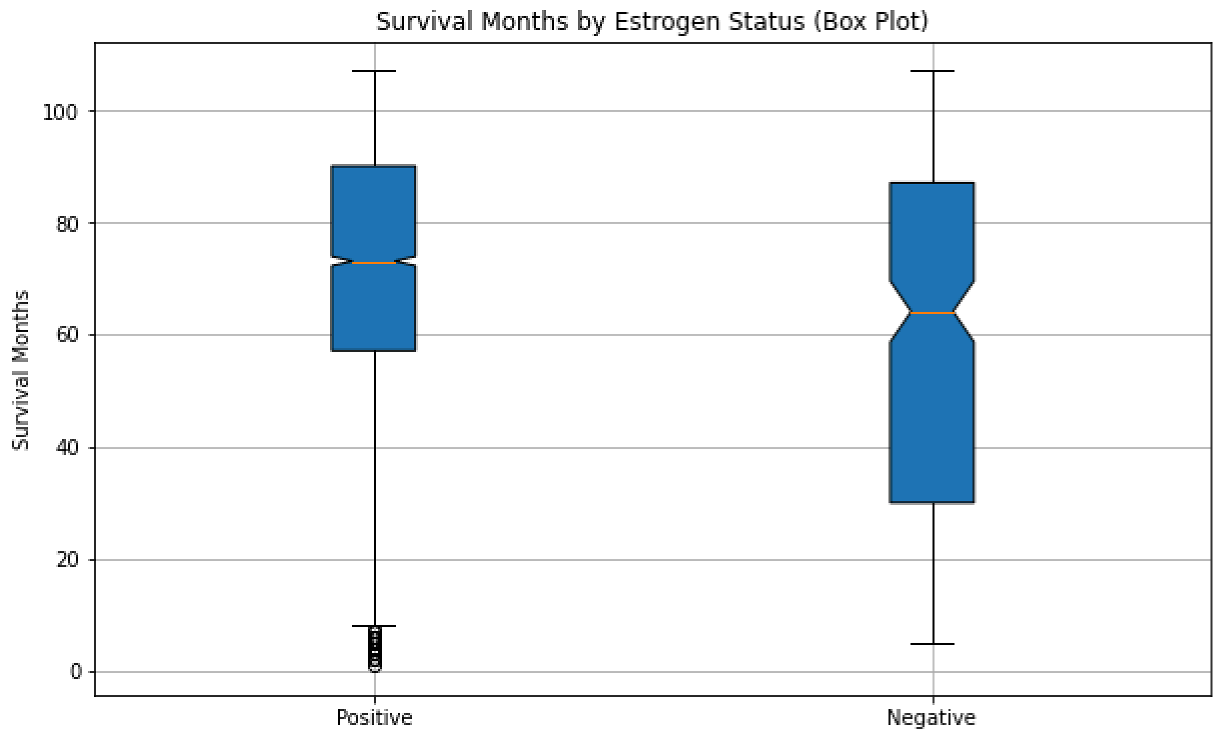
In [122]:
```
#ploting the Survival Months based on grade
df = pd.read_csv('../data/Breast_Cancer.csv')
## Define the order of grades
grade_order = ['1', '2', '3', ' anaplastic; Grade IV']

## Plot the correlation between Grade and Survival Months using a box plot
plt.figure(figsize=(10, 6))
sns.boxplot(x='Grade', y='Survival Months', data=df, order=grade_order, palette='Set3')
plt.title('Correlation between Grade and Survival Months')
plt.xlabel('Grade')
plt.ylabel('Survival Months')

## Adjust y-axis limits
plt.ylim(bottom=0, top=df['Survival Months'].max() + 10)

## Perform Kruskal-Wallis H-test
grades = [df[df['Grade'] == grade]['Survival Months'] for grade in grade_order]
H, p_value = kruskal(*grades)

## Annotate with p-value
plt.text(2.5, df['Survival Months'].max() - 20, f'p = {p_value:.4f}', ha='center')

## Determine significance based on p-value
if p_value < 0.05:
    plt.text(2.5, df['Survival Months'].max() - 50, 'Significant', ha='center', color='red')
else:
    plt.text(2.5, df['Survival Months'].max() - 50, 'Not Significant', ha='center', color='green')
##save the plot
plt.savefig(fig_folder + "grade_survival_plot.png")
plt.grid(True)
## Display the plot
plt.show()
```



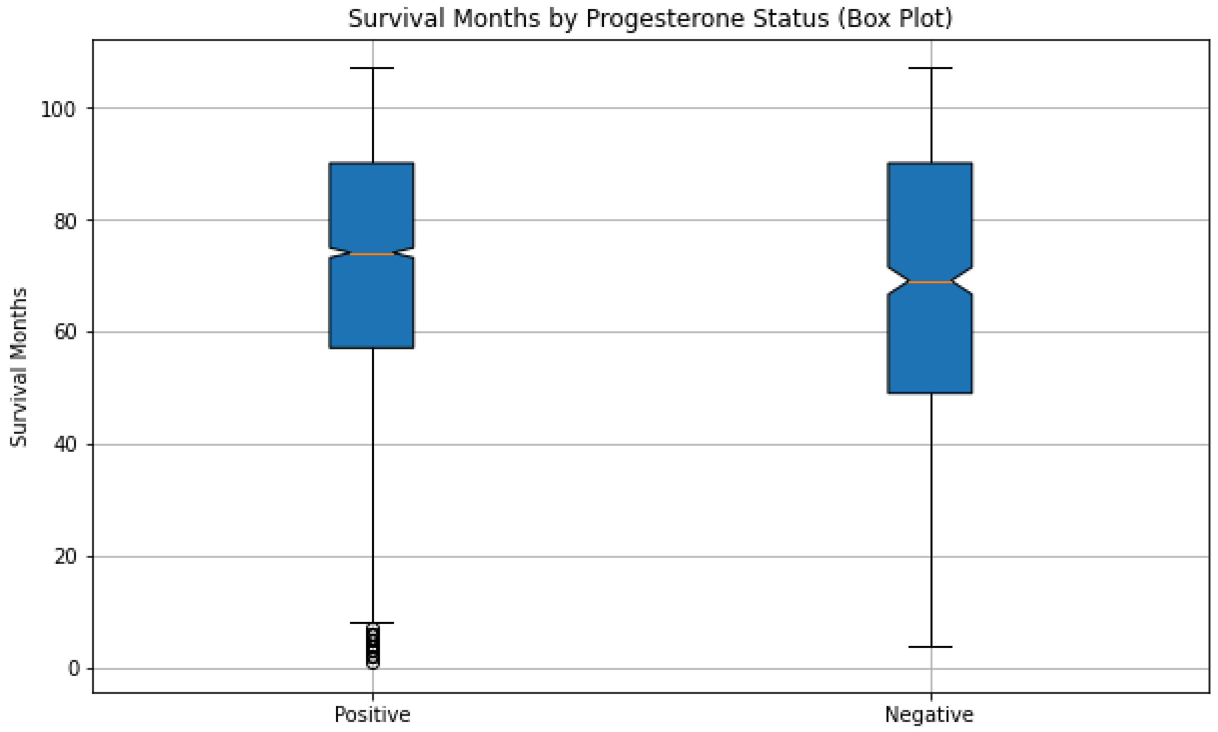
In [123]:
```
#Kruskal-Wallis H-test for survival months based on grade

## Load the dataset
df = pd.read_csv('../data/Breast_Cancer.csv')

## Perform Kruskal-Wallis H-test
grades = [df[df['Grade'] == grade]['Survival Months'] for grade in ['1', '2', '3', ' anaplastic; Grade IV']]
H, p_value = kruskal(*grades)

## Print the p-value
print("P-value of the Kruskal-Wallis H-test:", p_value)
```

```
P-value of the Kruskal-Wallis H-test: 0.007483500369062529
```

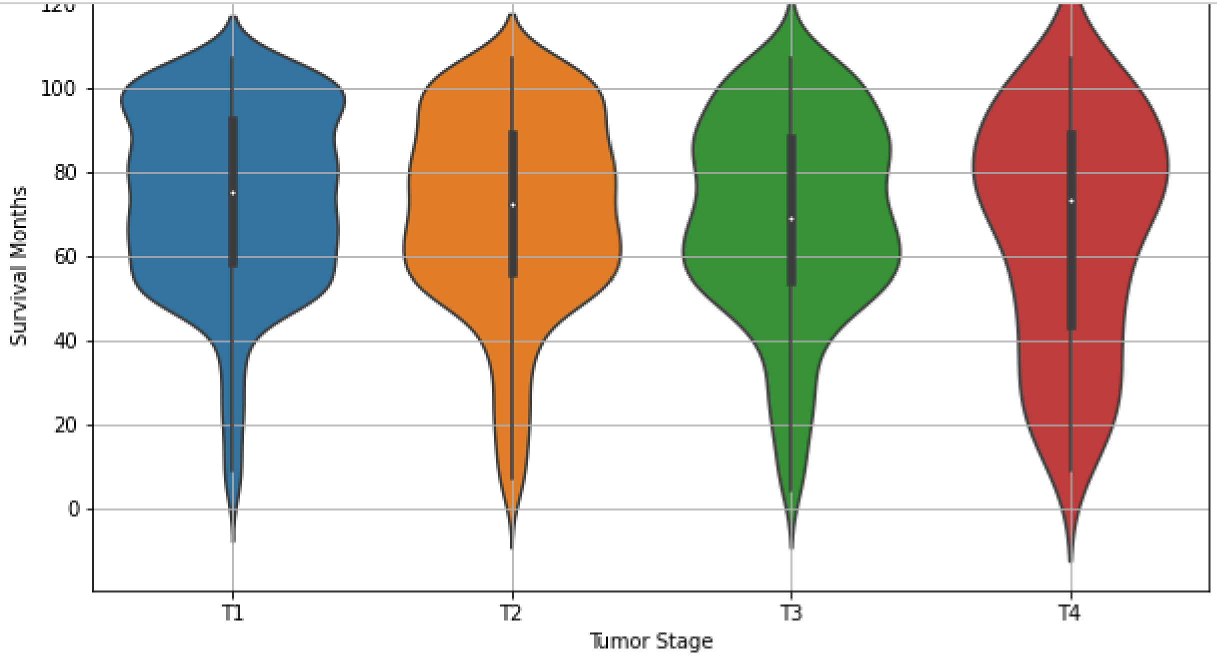
In [124]:
```
#box plot of survival months based on estrogen status
##Defining a function to create the plot
plt.figure(figsize=(10, 6))
plt.boxplot(
    [df[df['Estrogen Status'] == 'Positive']['Survival Months'],
     df[df['Estrogen Status'] == 'Negative']['Survival Months']],
    labels=['Positive', 'Negative'],
    notch=True,
    vert=True,
    patch_artist=True
)
plt.title('Survival Months by Estrogen Status (Box Plot)')
plt.ylabel('Survival Months')
plt.grid(True)
##save the plot
plt.savefig(fig_folder + "Estrogen_survival.png")
## Display the plot
plt.show()
```



In [125]:
```
#box plot of survival months based on progesterone status
##Defining a function to create the plot
plt.figure(figsize=(10, 6))
plt.boxplot(
    [df[df['Progesterone Status'] == 'Positive']['Survival Months'],
     df[df['Progesterone Status'] == 'Negative']['Survival Months']],
    labels=['Positive', 'Negative'],
    notch=True,
    vert=True,
    patch_artist=True
)
plt.title('Survival Months by Progesterone Status (Box Plot)')
plt.ylabel('Survival Months')
plt.grid(True)
##save the plot
plt.savefig(fig_folder + "Progesterone_survival.png")
## Display the plot
plt.show()
```


Survival Months by Progesterone Status (Box Plot)
Survival Months
0
20
40
60
80
100
Positive
Negative

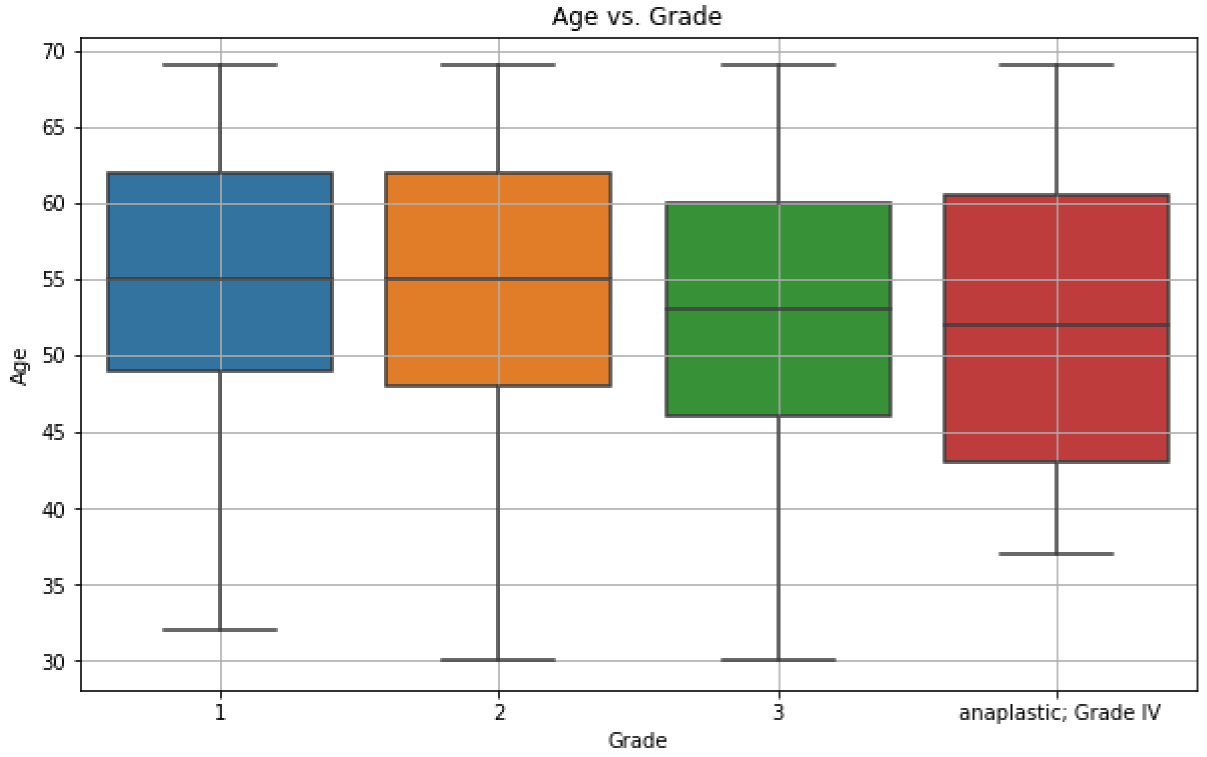
In [126]:
```
# Plot using a violin plot for Tumor Stage vs. Survival Months
plt.figure(figsize=(10, 6))
sns.violinplot(x='T Stage ', y='Survival Months', data=df, order=['T1', 'T2', 'T3', 'T4'])
plt.title('Tumor Stage vs. Survival Months')
plt.xlabel('Tumor Stage')
plt.ylabel('Survival Months')
plt.grid(True)
##save the plot
plt.savefig(fig_folder + "Tumor_Stage_survival.png")
## Display the plot
plt.show()
```



In [127]:
```
# Perform t-test for each pair of tumor stages
stages = df['T Stage '].unique()
for i in range(len(stages)):
    for j in range(i+1, len(stages)):
         # Extract survival months for each stage pair
        stage1 = df[df['T Stage '] == stages[i]]['Survival Months']
        stage2 = df[df['T Stage '] == stages[j]]['Survival Months']
        # Perform t-test to compare survival months between the two stages
        t_stat, p_val = ttest_ind(stage1, stage2)
        print(f"T-test between {stages[i]} and {stages[j]}: p-value = {p_val:.4f}")
```

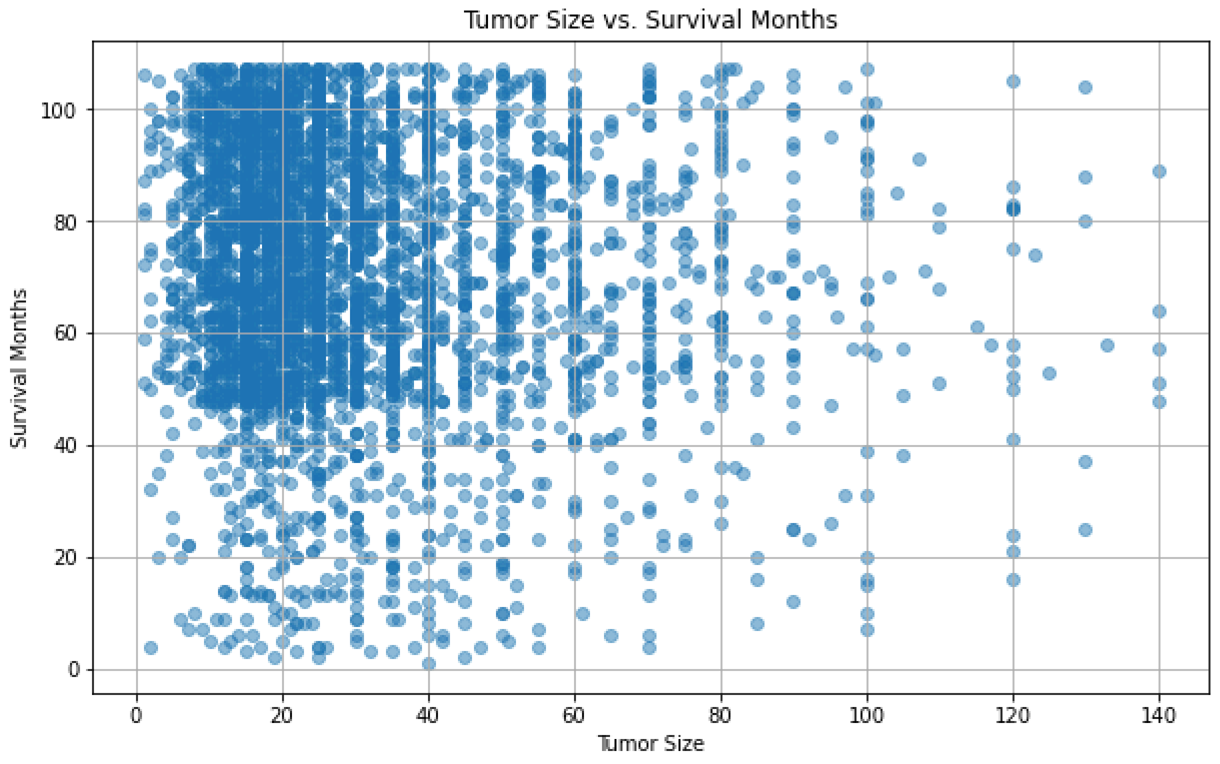
```
T-test between T1 and T2: p-value = 0.0000
T-test between T1 and T3: p-value = 0.0000
T-test between T1 and T4: p-value = 0.0005
T-test between T2 and T3: p-value = 0.2199
T-test between T2 and T4: p-value = 0.0575
T-test between T3 and T4: p-value = 0.2300
```

```
In [128]: # Plot using a box plot for Age vs. Grade
plt.figure(figsize=(10, 6))
sns.boxplot(x='Grade', y='Age', data=df, order=['1', '2', '3', ' anaplastic; Grade IV'])
plt.title('Age vs. Grade')
plt.xlabel('Grade')
plt.ylabel('Age')
plt.grid(True)
##save the plot
plt.savefig(fig_folder + "age_grade.png")
##Display the plot
plt.show()

## Perform t-tests
grades = ['1', '2', '3', ' anaplastic; Grade IV']
for i in range(len(grades)):
    for j in range(i+1, len(grades)):
        grade_1 = df[df['Grade'] == grades[i]]['Age']
        grade_2 = df[df['Grade'] == grades[j]]['Age']
        t_stat, p_value = ttest_ind(grade_1, grade_2)
        significance = "Significant" if p_value < 0.05 else "Not Significant"
        print(f"t-test between Grade {grades[i]} and Grade {grades[j]}: p-value = {p_value:.4f}, {significanc
```

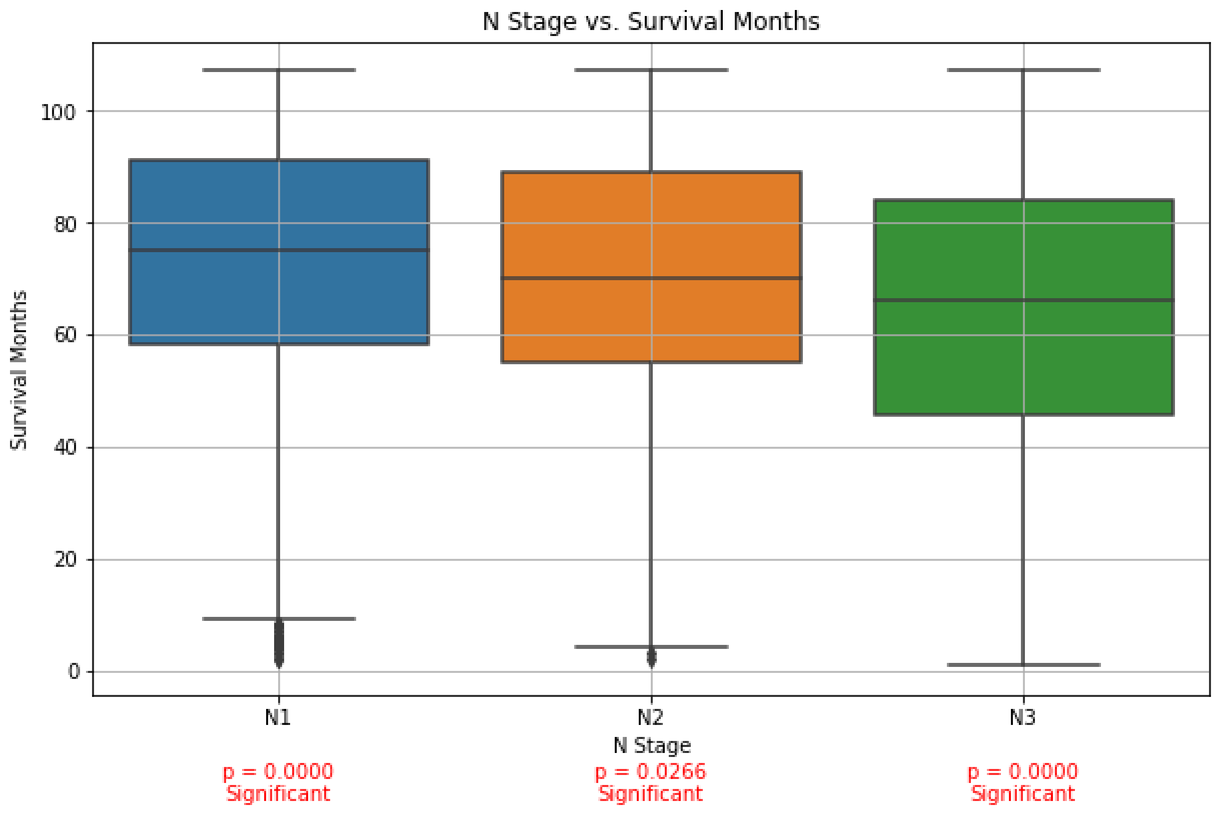


```
t-test between Grade 1 and Grade 2: p-value = 0.0203, Significant
t-test between Grade 1 and Grade 3: p-value = 0.0000, Significant
t-test between Grade 1 and Grade  anaplastic; Grade IV: p-value = 0.1327, Not Significant
t-test between Grade 2 and Grade 3: p-value = 0.0000, Significant
t-test between Grade 2 and Grade  anaplastic; Grade IV: p-value = 0.3246, Not Significant
t-test between Grade 3 and Grade  anaplastic; Grade IV: p-value = 0.8899, Not Significant
```

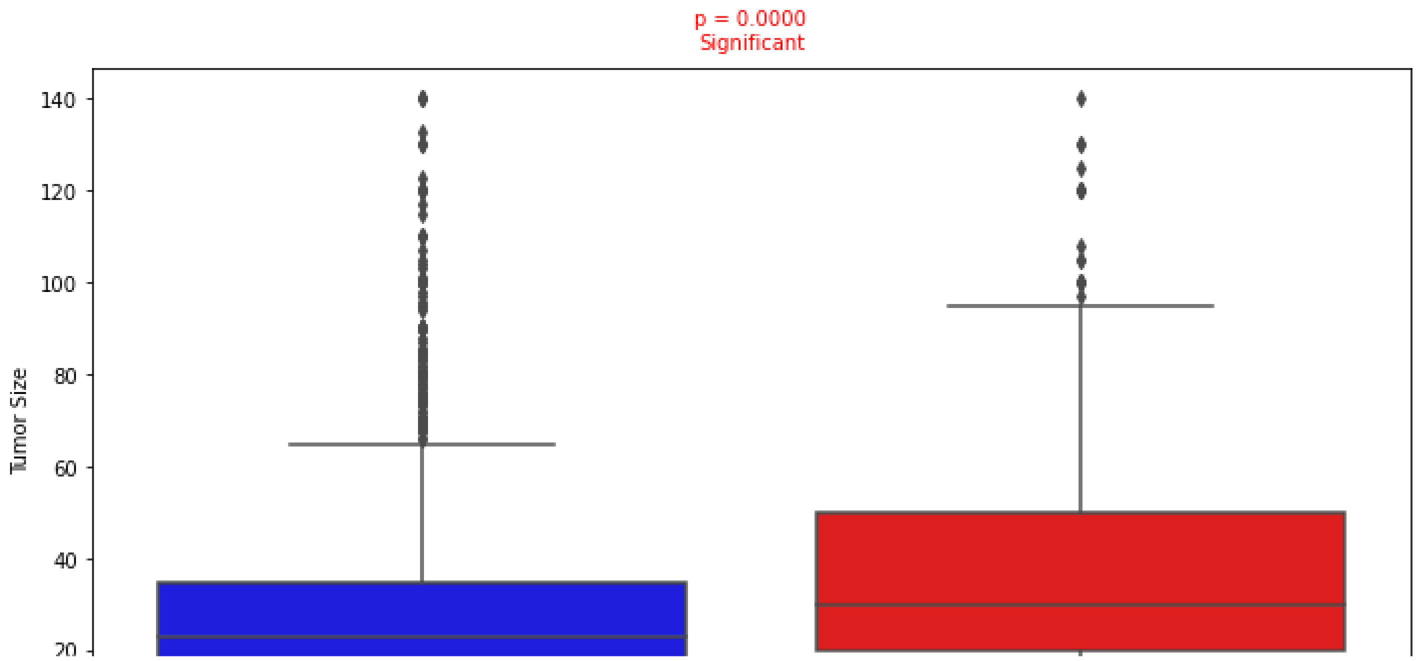
In [129]:
```
# Plot using a scatter plot Tumer size vs. Survival Months
plt.figure(figsize=(10, 6))
plt.scatter(df['Tumor Size'], df['Survival Months'], alpha=0.5)
plt.title('Tumor Size vs. Survival Months')
plt.xlabel('Tumor Size')
plt.ylabel('Survival Months')
plt.grid(True)
#save and show the plot
plt.savefig(fig_folder + "Tumor_Size_survival.png")
#Display the plot
plt.show()
```



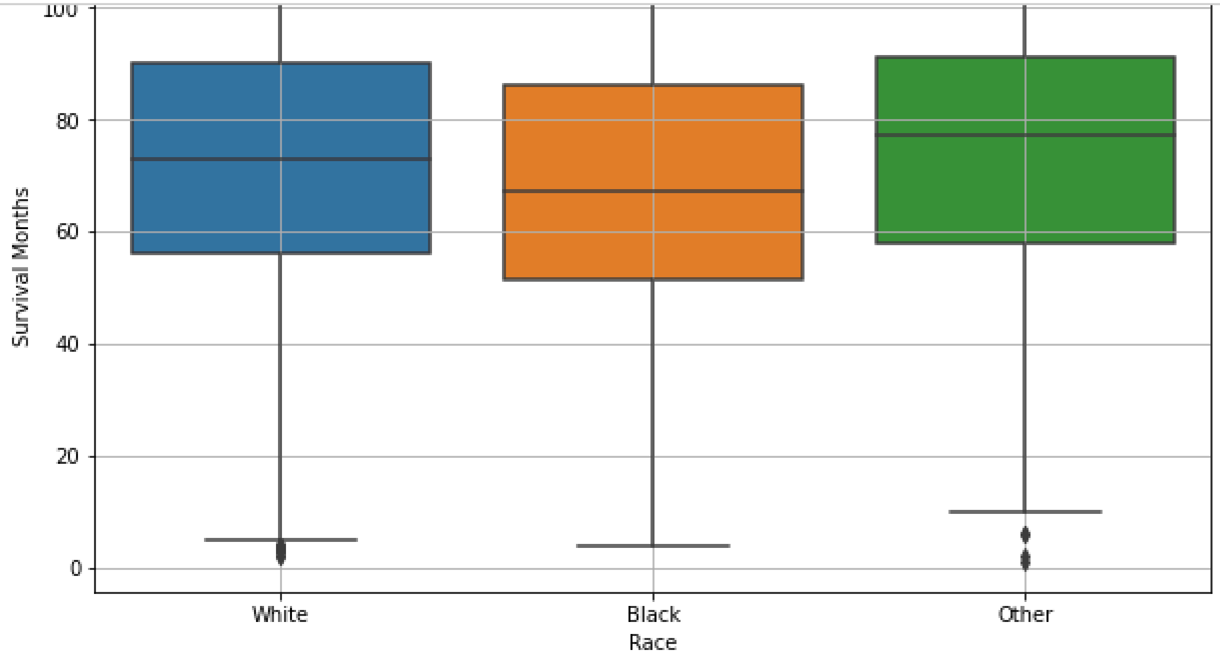
In [130]:
```
# Plot N Stage vs. Survival Months using a box plot
plt.figure(figsize=(10, 6))
sns.boxplot(x='N Stage', y='Survival Months', data=df)
plt.title('N Stage vs. Survival Months')
plt.xlabel('N Stage')
plt.ylabel('Survival Months')
plt.grid(True)

## Perform t-test for each N stage against all other stages
stages = df['N Stage'].unique()
for stage in stages:
    stage_data = df[df['N Stage'] == stage]['Survival Months']
    other_data = df[df['N Stage'] != stage]['Survival Months']
    t_stat, p_val = ttest_ind(stage_data, other_data)
    if p_val < 0.05:
        significance = 'Significant'
    else:
        significance = 'Not Significant'
    plt.text(stages.tolist().index(stage), df['Survival Months'].min() - 25, f'p = {p_val:.4f}\n{significance
             ha='center', va='bottom', color='red')
##save he plot
plt.savefig(fig_folder + "N_Stage_survival.png")
## Display the plot
plt.show()
```


N Stage vs. Survival Months
Survival Months
0
20
40
60
80
100
N1
N2
N3
N Stage
p = 0.0000
Significant
p = 0.0266
Significant
p = 0.0000
Significant

In [131]:
```
# plot the Alive, dead status using a box plot
# Split the dataset into two groups based on "Status"
alive_data = df[df['Status'] == 'Alive']['Tumor Size']
dead_data = df[df['Status'] == 'Dead']['Tumor Size']

# Plot overlapping box plots
plt.figure(figsize=(10, 6))
sns.boxplot(data=[alive_data, dead_data], palette=['blue', 'red'])

plt.xlabel('Status')
plt.ylabel('Tumor Size')
plt.xticks([0, 1], ['Alive', 'Dead'])

# Perform t-test
t_stat, p_val = ttest_ind(alive_data, dead_data)
if p_val < 0.05:
    significance = 'Significant'
else:
    significance = 'Not Significant'

# Add significance note to the plot
plt.text(0.5, max(alive_data.max(), dead_data.max()) + 10, f'p = {p_val:.4f}\n{significance}',
         ha='center', va='bottom', color='red')

plt.tight_layout()  # Adjust layout to prevent overlap
#save the plot
plt.savefig(fig_folder + "Alive_dead.png")
#Display the plot
plt.show()
```


p = 0.0000
Significant
Tumor Size
140
120
100
80
60
40
20

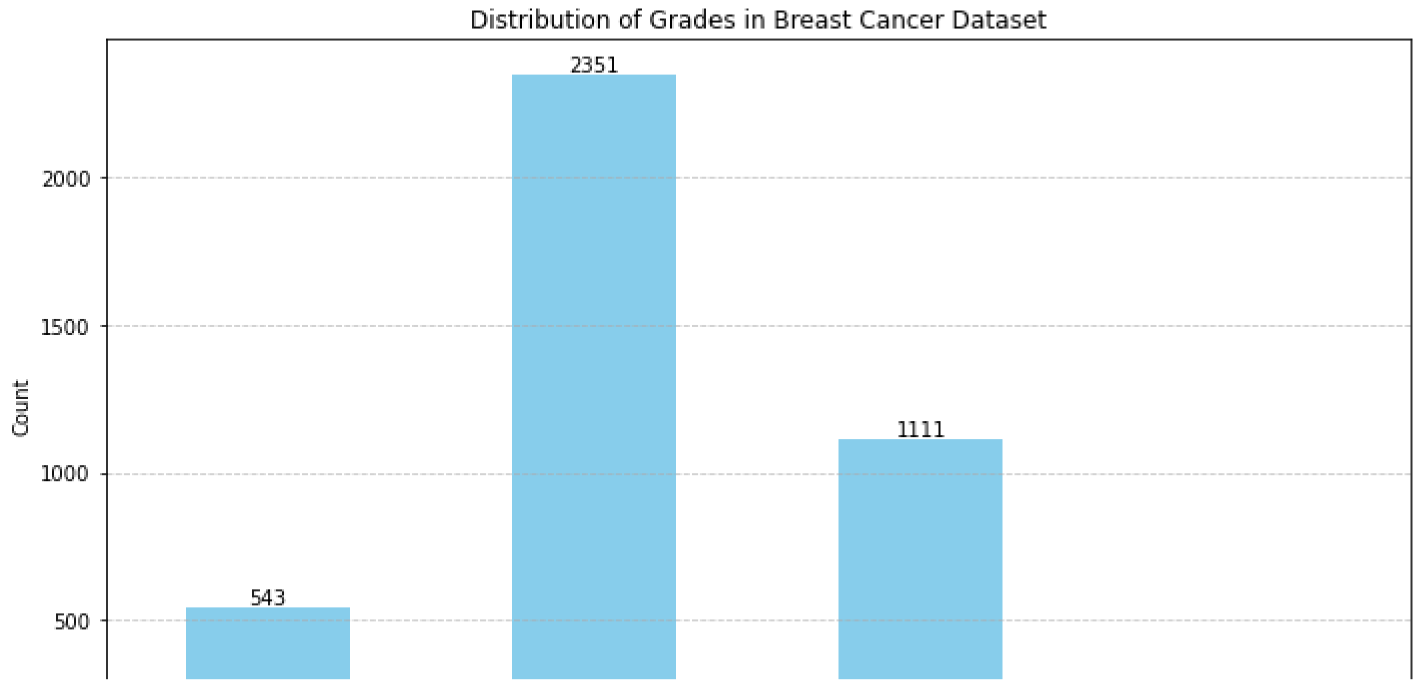
In [132]:
```
# Plot Survival Months by Race using box plot
plt.figure(figsize=(10, 6))
sns.boxplot(x='Race', y='Survival Months', data=df)
plt.title('Survival Months by Race')
plt.xlabel('Race')
plt.ylabel('Survival Months')
plt.grid(True)
#save the plot
plt.savefig(fig_folder + "race_survival_month.png")
#Display the plot
plt.show()
```



In [133]:
```
# Perform t-tests between each racial group (assuming 3 groups: White, Black, Other)
white_black_t_test = stats.ttest_ind(df[df['Race'] == "White"]["Survival Months"], df[df['Race'] == "Black"]
white_other_t_test = stats.ttest_ind(df[df['Race'] == "White"]["Survival Months"], df[df['Race'] == "Other"]
black_other_t_test = stats.ttest_ind(df[df['Race'] == "Black"]["Survival Months"], df[df['Race'] == "Other"]

# Print the t-test results
print("T-test between White and Black (p-value):", white_black_t_test.pvalue)
print("T-test between White and Other (p-value):", white_other_t_test.pvalue)
print("T-test between Black and Other (p-value):", black_other_t_test.pvalue)
```

```
T-test between White and Black (p-value): 0.00044919890603665357
T-test between White and Other (p-value): 0.19961014808886698
T-test between Black and Other (p-value): 0.0006868397864836594
```

In [134]:
```
#Plotting the grade based on age
# Define the order of grades
grade_order = ['1', '2', '3', ' anaplastic; Grade IV']

# Convert Grade column to categorical with specified order
df['Grade'] = pd.Categorical(df['Grade'], categories=grade_order, ordered=True)

# Plotting the column "Grade"
plt.figure(figsize=(10, 6))
ax = df['Grade'].value_counts().sort_index().plot(kind='bar', color='skyblue') # Assuming Grade is categorica
plt.title('Distribution of Grades in Breast Cancer Dataset')
plt.xlabel('Grade')
plt.ylabel('Count')
plt.xticks(rotation=0)  # Rotate x-axis labels if needed
plt.grid(axis='y', linestyle='--', alpha=0.7)

# Add value on top of each bar
for p in ax.patches:
    ax.annotate(str(p.get_height()), (p.get_x() + p.get_width() / 2., p.get_height()),
                ha='center', va='center', xytext=(0, 5), textcoords='offset points')

plt.tight_layout()
#save the plot
plt.savefig(fig_folder + "Grade_distribution.png")
#display the plot
plt.show()
```


Distribution of Grades in Breast Cancer Dataset
2351
1111
543
2000
1500
1000
500
Count

```
In [ ]:
```