Factors Influencing Heart Disease Deaths

Outhai Xayavongsa and Aaron Ramirez

University of San Diego

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Professor Leon Shpaner

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Heart disease is the predominant cause of mortality in the U.S. indicated by CDC's analysis, overshadowing other significant causes such as cancer and the recent COVID-19 pandemic. In the year 2021 alone, heart disease was responsible for one-fifth of all deaths, reflecting its significant impact on public health. The CDC employs a comprehensive definition for heart disease, including various cardiovascular conditions: Heart attacks, known as Acute myocardial infarction, arise when a segment of the heart muscle is deprived of blood; coronary artery disease is when an accumulation of fatty deposits inside the coronary arteries leads to reduction of blood flow; heart failure describes the heart cannot pump blood efficiently; and strokes occur when the blood supply to the brain is obstructed (Xu et al., 2022).

The dataset selected for analysis offers a nuanced view of heart disease mortality for the year 2014, specifically targeting the demographic aged 35 and older across different U.S. counties (U.S. Department of Health & Human Services, 2023). It employs age adjustment to mortality rates, a critical statistical method allowing equitable comparisons across diverse population age structures. By averaging mortality data over three years, the dataset aims to eliminate year-to-year fluctuations, providing a more consistent and dependable portrayal of the heart disease mortality landscape.

Demographic details such as gender and race are included within each county's data, which are vital for recognizing mortality trends and patterns among distinct population groups. Including geographical coordinates for each county opens avenues for spatial analysis, potentially linking heart disease mortality rates to environmental, economic, and healthcare accessibility factors. The study's purpose is twofold: exploratory and preventive. It intends to investigate how demographic and geographical factors contribute to the risk and outcomes of

heart disease. The overarching goal is to inform public health strategies that could mitigate the risk factors associated with heart disease, improve health outcomes, and pinpoint populations that might benefit from enhanced preventive healthcare services.

Data Cleaning and Preparation

The initial dataset contained 59,077 unique rows and 19 columns. The project commenced with the importation of the dataset, followed by the observation of numerous columns containing blank or invalid data, along with a column labeling row with insufficient data. Subsequently, these columns were eliminated. Next, rows labeled with the "overall" tag within stratifications 1 and 2 (pertaining to gender and race) were excluded, with the focus redirected towards individual-level data for improved inferential testing. Moreover, emphasis was placed solely on retaining county-specific data, disregarding broader state or national data for the test. Finally, column names were modified for enhanced readability and ease of testing.

A parallel dataset was also subjected to cleanup, intended for overall exploratory data and visual analysis. The process mirrored that described previously, albeit with a reverse approach, retaining only overall data for stratifications 1 and 2. The subsequent step involved outlier identification within each dataset, focusing on the column detailing heart disease mortality rates. Outliers were addressed by employing a function to calculate the interquartile range, as well as the first and third quartiles, subsequently determining lower and upper bounds using the formulas:

Lower bound = Q1 - 1.5IQR

Upper bound = Q3 + 1.5IQR

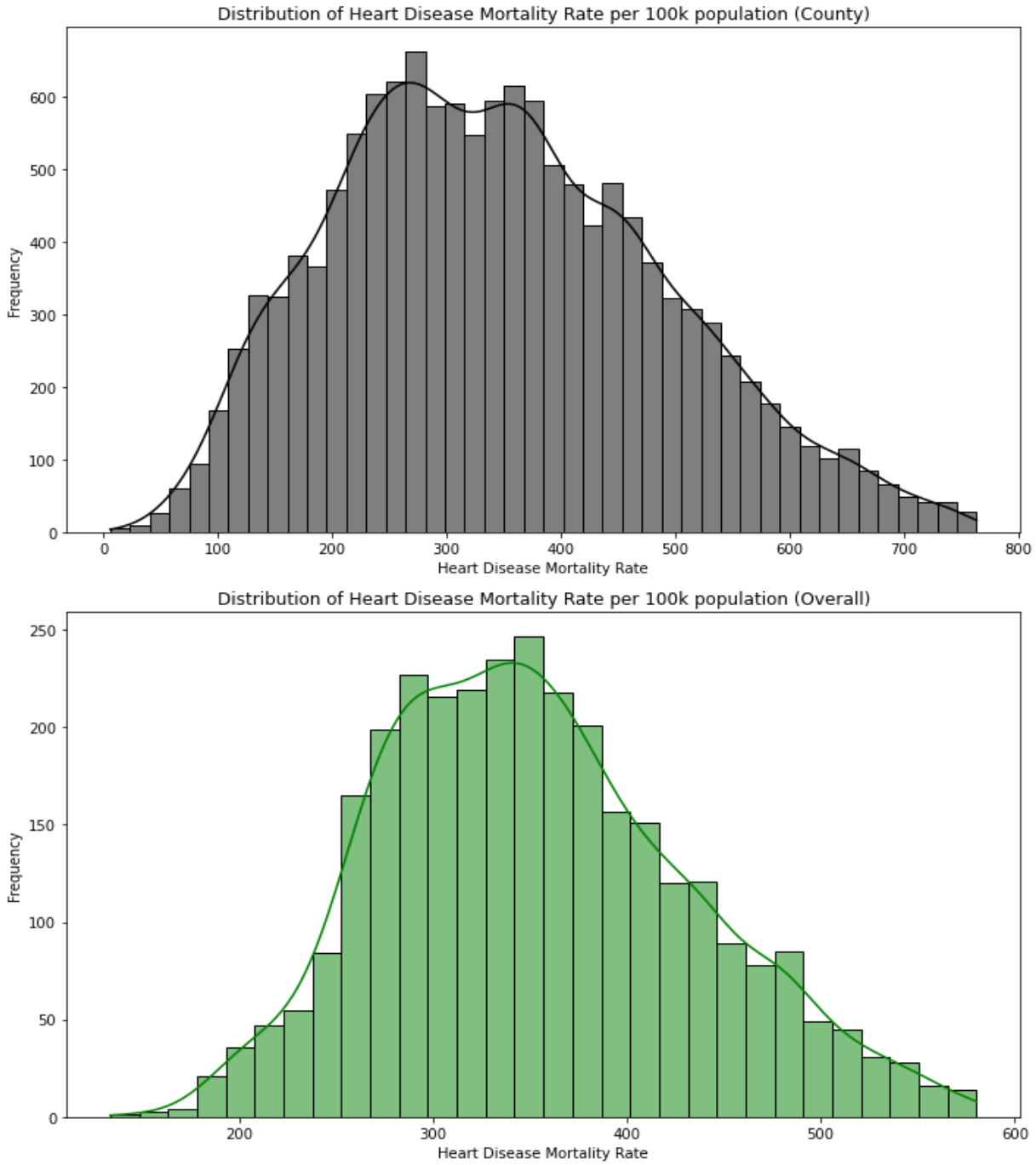
This methodology effectively captured over 95% of the data while eliminating outliers beyond the specified lower and upper bounds. The outlier removal process was applied to both datasets, resulting in two clean datasets poised for analysis and interpretation.

Exploratory Data Analysis

As the data analysis commenced, the focus initially turned to examining the five-number summary for the cleaned-up datasets. It was observed that the mean heart disease mortality rate for the individual-level data stood at approximately 347 individuals per 100,000 population, while the overall dataset indicated a rate of about 353 individuals. Additionally, the standard error rate was calculated to be 0.68 units (individuals), denoting a low level of variability. These findings suggest a notable similarity between the individual-level and overall datasets. Subsequently, attention was directed towards assessing the distribution of heart disease mortality rates. The results are presented below.

Figure 1

Histogram Distributions on Heart Disease Mortality Rate per 100k for the County and Overall



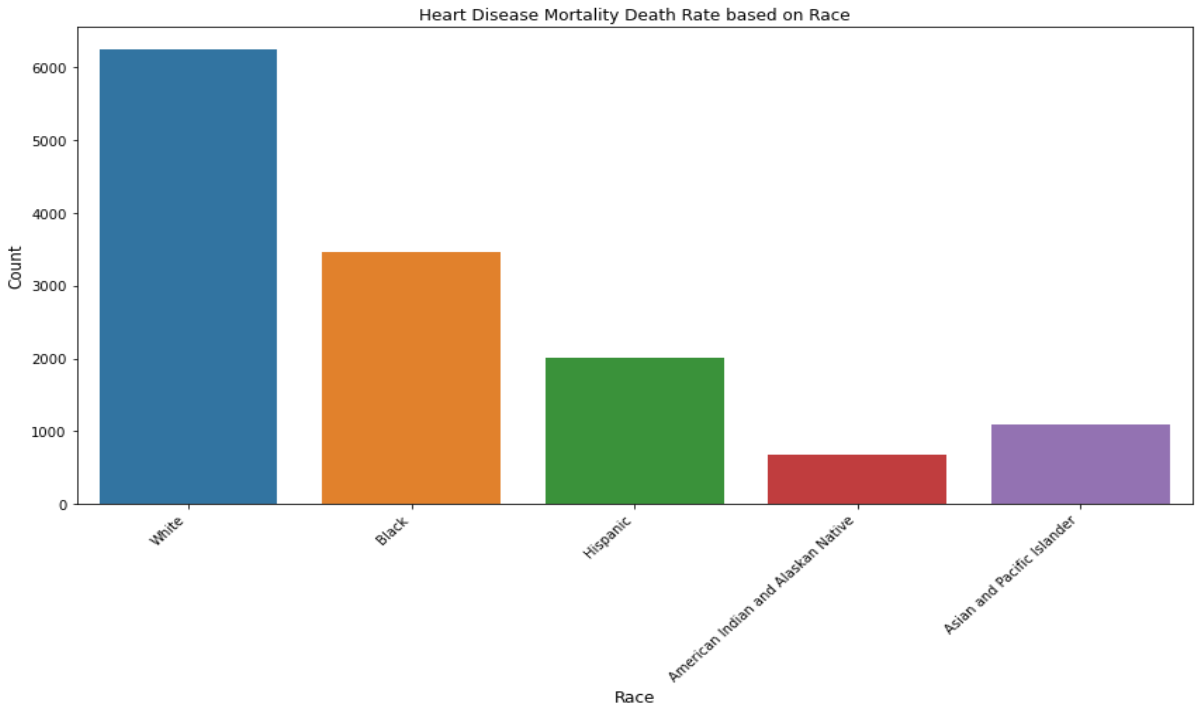
Note. The two graphs illustrate that both datasets exhibit a normal distribution, indicating adherence to the central limit theorem. This suggests that our data can be effectively utilized for

testing and modeling purposes in discerning the factors influencing high or low heart disease mortality rates among individuals aged over 35 years.

Subsequently, the examination delved into assessing the association between independent variables and mortality rates through bar graphs.

Figure 2

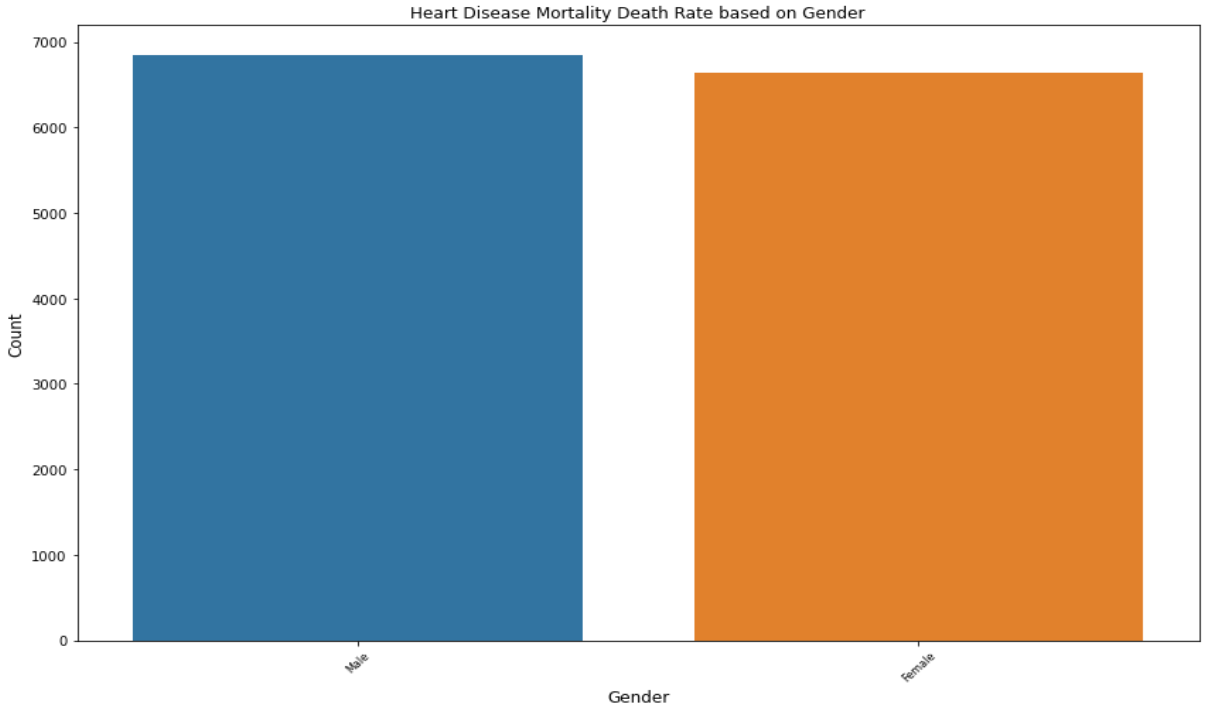
Bar Plot on Heart Disease Mortality Death Rate based on Race.



Note. The graph presented above delineates the distribution of individuals across different racial categories within the dataset. As indicated, individuals identifying as White constitute the highest count in the mortality rate statistics, whereas the count is lowest for those identifying as American Indian and Alaskan Native. Consequently, White race will be utilized as the default category for subsequent testing purposes.

Figure 3

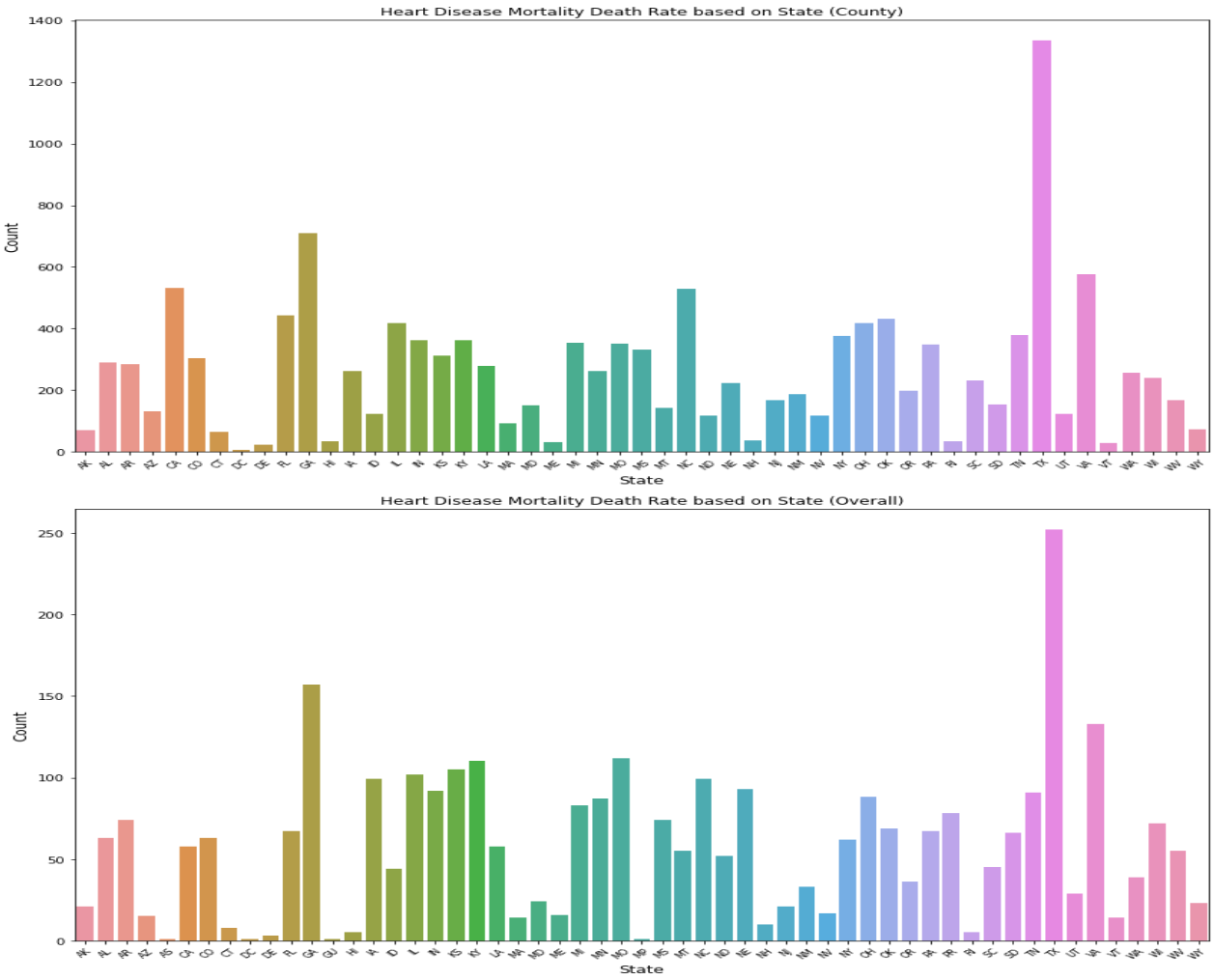
Bar Plot of Heart Disease Mortality Death Rate on Gender



Note. The graph depicted above showcases the count of individuals categorized by gender in relation to the mortality rate. It is evident from the graph that the counts for males and females are closely balanced, indicating a satisfactory representation of each gender within the dataset.

Figure 4

Heart Disease Mortality Death Rate by State Comparison

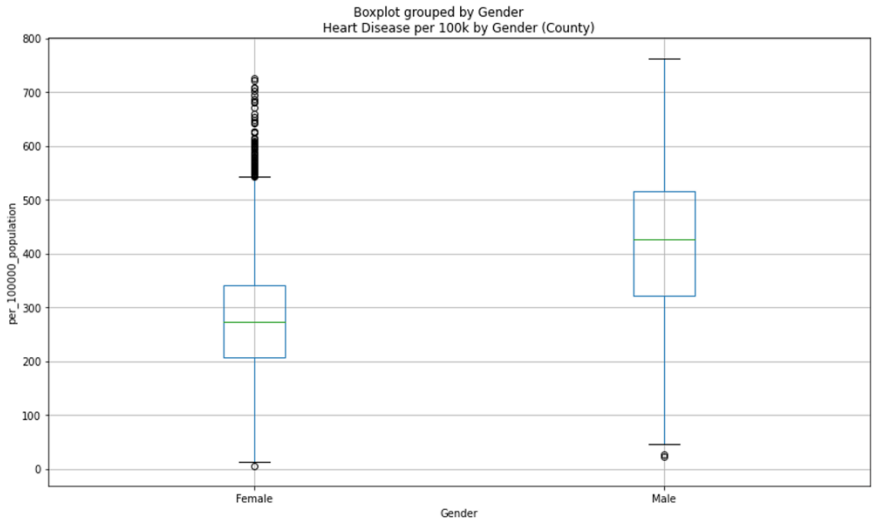


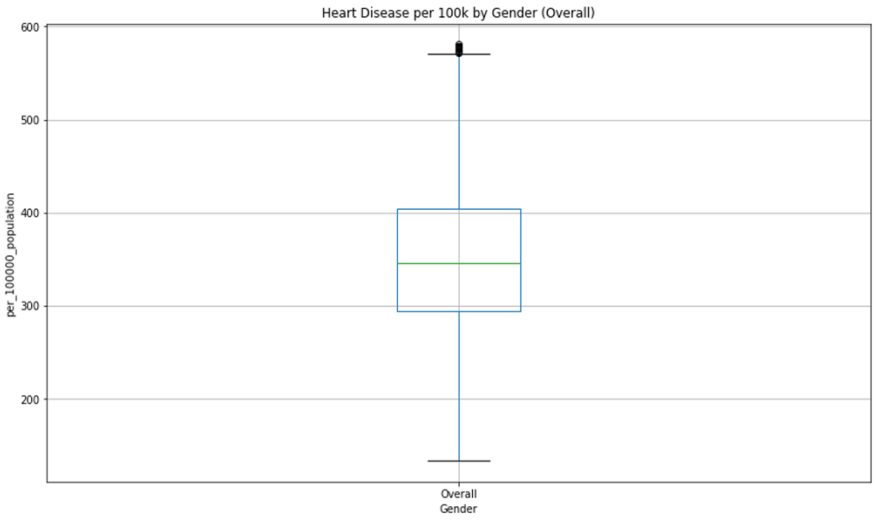
Note. An analysis was conducted to examine the count of individuals by state, incorporating both individual and overall datasets to discern any discrepancies among states. The observation revealed that certain states were not adequately represented in the individual-level data, attributed to insufficient data collection concerning independent variables and mortality rates. Notably, this discrepancy appeared to align with the general population distribution of each state, exemplified by larger states such as Texas exhibiting higher counts, while smaller states like Hawaii demonstrated lower counts.

Furthermore, boxplots were generated to explore the relationship between independent variables and mortality rates, aiming to identify outliers and discern the distribution patterns. Both individual and overall datasets were utilized for comparison, facilitating an assessment of how individual-level statistics contrasted with aggregated data.

Figure 5

Box Plots on Heart Disease per 100k by Gender based on County and Overall



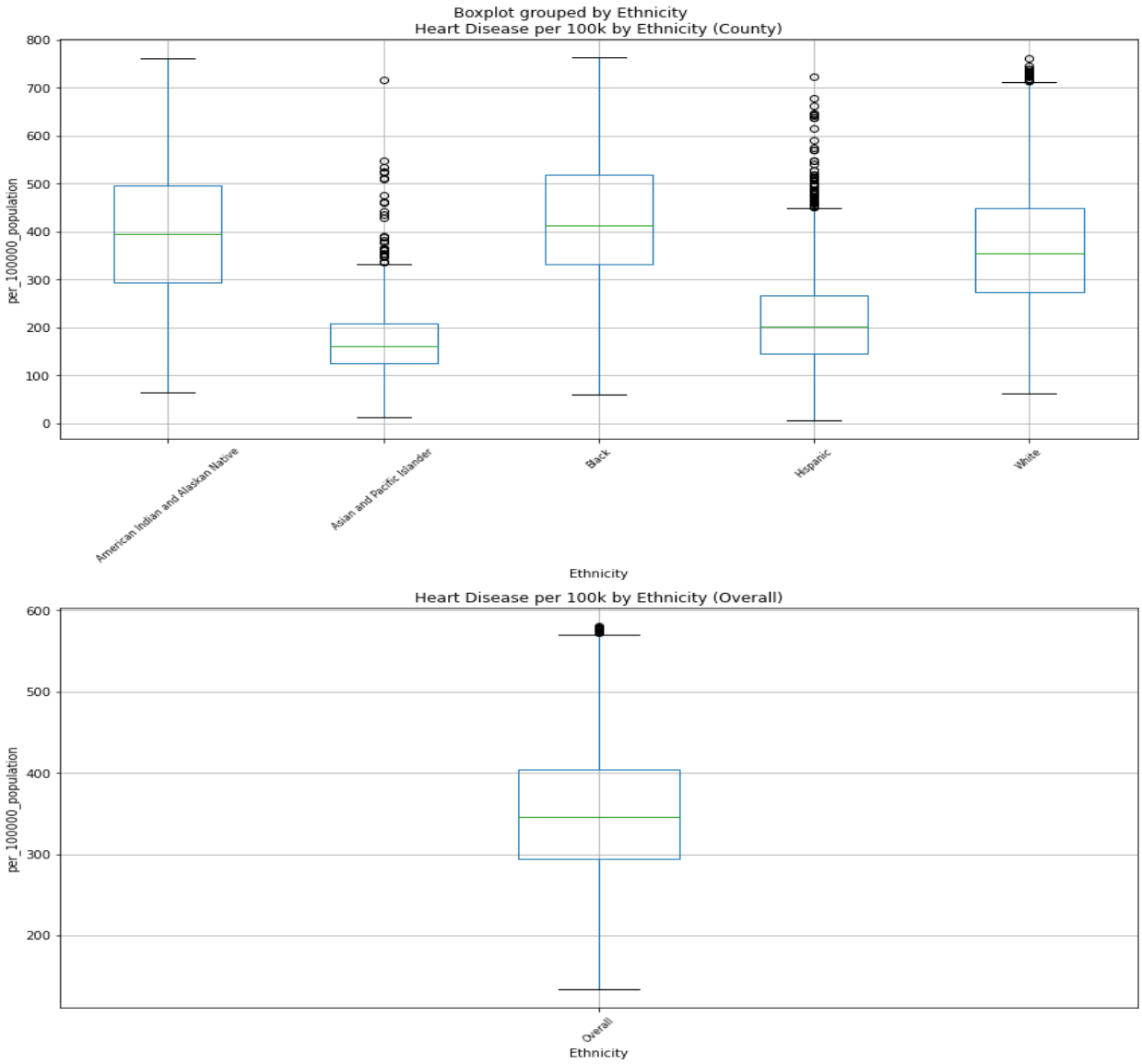


Note. The boxplot analysis reveals that the number of heart disease cases is greater among males than females. Additionally, the data for females includes a significant number of outliers.

A comparison with the aggregated data highlights that the maximum value in the overall dataset is around 600, which is lower than the individual-level data where the maximum reaches approximately 750. This suggests a discrepancy between the individual and aggregated data points, with individual records showing higher extremes.

Figure 6

Box Plots of Heart Disease per 100k by Each Ethnicity and Overall



Note. It becomes apparent that Black individuals exhibit the highest average mortality rate among all races.

Notably, Black individuals do not have any outliers, a trend shared with American Indian and Alaskan Natives, despite their initially low count. Surprisingly, American Indians and

Alaskan Natives display similar results to Black individuals, which is noteworthy given their comparatively lower count. Subsequently, White individuals fall within the middle range with minimal outliers. Conversely, Hispanic individuals emerge with the highest number of outliers, with some counties nearly reaching the ceiling. Lastly, Asian and Pacific Islanders present the lowest average mortality rate, albeit with one outlier that significantly exceeds the others, with one county registering an average of approximately 720. Comparing these findings to the overall statistics, White individuals display the closest average, while the ceiling is notably lower, approaching 600 rather than 800 as observed in the individual-level data.

Following the visual analysis, chi-square tests were conducted to examine the association between the assumed independent variables and to formulate hypotheses for subsequent testing. Additionally, z-tests were employed to assess whether there was any significant impact on heart rate in relation to the other categories.

Table 1

Chi-Square test results

Category	**Chi-square statistic**	**p-value**
Gender	7.171499e+03	3.097805e-69
Ethnicity	2.560000e+04	2.355235e-111
County	9.512658e+06	1.000000e+00
State	2.557907e+05	9.999865e-01

The results indicate that gender and ethnicity exhibit highly significant associations with mortality rate. The substantial chi-square statistics and minuscule p-values underscore the strength of these relationships. Conversely, there is no statistical association observed for county, as evidenced by a p-value of 1.00. Similarly, state demonstrates a p-value extremely close to 1.00, indicating a lack of association akin to county.

In the z-testing conducted for gender, it was observed that females exhibited a p-value of less than 0.05, with a z-statistic of -56, indicating a significant impact on mortality rate, resulting in lower rates for females. Conversely, for males, despite a count of 39, the p-value was 2.0, suggesting no significant association. The significant impact observed for females implies a notable difference that warrants further hypothesis testing during subsequent modeling and analysis phases.

Similarly, in the z-testing for race, significance was observed for Hispanic and Asian and Pacific Islander categories. Specifically, Hispanic individuals displayed a z-statistic of -58, while Asian and Pacific Islanders exhibited -81, both indicating significant impacts due to p-value being less than .05 resulting in lower averages. This suggests the potential for hypothesis testing on these variables in subsequent modeling endeavors.

Additionally, z-testing was conducted for states to assess any significant impacts on mortality rate. However, it is worth noting that the small p-values obtained from the chi-square test could potentially be attributed to random chance rather than statistical significance. Nonetheless, the z-testing revealed statistical significance for numerous states including Arizona, California, Colorado, Connecticut, Delaware, Florida, Iowa, Idaho, Louisiana, Massachusetts, Maryland, Maine, Minnesota, North Carolina, North Dakota, Nebraska, New Hampshire, New

Jersey, New Mexico, Nevada, New York, Oregon, Pennsylvania, Rhode Island, Utah, Virginia, Vermont, Washington, and Wisconsin.

As the analysis transitions to the next phase of modeling, it is evident that gender and race emerge as the most promising variables due to significant associations identified through the chi-square test, coupled with the significant impacts observed in certain categories within each variable. While testing on state variables is plausible, its significance is somewhat diminished by the chi-square p-value. Nonetheless, exploring the modeling of the states could still yield valuable insights.

Model Selection

When considering suitable models for analyzing gender and race in relation to heart disease mortality rate, several factors come into play. Heart disease mortality rate constitutes continuous float data, while ethnicity, gender, and state are categorical variables. Given these considerations, the models under consideration included linear regression/multilinear regression, logistic regression, clustering, and naïve Bayes.

Eliminating naïve Bayes from consideration was due to it primarily focus being on categorical data, which does not align with our target variable of continuous data. Similarly, logistic regression, which emphasizes classification outcomes, was deemed less applicable to our goal of analyzing continuous data.

Multilinear regression emerged as a promising choice, as it facilitates an examination of the impact of gender and ethnicity on the target variable (mortality rate), allowing for predictions based on these independent variables. This model enables the assessment of the combined effects of both independent variables on the target variable.

Furthermore, clustering was retained as a potential model to explore patterns and identify grouped observations that may contribute to variations in mortality rate. This approach aims to uncover any underlying patterns driving mortality rate trends, thereby providing insights beyond what is currently known.

Model Analysis

Upon selecting multi/linear regression and clustering as our models, we proceeded to format our dataset, accordingly, necessitating the hot encoding of all categorical variables. Subsequently, hypotheses were formulated to align with the significant data previously identified and the chosen models.

Hypothesis 1: There is a significant difference in heart disease mortality rates between genders.

- Null Hypothesis (H0): There is no significant difference in heart disease mortality rates between genders.
- Alternative Hypothesis (H1): There is a significant difference in heart disease mortality rates between genders.

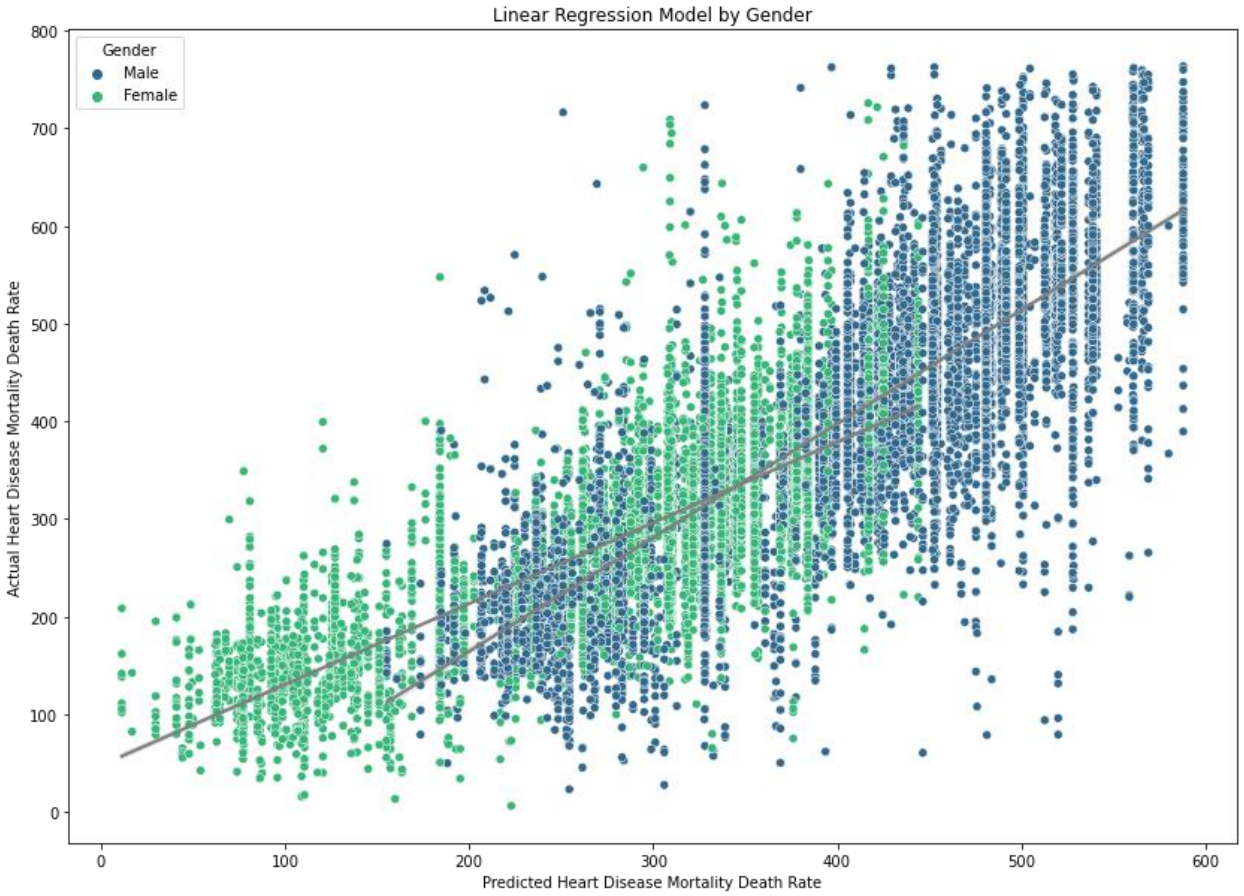
**All genders are tested but females were the primary subject to see their significant impact*

Linear regression was employed to test this hypothesis. Analysis of the results revealed that the model accounted for 23.6% of the variation in predicting the dependent mortality rate, indicating a relatively low explanatory power. The model indicated a default mortality rate of 276 individuals per 100,000 population for females (const), with males exhibiting a significantly higher rate, reflecting an increase of 140 individuals. Furthermore, the p-values for each gender were found to be significant, and the condition number indicated the absence of multicollinearity. Consequently, the results supported the rejection of the null hypothesis and the

acceptance of the alternative hypothesis, signifying a significant difference in heart disease mortality rates between genders. Females are the lower sloped line.

Figure 7

Linear Regression Model by Gender



Hypothesis 2: There is a significant difference in heart disease mortality rates between ethnicities.

- Null Hypothesis (H0): There is no significant difference in heart disease mortality rates between ethnicities.

- Alternative Hypothesis (H1): There is a significant difference in heart disease mortality rates between ethnicities.

**All ethnicities are tested but the main subjects were Hispanic and Asian and Pacific Islanders*

In examining the initial results, indications of multicollinearity emerged, evidenced by a condition number of 1.44e+15. To address this issue, the test was rerun after eliminating multicollinearity through several methods. Firstly, the 'const' column was replaced with 'White', aiding in the initial hot encoding process. Subsequently, the variance inflation factor (VIF) was calculated to detect additional multicollinearity among ethnicities. Any VIF values exceeding 10 were removed to prevent unstable and unreliable estimates.

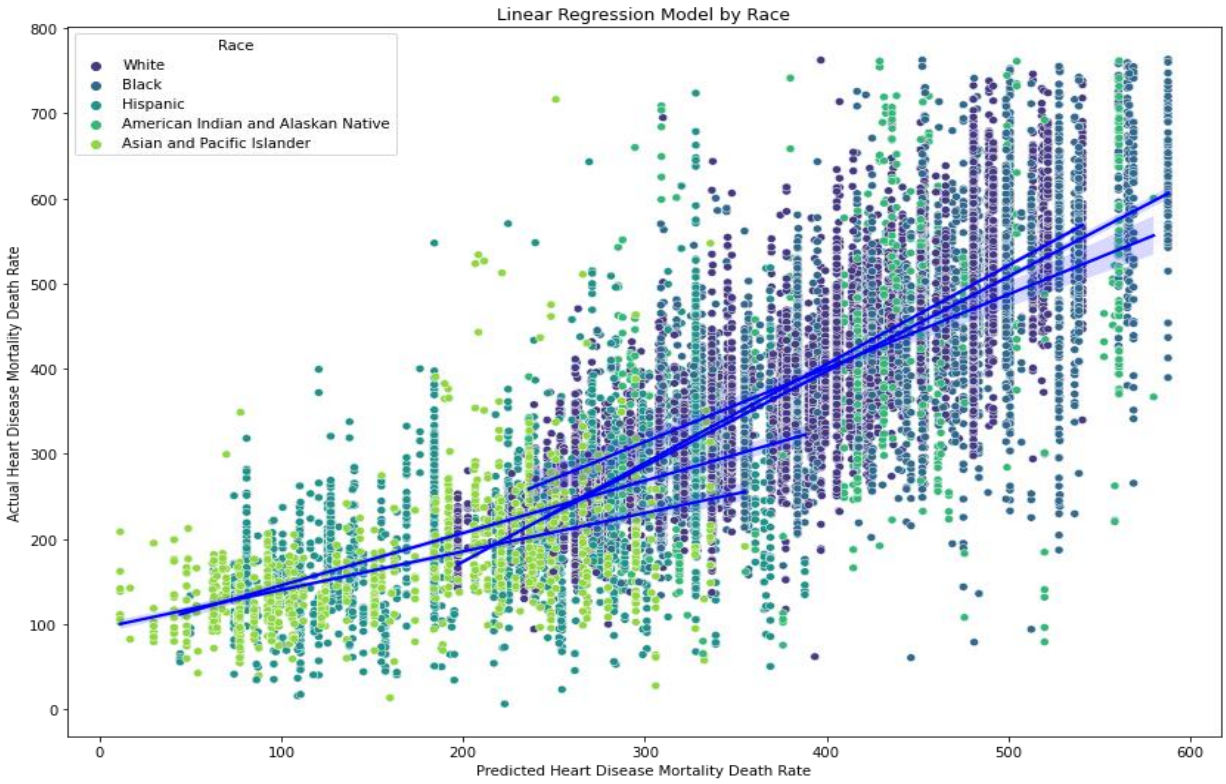
The revised model, which accounted for 34% of the variation in predicting the dependent mortality rate, demonstrated moderate explanatory power, explaining a considerable portion of the mortality rate. Notably, the 'White' ethnicity exhibited a default mortality rate of 368 individuals per 100,000 population, while Black and American Indian and Alaskan Native displayed increased rates of 60 and 35 individuals, respectively. Furthermore, significant impacts were observed for Hispanic and Asian and Pacific Islander, with both ethnicities exhibiting decreases of 151 and 195 individuals, respectively. These reductions in mortality rates for Hispanic and Asian and Pacific Islander ethnicities signify significantly lower rates compared to the other three.

Additionally, the p-values for each ethnicity were significant, further supporting the rejection of the null hypothesis and acceptance of the alternative hypothesis. Notably, the condition number indicated the absence of multicollinearity, thus resolving the initial issue. These findings underscore the significant impacts of Hispanic and Asian and Pacific Islander

ethnicities on heart disease mortality rates, aligning with the earlier z-test results and providing valuable insights for further exploration.

Figure 8

Linear Regression Model by Race



Note. The two lower sloped lines are Hispanic and Asian and Pacific Islander. The graph shows how they are significantly different from the other ethnicities.

Hypothesis 3: There is a significant interaction effect between gender and ethnicity on heart disease mortality rates.

- Null Hypothesis (H0): There is no significant interaction effect between gender and ethnicity on heart disease mortality rates.

- Alternative Hypothesis (H1): There is a significant interaction effect between gender and ethnicity on heart disease mortality rates.

The selected model for this hypothesis was multilinear regression. Upon examination of the results, the model demonstrated an explanatory power of 58.6%, indicating a moderate ability to predict the dependent mortality rate. Like the approach used for ethnicity, multicollinearity was addressed.

The model revealed that white females (const) had a default mortality rate of 297 individuals per 100,000 population. Males exhibited a significantly higher rate, with an increase of 140 individuals, with black males showing the highest among all groups. Conversely, Asian or Pacific Islander females displayed the lowest mortality rate. Additionally, Hispanic ethnicity continued to exhibit a significant impact, with a coefficient of -155.

The p-values for each variable were found to be significant, confirming their individual contributions to the model. Moreover, the condition number indicated the absence of multicollinearity, affirming the reliability of the results. Notably, the variables demonstrating significant impact trended towards lower mortality rates, as observed in the preceding graphs. These findings support the rejection of the null hypothesis and the acceptance of the alternative hypothesis, reinforcing the significant differences observed in heart disease mortality rates among genders and ethnicities.

Hypothesis 4: There is a significant difference in heart disease mortality rates between states.

- Null Hypothesis (H0): There is no significant difference in heart disease mortality rates between states.
- Alternative Hypothesis (H1): There is a significant difference in heart disease mortality rates between states.

**All states are test, but the subjects were Arizona, California, Colorado, Connecticut, Delaware, Florida, Iowa, Idaho, Louisiana, Massachusetts, Maryland, Maine, Minnesota, North Carolina, North Dakota, Nebraska, New Hampshire, New Jersey, New Mexico, Nevada, New York, Oregon, Pennsylvania, Rhode Island, Utah, Virginia, Vermont, Washington, and Wisconsin primary subjects for significant impact.*

Regarding the fourth hypothesis, which assesses the influence of states on mortality rates, the results are inconclusive. The Chi-Square test indicated a lack of association, whereas the linear regression suggested a minor influence of certain states, though they accounted for a small portion (16.6%) of the model's predictive capacity. The hypothesis was tested using linear regression, focusing primarily on states identified as statistically significant in the preceding z-test. Attempted measures to address multicollinearity involved applying the method utilized for ethnicity variables. While this approach successfully removed Georgia and Texas, multicollinearity persisted, indicated by a condition number exceeding the threshold of 30, reaching 41.6.

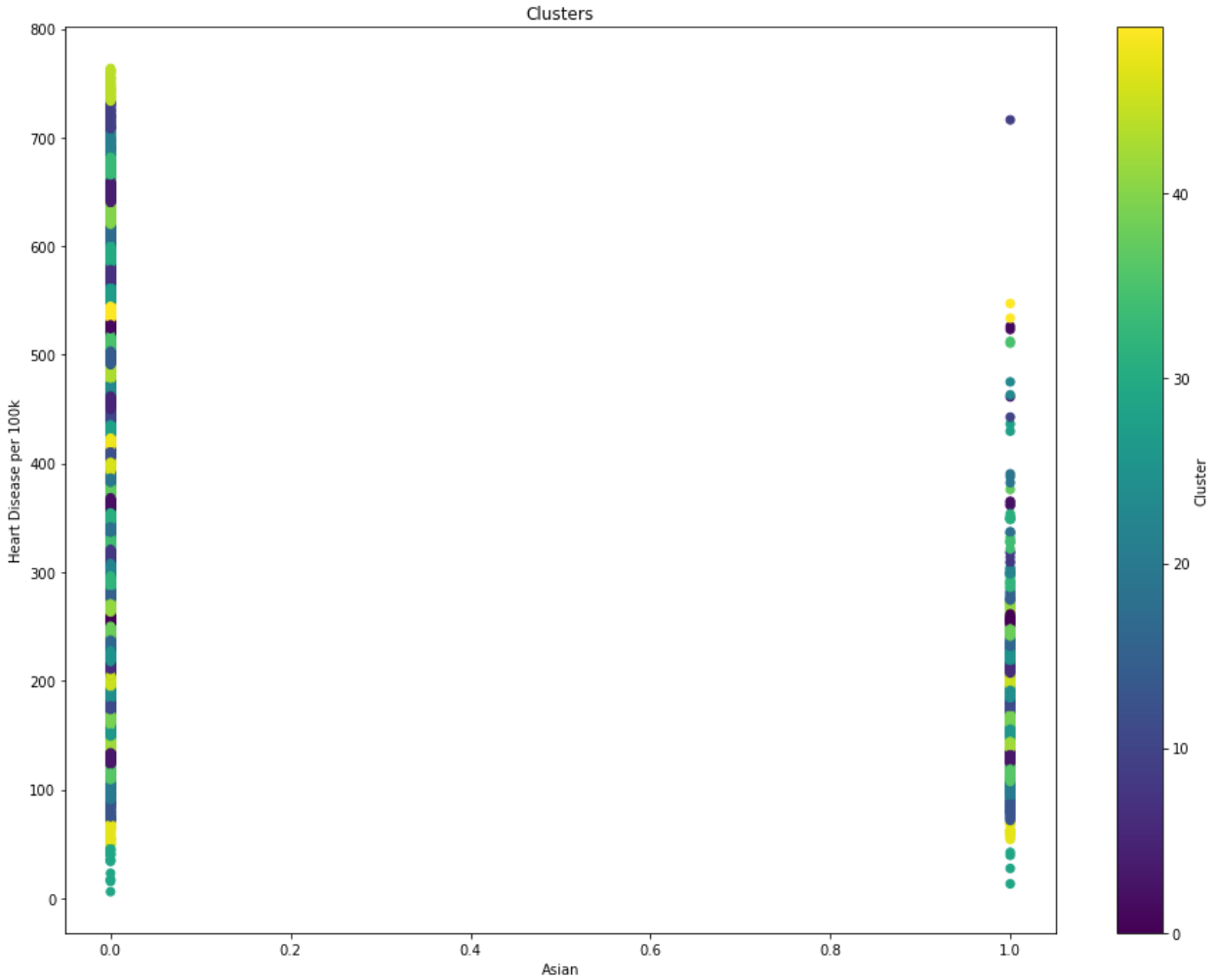
Analysis of the results revealed that the model accounted for 16.6% of the variation in predicting the dependent mortality rate, signifying a low explanatory power. Notably, states identified as significant in the z-test exhibited significant findings based on their p-values. However, given the observed multicollinearity and the potential for unreliable results, further testing is warranted to make informed decisions regarding this hypothesis. The considerable variability observed suggests the need for additional exploration before drawing definitive conclusions.

Regarding clustering analysis, notable patterns emerged that could be associated with the findings discussed above. These patterns appeared to be aligned with our earlier observations and

analyses. Further exploration of these patterns could provide valuable insights into the factors influencing heart disease mortality rates.

Figure 9

Cluster chart of the Asian Ethnicity

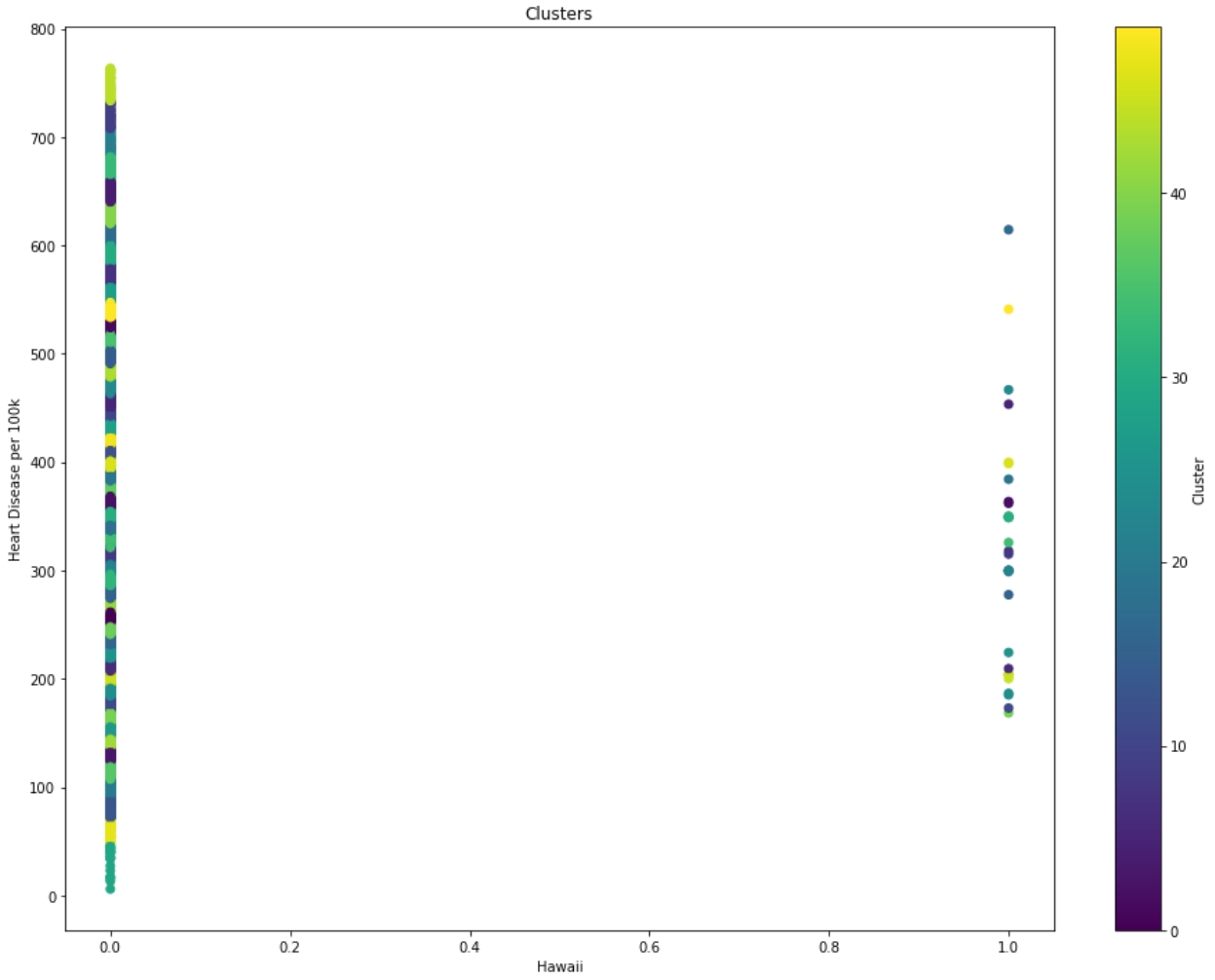


Note. Asians exhibited the lowest ceiling, as evidenced by both the box plot and the cluster chart.

Moreover, the cluster chart indicated a majority clustered closer to their floor and ceiling. These findings align with observations made for other ethnicities, suggesting a consistent pattern across different analyses and visualizations.

Figure 10

Cluster chart of the State of Hawaii



Note. The data from Hawaii appears to be sparse and widely spread out. The clustering pattern is not clearly discernible, and there exists a significant gap between the floor and ceiling values.

Conclusion

In the conclusion of the study, we observe a distinct pattern in the mortality rates due to heart disease that correlates with gender and ethnicity. Women, as well as individuals from Asian and Pacific Islander and Hispanic backgrounds, tend to show lower mortality rates. Conversely, African American males are highlighted as the group with the highest mortality rates. To gain a deeper understanding of these patterns, it is proposed that future research should delve into the significant variables that contribute to these lower rates. Cultural practices, including dietary customs among different ethnic groups, warrant further examination. For women, it would be beneficial to explore how their diet differs from that of men, along with the potential influences of living conditions and cultural expectations.

For a more comprehensive analysis, future studies could compare ethnic groups globally to discern any patterns that might correlate with environmental conditions. Examining the impact of different climates, such as colder regions or areas with high humidity, on heart disease mortality could be particularly revealing. Furthermore, socio-economic factors, healthcare access, and lifestyle choices, such as smoking and physical activity levels, across states could provide a clearer picture of the underlying causes of heart disease. By addressing these additional factors, researchers may uncover more nuanced insights into the prevalence of heart disease among adults over the age of 35 and the disparities seen across different demographic groups. This would not only contribute to the academic understanding of heart disease but could also inform public health policies and interventions aimed at reducing the burden of this disease (Nagar et al., 2023).

Recommendations

Based on the findings of the study, it is recommended that public health interventions should be tailored to address the specific needs of high-risk groups identified in the analysis. Given that African American males have the highest mortality rates, targeted prevention strategies such as community-based health education programs, improved access to early screening, and culturally sensitive healthcare services should be prioritized.

Moreover, the lower mortality rates observed among women, Asians Pacific Islanders, and Hispanics suggest that there may be protective cultural, dietary, or lifestyle factors at play. It is recommended that these factors be researched further to isolate the beneficial practices that could be promoted more widely. Public health campaigns might focus on the adoption of heart-healthy diets and lifestyles that mirror the positive aspects found within these communities.

Considering the inconclusive impacts of state-level factors, it would be prudent to conduct a more granular investigation into the socioeconomic and environmental factors that vary across states, which could be influencing heart disease mortality rates. This might include an in-depth analysis of healthcare infrastructure, the prevalence of risk factors like smoking and obesity, and even state-specific policies on healthcare. The goal would be to identify actionable policy levers that state governments can pull to improve heart health outcomes among their populations.

References

Nagar, K., Darji, J., Christian, A., & Patel, N. (2023). A Household Survey To Assess Prevalence of Communicable and Non-Communicable Disease and Standard of Living Patterns among Rural Peoples Residing in Rural Area of Kheda District, Gujarat. *Journal of Coastal Life Medicine*, *11*(1). https://www.jclmm.com/index.php/journal/article/view/558

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Xu, J., Murphy, S. L., Kochanek, K. D., & Arias, E. (2022, December 22). *Mortality in the United States, 2021*. Center for Disease Control and Prevention. Retrieved February 24, 2024, from https://stacks.cdc.gov/view/cdc/122516

Cleaning the Data

In [29]:
```
import pandas as pd
```

In [30]:
```
# This gets data for county off of gender, ethnicity and removing nation and state levels

master_df = pd.read_csv("Heart_Disease_Mortality_Data_Among_US_Adults__35____by_State_Territo

# removes the insufficient data columns
rem_null_overall_df = master_df[master_df['Data_Value_Footnote'].isnull()]

# gets only male/female
only_gen_overall_df = rem_null_overall_df[rem_null_overall_df['Stratification1'] != 'Overall']

# removes the overall for the ethnicity
only_eth_overall_df = only_gen_overall_df[only_gen_overall_df['Stratification2'] != 'Overall']

# only gets the county
only_county_overall_df = only_eth_overall_df[only_eth_overall_df['GeographicLevel'] == 'County']

# get the columns we are only using
desired_columns = ['LocationAbbr', 'LocationDesc', 'Data_Value', 'Stratification1', 'Stratification2']
cleaned_county_df = only_county_overall_df[desired_columns]

# Renamed the columns to better naming for the project
cleaned_county_df.columns = ['State', 'County', 'Heart Disease per 100k', 'Gender', 'Ethnicity']

# Validated the column total (I checked against the excel and made sure this was correct)
# print(len(cleaned_county_df))

# Checking the data
cleaned_county_df.head()
```

Out[30]:

	State	County	Heart Disease per 100k	Gender	Ethnicity
102	AK	Anchorage	317.5	Male	White
105	AK	Denali	400.7	Male	White
106	AK	Fairbanks North Star	401.0	Male	White
107	AK	Haines	385.5	Male	White
108	AK	Juneau	281.6	Male	White

In [31]:
```
# This block is to get the clean county overall data only

rem_null_overall_df = master_df[master_df['Data_Value_Footnote'].isnull()]

# gets overall for gender
only_gen_overall_df = rem_null_overall_df[rem_null_overall_df['Stratification1'] == 'Overall']

# gets overall for ethnicity
only_eth_overall_df = only_gen_overall_df[only_gen_overall_df['Stratification2'] == 'Overall']

# only gets the county
```

```
only_county_overall_df = only_eth_overall_df[only_eth_overall_df['GeographicLevel'] == 'County']

# get the columns we are only using
cleaned_county_overall_df = only_county_overall_df[desired_columns]

# Renamed the columns to better naming for the project
cleaned_county_overall_df.columns = ['State', 'County', 'Heart Disease per 100k', 'Gender', 'Ethnicity']

# Validated the column total (Verified the excel and it's correct)
# print(len(cleaned_county_overall_df))

cleaned_county_overall_df.head()
```

Out[31]:

	State	County	Heart Disease per 100k	Gender	Ethnicity
0	AK	Aleutians East	105.3	Overall	Overall
1	AK	Aleutians West	211.9	Overall	Overall
2	AK	Anchorage	257.9	Overall	Overall
3	AK	Bethel	351.6	Overall	Overall
5	AK	Denali	305.5	Overall	Overall

In [32]:

```
# This function finds the outliers using the interquartile range method
def find_outliers_iqr(df, column):
    # Extract the data column
    data = df[column]

    # Calculate the quartiles
    Q1 = data.quantile(0.25)
    Q3 = data.quantile(0.75)

    # Calculate the interquartile range (IQR)
    IQR = Q3 - Q1

    # Calculate the lower bound and upper bound for outliers
    lower_bound = Q1 - 1.5 * IQR
    upper_bound = Q3 + 1.5 * IQR

    # Find outliers based on the bounds
    outliers = (data < lower_bound) | (data > upper_bound)

    # Remove outliers from the DataFrame
    df = df[~outliers]

    return df

# Clean outliers from cleaned_county_df DataFrame
cleaned_county_df = find_outliers_iqr(cleaned_county_df, 'Heart Disease per 100k')

# Clean outliers from cleaned_county_overall_df DataFrame
cleaned_county_overall_df = find_outliers_iqr(cleaned_county_overall_df, 'Heart Disease per 100k')
```

Exploratory Data Analysis

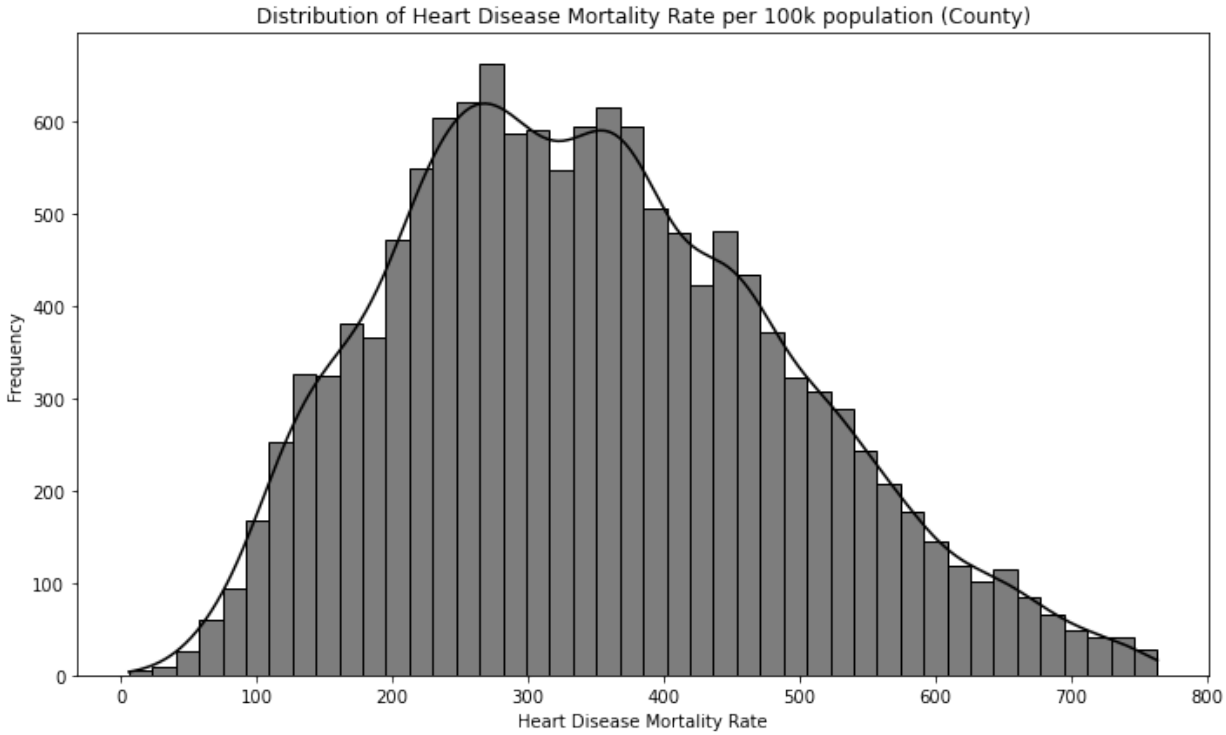
In [33]:
```
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
from scipy.stats import chi2_contingency
from scipy import stats
```

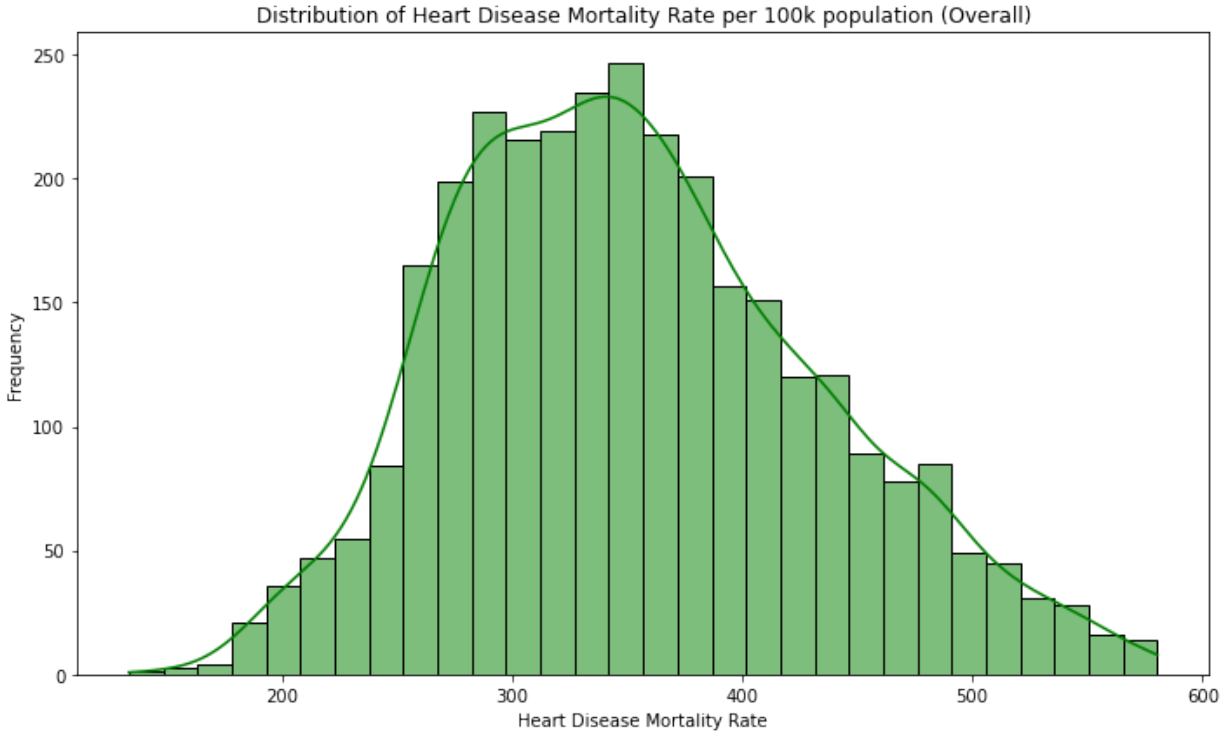
In [34]:
```
# Print 5 Number Summary for cleaned data with no outliers
print("5 Number Summary for cleaned data with no outliers\n", cleaned_county_df.describe())

# Print 5 Number Summary for cleaned data overall with no outliers
print("\n5 Number Summary for cleaned data overall with no outliers\n", cleaned_county_overall_df.de

# Calculate statistics for overall cleaned data
overall_mean = np.mean(cleaned_county_overall_df['Heart Disease per 100k'])
overall_std = np.std(cleaned_county_overall_df['Heart Disease per 100k'], ddof=1)
overall_size = len(cleaned_county_overall_df)

# Calculate statistics for individual cleaned data
indv_mean = np.mean(cleaned_county_df['Heart Disease per 100k'])
indv_size = len(cleaned_county_df)

# Calculate standard error for the sample
se_indv = overall_std / np.sqrt(indv_size)

# Print calculated statistics
print("Population Mean:", overall_mean)
print("Sample Mean:", indv_mean)
print("Standard Error for the Sample:", se_indv)
```

```
5 Number Summary for cleaned data with no outliers
       Heart Disease per 100k
count            13484.000000
mean               347.002648
std                143.989750
min                  6.000000
25%                239.675000
50%                335.900000
75%                445.800000
max                763.500000

5 Number Summary for cleaned data overall with no outliers
       Heart Disease per 100k
count             3162.000000
mean               353.284756
std                 79.606042
min                133.500000
25%                294.025000
50%                345.850000
75%                404.575000
max                580.400000
Population Mean: 353.2847564832387
Sample Mean: 347.0026475823194
Standard Error for the Sample: 0.6855460914644189
```

In [35]:
```
# Create a figure and axes with a 2x1 layout
fig, axes = plt.subplots(nrows=2, ncols=1, figsize=(10, 12))

# Subplot 1: Histogram for cleaned_county_df
sns.histplot(cleaned_county_df['Heart Disease per 100k'], bins='auto', kde=True, color='black', ax=axes[0]
```

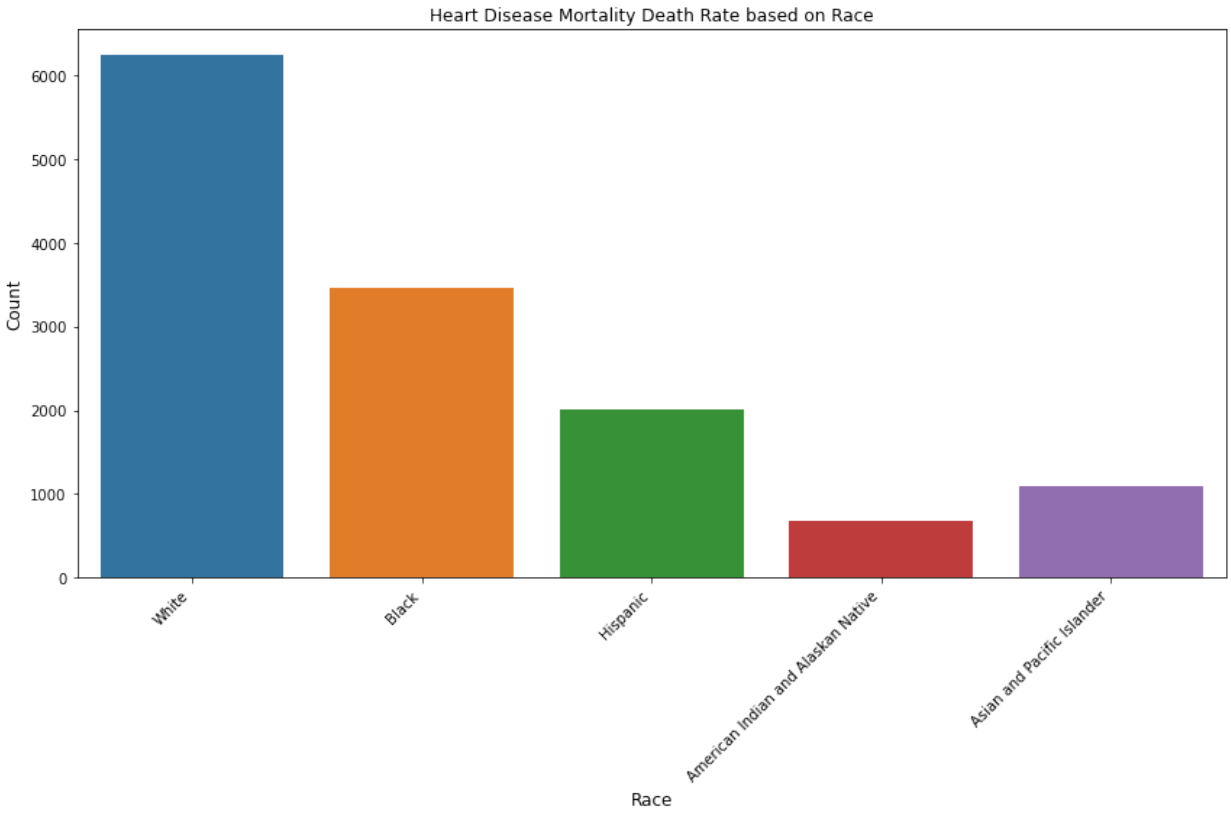
```
axes[0].set_title('Distribution of Heart Disease Mortality Rate per 100k population (County)')
axes[0].set_xlabel('Heart Disease Mortality Rate')
axes[0].set_ylabel('Frequency')

# Subplot 2: Histogram for cleaned_county_overall_df
sns.histplot(cleaned_county_overall_df['Heart Disease per 100k'], bins='auto', kde=True, color='green', ax
axes[1].set_title('Distribution of Heart Disease Mortality Rate per 100k population (Overall)')
axes[1].set_xlabel('Heart Disease Mortality Rate')
axes[1].set_ylabel('Frequency')

plt.tight_layout()  # Adjust layout to prevent overlapping
plt.show()
```

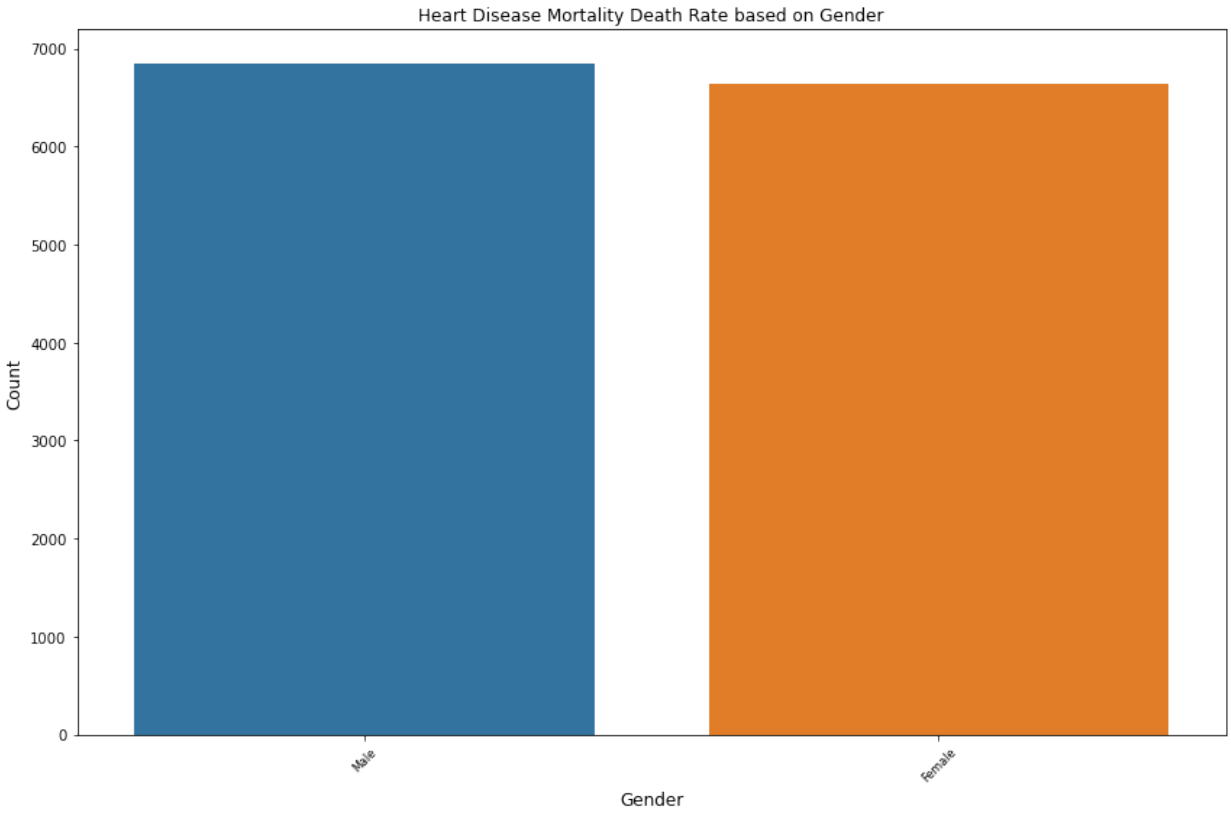


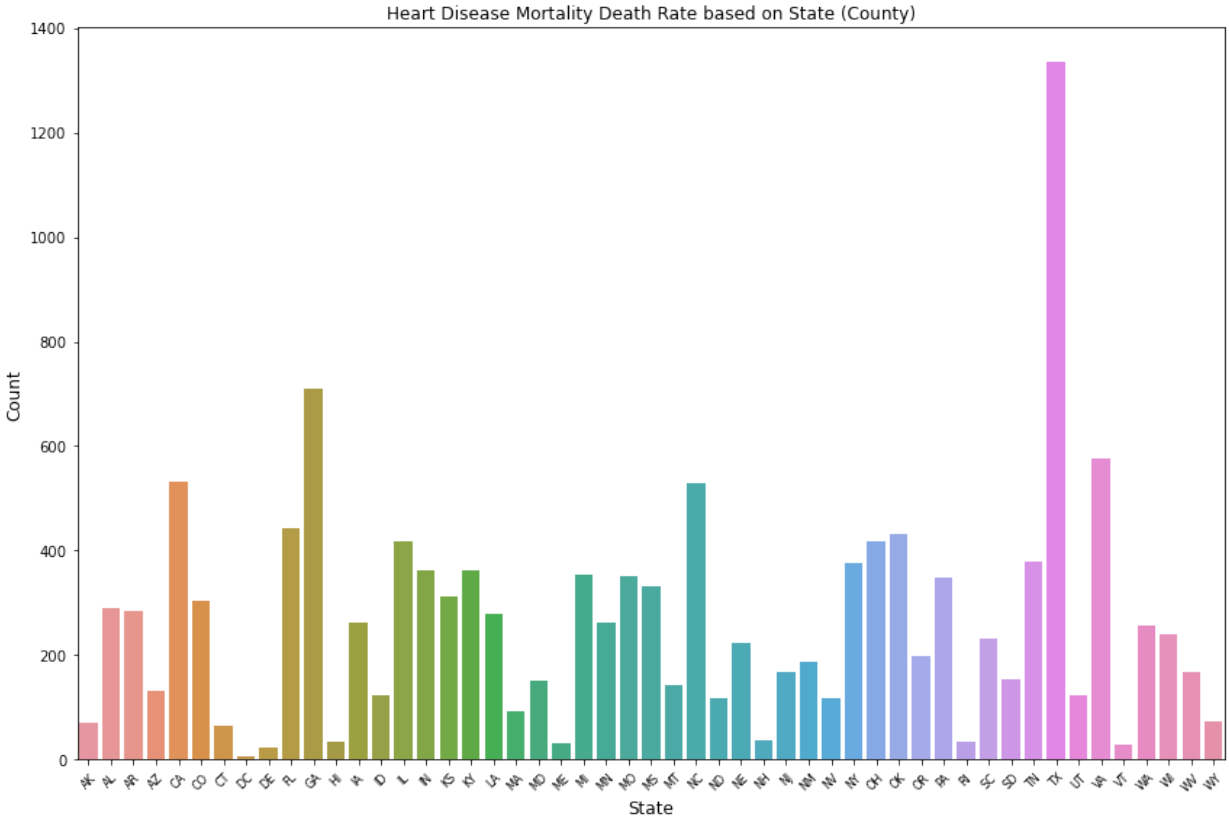


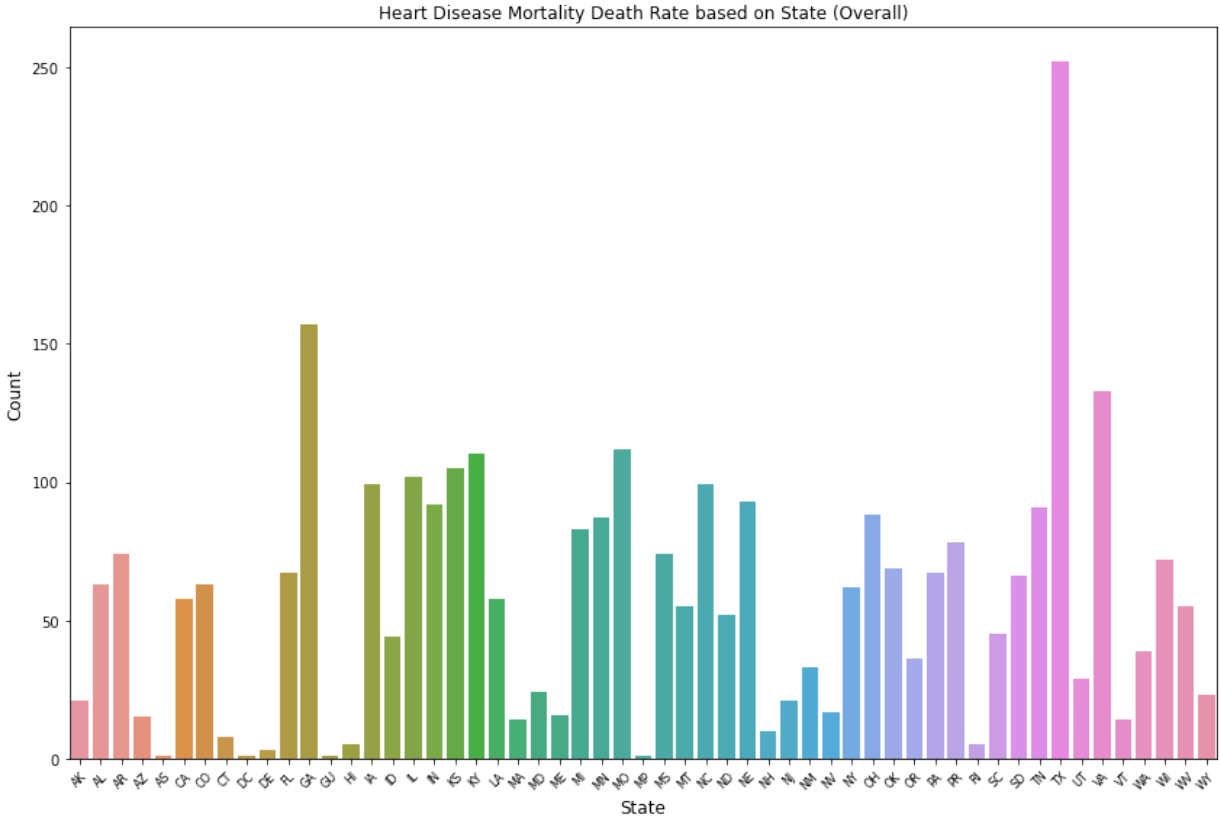
In [36]:
```
# Plot for Ethnicity
plt.figure(figsize=(12, 8))  # Countplot for Ethnicity
sns.countplot(data=cleaned_county_df, x='Ethnicity')
plt.title('Heart Disease Mortality Death Rate based on Race', fontsize=12)
plt.xticks(rotation=45, ha='right', fontsize=10)  # Rotate labels by 45 degrees and align them to the righ
plt.xlabel('Race', fontsize=12)
plt.ylabel('Count', fontsize=12)
plt.tight_layout()  # Adjust layout to prevent overlapping
plt.show()

# Plot for Gender
plt.figure(figsize=(12, 8))  # Countplot for Gender
sns.countplot(data=cleaned_county_df, x='Gender')
plt.title('Heart Disease Mortality Death Rate based on Gender', fontsize=12)
plt.xticks(rotation=45, fontsize=8)  # Decrease font size
plt.xlabel('Gender', fontsize=12)
plt.ylabel('Count', fontsize=12)
plt.tight_layout()  # Adjust layout to prevent overlapping
plt.show()

# Plot for States
fig, axs = plt.subplots(nrows=2, ncols=1, figsize=(12, 16))  # Create a figure and axes with a 2x1 layout

# Subplot 1: Countplot for State in cleaned_county_df
sns.countplot(data=cleaned_county_df, x='State', ax=axs[0])
axs[0].set_title('Heart Disease Mortality Death Rate based on State (County)', fontsize=12)
axs[0].tick_params(axis='x', labelrotation=45, labelsize=8)  # Rotate and decrease x-axis tick label size
axs[0].set_xlabel('State', fontsize=12)
axs[0].set_ylabel('Count', fontsize=12)

# Subplot 2: Countplot for State in cleaned_county_overall_df
sns.countplot(data=cleaned_county_overall_df, x='State', ax=axs[1])
axs[1].set_title('Heart Disease Mortality Death Rate based on State (Overall)', fontsize=12)
axs[1].tick_params(axis='x', labelrotation=45, labelsize=8)  # Rotate and decrease x-axis tick label size
axs[1].set_xlabel('State', fontsize=12)
axs[1].set_ylabel('Count', fontsize=12)

plt.tight_layout()  # Adjust layout to prevent overlapping
plt.show()

# Plot for top 10 counties
top_counties = cleaned_county_df['County'].value_counts().nlargest(10).index  # Calculate the top 10 co
top_counties_overall = cleaned_county_overall_df['County'].value_counts().nlargest(10).index

top_county_data = cleaned_county_df[cleaned_county_df['County'].isin(top_counties)]  # Filter the dat
top_county_data_overall = cleaned_county_overall_df[cleaned_county_overall_df['County'].isin(top_cou

fig, axs = plt.subplots(nrows=2, ncols=1, figsize=(12, 16))  # Create a figure and axes with a 2x1 layout

# Subplot 1: Countplot for top 10 counties' heart disease mortality death rates
sns.countplot(data=top_county_data, x='County', order=top_counties, ax=axs[0])
axs[0].set_title('Top 10 Heart Disease Mortality Death Rate by County', fontsize=12)
axs[0].tick_params(axis='x', labelrotation=45, labelsize=8)  # Rotate and decrease x-axis tick label size
axs[0].set_xlabel('County', fontsize=12)
axs[0].set_ylabel('Count', fontsize=12)

# Subplot 2: Countplot for top 10 counties' heart disease mortality death rates (overall)
sns.countplot(data=top_county_data_overall, x='County', order=top_counties_overall, ax=axs[1])
axs[1].set_title('Top 10 Heart Disease Mortality Death Rate by County (Overall)', fontsize=12)
```

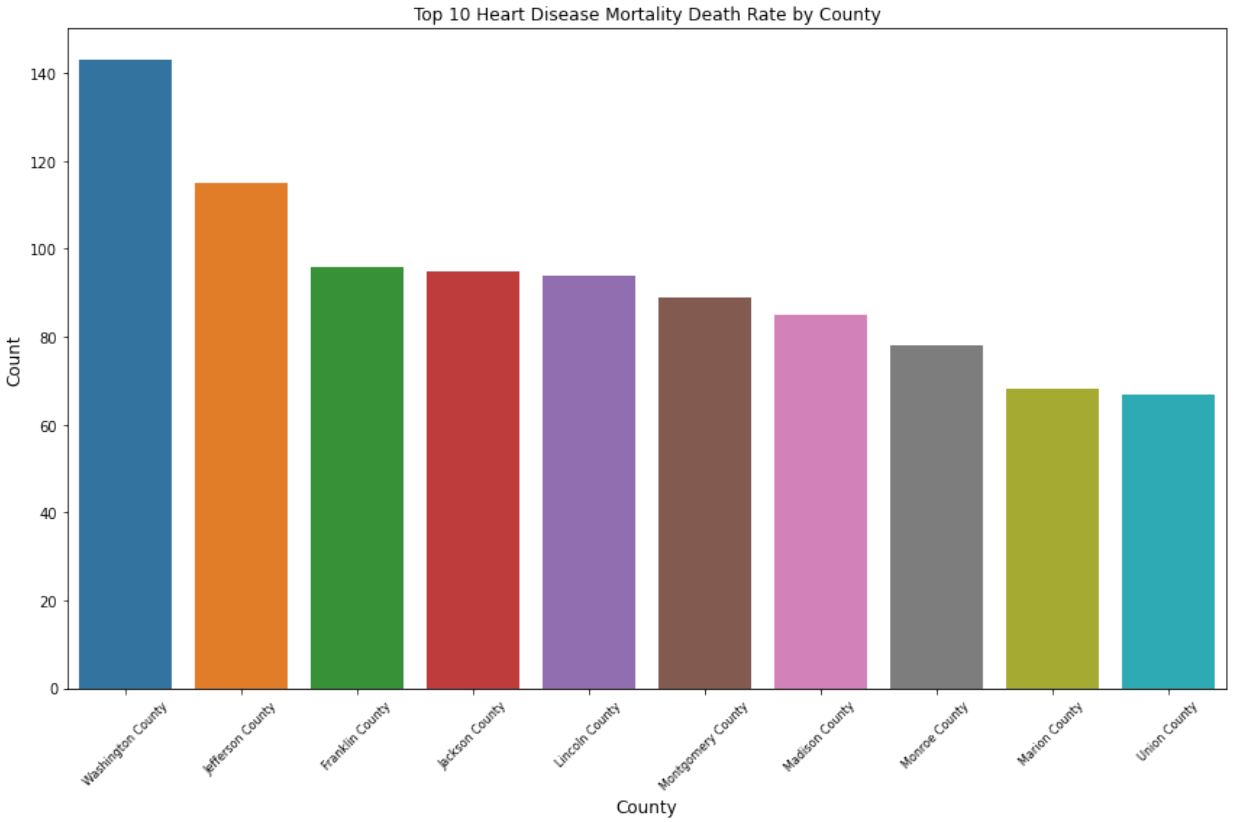
```
axs[1].tick_params(axis='x', labelrotation=45, labelsize=8)  # Rotate and decrease x-axis tick label size
axs[1].set_xlabel('County', fontsize=12)
axs[1].set_ylabel('Count', fontsize=12)

plt.tight_layout()  # Adjust layout to prevent overlapping
plt.show()
```

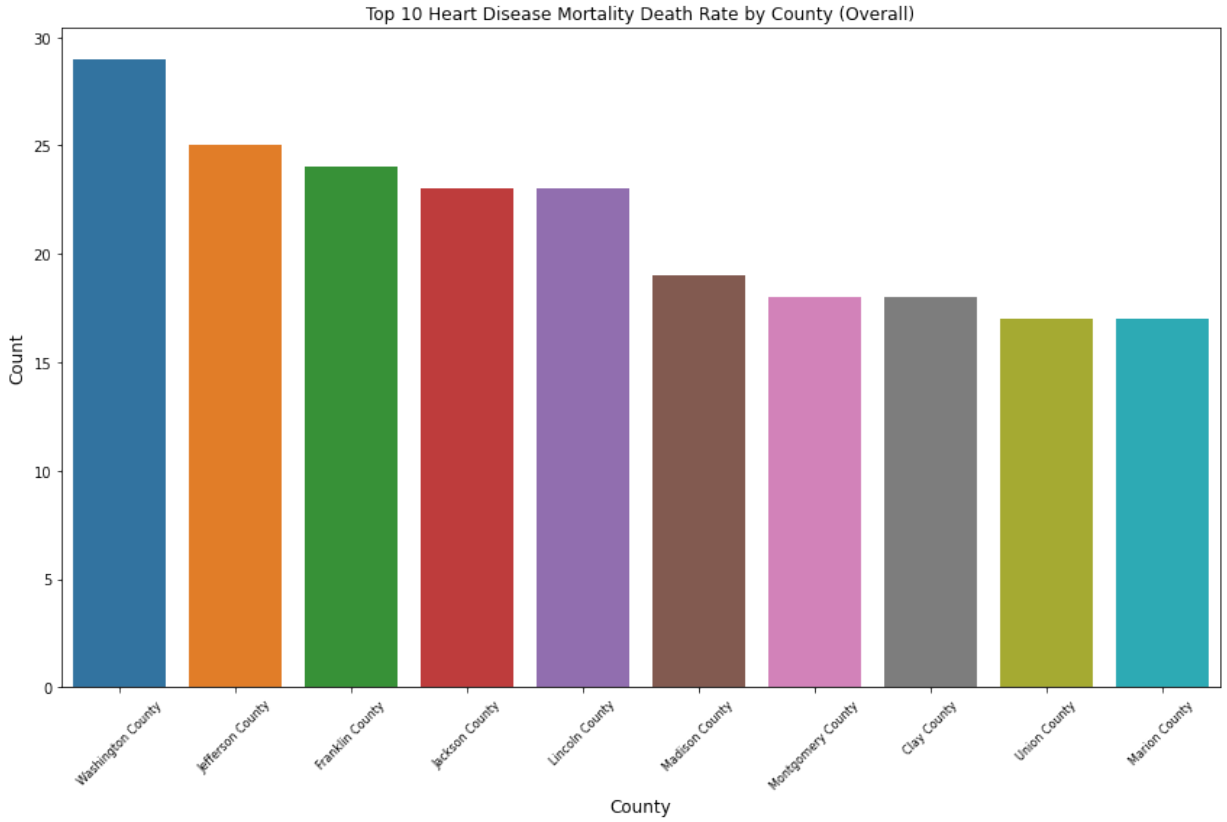





Heart Disease Mortality Death Rate based on State (County)
Count
State
0
200
400
600
800
1000
1200
1400

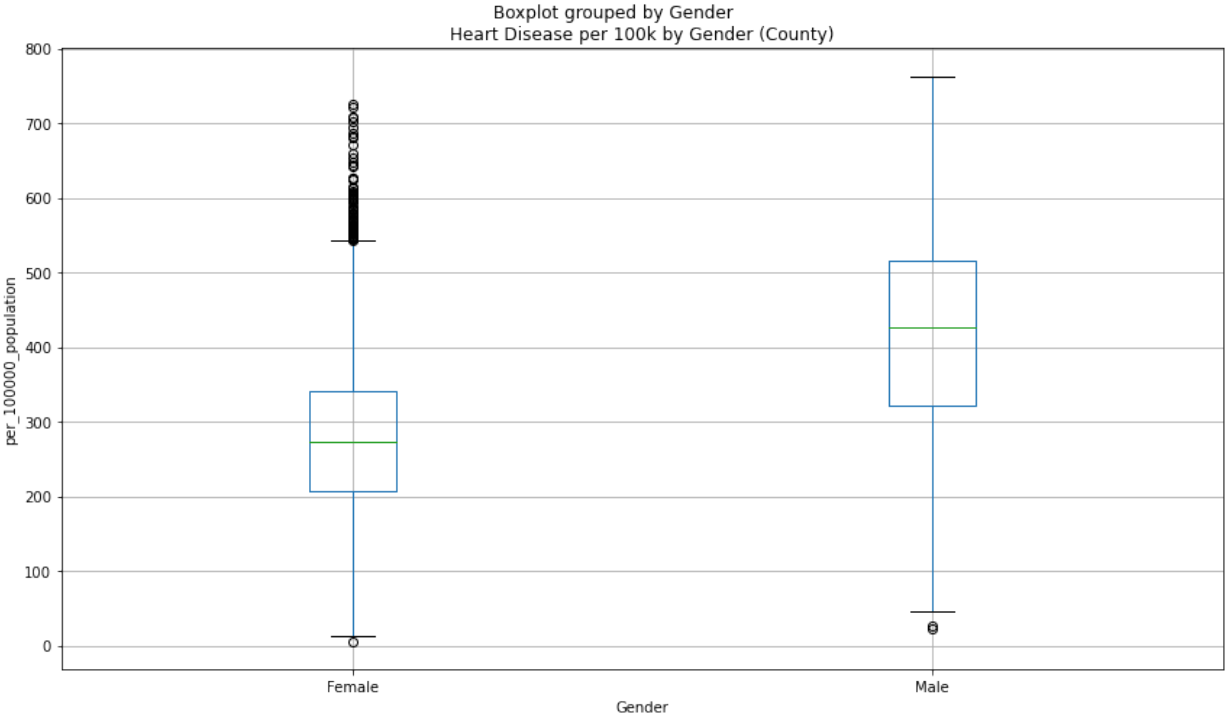

Heart Disease Mortality Death Rate based on State (Overall)
Count
State
0
50
100
150
200
250

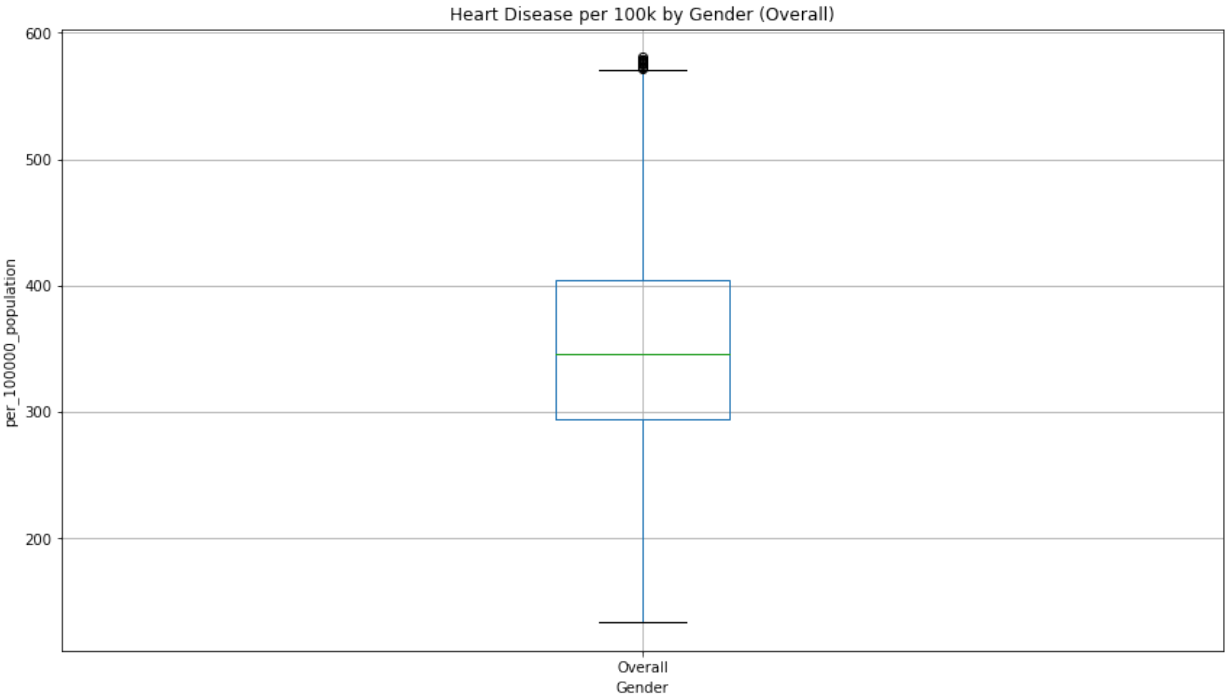


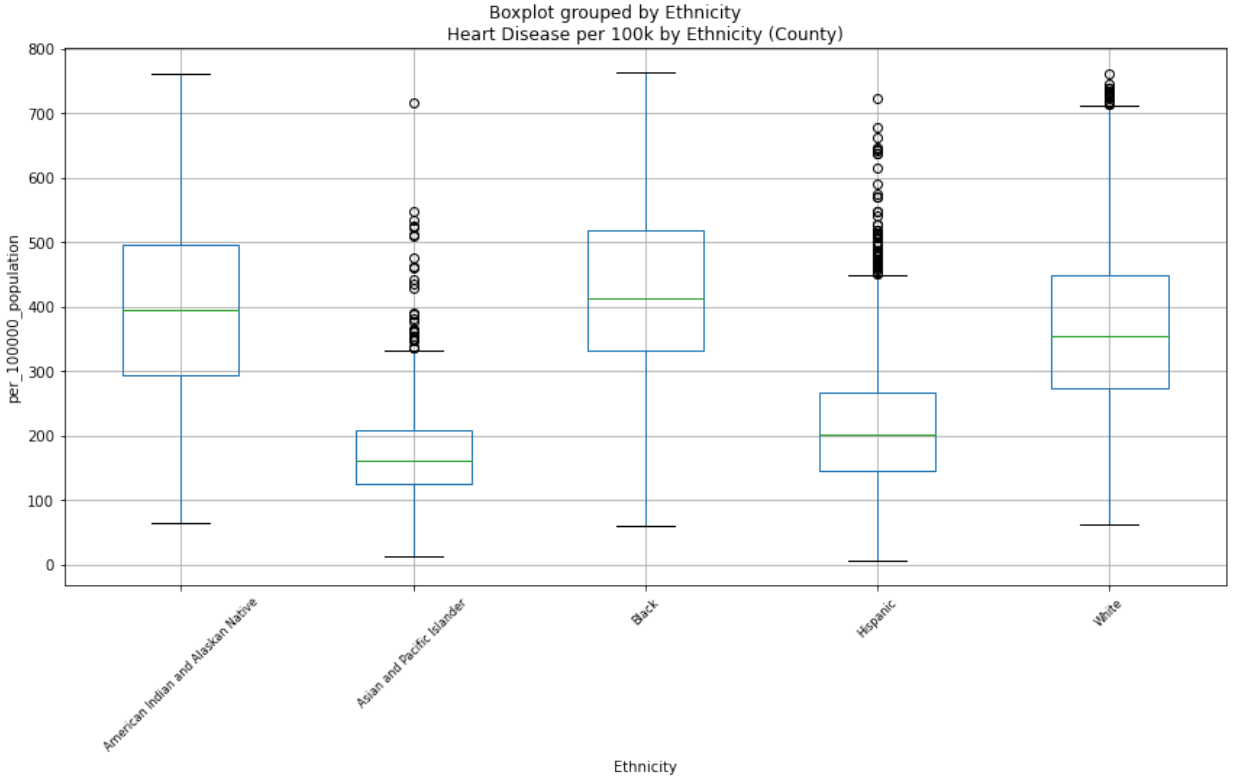


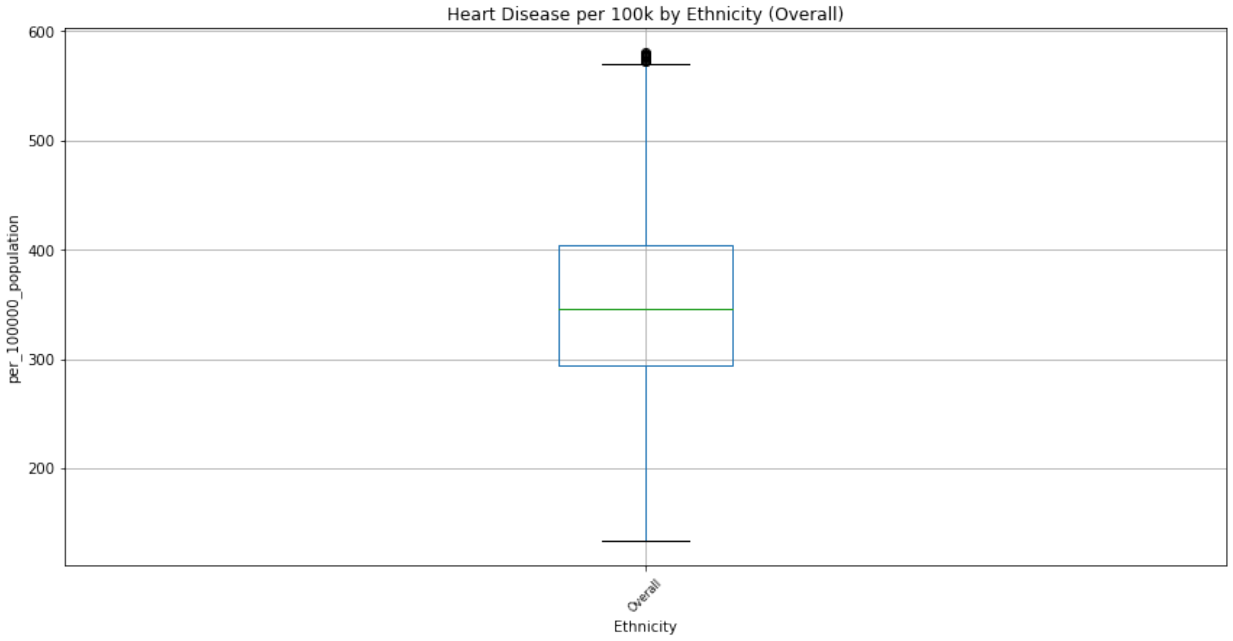
In [37]:
```
# Create a figure and axes for the first set of subplots
fig, axes1 = plt.subplots(nrows=2, ncols=1, figsize=(12, 14))

# Subplot 1: Box plot for Heart Disease per 100k by Gender in cleaned_county_df
cleaned_county_df.boxplot(column='Heart Disease per 100k', by='Gender', ax=axes1[0])
axes1[0].set_title('Heart Disease per 100k by Gender (County)')
axes1[0].set_ylabel('per_100000_population')
```

```
# Subplot 2: Box plot for Heart Disease per 100k by Gender in cleaned_county_overall_df
cleaned_county_overall_df.boxplot(column='Heart Disease per 100k', by='Gender', ax=axes1[1])
axes1[1].set_title('Heart Disease per 100k by Gender (Overall)')
axes1[1].set_ylabel('per_100000_population')

plt.tight_layout()  # Adjust layout to prevent overlapping
plt.show()

# Create a new figure and axes for the second set of subplots
fig, axes2 = plt.subplots(nrows=2, ncols=1, figsize=(12, 14))

# Subplot 1: Box plot for Heart Disease per 100k by Ethnicity in cleaned_county_df
cleaned_county_df.boxplot(column='Heart Disease per 100k', by='Ethnicity', ax=axes2[0])
axes2[0].set_title('Heart Disease per 100k by Ethnicity (County)')
axes2[0].set_ylabel('per_100000_population')
axes2[0].tick_params(axis='x', rotation=45, labelsize=8)  # Rotate and decrease x-axis tick label size

# Subplot 2: Box plot for Heart Disease per 100k by Ethnicity in cleaned_county_overall_df
cleaned_county_overall_df.boxplot(column='Heart Disease per 100k', by='Ethnicity', ax=axes2[1])
axes2[1].set_title('Heart Disease per 100k by Ethnicity (Overall)')
axes2[1].set_ylabel('per_100000_population')
axes2[1].tick_params(axis='x', rotation=45, labelsize=8)  # Rotate and decrease x-axis tick label size

plt.tight_layout()  # Adjust layout to prevent overlapping
plt.show()
```


Boxplot grouped by Gender
Heart Disease per 100k by Gender (County)
per_100000_population
800
700
600
500
400
300
200
100
0
Female
Male
Gender


Heart Disease per 100k by Gender (Overall)
per_100000_population
600
500
400
300
200
Overall
Gender





In [38]:
```
# Chi-square test for gender
contingency_gender = pd.crosstab(cleaned_county_df['Heart Disease per 100k'], cleaned_county_df['Ge
chi2_stat_gender, p_val_gender, _, _ = chi2_contingency(contingency_gender)

# Chi-square test for race
contingency_race = pd.crosstab(cleaned_county_df['Heart Disease per 100k'], cleaned_county_df['Ethni
chi2_stat_race, p_val_race, _, _ = chi2_contingency(contingency_race)

# Chi-square test for county
contingency_geo = pd.crosstab(cleaned_county_df['Heart Disease per 100k'], cleaned_county_df['County
chi2_stat_geo, p_val_geo, _, _ = chi2_contingency(contingency_geo)

# Chi-square test for state
contingency_state = pd.crosstab(cleaned_county_df['Heart Disease per 100k'], cleaned_county_df['State
chi2_stat_state, p_val_state, _, _ = chi2_contingency(contingency_state)
```

```
# Create a DataFrame for the chi-square statistics and p-values
data = {
    'Category': ['Gender', 'Ethnicity', 'County', 'State'],
    'Chi-square statistic': [chi2_stat_gender, chi2_stat_race, chi2_stat_geo, chi2_stat_state],
    'p-value': [p_val_gender, p_val_race, p_val_geo, p_val_state]
}

# Create the DataFrame for Chi-Square test
chi_square_df = pd.DataFrame(data)

# Print the DataFrame
print(chi_square_df)
```

```
    Category  Chi-square statistic       p-value
0     Gender          7.171499e+03   3.097805e-69
1  Ethnicity          2.560000e+04  2.355235e-111
2     County          9.512658e+06   1.000000e+00
3      State          2.557907e+05   9.999865e-01
```

In [39]:

```
# Calculate the overall mean heart disease rate
mean_heart_disease = cleaned_county_df['Heart Disease per 100k'].mean()

# Iterate through each state and perform the Z-test
for state in cleaned_county_df['State'].unique():
    heart_disease_state = cleaned_county_df[cleaned_county_df['State'] == state]['Heart Disease per 10

    # Performing the Z-test
    z_stat = (heart_disease_state.mean() - mean_heart_disease) / (heart_disease_state.std() / np.sqrt
    p_value = stats.norm.cdf(z_stat) * 2  # two-tailed test

    # Round Z-statistic and P-value to two decimals
    z_stat_rounded = round(z_stat, 2)
    p_value_rounded = round(p_value, 2)

    # Outputting the result
    print(f"Z-test for {state}:")
    print(f"Z-statistic: {z_stat_rounded}")
    print(f"P-value: {p_value_rounded}")
    if p_value < 0.05:
        print("The mean heart disease rate for this state is significantly different from the overall mean.
    else:
        print("The mean heart disease rate for this state is not significantly different from the overall m
    print()

# Z-test for Ethnicity
# Iterate through each ethnicity and perform the Z-test
for ethnicity in cleaned_county_df['Ethnicity'].unique():
    heart_disease_ethnicity = cleaned_county_df[cleaned_county_df['Ethnicity'] == ethnicity]['Heart Dis

    # Performing the Z-test
    z_stat = (heart_disease_ethnicity.mean() - mean_heart_disease) / (heart_disease_ethnicity.std() /
    p_value = stats.norm.cdf(z_stat) * 2  # two-tailed test

    # Round Z-statistic and P-value to two decimals
    z_stat_rounded = round(z_stat, 2)
    p_value_rounded = round(p_value, 2)

    # Outputting the result
    print(f"Z-test for {ethnicity}:")
```

```
    print(f"Z-statistic: {z_stat_rounded}")
    print(f"P-value: {p_value_rounded}")
    if p_value < 0.05:
        print("The mean heart disease rate for this ethnicity is significantly different from the overall m
    else:
        print("The mean heart disease rate for this ethnicity is not significantly different from the overa
    print()

# Z-test for Gender
# Iterate through each gender and perform the Z-test
for gender in cleaned_county_df['Gender'].unique():
    heart_disease_gender = cleaned_county_df[cleaned_county_df['Gender'] == gender]['Heart Disease

    # Performing the Z-test
    z_stat = (heart_disease_gender.mean() - mean_heart_disease) / (heart_disease_gender.std() / np.
    p_value = stats.norm.cdf(z_stat) * 2  # two-tailed test

    # Round Z-statistic and P-value to two decimals
    z_stat_rounded = round(z_stat, 2)
    p_value_rounded = round(p_value, 2)

    # Outputting the result
    print(f"Z-test for {gender}:")
    print(f"Z-statistic: {z_stat_rounded}")
    print(f"P-value: {p_value_rounded}")
    if p_value < 0.05:
        print("The mean heart disease rate for this gender is significantly different from the overall mea
    else:
        print("The mean heart disease rate for this gender is not significantly different from the overall
    print()
```

Z-test for AK:
Z-statistic: -1.62
P-value: 0.11
The mean heart disease rate for this state is not significantly different from the overall mean.

Z-test for AL:
Z-statistic: 11.87
P-value: 2.0
The mean heart disease rate for this state is not significantly different from the overall mean.

Z-test for AR:
Z-statistic: 12.6
P-value: 2.0
The mean heart disease rate for this state is not significantly different from the overall mean.

Z-test for AZ:
Z-statistic: -7.56
P-value: 0.0
The mean heart disease rate for this state is significantly different from the overall mean.

Z-test for CA:
Z-statistic: -9.3
P-value: 0.0
The mean heart disease rate for this state is significantly different from the overall mean.

Z-test for CO:
Z-statistic: -19.56
P-value: 0.0
The mean heart disease rate for this state is significantly different from the overall mean.

Z-test for CT:
Z-statistic: -7.8
P-value: 0.0
The mean heart disease rate for this state is significantly different from the overall mean.

Z-test for DC:
Z-statistic: -1.08
P-value: 0.28
The mean heart disease rate for this state is not significantly different from the overall mean.

Z-test for DE:
Z-statistic: -3.04
P-value: 0.0
The mean heart disease rate for this state is significantly different from the overall mean.

Z-test for FL:
Z-statistic: -11.37
P-value: 0.0
The mean heart disease rate for this state is significantly different from the overall mean.

Z-test for GA:
Z-statistic: 5.96
P-value: 2.0
The mean heart disease rate for this state is not significantly different from the overall mean.

Z-test for HI:
Z-statistic: -1.89
P-value: 0.06
The mean heart disease rate for this state is not significantly different from the overall mean.

Z-test for IA:
Z-statistic: -0.69
P-value: 0.49
The mean heart disease rate for this state is not significantly different from the overall mean.

Z-test for ID:
Z-statistic: -8.2
P-value: 0.0
The mean heart disease rate for this state is significantly different from the overall mean.

Z-test for IL:
Z-statistic: -0.52
P-value: 0.6
The mean heart disease rate for this state is not significantly different from the overall mean.

Z-test for IN:
Z-statistic: 1.76
P-value: 1.92
The mean heart disease rate for this state is not significantly different from the overall mean.

Z-test for KS:
Z-statistic: -2.77
P-value: 0.01
The mean heart disease rate for this state is significantly different from the overall mean.

Z-test for KY:
Z-statistic: 11.18
P-value: 2.0
The mean heart disease rate for this state is not significantly different from the overall mean.

Z-test for LA:
Z-statistic: 9.9
P-value: 2.0
The mean heart disease rate for this state is not significantly different from the overall mean.

Z-test for MA:
Z-statistic: -11.18
P-value: 0.0
The mean heart disease rate for this state is significantly different from the overall mean.

Z-test for MD:
Z-statistic: -4.44
P-value: 0.0
The mean heart disease rate for this state is significantly different from the overall mean.

Z-test for ME:
Z-statistic: -2.19
P-value: 0.03
The mean heart disease rate for this state is significantly different from the overall mean.

Z-test for MI:
Z-statistic: 2.14
P-value: 1.97
The mean heart disease rate for this state is not significantly different from the overall mean.

Z-test for MN:
Z-statistic: -14.01
P-value: 0.0
The mean heart disease rate for this state is significantly different from the overall mean.

Z-test for MO:
Z-statistic: 7.69
P-value: 2.0
The mean heart disease rate for this state is not significantly different from the overall mean.

Z-test for MS:
Z-statistic: 18.52
P-value: 2.0
The mean heart disease rate for this state is not significantly different from the overall mean.

Z-test for MT:
Z-statistic: 0.18
P-value: 1.15
The mean heart disease rate for this state is not significantly different from the overall mean.

Z-test for NC:
Z-statistic: -4.3
P-value: 0.0
The mean heart disease rate for this state is significantly different from the overall mean.

Z-test for ND:
Z-statistic: -2.35
P-value: 0.02
The mean heart disease rate for this state is significantly different from the overall mean.

Z-test for NE:
Z-statistic: -6.8
P-value: 0.0
The mean heart disease rate for this state is significantly different from the overall mean.

Z-test for NH:
Z-statistic: -6.24
P-value: 0.0
The mean heart disease rate for this state is significantly different from the overall mean.

Z-test for NJ:
Z-statistic: -6.82
P-value: 0.0
The mean heart disease rate for this state is significantly different from the overall mean.

Z-test for NM:
Z-statistic: -6.32
P-value: 0.0
The mean heart disease rate for this state is significantly different from the overall mean.

Z-test for NV:
Z-statistic: -0.86
P-value: 0.39
The mean heart disease rate for this state is not significantly different from the overall mean.

Z-test for NY:
Z-statistic: -3.92
P-value: 0.0
The mean heart disease rate for this state is significantly different from the overall mean.

Z-test for OH:
Z-statistic: 1.78
P-value: 1.92
The mean heart disease rate for this state is not significantly different from the overall mean.

Z-test for OK:
Z-statistic: 12.53
P-value: 2.0
The mean heart disease rate for this state is not significantly different from the overall mean.

Z-test for OR:
Z-statistic: -13.78
P-value: 0.0
The mean heart disease rate for this state is significantly different from the overall mean.

Z-test for PA:
Z-statistic: -2.78
P-value: 0.01
The mean heart disease rate for this state is significantly different from the overall mean.

Z-test for RI:
Z-statistic: -5.72
P-value: 0.0
The mean heart disease rate for this state is significantly different from the overall mean.

Z-test for SC:
Z-statistic: 0.34
P-value: 1.27
The mean heart disease rate for this state is not significantly different from the overall mean.

Z-test for SD:
Z-statistic: -1.29
P-value: 0.2
The mean heart disease rate for this state is not significantly different from the overall mean.

Z-test for TN:
Z-statistic: 10.22
P-value: 2.0
The mean heart disease rate for this state is not significantly different from the overall mean.

Z-test for TX:
Z-statistic: 3.04
P-value: 2.0
The mean heart disease rate for this state is not significantly different from the overall mean.

Z-test for UT:
Z-statistic: -9.95
P-value: 0.0
The mean heart disease rate for this state is significantly different from the overall mean.

Z-test for VA:
Z-statistic: -3.89
P-value: 0.0
The mean heart disease rate for this state is significantly different from the overall mean.

Z-test for VT:
Z-statistic: -2.24
P-value: 0.03
The mean heart disease rate for this state is significantly different from the overall mean.

Z-test for WA:
Z-statistic: -9.59
P-value: 0.0
The mean heart disease rate for this state is significantly different from the overall mean.

Z-test for WI:
Z-statistic: -5.06
P-value: 0.0
The mean heart disease rate for this state is significantly different from the overall mean.

Z-test for WV:
Z-statistic: 5.87
P-value: 2.0
The mean heart disease rate for this state is not significantly different from the overall mean.

Z-test for WY:
Z-statistic: -1.04
P-value: 0.3
The mean heart disease rate for this state is not significantly different from the overall mean.

Z-test for White:
Z-statistic: 14.14
P-value: 2.0
The mean heart disease rate for this ethnicity is not significantly different from the overall mean.

Z-test for Black:
Z-statistic: 37.39
P-value: 2.0
The mean heart disease rate for this ethnicity is not significantly different from the overall mean.

Z-test for Hispanic:
Z-statistic: -58.1
P-value: 0.0
The mean heart disease rate for this ethnicity is significantly different from the overall mean.

Z-test for American Indian and Alaskan Native:
Z-statistic: 9.97
P-value: 2.0
The mean heart disease rate for this ethnicity is not significantly different from the overall mean.

Z-test for Asian and Pacific Islander:
Z-statistic: -81.73
P-value: 0.0
The mean heart disease rate for this ethnicity is significantly different from the overall mean.

Z-test for Male:
Z-statistic: 39.28
P-value: 2.0
The mean heart disease rate for this gender is not significantly different from the overall mean.

Z-test for Female:
Z-statistic: -56.6
P-value: 0.0
The mean heart disease rate for this gender is significantly different from the overall mean.

Model Selection and Analysis

Linear Regression and Clustering

In [40]:
```
import statsmodels.api as sm
from statsmodels.stats.outliers_influence import variance_inflation_factor

from sklearn.preprocessing import StandardScaler
from sklearn.cluster import KMeans
```

In [41]:
```
# Create a copy of cleaned_county_df for regression analysis
gender_regression_df = cleaned_county_df.copy()

# Convert 'Gender' to dummy variables
# Now 'Gender' will be encoded as 1 for Male and 0 for Female
gender_regression_df['Gender'] = pd.get_dummies(gender_regression_df['Gender'], drop_first=True)

# Define the independent variable (X) and dependent variable (Y)
x_gender = gender_regression_df['Gender']
y_heart = gender_regression_df['Heart Disease per 100k']

# Add a constant term to the independent variable
x_gender = sm.add_constant(x_gender)

# Fit the regression model
gender_regression_model = sm.OLS(y_heart, x_gender).fit()

# Print the summary of the regression model
print(gender_regression_model.summary())

# Notes for the presentation
# R-Squared shows 23.6% of variability of the heart disease is explained by gender
# F statistic 4167 the model is significantly better fit than a model with no predictors
# prob of F statistics is close to 0 which proves that gender is related to heart disease
# Log-likelihood is for model comparison. Higher is better
# AIC, BIC are for other model comparisons. The lower is better

# males = 1
# females 0
# Const coef: this is to show when all values are 0 (Gender = 0 = female) which shows female average
# Gender Coef: males have a higher disease mortality rate by 139.94 units
# t stat: shows gender is statistically significant
# P>|t|: shows the p-values are close to .00 so are significant
# omnibus: this is small so it is normally distributed
# prob(omnibus): higher values show it is normal
# Durbin-Watson: Since it is not close to two this shows significant autocorrelation
# Cond. No. : This measures multicollinearity. Values greater than 30 indicate multicollinearity

# MODEL AND DATA IS SIGNIFICANT
```

```
                            OLS Regression Results
==============================================================================
Dep. Variable:     Heart Disease per 100k   R-squared:                       0.236
Model:                            OLS   Adj. R-squared:                  0.236
Method:                 Least Squares   F-statistic:                     4167.
Date:                Sat, 24 Feb 2024   Prob (F-statistic):               0.00
Time:                        18:18:23   Log-Likelihood:                -84329.
No. Observations:               13484   AIC:                         1.687e+05
Df Residuals:                   13482   BIC:                         1.687e+05
Df Model:                           1
Covariance Type:            nonrobust
==============================================================================
                 coef    std err          t      P>|t|      [0.025      0.975]
------------------------------------------------------------------------------
const        275.9017      1.545    178.542      0.000     272.873     278.931
Gender       139.9395      2.168     64.550      0.000     135.690     144.189
==============================================================================
Omnibus:                        0.196   Durbin-Watson:                   0.726
Prob(Omnibus):                  0.907   Jarque-Bera (JB):                0.217
Skew:                          -0.005   Prob(JB):                        0.897
Kurtosis:                       2.983   Cond. No.                         2.64
==============================================================================

Notes:
[1] Standard Errors assume that the covariance matrix of the errors is correctly specified.
```

```
c:\Users\User\anaconda3\lib\site-packages\statsmodels\tsa\tsatools.py:142: FutureWarning: In a futur
e version of pandas all arguments of concat except for the argument 'objs' will be keyword-only
  x = pd.concat(x[::order], 1)
```

In [42]:

```
# Create a copy of cleaned_county_df for regression analysis
ethnicity_regression_df = cleaned_county_df.copy()

# One-hot encode the 'Ethnicity' column
ethnicity_dummies = pd.get_dummies(ethnicity_regression_df['Ethnicity'])

# Concatenate the dummy variables with the original DataFrame
ethnicity_regression_dummies = pd.concat([ethnicity_regression_df, ethnicity_dummies], axis=1)

# Define the independent variables (X) and dependent variable (Y)
x_ethnicity = ethnicity_regression_dummies[['White', 'Black', 'Hispanic', 'American Indian and Alaskan Na
y_heart = ethnicity_regression_dummies['Heart Disease per 100k']

# Add a constant term to the independent variables
x_ethnicity = sm.add_constant(x_ethnicity)

# Fit the regression model
ethnicity_regression_model = sm.OLS(y_heart, x_ethnicity).fit()

# Print the summary of the regression model
print(ethnicity_regression_model.summary())

# R-Squared: 28% of the data is explained by ethnicity
# F statistic: 1329 shows the model is significant
# Prob of F statistics: is close to 0 which shows it's significant

# Log-likelihood: is for model comparison. Higher is better
# AIC, BIC: are for other model comparisons. The lower is better

# Const coef: the average when no one has ethnicity (the default is assumed white)
# Rest of Coef: average heart disease for each ethnicity
```

```
# t stat: larger absolute values indicate greater evidence against the null hypothesis
# P>|t|: no significance since close to 1

# MODEL is significant but the data is not
```

```
                            OLS Regression Results
==============================================================================
Dep. Variable:      Heart Disease per 100k   R-squared:                       0.340
Model:                             OLS   Adj. R-squared:                  0.340
Method:                  Least Squares   F-statistic:                     1737.
Date:                 Sat, 24 Feb 2024   Prob (F-statistic):               0.00
Time:                         18:18:23   Log-Likelihood:                -83342.
No. Observations:                13484   AIC:                         1.667e+05
Df Residuals:                    13479   BIC:                         1.667e+05
Df Model:                            4
Covariance Type:            nonrobust
================================================================================================
                                   coef    std err          t      P>|t|      [0.025      0.975]
------------------------------------------------------------------------------------------------
const                          265.1469      1.126    235.436      0.000     262.939     267.354
White                          103.0378      1.653     62.343      0.000      99.798     106.277
Black                          163.3917      1.976     82.673      0.000     159.518     167.266
Hispanic                       -47.6185      2.408    -19.779      0.000     -52.338     -42.899
American Indian and Alaskan Native  138.5605      3.845     36.036      0.000     131.024     146.097
Asian and Pacific Islander         -92.2246      3.092    -29.824      0.000     -98.286     -86.163
==============================================================================
Omnibus:                      570.105   Durbin-Watson:                   0.821
Prob(Omnibus):                  0.000   Jarque-Bera (JB):              644.453
Skew:                           0.534   Prob(JB):                    1.14e-140
Kurtosis:                       3.081   Cond. No.                     1.44e+15
==============================================================================

Notes:
[1] Standard Errors assume that the covariance matrix of the errors is correctly specified.
[2] The smallest eigenvalue is 8.69e-27. This might indicate that there are
strong multicollinearity problems or that the design matrix is singular.
```

```
c:\Users\User\anaconda3\lib\site-packages\statsmodels\tsa\tsatools.py:142: FutureWarning: In a futur
e version of pandas all arguments of concat except for the argument 'objs' will be keyword-only
  x = pd.concat(x[::order], 1)
```

In [43]:
```
# Make a copy of the dummy data without the 'White' column to remove multicollinearity
ethnicity_regression_dummies_noCol = ethnicity_regression_dummies.drop(columns=['White'])

# Define the predictor variables after removing 'White' to address multicollinearity
x_no_white = ethnicity_regression_dummies_noCol[['Black', 'Hispanic', 'American Indian and Alaskan Nati

# Define the target variable
y_heart = ethnicity_regression_dummies['Heart Disease per 100k']

# Calculate Variance Inflation Factor (VIF) to detect multicollinearity
vif_data = sm.add_constant(x_no_white)
vif = pd.DataFrame()
vif["Variable"] = vif_data.columns
vif["VIF"] = [variance_inflation_factor(vif_data.values, i) for i in range(vif_data.shape[1])]

# Identify variables with VIF greater than 10 (common threshold indicating multicollinearity)
high_vif_variables = vif[vif["VIF"] > 10]["Variable"].tolist()
```

```
# Drop high VIF variables from the predictor variables
x_no_white = x_no_white.drop(columns=high_vif_variables)
x_no_white = sm.add_constant(x_no_white)

# Fit Ordinary Least Squares (OLS) regression model using the updated predictor variables
# and the target variable y_heart
model = sm.OLS(y_heart, x_no_white).fit()

# Print the summary of the regression model
print("\nModel Summary After Addressing Multicollinearity:")
print(model.summary())

# R-Squared: 31% of the data is explained by ethnicity
# F statistic: 1529 shows the model is significant
# Prob of F statistics: is close to 0 which shows it's significant

# Log-likelihood (negative does not matter): is for model comparison. Higher is better
# AIC, BIC: are for other model comparisons. The lower is better

# Const coef: the average when no one has ethnicity (the default is assumed white)
# black coef: higher than white
# hispanic coef: lower than white
# indian coef: higher than white
# asian coef: worse than white
# t stat: larger absolute values indicate greater evidence against the null hypothesis
# P>|t|: significance since close to .00

# MODEL AND DATA IS SIGNIFICANT
```

```
Model Summary After Addressing Multicollinearity:
                            OLS Regression Results
==============================================================================
Dep. Variable:     Heart Disease per 100k   R-squared:                       0.340
Model:                            OLS   Adj. R-squared:                  0.340
Method:                 Least Squares   F-statistic:                     1737.
Date:                Sat, 24 Feb 2024   Prob (F-statistic):               0.00
Time:                        18:18:23   Log-Likelihood:                -83342.
No. Observations:               13484   AIC:                         1.667e+05
Df Residuals:                   13479   BIC:                         1.667e+05
Df Model:                           4
Covariance Type:            nonrobust
================================================================================================
=====
                                   coef    std err          t      P>|t|      [0.025      0.975]
------------------------------------------------------------------------------------------------
---
const                          368.1847      1.482    248.516      0.000     365.281     371.089
Black                           60.3540      2.480     24.334      0.000      55.492      65.216
Hispanic                      -150.6563      2.998    -50.256      0.000    -156.532    -144.780
American Indian and Alaskan Native    35.5227      4.740      7.494      0.000      26.231      44.814
Asian and Pacific Islander       -195.2623      3.826    -51.039      0.000    -202.761    -187.763
==============================================================================
Omnibus:                      570.105   Durbin-Watson:                   0.821
Prob(Omnibus):                  0.000   Jarque-Bera (JB):              644.453
Skew:                           0.534   Prob(JB):                    1.14e-140
Kurtosis:                       3.081   Cond. No.                         5.19
==============================================================================

Notes:
[1] Standard Errors assume that the covariance matrix of the errors is correctly specified.
```

```
c:\Users\User\anaconda3\lib\site-packages\statsmodels\tsa\tsatools.py:142: FutureWarning: In a futur
e version of pandas all arguments of concat except for the argument 'objs' will be keyword-only
  x = pd.concat(x[::order], 1)
```

In [44]:

```
# Make a copy of the original dataframe
state_regression_df = cleaned_county_df.copy()

# Create hot encoded data, dropping the first state (AK)
state_regression_encode = pd.get_dummies(state_regression_df, columns=['State'], drop_first=True)

# Define predictor variables (hot encoded states) and target variable (heart disease rate)
x_hot_encoded_state = state_regression_encode.drop(['Heart Disease per 100k', 'County', 'Gender', 'Ethr
y_heart = state_regression_encode['Heart Disease per 100k']

# Calculate Variance Inflation Factor (VIF) to detect multicollinearity
vif_data_state = sm.add_constant(x_hot_encoded_state)
vif_state = pd.DataFrame()
vif_state["Variable"] = vif_data_state.columns
vif_state["VIF"] = [variance_inflation_factor(vif_data_state.values, i) for i in range(vif_data_state.shape

# Identify variables with VIF greater than 10 (common threshold indicating multicollinearity)
high_vif_variables = vif_state[vif_state["VIF"] > 10]["Variable"].tolist()

# Remove constant from high VIF variables list
high_vif_variables.remove('const')

# Drop variables with high VIF
x_hot_encoded_state = x_hot_encoded_state.drop(high_vif_variables, axis=1)

# Add constant
x_hot_encoded_state = sm.add_constant(x_hot_encoded_state)

# Fit Ordinary Least Squares (OLS) regression model using the updated predictor variables and the tar
model = sm.OLS(y_heart, x_hot_encoded_state).fit()

# Print the summary of the regression model
print("\nModel Summary After Addressing Multicollinearity:")
print(model.summary())


# R-Squared: 16% of the data is explained by the ethnicity
# F statistic: 54 shows the model is significant
# Prob of F statistics: is close to 0 which shows it's significant

# Log-likelihood (negative does not matter): is for model comparison. Higher is better
# AIC, BIC: are for other model comparisons. The lower is better

# Const coef: the average when no one has the state (the default is assumed Alaska)
# t stat: larger absolute values indicate greater evidence against the null hypothesis
# P>|t|: Depends on the state, some of them are not significant. These would be the states to study

# MODEL AND DATA ARE SIGNIFICANT (depending on state)

# Based on the chi-square test, these results for significant contribution to heart disease mortality
# can be due to random chance. It is best to examine the counties that do not have significance if you
# deep dive more and go under the assumption that this is not due to random chance.

# Texas and Georgia were removed due to high VIF.
```

```
c:\Users\User\anaconda3\lib\site-packages\statsmodels\tsa\tsatools.py:142: FutureWarning: In a futur
e version of pandas all arguments of concat except for the argument 'objs' will be keyword-only
  x = pd.concat(x[::order], 1)
```

Model Summary After Addressing Multicollinearity:

OLS Regression Results

Dep. Variable:	Heart Disease per 100k	R-squared:	0.165
Model:	OLS	Adj. R-squared:	0.162
Method:	Least Squares	F-statistic:	55.22
Date:	Sat, 24 Feb 2024	Prob (F-statistic):	0.00
Time:	18:18:24	Log-Likelihood:	-84931.
No. Observations:	13484	AIC:	1.700e+05
Df Residuals:	13435	BIC:	1.703e+05
Df Model:	48		
Covariance Type:	nonrobust		

	coef	std err	t	P>|t|	[0.025	0.975]
const	364.7796	2.867	127.256	0.000	359.161	370.398
State_AL	88.6038	8.267	10.717	0.000	72.398	104.809
State_AR	88.5869	8.331	10.633	0.000	72.257	104.917
State_AZ	-90.5651	11.869	-7.630	0.000	-113.830	-67.300
State_CA	-66.5237	6.399	-10.396	0.000	-79.066	-53.981
State_CO	-116.3073	8.098	-14.363	0.000	-132.180	-100.435
State_CT	-115.3390	16.726	-6.896	0.000	-148.124	-82.554
State_DC	-94.7171	46.696	-2.028	0.043	-186.248	-3.186
State_DE	-102.2251	28.252	-3.618	0.000	-157.602	-46.848
State_FL	-82.7003	6.882	-12.017	0.000	-96.189	-69.211
State_HI	-52.1943	22.789	-2.290	0.022	-96.865	-7.524
State_IA	-22.6363	8.649	-2.617	0.009	-39.589	-5.683
State_ID	-85.7739	12.227	-7.015	0.000	-109.741	-61.807
State_IL	-20.9818	7.063	-2.970	0.003	-34.827	-7.136
State_IN	-5.6106	7.507	-0.747	0.455	-20.326	9.104
State_KS	-35.5576	7.984	-4.454	0.000	-51.207	-19.908
State_KY	61.3907	7.507	8.178	0.000	46.676	76.106
State_LA	76.7923	8.410	9.131	0.000	60.307	93.277
State_MA	-136.2924	13.896	-9.808	0.000	-163.530	-109.055
State_MD	-70.5372	11.104	-6.352	0.000	-92.303	-48.771
State_ME	-50.2948	23.127	-2.175	0.030	-95.626	-4.963
State_MI	-1.7622	7.561	-0.233	0.816	-16.583	13.059
State_MN	-107.0522	8.619	-12.420	0.000	-123.948	-90.157
State_MO	39.4462	7.589	5.198	0.000	24.571	54.321
State_MS	121.7279	7.782	15.642	0.000	106.474	136.982
State_MT	-15.8614	11.391	-1.393	0.164	-38.189	6.466
State_NC	-44.9266	6.413	-7.005	0.000	-57.498	-32.356
State_ND	-42.9216	12.420	-3.456	0.001	-67.267	-18.577
State_NE	-62.2146	9.282	-6.703	0.000	-80.408	-44.021
State_NH	-124.1877	21.861	-5.681	0.000	-167.039	-81.337
State_NJ	-85.2237	10.567	-8.065	0.000	-105.936	-64.511
State_NM	-67.7342	10.057	-6.735	0.000	-87.448	-48.020
State_NV	-29.6679	12.420	-2.389	0.017	-54.013	-5.323
State_NY	-42.7607	7.386	-5.789	0.000	-57.239	-28.282
State_OH	-5.9818	7.056	-0.848	0.397	-19.813	7.850
State_OK	72.8691	6.954	10.479	0.000	59.239	86.499
State_OR	-117.0711	9.775	-11.977	0.000	-136.231	-97.911
State_PA	-38.1785	7.626	-5.006	0.000	-53.126	-23.231
State_RI	-109.8884	22.789	-4.822	0.000	-154.559	-65.218
State_SC	-14.3324	9.100	-1.575	0.115	-32.169	3.504
State_SD	-31.6919	10.970	-2.889	0.004	-53.194	-10.190
State_TN	56.9666	7.353	7.747	0.000	42.553	71.380
State_UT	-98.2617	12.227	-8.036	0.000	-122.229	-74.295
State_VA	-38.7069	6.200	-6.243	0.000	-50.860	-26.554
State_VT	-50.6996	24.238	-2.092	0.036	-98.210	-3.189

```
State_WA      -91.4170      8.708    -10.497      0.000    -108.487     -74.347
State_WI      -58.0087      8.963     -6.472      0.000     -75.577     -40.441
State_WV       30.1527     10.596      2.846      0.004       9.383      50.923
State_WY      -31.8337     15.590     -2.042      0.041     -62.393      -1.274
==============================================================================
Omnibus:                      137.350   Durbin-Watson:                   0.697
Prob(Omnibus):                  0.000   Jarque-Bera (JB):              131.983
Skew:                           0.215   Prob(JB):                     2.19e-29
Kurtosis:                       2.775   Cond. No.                         41.6
==============================================================================

Notes:
[1] Standard Errors assume that the covariance matrix of the errors is correctly specified.
```

In [45]:

```python
# Define states of interest
states_of_interest = ['AZ', 'CA', 'CO', 'CT', 'DE', 'FL', 'IA', 'ID', 'LA', 'MA',
                      'MD', 'ME', 'MN', 'NC', 'ND', 'NE', 'NH', 'NJ', 'NM', 'NV',
                      'NY', 'OR', 'PA', 'RI', 'UT', 'VA', 'VT', 'WA', 'WI']

# Initialize dictionaries to store coefficients and p-values
coefficients = {}
p_values = {}

# Extract coefficients and p-values from Table 1
table_data = model.summary().tables[1].data
for row in table_data[2:]:  # Skip the first two rows as they contain headers
    state = row[0].split('_')[1]  # Extract state abbreviation
    if state in states_of_interest:
        coef = float(row[1])  # Extract coefficient value
        p_val = float(row[4])  # Extract p-value
        coefficients[state] = coef
        p_values[state] = p_val

# Print coefficients and p-values for the specified states
for state in states_of_interest:
    print(f"State: {state}, Coefficient: {coefficients[state]}, P-value: {p_values[state]}")

# Comments:
# The code extracts coefficients and p-values from Table 1 of the regression model summary and prints
# The specified states of interest are those in the list 'states_of_interest'.
# Coefficients are stored in the 'coefficients' dictionary, and p-values are stored in the 'p_values' dictio
# The code ensures that only coefficients and p-values for the specified states are extracted and print
# The loop iterates through the table data, skipping the first two rows (which contain headers), and spl
# It then checks if the state is in the list of states of interest and extracts the coefficient and p-value
```

```
State: AZ, Coefficient: -90.5651, P-value: 0.0
State: CA, Coefficient: -66.5237, P-value: 0.0
State: CO, Coefficient: -116.3073, P-value: 0.0
State: CT, Coefficient: -115.339, P-value: 0.0
State: DE, Coefficient: -102.2251, P-value: 0.0
State: FL, Coefficient: -82.7003, P-value: 0.0
State: IA, Coefficient: -22.6363, P-value: 0.009
State: ID, Coefficient: -85.7739, P-value: 0.0
State: LA, Coefficient: 76.7923, P-value: 0.0
State: MA, Coefficient: -136.2924, P-value: 0.0
State: MD, Coefficient: -70.5372, P-value: 0.0
State: ME, Coefficient: -50.2948, P-value: 0.03
State: MN, Coefficient: -107.0522, P-value: 0.0
State: NC, Coefficient: -44.9266, P-value: 0.0
State: ND, Coefficient: -42.9216, P-value: 0.001
State: NE, Coefficient: -62.2146, P-value: 0.0
State: NH, Coefficient: -124.1877, P-value: 0.0
State: NJ, Coefficient: -85.2237, P-value: 0.0
State: NM, Coefficient: -67.7342, P-value: 0.0
State: NV, Coefficient: -29.6679, P-value: 0.017
State: NY, Coefficient: -42.7607, P-value: 0.0
State: OR, Coefficient: -117.0711, P-value: 0.0
State: PA, Coefficient: -38.1785, P-value: 0.0
State: RI, Coefficient: -109.8884, P-value: 0.0
State: UT, Coefficient: -98.2617, P-value: 0.0
State: VA, Coefficient: -38.7069, P-value: 0.0
State: VT, Coefficient: -50.6996, P-value: 0.036
State: WA, Coefficient: -91.417, P-value: 0.0
State: WI, Coefficient: -58.0087, P-value: 0.0
```

In [46]:

```
# Drop the constant column from x_no_white as it's not needed in this context
default_white_race = x_no_white.drop(columns='const')

# Combine gender and race with heart disease data
combined = pd.concat([gender_regression_df[['Gender', 'Heart Disease per 100k']], default_white_race],

# Separate predictors (x_comb) and target (y_comb)
x_comb = combined.drop('Heart Disease per 100k', axis=1)
y_comb = combined['Heart Disease per 100k']

# Add constant for the intercept term
x_comb = sm.add_constant(x_comb)

# Fit Ordinary Least Squares (OLS) regression model
model = sm.OLS(y_comb, x_comb).fit()

# Print model summary
print(model.summary())


# R-Squared: 58% of the data is explained by ethnicity
# F statistic: 3816 show model is significant
# prob of F statistics: is close to 0 which shows it significant

# Log-likelohood(neg does not matter): is for model comparison. Higher is better
# AIC, BIC: are for other model comparisons. the lower is better

# Const coef: the average when someone is a white female (all other refs are 0)
# Gender coef: being male increases 142 units
# black coef: being black incerease by 60
```

```
# hispanic coef: lowers by 155
# indian coef: higher by 28
# asian coef: being asian lowers by 196
# t stat: larger absolutes values indicate greater evidence against the null hypothesis
# P>|t|: significance since close to .00

# MODEL AND DATA IS SIGNIFICANT
```

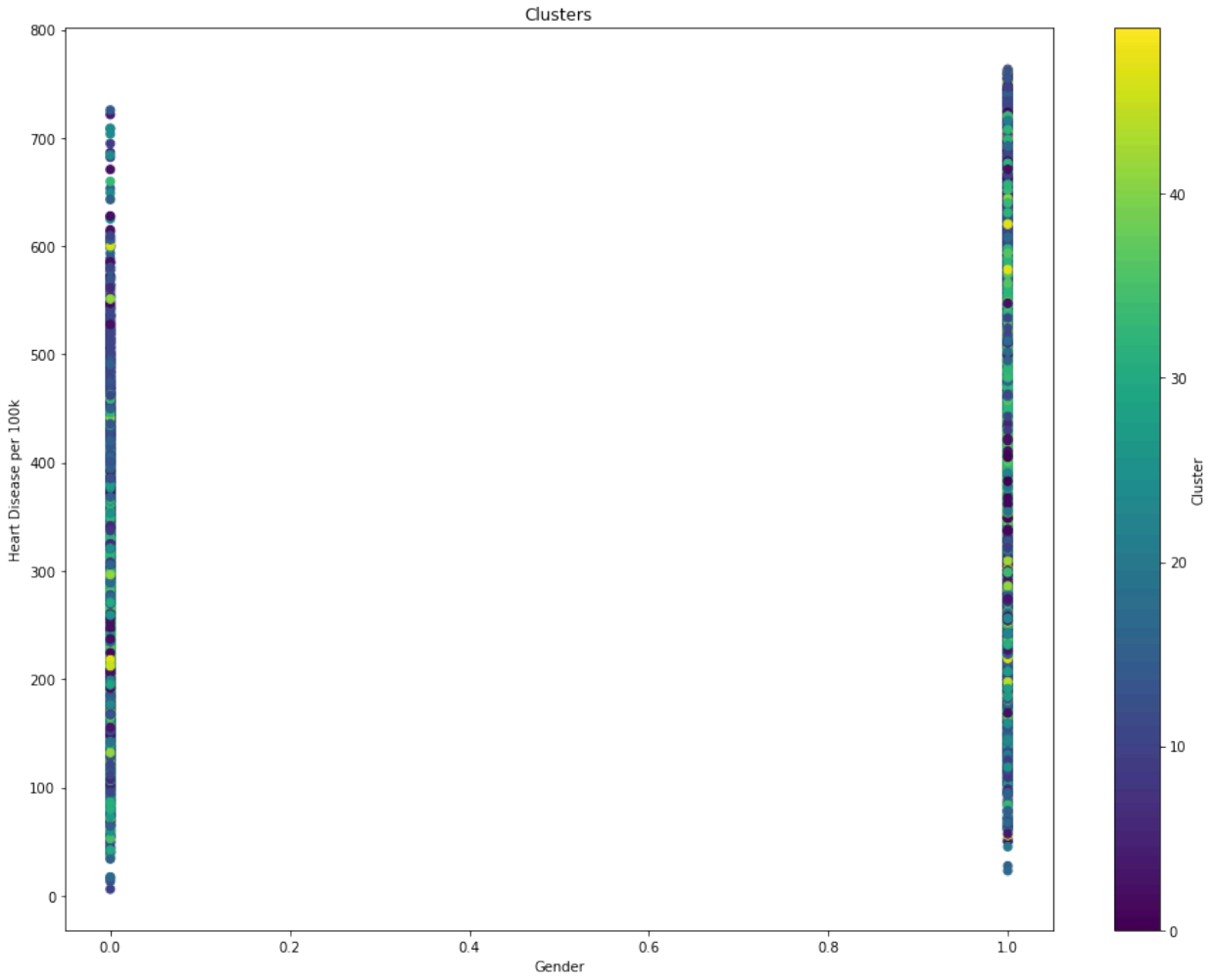
```
                            OLS Regression Results
==============================================================================
Dep. Variable:     Heart Disease per 100k   R-squared:                       0.586
Model:                                OLS   Adj. R-squared:                  0.586
Method:                     Least Squares   F-statistic:                     3816.
Date:                    Sat, 24 Feb 2024   Prob (F-statistic):               0.00
Time:                            18:18:24   Log-Likelihood:                -80198.
No. Observations:                   13484   AIC:                         1.604e+05
Df Residuals:                       13478   BIC:                         1.605e+05
Df Model:                               5
Covariance Type:                nonrobust
================================================================================================
                                   coef    std err          t      P>|t|      [0.025      0.975]
------------------------------------------------------------------------------------------------
const                          296.8629      1.419    209.274      0.000     294.082     299.643
Gender                         142.8956      1.597     89.485      0.000     139.766     146.026
Black                           60.2072      1.964     30.648      0.000      56.357      64.058
Hispanic                      -155.7819      2.375    -65.589      0.000    -160.437    -151.126
American Indian and Alaskan Native    28.7282      3.755      7.650      0.000      21.367      36.089
Asian and Pacific Islander      -196.9472      3.030    -64.994      0.000    -202.887    -191.008
==============================================================================
Omnibus:                      518.354   Durbin-Watson:                   1.229
Prob(Omnibus):                  0.000   Jarque-Bera (JB):              753.898
Skew:                           0.378   Prob(JB):                    1.96e-164
Kurtosis:                       3.878   Cond. No.                         5.87
==============================================================================

Notes:
[1] Standard Errors assume that the covariance matrix of the errors is correctly specified.
```

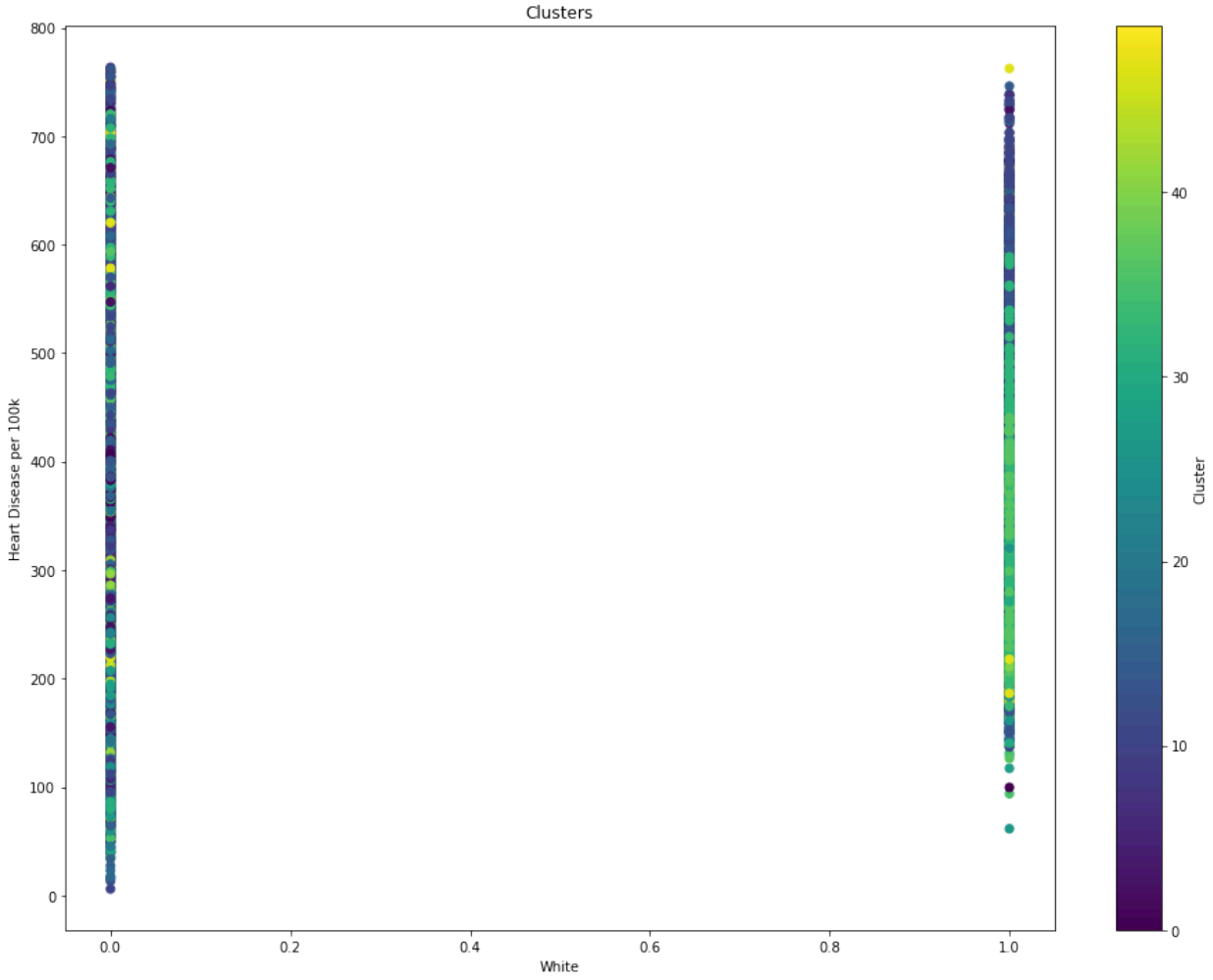
```
c:\Users\User\anaconda3\lib\site-packages\statsmodels\tsa\tsatools.py:142: FutureWarning: In a futur
e version of pandas all arguments of concat except for the argument 'objs' will be keyword-only
  x = pd.concat(x[::order], 1)
```

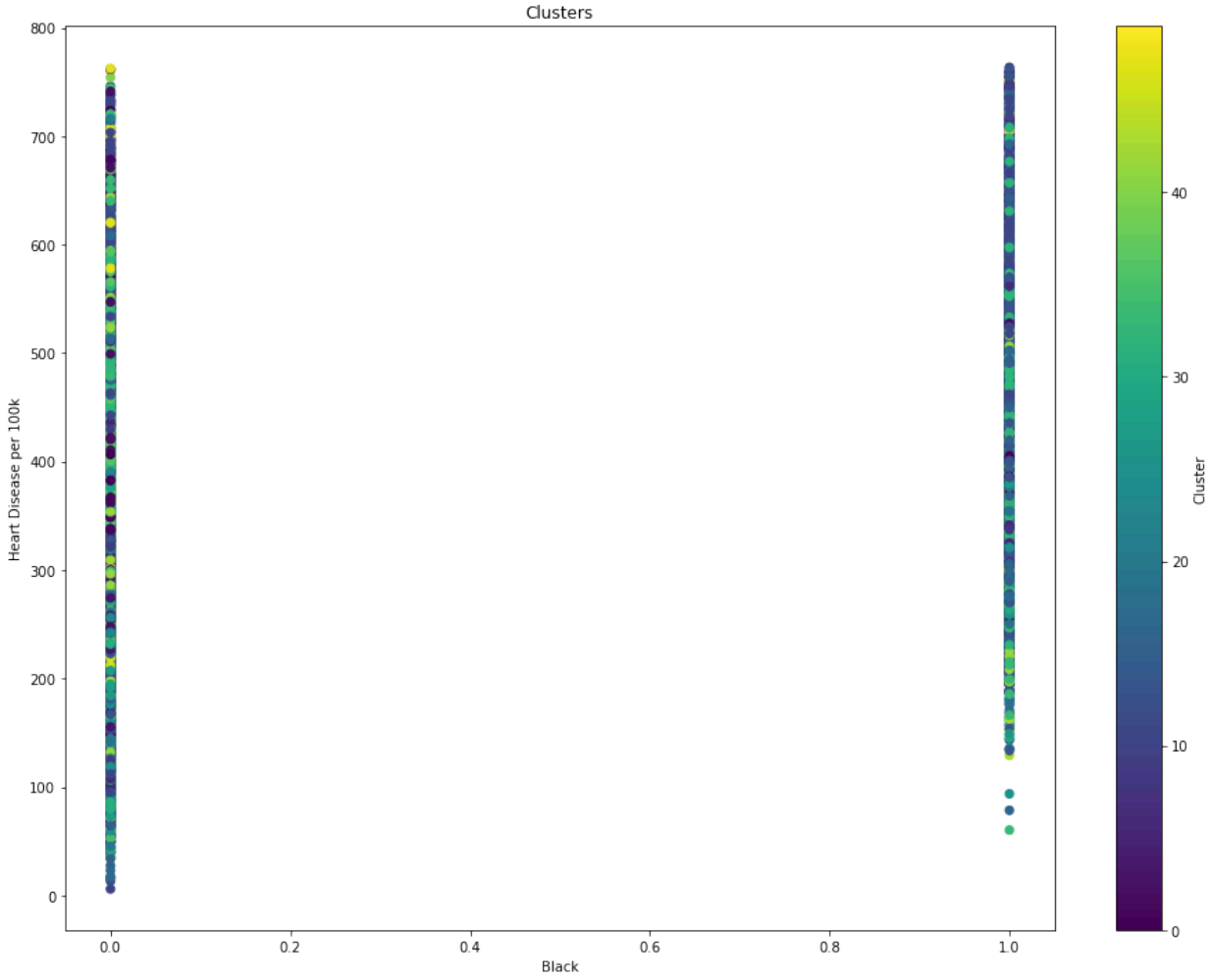
In [47]:
```
# Extracting necessary data
all_races = ethnicity_regression_dummies.copy()
all_races_only = all_races[['Black', 'Hispanic', 'American Indian and Alaskan Native', 'Asian and Pacific Isl

gender_bi = gender_regression_df.copy()
gender_bi = gender_bi[['Gender', 'Heart Disease per 100k']]

all_state = pd.get_dummies(state_regression_df, columns=['State'])
all_state_only = all_state.drop(['Heart Disease per 100k', 'County', 'Gender', 'Ethnicity'], axis=1)

# Combine all data for clustering
combined_cluster_no_state = combined.copy()
default_state = x_hot_encoded_state.drop(columns='const')
combined_cluster = pd.concat([all_races_only, gender_bi, all_state_only], axis=1)

# Standardize the features
scaler = StandardScaler()
```

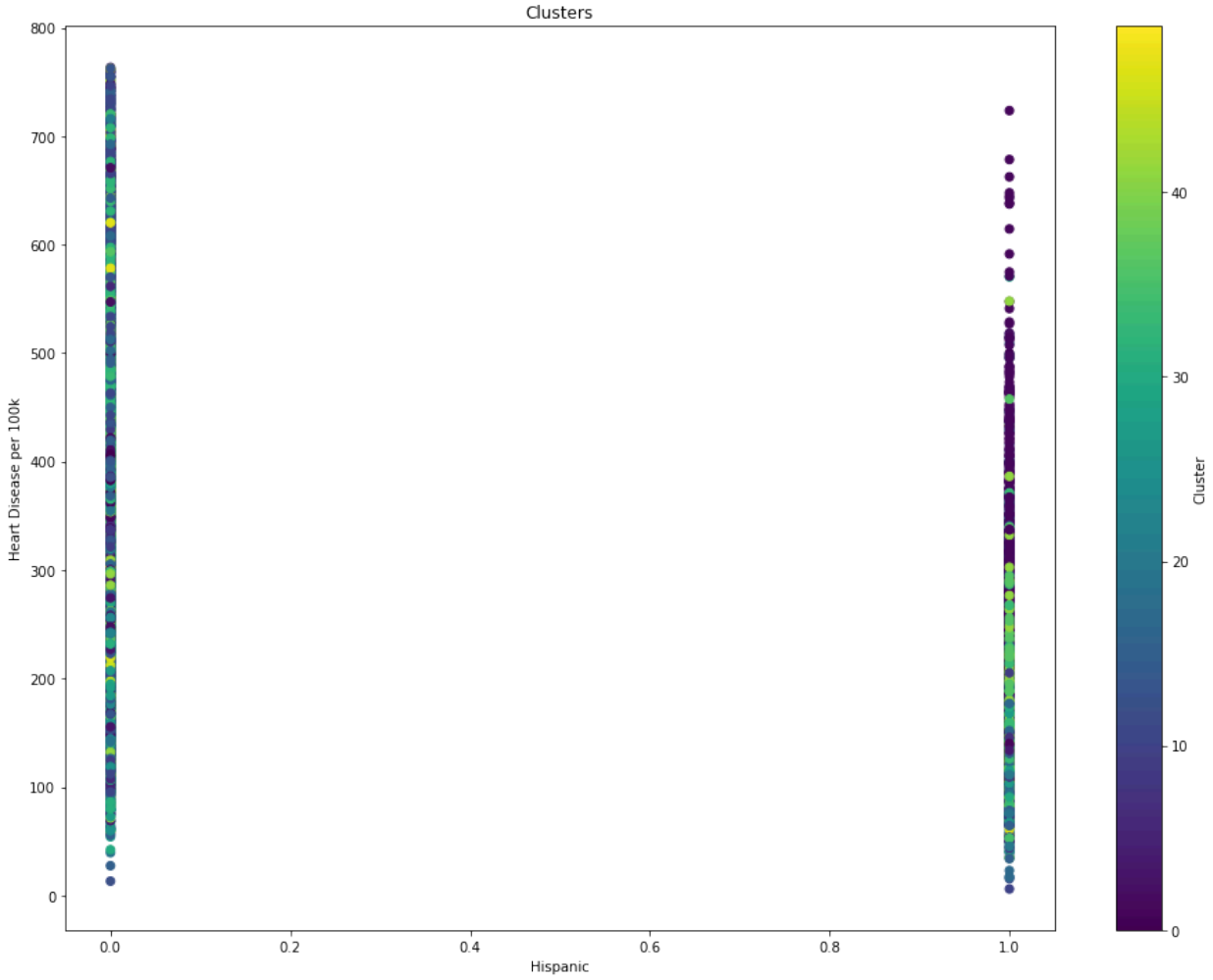
```
combined_cluster_scaled = scaler.fit_transform(combined_cluster)

# Choose the number of clusters
num_clusters = 50

# Initialize and fit the KMeans model
kmeans = KMeans(n_clusters=num_clusters, random_state=42)
kmeans.fit(combined_cluster_scaled)

# Get cluster labels for each data point
cluster_labels = kmeans.labels_

# Add cluster labels to the DataFrame
combined_cluster['Cluster'] = cluster_labels

# Get centroids
centroids = kmeans.cluster_centers_

# Create a DataFrame to display centroid values
centroid_df = pd.DataFrame(centroids, columns=combined_cluster.columns[:-1])  # Exclude the 'Cluster' c

# Display centroid values
#print("Centroid Values for Each Cluster:")
#print(centroid_df)

# Scatter plot for Gender
plt.figure(figsize=(16, 12))
plt.scatter(combined_cluster['Gender'], combined_cluster['Heart Disease per 100k'], c=cluster_labels, cm
plt.title('Clusters')
plt.xlabel('Gender')
plt.ylabel('Heart Disease per 100k')
plt.colorbar(label='Cluster')
plt.show()

# Scatter plot for White race
plt.figure(figsize=(16, 12))
plt.scatter(combined_cluster['White'], combined_cluster['Heart Disease per 100k'], c=cluster_labels, cma
plt.title('Clusters')
plt.xlabel('White')
plt.ylabel('Heart Disease per 100k')
plt.colorbar(label='Cluster')
plt.show()

# Scatter plot for Black race
plt.figure(figsize=(16, 12))
plt.scatter(combined_cluster['Black'], combined_cluster['Heart Disease per 100k'], c=cluster_labels, cmap
plt.title('Clusters')
plt.xlabel('Black')
plt.ylabel('Heart Disease per 100k')
plt.colorbar(label='Cluster')
plt.show()

# Scatter plot for Hispanic race
plt.figure(figsize=(16, 12))
plt.scatter(combined_cluster['Hispanic'], combined_cluster['Heart Disease per 100k'], c=cluster_labels, cm
plt.title('Clusters')
plt.xlabel('Hispanic')
plt.ylabel('Heart Disease per 100k')
plt.colorbar(label='Cluster')
plt.show()
```

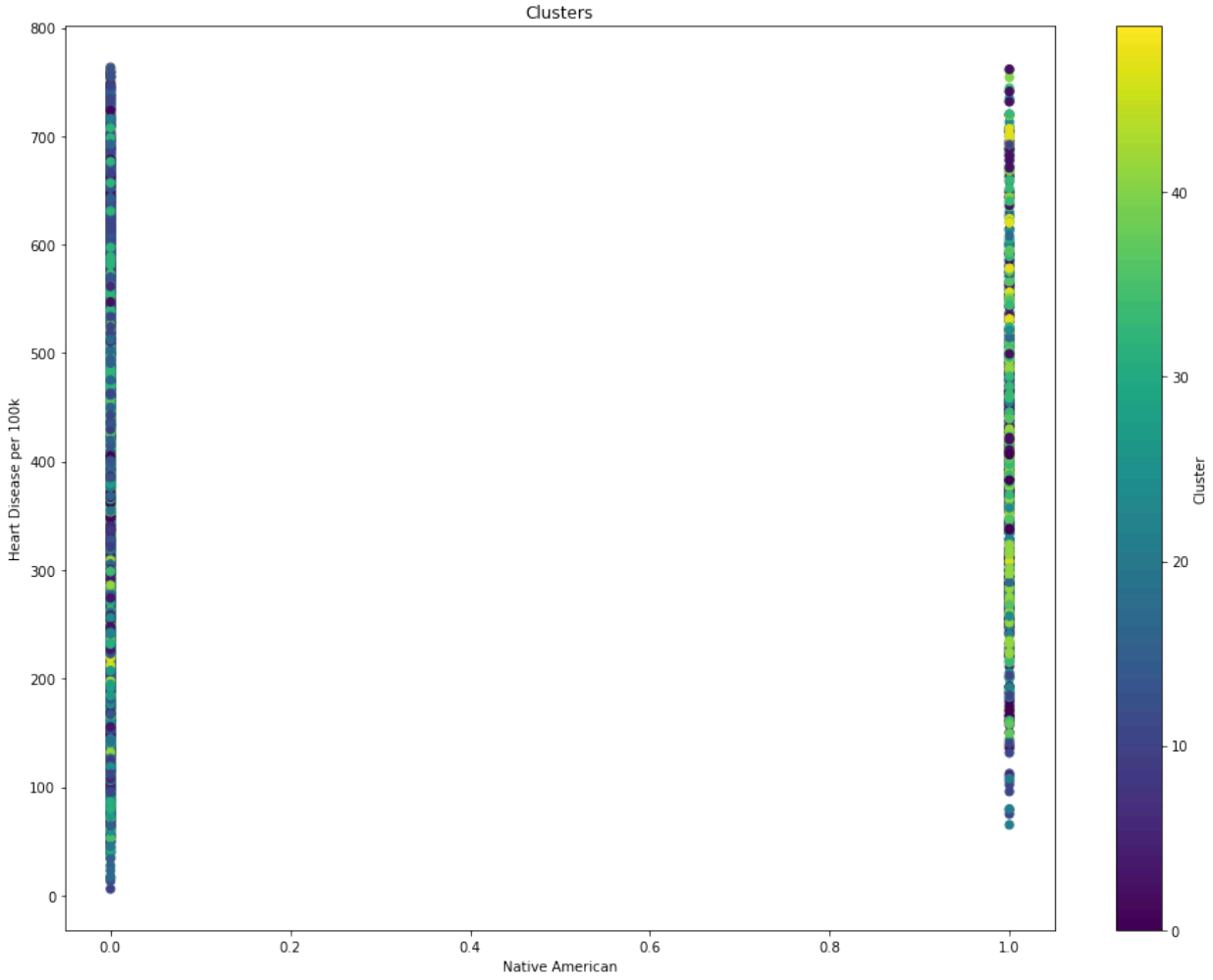
```
# Scatter plot for American Indian and Alaskan Native race
plt.figure(figsize=(16, 12))
plt.scatter(combined_cluster['American Indian and Alaskan Native'], combined_cluster['Heart Disease per
plt.title('Clusters')
plt.xlabel('Native American')
plt.ylabel('Heart Disease per 100k')
plt.colorbar(label='Cluster')
plt.show()

# Scatter plot for Asian and Pacific Islander race
plt.figure(figsize=(16, 12))
plt.scatter(combined_cluster['Asian and Pacific Islander'], combined_cluster['Heart Disease per 100k'], c=
plt.title('Clusters')
plt.xlabel('Asian')
plt.ylabel('Heart Disease per 100k')
plt.colorbar(label='Cluster')
plt.show()

# Scatter plot for State (Hawaii)
plt.figure(figsize=(16, 12))
plt.scatter(combined_cluster['State_HI'], combined_cluster['Heart Disease per 100k'], c=cluster_labels, c
plt.title('Clusters')
plt.xlabel('Hawaii')
plt.ylabel('Heart Disease per 100k')
plt.colorbar(label='Cluster')
plt.show()
```

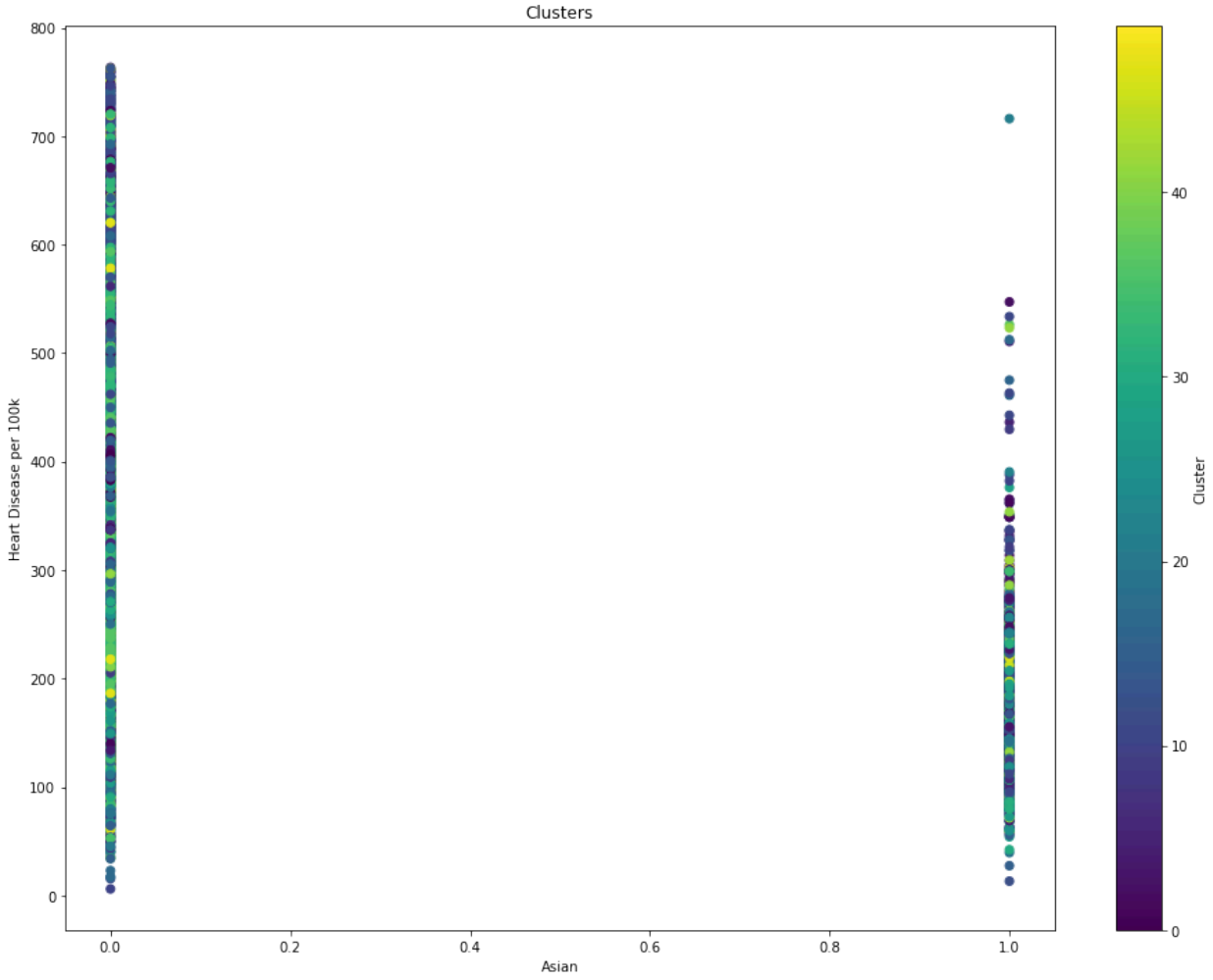


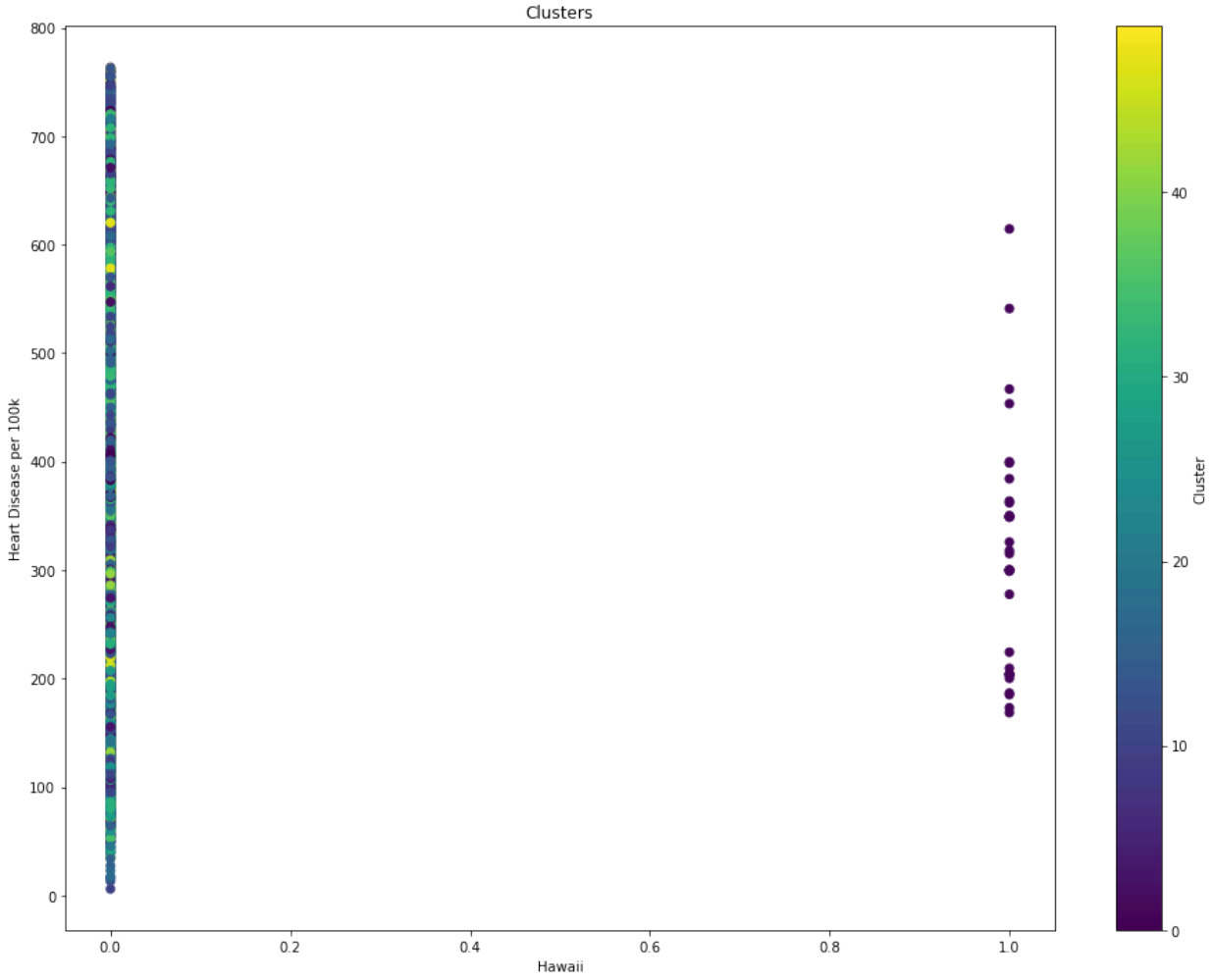

Clusters
Heart Disease per 100k
White
Cluster
800
700
600
500
400
300
200
100
0
0.0
0.2
0.4
0.6
0.8
1.0
40
30
20
10
0


Clusters
Heart Disease per 100k
Black
Cluster
800
700
600
500
400
300
200
100
0
0.0
0.2
0.4
0.6
0.8
1.0
40
30
20
10
0


Clusters
Heart Disease per 100k
Hispanic
Cluster
800
700
600
500
400
300
200
100
0
0.0
0.2
0.4
0.6
0.8
1.0
40
30
20
10
0


Clusters
Heart Disease per 100k
Native American
Cluster
800
700
600
500
400
300
200
100
0
0.0
0.2
0.4
0.6
0.8
1.0
40
30
20
10
0


Clusters
Heart Disease per 100k
Asian
Cluster
800
700
600
500
400
300
200
100
0
0.0
0.2
0.4
0.6
0.8
1.0
40
30
20
10
0

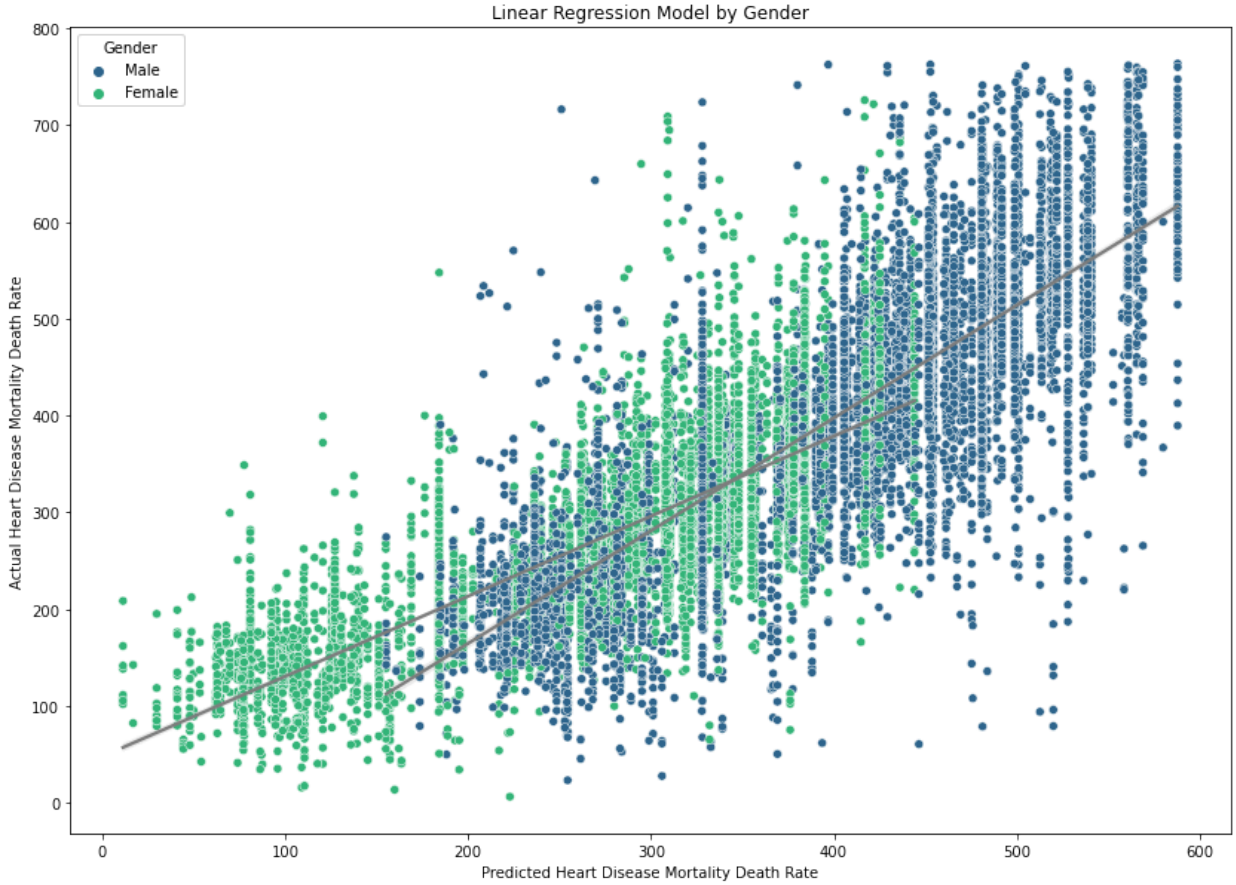


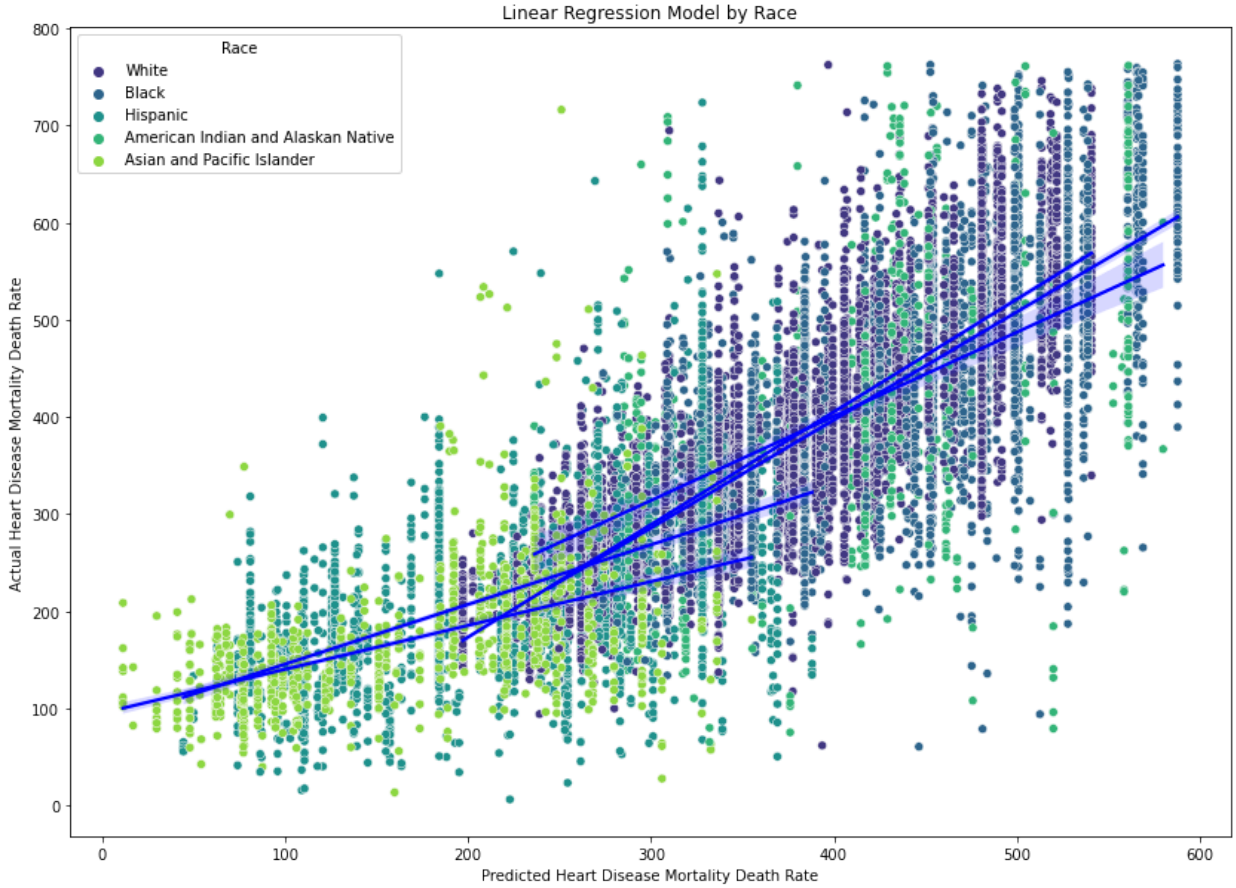
Linear Regression Visual Modeling

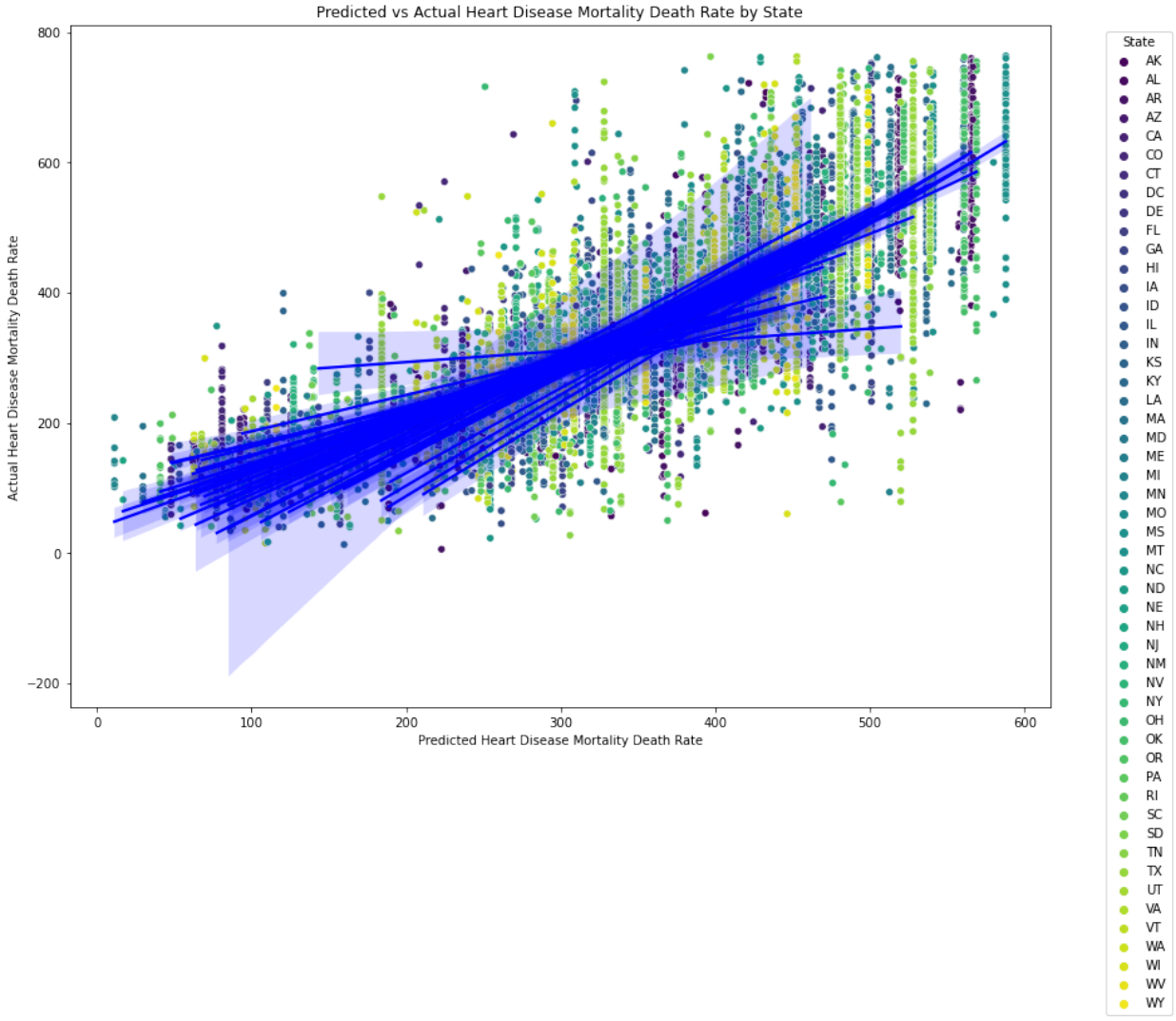
In [48]:
```
from sklearn.linear_model import LinearRegression
from sklearn.preprocessing import OneHotEncoder
from sklearn.compose import ColumnTransformer
from sklearn.pipeline import Pipeline
```

In [49]:
```
# Selecting relevant columns
X = cleaned_county_df[['Gender', 'Ethnicity', 'State']]
y = cleaned_county_df['Heart Disease per 100k']

# Define preprocessing steps for encoding categorical variables
preprocessor = ColumnTransformer(
    transformers=[
        ('cat', OneHotEncoder(), ['Gender', 'Ethnicity', 'State'])  # One-hot encode categorical variables
    ],
    remainder='passthrough'  # Pass through any remaining columns
)

# Create a pipeline with preprocessing and linear regression model
pipeline = Pipeline([
    ('preprocessor', preprocessor),
    ('regressor', LinearRegression())  # Linear regression model
])

# Fit the pipeline on the data
```

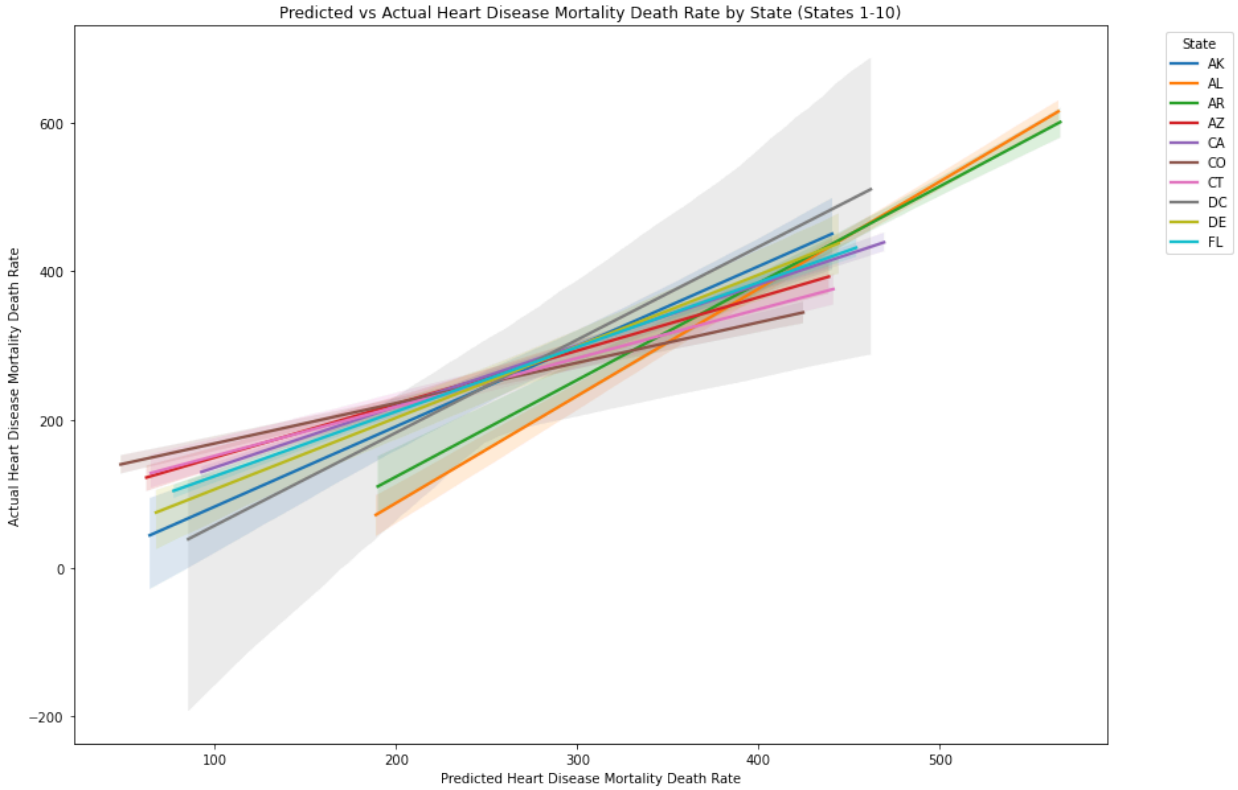
```
pipeline.fit(X, y)

# Predict heart disease mortality death rate
y_pred = pipeline.predict(X)


# Plot for Gender
plt.figure(figsize=(14, 10))
sns.scatterplot(data=cleaned_county_df, x=y_pred, y=y, hue='Gender', palette='viridis', legend='full')
for category in cleaned_county_df['Gender'].unique():
    category_mask = (cleaned_county_df['Gender'] == category)
    sns.regplot(x=y_pred[category_mask], y=y[category_mask], scatter=False, color='gray')
plt.xlabel('Predicted Heart Disease Mortality Death Rate')
plt.ylabel('Actual Heart Disease Mortality Death Rate')
plt.title('Linear Regression Model by Gender')
plt.legend(title='Gender')
plt.show()

# Plot for Race
plt.figure(figsize=(14, 10))
sns.scatterplot(data=cleaned_county_df, x=y_pred, y=y, hue='Ethnicity', palette='viridis', legend='full')
for category in cleaned_county_df['Ethnicity'].unique():
    category_mask = (cleaned_county_df['Ethnicity'] == category)
    sns.regplot(x=y_pred[category_mask], y=y[category_mask], scatter=False, color='blue')
plt.xlabel('Predicted Heart Disease Mortality Death Rate')
plt.ylabel('Actual Heart Disease Mortality Death Rate')
plt.title('Linear Regression Model by Race')
plt.legend(title='Race')
plt.show()

# Plot for State
plt.figure(figsize=(14, 10))
sns.scatterplot(data=cleaned_county_df, x=y_pred, y=y, hue='State', palette='viridis')
for category in cleaned_county_df['State'].unique():
    category_mask = (cleaned_county_df['State'] == category)
    sns.regplot(x=y_pred[category_mask], y=y[category_mask], scatter=False, color='blue')
plt.xlabel('Predicted Heart Disease Mortality Death Rate')
plt.ylabel('Actual Heart Disease Mortality Death Rate')
plt.title('Predicted vs Actual Heart Disease Mortality Death Rate by State')
plt.legend(title='State', bbox_to_anchor=(1.05, 1), loc='upper left')
plt.show()
```

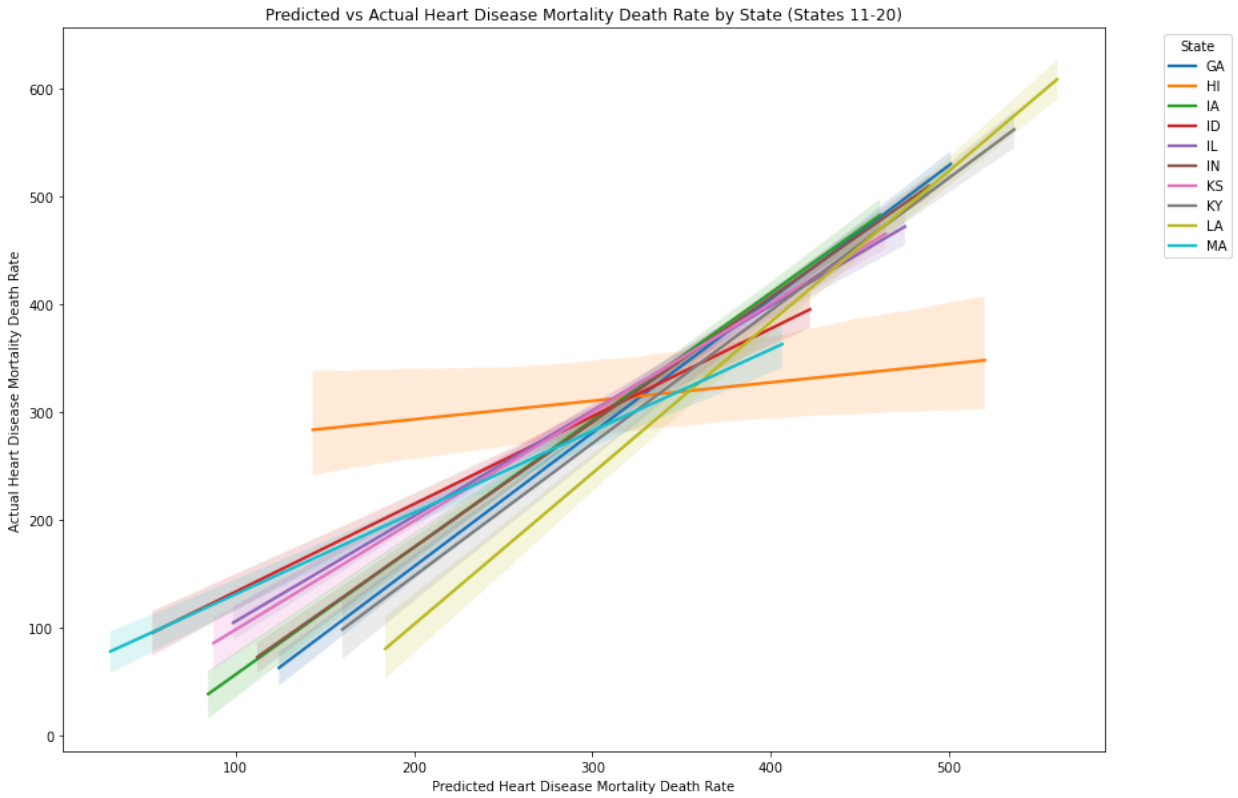

Linear Regression Model by Gender
Gender
Male
Female
Actual Heart Disease Mortality Death Rate
Predicted Heart Disease Mortality Death Rate
0
100
200
300
400
500
600
700
800

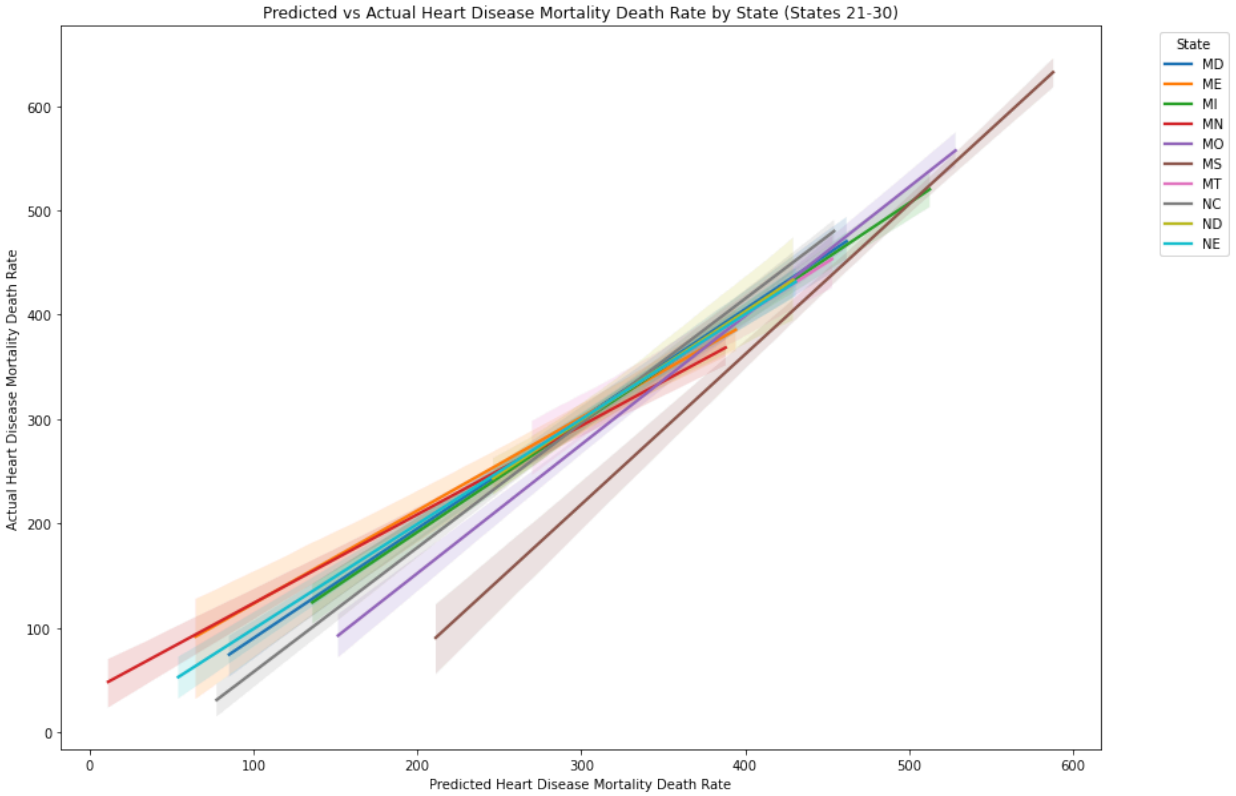

Linear Regression Model by Race
Race
White
Black
Hispanic
American Indian and Alaskan Native
Asian and Pacific Islander
Actual Heart Disease Mortality Death Rate
Predicted Heart Disease Mortality Death Rate
0
100
200
300
400
500
600
700
800

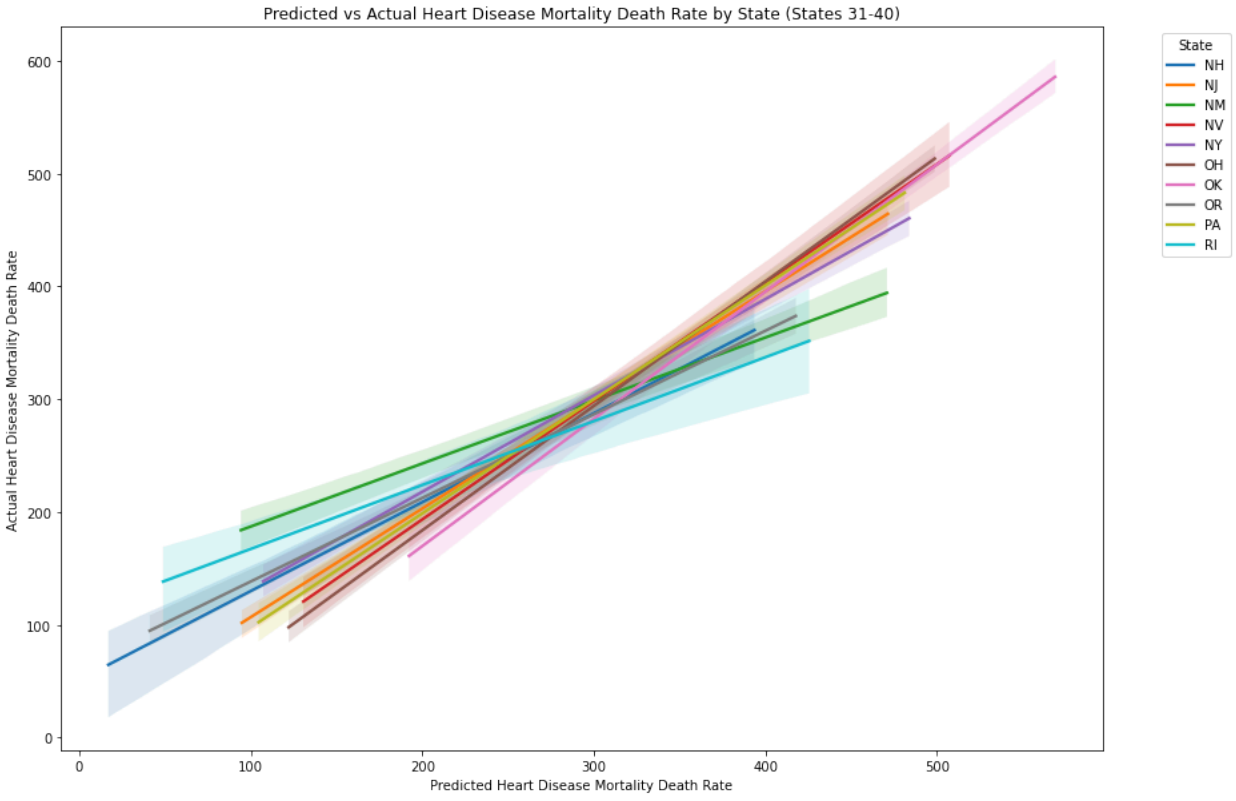


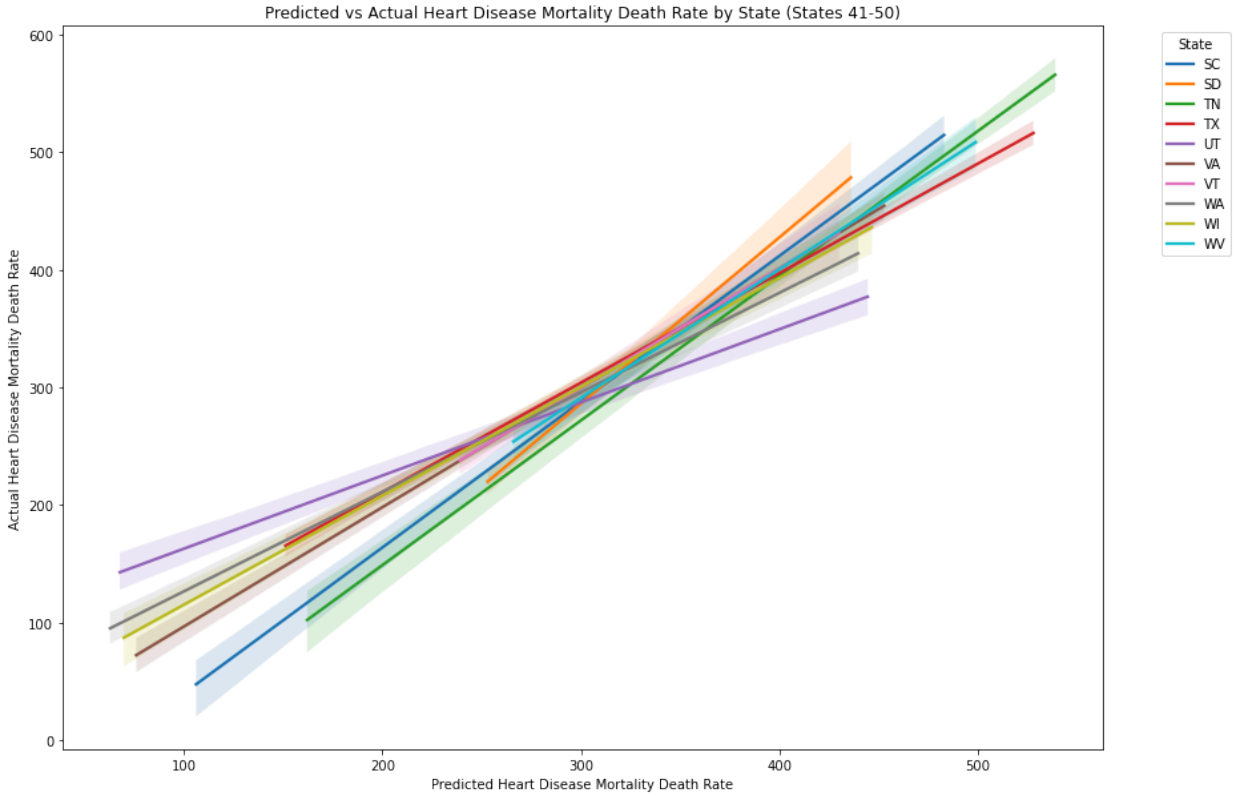
In [50]:
```
# Determine the number of groups (graphs) needed
num_states = len(cleaned_county_df['State'].unique())
num_groups = int(np.ceil(num_states / 10))  # Round up to the nearest integer

# Plot for each group of states
for i in range(num_groups):
    start_index = i * 10
    end_index = min((i + 1) * 10, num_states)  # Ensure not to exceed the number of states
    states_subset = list(cleaned_county_df['State'].unique())[start_index:end_index]

    plt.figure(figsize=(14, 10))
    for category in states_subset:
        category_mask = (cleaned_county_df['State'] == category)
        sns.regplot(x=y_pred[category_mask], y=y[category_mask], scatter=False, label=category)

    plt.xlabel('Predicted Heart Disease Mortality Death Rate')
    plt.ylabel('Actual Heart Disease Mortality Death Rate')
    plt.title(f'Predicted vs Actual Heart Disease Mortality Death Rate by State (States {start_index+1}-{e
    plt.legend(title='State', bbox_to_anchor=(1.05, 1), loc='upper left')
    plt.show()

    # Assumption for Hawaii. It is the amount of data collected (seen in clustering) and
    # assuming the population is majority Asian
```

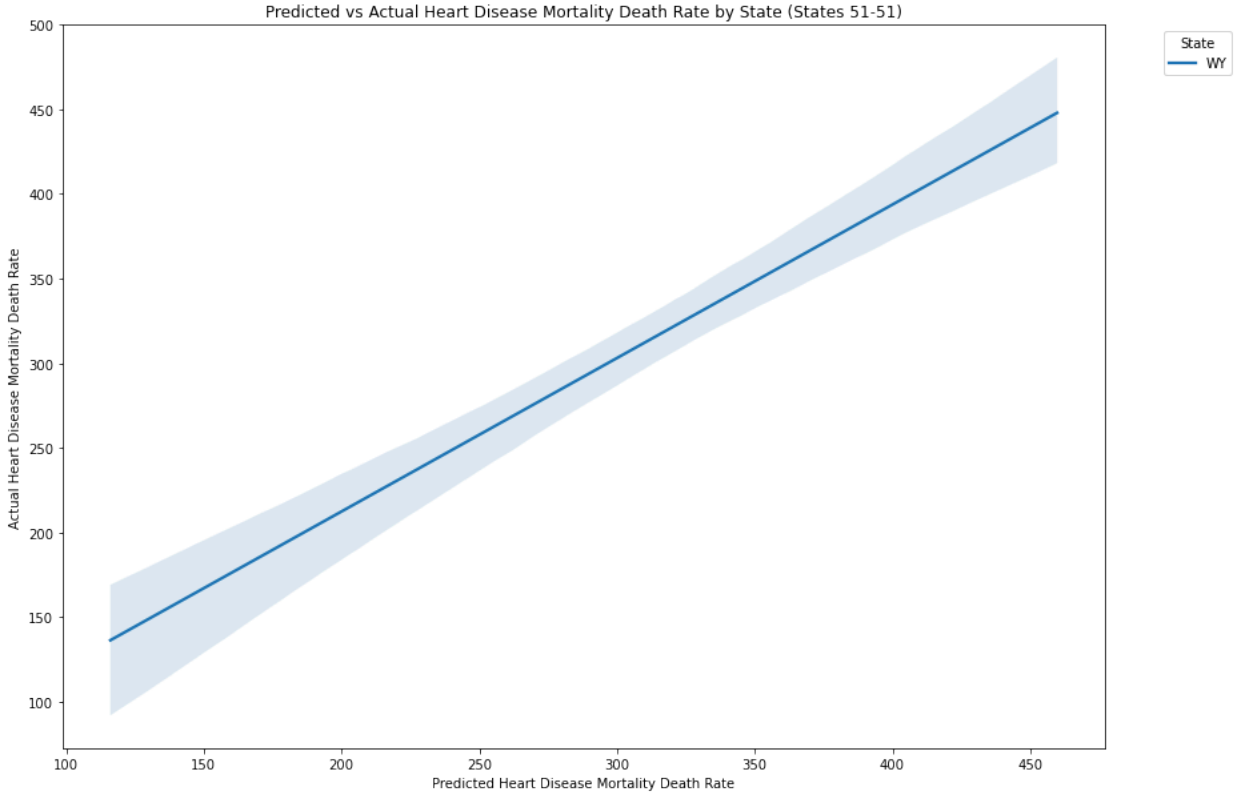

Predicted vs Actual Heart Disease Mortality Death Rate by State (States 1-10)
Actual Heart Disease Mortality Death Rate
Predicted Heart Disease Mortality Death Rate
State
AK
AL
AR
AZ
CA
CO
CT
DC
DE
FL


Predicted vs Actual Heart Disease Mortality Death Rate by State (States 11-20)
Actual Heart Disease Mortality Death Rate
Predicted Heart Disease Mortality Death Rate
State
GA
HI
IA
ID
IL
IN
KS
KY
LA
MA


Predicted vs Actual Heart Disease Mortality Death Rate by State (States 21-30)
Actual Heart Disease Mortality Death Rate
Predicted Heart Disease Mortality Death Rate
0
100
200
300
400
500
600
State
MD
ME
MI
MN
MO
MS
MT
NC
ND
NE


Predicted vs Actual Heart Disease Mortality Death Rate by State (States 31-40)
Actual Heart Disease Mortality Death Rate
Predicted Heart Disease Mortality Death Rate
0
100
200
300
400
500
600
State
NH
NJ
NM
NV
NY
OH
OK
OR
PA
RI


Predicted vs Actual Heart Disease Mortality Death Rate by State (States 41-50)
Actual Heart Disease Mortality Death Rate
Predicted Heart Disease Mortality Death Rate
State
SC
SD
TN
TX
UT
VA
VT
WA
WI
WV


Predicted vs Actual Heart Disease Mortality Death Rate by State (States 51-51)
Actual Heart Disease Mortality Death Rate
Predicted Heart Disease Mortality Death Rate
State
WY