Introduction

In our project we explore and analyze the correlation between heart disease mortality rates and many different behavioral and environmental factors. We hope to discover how the things in our control (such as exercise and smoking) and things out of our control (gender and certain health problems) are related to the cardiovascular mortalities in the US.

In particular we hope to answer the following questions:

- Does gender or ethnicity play a role in heart-related deaths?
- Do heart-related deaths cluster in certain parts of the US?
- Can we use income data to explain how cardiovascular mortalities scatter throughout the US?
- What are the highest correlated features of CDC survey participants with the mortalities and do they follow a similar pattern of geographical clusters formed by death statistics?

Data Importing, Cleaning, Imputing, and Manipulation

Installing the required packages:

```
#Kindly note:

# We have included the requirements.txt in our data folder so that the !pip install -r requirements.txt command would work if
# you are using the data folder as the directory, although it seems that running the file is not necessary.
# Also, our code downloads the files from the internet and places them into the current directory folder so the data
# files we provided in the .zip are not necessary. We have also tried our best to follow Pep 8 guidelines. Google Colab
# does have a wider screen than jupyter notebook so some of our code is a little wide for jupyter but it looks fine in Jupyter
# and great in Google colab :). Lastly, we were told that the error after importing was ok by our counselor as it does not impact code.
# We hope that our documentation process is accessible enough to understand. Thanks for reading!


!pip install altair==5.1.2 jsonschema==4.17.3 vega==1.3
!pip install -r requirements.txt
!pip install vega-datasets
```

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Requirement already satisfied: altair==5.1.2 in /usr/local/lib/python3.10/dist-packages (5.1.2)
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Requirement already satisfied: gitpython!=3.1.19,<4,>=3.0.7 in /usr/local/lib/python3.10/dist-packages (from streamlit==1.31.1->-r requirements.txt
Requirement already satisfied: pydeck<1,>=0.8.0b4 in /usr/local/lib/python3.10/dist-packages (from streamlit==1.31.1->-r requirements.txt (line 2))
Requirement already satisfied: tornado<7,>=6.0.3 in /usr/local/lib/python3.10/dist-packages (from streamlit==1.31.1->-r requirements.txt (line 2))
```

Importing the usual suspects and adjusting a few visualization settings:

```python
import os
import requests
from zipfile import ZipFile
from urllib.request import urlretrieve
import pandas as pd
import numpy as np
import csv
import altair as alt
from vega_datasets import data
from math import cos, asin, sqrt
from sklearn.neighbors import BallTree
%matplotlib inline
import seaborn as sns
sns.set()
import matplotlib.pyplot as plt
from sklearn.preprocessing import StandardScaler
import statsmodels.api as sm
alt.data_transformers.disable_max_rows()
from sklearn.feature_selection import RFECV
from sklearn.ensemble import RandomForestRegressor
from scipy.stats import t
from sklearn.linear_model import LinearRegression
from sklearn.preprocessing import PolynomialFeatures
pd.set_option('display.max_columns', None)
```

```python
def download_file(download_f, filename, force=False):
    """
    Downloads a file using a dynamic function.

    :param download_f: Function to be used for the actual download operation
    :param filename: File name for saving
    :param force: Whether to overwrite an existing file
    """
    if force or not os.path.exists(filename):
        download_f(filename)
```

```
def download_annual_personal_income_by_county(filename):
    """
    Downloads the personal income dataset and extracts it.

    :param filename: File name for saving
    """
    def download(filename):
        """
        Actual download logic for the personal income dataset

        :param filename: File name for saving
        """
        url = 'https://apps.bea.gov/regional/downloadzip.cfm'
        payload = {
          'selFilename': 'CAINC1',
          'sbmtButton': 'Download'
          }
        res = requests.post(url, params=payload)
        with open(filename, 'wb') as f:
            f.write(res.content)
    download_file(download, filename)
    with ZipFile(filename, 'r') as zObject:
        zObject.extractall(path='./income_unzipped/')


def download_heart_disease_mortality_by_county(filename):
    """
    Downloads the mortality dataset.

    :param filename: File name for saving
    """
    def download(filename):
        """
        Actual download logic for the personal income dataset

        :param filename: File name for saving
        """
        url = 'https://data.cdc.gov/resource/jiwm-ppbh.csv?$limit=100000'
        urlretrieve(url, filename)
    download_file(download, filename)


def download_cdc_survey(filename):
    """
    Downloads the cdc survey dataset.

    :param filename: File name for saving
    """
    def download(filename):
        """
        Actual download logic for the personal cdc survey dataset
        :param filename: File name for saving
        """
        url = 'https://www.cdc.gov/brfss/annual_data/2022/files/LLCP2022ASC.zip'
        urlretrieve(url, filename)
    download_file(download, filename)
    with ZipFile(filename, 'r') as zObject:
        zObject.extractall(path='./cdc_survey_unzipped/')
```

Downloading (and extrating if necessary) all three datasets:

```
annual_personal_income_by_county_zip_filename = 'CAINC1.zip'
download_annual_personal_income_by_county(annual_personal_income_by_county_zip_filename)

heart_disease_mortality_by_county_csv_filename = 'mortality.csv'
download_heart_disease_mortality_by_county(heart_disease_mortality_by_county_csv_filename)

cdc_survey_zip_filename = 'cdc_survey.zip'
download_cdc_survey(cdc_survey_zip_filename)
```

```
state_code_to_abbr = {
    1: 'AL', 2: 'AK', 4: 'AZ', 5: 'AR', 6: 'CA', 8: 'CO', 9: 'CT', 10: 'DE', 11: 'DC', 12: 'FL', 13: 'GA', 15: 'HI', 16: 'ID', 17: 'IL', 18: 'IN', 19: 'I
    21: 'KY', 22: 'LA', 23: 'ME', 24: 'MD', 25: 'MA', 26: 'MI', 27: 'MN', 28: 'MS', 29: 'MO', 30: 'MT', 31: 'NE', 32: 'NV', 33: 'NH', 34: 'NJ', 35: 'NM',
    37: 'NC', 38: 'ND', 39: 'OH', 40: 'OK', 41: 'OR', 42: 'PA', 44: 'RI', 45: 'SC', 46: 'SD', 47: 'TN', 48: 'TX', 49: 'UT', 50: 'VT', 51: 'VA', 53: 'WA',
    }

def parse_cdc_survey():
  """
  Reads the CDC survey input file and parses the contents using ASCII format.

  :return: CDC survey dataframe.
  """
  rows = []
  with open('./cdc_survey_unzipped/LLCP2022.ASC ', 'r') as f:
    count = 0
    for line in f:
      row = {}
      state_code = int(line[:2])
      interview_completed = line[31:35] == '1100'
      if interview_completed and state_code in state_code_to_abbr:
        row['State Abbr.'] = state_code_to_abbr[state_code]
        row['Interview Year'] = line[22:26]

        age_older_18_landline = line[67]
        if age_older_18_landline == '1':
          row['Is Adult Landline'] = True
        elif age_older_18_landline == '2':
          row['Is Adult Landline'] = False

        gender = line[1979]
        if gender == '1':
          row['Gender'] = 'Male'
        elif gender == '2':
          row['Gender'] = 'Female'

        num_of_adults_landline = line[69:71].strip()
        if num_of_adults_landline:
          row['Num of Adults Landline'] = int(num_of_adults_landline)


        age_older_18_cell = line[80]
        if age_older_18_cell == '1':
          row['Is Adult Cell'] = True

        num_of_adults_cell = line[88:90].strip()
        if num_of_adults_cell and int(num_of_adults_cell) <= 76:
          row['Num of Adults Cell'] = int(num_of_adults_cell)

        general_health = line[100].strip()
        if general_health == '1':
          row['General Health'] = 'Excellent'
        elif general_health == '2':
```

```
      row['General Health'] = 'Very good'
    elif general_health == '3':
      row['General Health'] = 'Good'
    elif general_health == '4':
      row['General Health'] = 'Fair'
    elif general_health == '5':
      row['General Health'] = 'Poor'

    health_care_access = line[107:109].strip()
    if health_care_access:
      health_care_access_code = int(health_care_access)
      if health_care_access_code == 1:
        row['Health Care Access'] = 'from_employer'
      elif health_care_access_code == 2:
        row['Health Care Access'] = 'from_own_pocket'
      elif health_care_access_code == 3:
        row['Health Care Access'] = 'medicare'
      elif health_care_access_code == 4:
        row['Health Care Access'] = 'medigap'
      elif health_care_access_code == 5:
        row['Health Care Access'] = 'medicaid'
      elif health_care_access_code == 6:
        row['Health Care Access'] = 'children_health_insurance_program'
      elif health_care_access_code == 7:
        row['Health Care Access'] = 'military'
      elif health_care_access_code == 8:
        row['Health Care Access'] = 'indian_health'
      elif health_care_access_code == 9:
        row['Health Care Access'] = 'state_sponsored'
      elif health_care_access_code == 10:
        row['Health Care Access'] = 'other_government'
      elif health_care_access_code == 88:
        row['Health Care Access'] = 'no_coverage'

    could_afford_doctor = line[110].strip()
    if could_afford_doctor:
      could_afford_doctor_code = int(could_afford_doctor)
      if could_afford_doctor_code == 1:
        row['Could Afford Doctor'] = True
      elif could_afford_doctor_code == 2:
        row['Could Afford Doctor'] = False

    how_many_years_since_last_checkup = line[111].strip()
    if how_many_years_since_last_checkup:
      how_many_years_since_last_checkup_code = int(how_many_years_since_last_checkup)
      if how_many_years_since_last_checkup_code == 1:
        row['Years Since Last Checkup'] = 'within_past_year'
      elif how_many_years_since_last_checkup_code == 2:
        row['Years Since Last Checkup'] = 'within_past_two_years'
      elif how_many_years_since_last_checkup_code == 3:
        row['Years Since Last Checkup'] = 'within_past_five_years'
      elif how_many_years_since_last_checkup_code == 4:
```

```
        row['Years Since Last Checkup'] = 'five_or_more_years'

    exercise_in_past_30_days = line[112].strip()
    if exercise_in_past_30_days:
      exercise_in_past_30_days_code = int(exercise_in_past_30_days)
      if exercise_in_past_30_days_code == 1:
        row['Exercise in Past 30 Days'] = True
      elif exercise_in_past_30_days_code == 2:
        row['Exercise in Past 30 Days'] = False

    hours_of_sleeping = line[113:115].strip()
    if hours_of_sleeping:
      hours_of_sleeping_code = int(hours_of_sleeping)
      if hours_of_sleeping_code <= 24:
        row['Hours of Sleeping'] = hours_of_sleeping_code

    how_many_years_since_last_dentist_visit = line[115].strip()
    if how_many_years_since_last_dentist_visit:
      how_many_years_since_last_dentist_visit_code = int(how_many_years_since_last_dentist_visit)
      if how_many_years_since_last_dentist_visit_code == 1:
        row['Years Since Last Dentist Visit'] = 'within_past_year'
      elif how_many_years_since_last_dentist_visit_code == 2:
        row['Years Since Last Dentist Visit'] = 'within_past_two_years'
      elif how_many_years_since_last_dentist_visit_code == 3:
        row['Years Since Last Dentist Visit'] = 'within_past_five_years'
      elif how_many_years_since_last_dentist_visit_code == 4:
        row['Years Since Last Dentist Visit'] = 'five_or_more_years'

    heart_attack = line[117].strip()
    if heart_attack:
      if heart_attack == '1':
        row['Heart Attack'] = True
      elif heart_attack == '2':
        row['Heart Attack'] = False

    heart_disease = line[118].strip()
    if heart_disease:
      if heart_disease == '1':
        row['Heart Disease'] = True
      elif heart_disease == '2':
        row['Heart Disease'] = False

    stroke = line[119].strip()
    if stroke:
      if stroke == '1':
        row['Stroke'] = True
      elif stroke == '2':
        row['Stroke'] = False

    asthma = line[1908].strip()
    if asthma:
      if asthma == '1':
```

```
        row['Asthma'] = False
      elif asthma == '2':
        row['Asthma'] = True

    asthma_in_effect = line[1909].strip()
    if asthma_in_effect:
      if asthma_in_effect == '2':
        row['Asthma in Effect'] = True
      elif asthma_in_effect == '1':
        row['Asthma in Effect'] = False

    depression = line[125].strip()
    if depression:
      if depression == '1':
        row['Depression'] = True
      elif depression == '2':
        row['Depression'] = False

    kidney_disease = line[126].strip()
    if kidney_disease:
      if kidney_disease == '1':
        row['Kidney Disease'] = True
      elif kidney_disease == '2':
        row['Kidney Disease'] = False

    arthritis = line[1911].strip()
    if arthritis:
      if arthritis == '1':
        row['Arthritis'] = True
      elif arthritis == '2':
        row['Arthritis'] = False

    diabetes = line[128].strip()
    if diabetes:
      if diabetes == '1':
        row['Diabetes'] = True
      elif diabetes in ['2', '3', '4']:
        row['Diabetes'] = False

    weight_in_pounds = line[188:192].strip()
    if weight_in_pounds:
      weight_in_pounds_code = int(weight_in_pounds)
      if weight_in_pounds_code >= 50 and weight_in_pounds_code <= 776:
        row['Weight in Pounds'] = weight_in_pounds_code

    height_in_inches = line[1986:1989].strip()
    if height_in_inches:
      height_in_inches_code = int(height_in_inches)
      row['Height in Inches'] = height_in_inches_code


    smoking = line[223].strip()
```

```
        if smoking:
          if smoking == '1':
            row['Smoking'] = 'every_day'
          elif smoking == '2':
            row['Smoking'] = 'some_days'
          elif smoking == '3':
            row['Smoking'] = 'never'

        cigarettes_per_day = line[232:235].strip()
        if cigarettes_per_day:
          cigarettes_per_day_code = int(cigarettes_per_day)
          if cigarettes_per_day_code <= 300:
            row['Cigarettes per Day'] = cigarettes_per_day_code

        drinks_last_30_day = line[241:243].strip()
        if drinks_last_30_day:
          drinks_last_30_day_code = int(drinks_last_30_day)
          if drinks_last_30_day_code <= 76:
            row['Drinks in Last 30 Days'] = drinks_last_30_day_code

        pre_diabetes = line[269].strip()
        if pre_diabetes:
          if pre_diabetes == '1':
            row['Prediabetes'] = True
          elif pre_diabetes in ['2', '3']:
            row['Prediabetes'] = False

        diabetes = line[270].strip()
        if diabetes:
          if diabetes in ['1', '2']:
            row['Diabetes'] = True

        shortness_of_breath = line[305].strip()
        if shortness_of_breath:
          if shortness_of_breath == '1':
            row['Shortness of Breath'] = True
          elif shortness_of_breath == '2':
            row['Shortness of Breath'] = False

        life_satisfaction = line[360].strip()
        if life_satisfaction:
          if life_satisfaction == '1':
            row['Life Satisfaction'] = 'very_satisfied'
          elif life_satisfaction == '2':
            row['Life Satisfaction'] = 'satisfied'
          elif life_satisfaction == '3':
            row['Life Satisfaction'] = 'dissatisfied'
          elif life_satisfaction == '4':
            row['Life Satisfaction'] = 'very_dissatisfied'

        ethnicity = line[1975].strip()
        if ethnicity:
```

```
          if ethnicity == '1':
            row['Ethnicity'] = 'White'
          elif ethnicity == '2':
            row['Ethnicity'] = 'Black'
          elif ethnicity == '3':
            row['Ethnicity'] = 'American Indian and Alaskan Native'
          elif ethnicity in ['4', '5']:
            row['Ethnicity'] = 'Asian and Pacific Islander'
          elif ethnicity == '8':
            row['Ethnicity'] = 'Hispanic'
          elif ethnicity == '7':
            row['Ethnicity'] = 'Multiracial, non-Hispanic'

        metropolitan = line[1401].strip()
        if metropolitan:
          if metropolitan == '1':
            row['Metropolitan'] = True
          elif metropolitan == '2':
            row['Metropolitan'] = False

        age_group = line[1985].strip()
        if age_group:
          if age_group == '1':
            row['Age Group'] = 'between_18_and_24'
          elif age_group == '2':
            row['Age Group'] = 'between_25_and_34'
          elif age_group == '3':
            row['Age Group'] = 'between_35_and_44'
          elif age_group == '4':
            row['Age Group'] = 'between_45_and_54'
          elif age_group == '5':
            row['Age Group'] = 'between_55_and_64'
          elif age_group == '6':
            row['Age Group'] = 'older_than_65'

        bmi_category = line[2001].strip()
        if bmi_category:
          if bmi_category == '1':
            row['BMI Category'] = 'underweight'
          elif bmi_category == '2':
            row['BMI Category'] = 'normal_weight'
          elif bmi_category == '3':
            row['BMI Category'] = 'over_weight'
          elif bmi_category == '4':
            row['BMI Category'] = 'obese'

        education = line[2004].strip()
        if education:
          if education == '1':
            row['Education'] = 'did_not_graduate_high_school'
          elif education == '2':
            row['Education'] = 'graduated_high_school'
```

```
          elif education == '3':
            row['Education'] = 'attended_college'
          elif education == '4':
            row['Education'] = 'graduated_college'

        income_level = line[2005].strip()
        if income_level:
          if income_level == '1':
            row['Income Level'] = 'less_than_15K'
          elif income_level == '2':
            row['Income Level'] = 'between_15K_and_25K'
          elif income_level == '3':
            row['Income Level'] = 'between_25K_and_35K'
          elif income_level == '4':
            row['Income Level'] = 'between_35K_and_50K'
          elif income_level == '5':
            row['Income Level'] = 'between_50K_and_100K'
          elif income_level == '6':
            row['Income Level'] = 'between_100K_and_200K'
          elif income_level == '7':
            row['Income Level'] = 'more_than_200K'

        heavy_alcohol_consumption = line[2047].strip()
        if heavy_alcohol_consumption:
          if heavy_alcohol_consumption == '1':
            row['Heavy Alcohol Consumption'] = False
          elif heavy_alcohol_consumption == '2':
            row['Heavy Alcohol Consumption'] = True

        rows.append(row)

    df = pd.DataFrame.from_dict(rows).astype({'Is Adult Landline': bool, 'Could Afford Doctor': bool, 'Exercise in Past 30 Days': bool, 'Heart Attack': b
                                              'Stroke': bool, 'Asthma': bool, 'Asthma in Effect': bool, 'Depression': bool, 'Kidney Disease': bool, 'Arth
                                              'Diabetes': bool, 'Metropolitan': bool, 'Heavy Alcohol Consumption': bool, 'Prediabetes': bool, 'Shortness
                                              }
                                             )

    return df

def parse_mortality():
    """
    Reads the mortality input file and parses the contents using CSV format.

    :return: Mortality dataframe.
    """
    df = pd.read_csv('mortality.csv')
    return df

def parse_income():
    """
    Reads the income data input file and parses the contents using CSV format.
    :return: Income dataframe.
    """
    df = pd.read_csv('income_unzipped/CAINC1__ALL_AREAS_1969_2022.csv', encoding='ISO-8859-1', skipfooter=4,
                     usecols=['GeoFIPS', 'Region', 'LineCode', 'Description', 'Unit', '2018', '2019', '2020'], na_values='(NA)', engine='python')
    df['2019'] = (df['2018'] + df['2019'] + df['2020']) / 3
    df['GeoFIPS'] = df['GeoFIPS'].replace({'["\']': ''}, regex=True)
    df.drop(['2018', '2020'], axis=1, inplace=True)
    return df.astype({'GeoFIPS': int})
```

Importing and peeking in the mortality data...

```
df_mortality = parse_mortality()
df_mortality.head()
```

	year	locationabbr	locationdesc	geographiclevel	datasource	class	topic	data_value	data_value_unit	data_value_type	data_value_footno
0	2019	AK	Aleutians East	County	NVSS	Cardiovascular Diseases	Heart Disease Mortality	182.4	per 100,000 population	Age-adjusted, Spatially Smoothed, 3-year Avera...	
1	2019	AK	Aleutians West	County	NVSS	Cardiovascular Diseases	Heart Disease Mortality	172.6	per 100,000 population	Age-adjusted, Spatially Smoothed, 3-year Avera...	
2	2019	AK	Anchorage	County	NVSS	Cardiovascular Diseases	Heart Disease Mortality	255.6	per 100,000 population	Age-adjusted, Spatially Smoothed, 3-year Avera...	
3	2019	AK	Bethel	County	NVSS	Cardiovascular Diseases	Heart Disease Mortality	343.4	per 100,000 population	Age-adjusted, Spatially Smoothed, 3-year Avera...	
4	2019	AK	Bristol Bay	County	NVSS	Cardiovascular Diseases	Heart Disease Mortality	NaN	per 100,000 population	Age-adjusted, Spatially Smoothed, 3-year Avera...	

Mortality dataset has statistics at both state and county levels. We will first focus our efforts on the counties.

25841 values (44.5%) from the **data_value** are missing in the mortality dataset at county level. We need imputation to avoid losing valuable information.

```
df_mortality_county = df_mortality[df_mortality['geographiclevel'] == 'County'].copy()

#Commented out for conciseness. Uncomment to see number of missing values per column.
#df_mortality_county.isnull().sum()
```

We will impute missing data by averaging the values from four closest neigbors. We first convert the lat and lon coordinates into radians because we will use those shortly for imputation.

```
for col in df_mortality_county[["y_lat", "x_lon"]]:
    rad = np.deg2rad(df_mortality_county[col].values)
    df_mortality_county[f'{col}_rad'] = rad

df_mortality_county_without_nan = df_mortality_county[df_mortality_county['data_value'].notna()].copy()
```

Ball tree is a data structure that can handle geospatial data for efficient search. With the help of a ball tree, we can reduce the search time for all missing data from $O(n^2)$ down to $O(nlogn)$.

Ball trees work on radian data and that is why we did that conversion above.

```
ball = BallTree(df_mortality_county_without_nan[['y_lat_rad', 'x_lon_rad']].values, metric='haversine')
```

The function below finds the four nearest neigbour counties and averages the data from them.

Note: It might take 30 seconds to execute.

```
def impute_from_neigbours(row):
    """
    Imputes missing information from the closest neigbors.

    :param row: Current row of the dataset to be processed.
    """
    if np.isnan(row['data_value']):
        _, indices = ball.query([row[['y_lat_rad', 'x_lon_rad']].values], k=4)
        row['data_value'] = df_mortality_county_without_nan.iloc[indices[0]]['data_value'].mean()
    return row

df_mortality_county_imputed = df_mortality_county.apply(impute_from_neigbours, axis=1)
```

Now, we no longer have missing data for the ***data_value*** column.

```
#Commented out for conciseness
#df_mortality_county_imputed.isnull().sum()
```

Importing and peeking in the income data...

```
df_income = parse_income()
df_income.head()
```

	GeoFIPS	Region	LineCode	Description	Unit	2019
0	0		1	Personal income (thousands of dollars)	Thousands of dollars	1.848933e+10
1	0		2	Population (persons) 1/	Number of persons	3.300956e+08
2	0		3	Per capita personal income (dollars) 2/	Dollars	5.600300e+04
3	1000	5	1	Personal income (thousands of dollars)	Thousands of dollars	2.172375e+08
4	1000	5	2	Population (persons) 1/	Number of persons	5.003725e+06

We will not do data imputation for missing rows here as only 84 out of 9600 (less than 1%) rows are missing data.

```
df_income.isnull().sum()
```

```
GeoFIPS         0
Region          0
LineCode        0
Description     0
Unit            0
2019           84
dtype: int64
```

Let's go ahead and drop those missing rows.

```
df_income_short = df_income.dropna()
```

Now let's rename the columns of the mortality data to have more meaningful titles.

```
df_mortality_county_imputed_short = df_mortality_county_imputed[
    ['locationabbr', 'locationdesc', 'geographiclevel', 'data_value', 'stratification1', 'stratification2', 'locationid', 'y_lat', 'x_lon']
    ].rename(columns={
    'locationabbr': 'State',
    'locationdesc': 'County',
    'data_value': 'Mortality Rate per 100K',
    'stratification1': 'Gender',
    'stratification2': 'Ethnicity'
    }
    )

df_mortality_county_imputed_short.head()
```

	State	County	geographiclevel	Mortality Rate per 100K	Gender	Ethnicity	locationid	y_lat	x_lon
0	AK	Aleutians East	County	182.400	Overall	Overall	2013	55.442393	-161.959930
1	AK	Aleutians West	County	172.600	Overall	Overall	2016	53.648343	-166.917533
2	AK	Anchorage	County	255.600	Overall	Overall	2020	61.159145	-149.104559
3	AK	Bethel	County	343.400	Overall	Overall	2050	60.923648	-159.753262
4	AK	Bristol Bay	County	269.825	Overall	Overall	2060	58.753496	-156.694662

We are interested in the specific values for the gender as well as race/ethnicity levels and not just the overall aggregations.

```
#Here we create a smorgasbord of dataframes to create our visualizations with. Certain columns such as 'Gender' and 'Ethnicity' have row values that are
#categories e.g. 'Male' and 'Female', but also have another category named 'Overall' whose rows show values for all of the categories. We create datafram
#with 'Overall' in them, and we also create dataframes that only include the variable names in them e.g. 'Male' and 'Female'. Depending on what the model
#visualization we are making calls for, we choose the appropriate dataframe.

df_mortality_county_imputed_short_overall = df_mortality_county_imputed_short[(df_mortality_county_imputed_short['Gender'] == 'Overall') &\
                                                                              (df_mortality_county_imputed_short['Ethnicity'] == 'Overall')
                                                                              ]

df_mortality_county_imputed_short_no_overall = df_mortality_county_imputed_short[(df_mortality_county_imputed_short['Gender'] != 'Overall') &\
                                                                                 (df_mortality_county_imputed_short['Ethnicity'] != 'Overall')
                                                                                 ]

df_mortality_county_imputed_short_just_gender = df_mortality_county_imputed_short[(df_mortality_county_imputed_short['Gender'] != 'Overall') &\
                                                                                  (df_mortality_county_imputed_short['Ethnicity'] == 'Overall')
                                                                                  ]

df_mortality_county_imputed_short_just_race = df_mortality_county_imputed_short[(df_mortality_county_imputed_short['Gender'] == 'Overall') &\
                                                                                (df_mortality_county_imputed_short['Ethnicity'] != 'Overall')
                                                                                ]

df_mortality_short_county_male = df_mortality_county_imputed_short[(df_mortality_county_imputed_short['Ethnicity'] == 'Overall') &\
                                                                   (df_mortality_county_imputed_short['Gender'] == 'Male')
                                                                   ]

df_mortality_short_county_female = df_mortality_county_imputed_short[(df_mortality_county_imputed_short['Ethnicity'] == 'Overall') &\
                                                                     (df_mortality_county_imputed_short['Gender'] == 'Female')
                                                                     ]

df_mortality_short_county_white = df_mortality_county_imputed_short[(df_mortality_county_imputed_short['Ethnicity'] == 'White') &\
                                                                    (df_mortality_county_imputed_short['Gender'] == 'Overall')
                                                                    ]

df_mortality_short_county_black = df_mortality_county_imputed_short[(df_mortality_county_imputed_short['Ethnicity'] == 'Black') &\
                                                                    (df_mortality_county_imputed_short['Gender'] == 'Overall')
                                                                    ]

df_mortality_short_county_hispanic = df_mortality_county_imputed_short[(df_mortality_county_imputed_short['Ethnicity'] == 'Hispanic') &\
                                                                       (df_mortality_county_imputed_short['Gender'] == 'Overall')
                                                                       ]

df_mortality_short_county_asian = df_mortality_county_imputed_short[(df_mortality_county_imputed_short['Ethnicity'] == 'Asian and Pacific Islander') &\
                                                                    (df_mortality_county_imputed_short['Gender'] == 'Overall')
                                                                    ]

df_mortality_short_county_native_american = df_mortality_county_imputed_short[(df_mortality_county_imputed_short['Ethnicity'] == 'American Indian and Ala
                                                                              (df_mortality_county_imputed_short['Gender'] == 'Overall')
                                                                              ]
```

Importing and peeking in the survey data...

```
df_cdc_survey = parse_cdc_survey()
df_cdc_survey.head()
```

	State Abbr.	Interview Year	Is Adult Landline	Gender	Num of Adults Landline	General Health	Could Afford Doctor	Years Since Last Checkup	Exercise in Past 30 Days	Hours of Sleeping	Heart Attack	Heart Disease	Stroke	Asthma	Asthma in Effect	Depression
0	AL	2022	True	Female	2.0	Very good	False	within_past_year	False	8.0	False	False	False	False	False	False
1	AL	2022	True	Female	2.0	Excellent	False	NaN	False	6.0	False	False	False	False	False	False
2	AL	2022	True	Female	1.0	Very good	False	within_past_year	True	5.0	False	False	False	False	False	False
3	AL	2022	True	Female	3.0	Excellent	False	within_past_year	True	7.0	False	False	False	True	True	False
4	AL	2022	True	Female	2.0	Fair	False	within_past_year	True	9.0	False	False	False	False	False	False

From the mortality dataframe, we will create two dataframes that only include information on the state level. This is so that we can merge them with the previously created CDC survey dataframe that exists only at the state level.

The reason we create two of them is because one of them includes the data while accounting for gender and race, and the other one doesn't. We want to include the dataset that accounts for gender and race for our multiple linear regression, but the caveat is that it has a higher percentage of missing rows. The second dataset that we create which doesn't account for gender or race only has 1 missing row, so we use this for other types of analysis because of it's completeness.

```
df_mortality_state = df_mortality[(df_mortality['geographiclevel'] == 'State')]
df_mortality_state_short = df_mortality_state[
    ['locationabbr', 'locationdesc', 'data_value', 'stratification1', 'stratification2', 'y_lat', 'x_lon']
    ].rename(columns={
    'locationabbr': 'State',
    'data_value': 'Mortality Rate per 100K',
    'stratification1': 'Gender',
    'stratification2': 'Ethnicity'
    }
    )
#The following df has 122 missing mortality rows, or 21.78%
df_mortality_state_short_no_overall = df_mortality_state_short[(df_mortality_state_short['Gender'] != 'Overall') & (df_mortality_state_short['Ethnicity']
#The following df only has 1 missing mortality row
df_mortality_state_short_overall = df_mortality_state_short[(df_mortality_state_short['Gender'] == 'Overall') & (df_mortality_state_short['Ethnicity'] ==
```

For the dataset that accounts for gender and race, it appears that 122 rows (21.78%) are missing the mortality rate value. Although the percent is fairly high, we will not try to impute these using our clustering method because the states are too big of a geographical area for it to make sense to approximate the values from neighbors. We could impute values by inserting the mean or by label propagation, however we believe removing the data will be sufficient.

```
df_mortality_state_short_no_overall.isnull().sum()
```

```
    State                        0
    locationdesc                 0
    Mortality Rate per 100K    122
    Gender                       0
    Ethnicity                    0
    y_lat                        0
    x_lon                        0
    dtype: int64
```

```
df_mortality_state_short_overall.dropna(inplace=True)
df_mortality_state_short_no_overall.dropna(inplace=True)
```

```
df_mortality_state_short_overall.isnull().sum()
```

```
    State                      0
    locationdesc               0
    Mortality Rate per 100K    0
    Gender                     0
    Ethnicity                  0
    y_lat                      0
    x_lon                      0
    dtype: int64
```

We now assign numeric values for the categorical variables pertaining to **smoking** and **bmi_category**.

```
df_cdc_survey=df_cdc_survey.replace({'BMI Category':{'over_weight':0,'obese':1,'normal_weight':0,'underweight':0},
                                     'Smoking':{'some_days':1,'every_day':1,'never':0}}).rename({'BMI Category':'Obesity'},axis=1)
df_cdc_survey.head()
```

	State Abbr.	Interview Year	Is Adult Landline	Gender	Num of Adults Landline	General Health	Could Afford Doctor	Years Since Last Checkup	Exercise in Past 30 Days	Hours of Sleeping	Heart Attack	Heart Disease	Stroke	Asthma	Asthma in Effect	Depression
0	AL	2022	True	Female	2.0	Very good	False	within_past_year	False	8.0	False	False	False	False	False	False
1	AL	2022	True	Female	2.0	Excellent	False	NaN	False	6.0	False	False	False	False	False	False
2	AL	2022	True	Female	1.0	Very good	False	within_past_year	True	5.0	False	False	False	False	False	False
3	AL	2022	True	Female	3.0	Excellent	False	within_past_year	True	7.0	False	False	False	True	True	False
4	AL	2022	True	Female	2.0	Fair	False	within_past_year	True	9.0	False	False	False	False	False	False

We will use the following columns from the CDC survey dataset for exploration.

```
cols_for_exploration = ['State Abbr.','Ethnicity','Gender', 'Could Afford Doctor', 'Exercise in Past 30 Days', 'Hours of Sleeping', 'Asthma','Stroke',
                        'Asthma in Effect', 'Depression', 'Kidney Disease', 'Arthritis', 'Diabetes', 'Metropolitan', 'Heavy Alcohol Consumption','Obesity
                        ]

df_cdc_survey_short = df_cdc_survey[cols_for_exploration].copy()
```

CDC survey data consists of individual subjects which makes it necessary to do aggregations. Taking the averages across states, gender, and race is our next step.

```
df_cdc_survey_state = df_cdc_survey_short.groupby(['State Abbr.']).mean(numeric_only=True).reset_index()
df_cdc_survey_state_gender_race = df_cdc_survey_short.groupby(['State Abbr.','Gender','Ethnicity']).mean(numeric_only=True).reset_index()
```

We are now ready to join the aggregated CDC survey data with the mortality data. There are two joins below:

1. At the state-gender-race/ethnicity level to explore the relations of all three with the mortality
2. At the state level to explore the relation of only state with the mortality

```
df_mortality_with_cdc_state_gender_race = df_mortality_state_short_no_overall.merge(df_cdc_survey_state_gender_race, how='inner',left_on=['State','Gender
                                                                                    right_on=['State Abbr.','Gender','Ethnicity']
                                                                                    )
df_mortality_with_cdc_state = df_mortality_state_short_overall.merge(df_cdc_survey_state, how='inner',left_on=['State'],right_on=['State Abbr.'])
```

The following is a list of numerical columns for correlation analysis.

```
corr_features = ['Could Afford Doctor', 'Exercise in Past 30 Days', 'Hours of Sleeping', 'Asthma','Stroke',
                 'Asthma in Effect', 'Depression', 'Kidney Disease', 'Arthritis', 'Diabetes', 'Metropolitan', 'Heavy Alcohol Consumption','Obesity','Smc
                 ]
correlation_df = df_mortality_with_cdc_state[corr_features + ['Mortality Rate per 100K']]
```

Downloading the topography data of counties and states for choropleth maps.

```
counties = alt.topo_feature(data.us_10m.url, 'counties')
states = alt.topo_feature(data.us_10m.url, feature='states')
```

```
def create_choropleth(title, data, map_source=counties, legend_title='Deaths per 100K', data_col='Mortality Rate per 100K',sort='ascending'):
    """
    Creates a choropleth map.

    :param title: Title of the visualization.
    :param data: Source dataframe for density calculation.
    :param map_source: Map data.
    :param legend_title: Title of the legend for density scale.
    :param data_col: Column name of the source dataframe for measurements.
    :param sort: Sorting choice for color highlighting.

    :return: Altair choropleth map.
    """
    return alt.Chart(map_source).mark_geoshape().encode(color=alt.Color('{}:Q'.format(data_col),sort=sort).title(legend_title)).properties(
               width=500,
               height=300,
               title=title
               ).transform_lookup(
                   lookup='id',
                  from_=alt.LookupData(data, 'locationid', [data_col])
               ).project('albersUsa')
```

Below is the color scheme for our visualizations.

```
range_ = ['#1276ce', '#18ce12', '#ce6a12', '#c812ce', '#ecfc0d', '#0d5390', '#05233e', '#a0c8eb','#56734a']
```

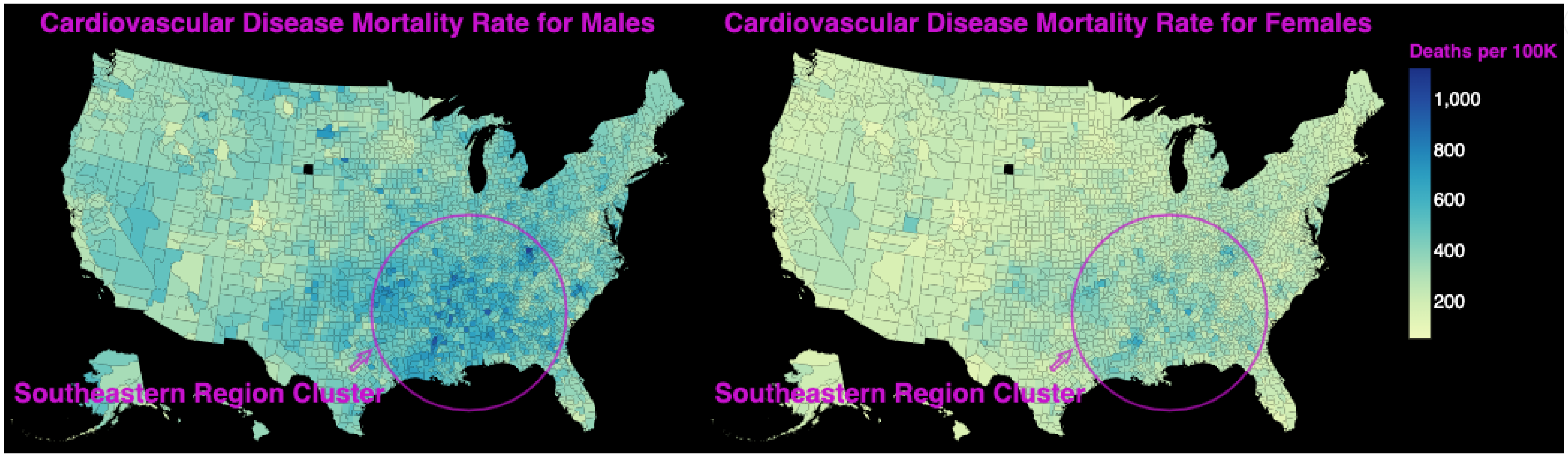
```
# define the theme by returning the dictionary of configurations
def dark_enhanced():
    lightColor = '#fff';
    medColor = '#888';
    return {
        'config': {
  'background': 'black',

  'view': {
    'stroke': 'black',
  },

  'title': {
    'color': range_[3],
    'subtitleColor': lightColor,
  },

  'style': {
    'guide-label': {
      'fill': lightColor,
    },
    'guide-title': {
      'fill': lightColor,
    },
  },

  'axis': {
    'domainColor': lightColor,
    'gridColor': medColor,
    'tickColor': lightColor,
  },
}
}


# registering the custom theme under a chosen name
alt.themes.register('dark_enhanced', dark_enhanced)

# enabling the newly registered theme
alt.themes.enable('dark_enhanced')
```

```
ThemeRegistry.enable('dark_enhanced')
```

Analysis

To start off, let's try to answer our first question about the connection between cardiovascular disease deaths and gender/ethnicity. Let's take a bird's eye view and look at the cardiovascular disease mortality rates in United States controlling for gender through the use of choropleth maps.

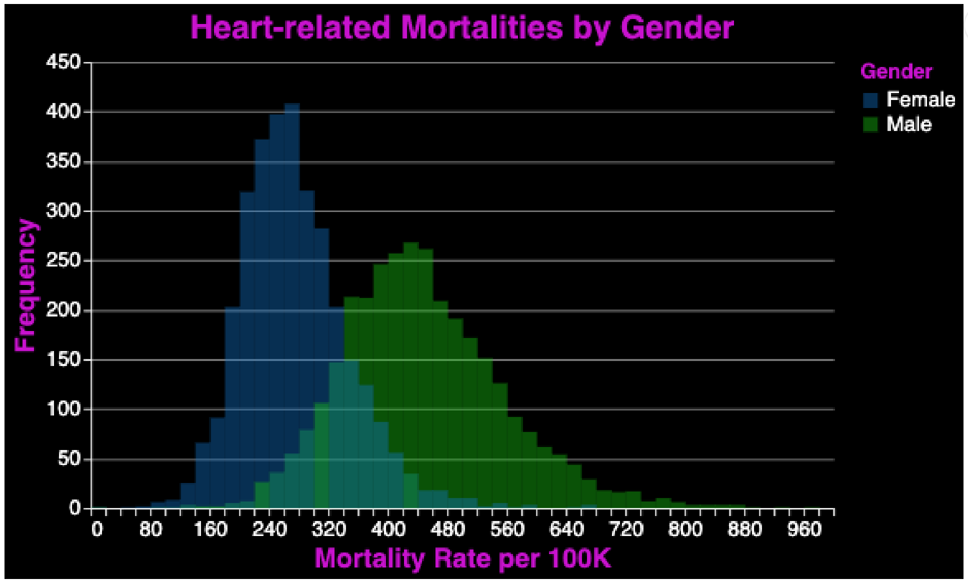
```
(create_choropleth('Cardiovascular Disease Mortality Rate for Males', df_mortality_short_county_male)  \

    #Adding annotations
    + alt.Chart().mark_point(size=21000,color=range_[3],filled=False,x=340,y=200,width=20000,height=1000) \
    + alt.Chart().mark_text(text='Southeastern Region Cluster',dx=-110,dy=110,fontSize=20,fontWeight='bold',color=range_[3]) \
    + alt.Chart().mark_point(shape='arrow',angle=45,size=400,color=range_[3],x=260,y=235) |\

    create_choropleth('Cardiovascular Disease Mortality Rate for Females', df_mortality_short_county_female)\

    + alt.Chart().mark_point(size=21000,color=range_[3],filled=False,x=340,y=200,width=20000,height=1000) \
    + alt.Chart().mark_text(text='Southeastern Region Cluster',dx=-110,dy=110,fontSize=20,fontWeight='bold',color=range_[3]) \
    + alt.Chart().mark_point(shape='arrow',angle=45,size=400,color=range_[3],x=260,y=235)

).configure_legend(titleFontSize=14,labelFontSize=14,titleColor=range_[3]).configure_title(fontSize=20,color=range_[3])
```


Cardiovascular Disease Mortality Rate for Males
Southeastern Region Cluster
Cardiovascular Disease Mortality Rate for Females
Southeastern Region Cluster
Deaths per 100K
1,000
800
600
400
200

As we can see, the mortality rate for males seems to be a lot higher than females throughout the US. We can also see some apparent clustering of deaths in the south-east region of the US for both genders. Now let's see if the histograms for the mortality rate for genders match what these maps show.

```
def mortality_histogram(src, col, title, opacity=0.6):
    """
    Creates a histogram.

    :param src: Source dataframe.
    :param col: Column of the source dataframe for histogram calculation.
    :param title: Title of the visualization.
    :param opacity: Opacity to have better visualizations with overlaps.

    :return: Altair histogram.
    """
    return alt.Chart(src).mark_bar(
        opacity=opacity,
        binSpacing=0,
        clip=True
        ).encode(
            alt.X('Mortality Rate per 100K:Q', title='Mortality Rate per 100K').bin(maxbins=100).scale(domain=(0, 1000)),
            alt.Y('count()',title='Frequency').stack(None),
            alt.Color('{}:N'.format(col)).scale(range=range_)
        ).properties(
            width=500,
            height=300,
            title=title
        )
```

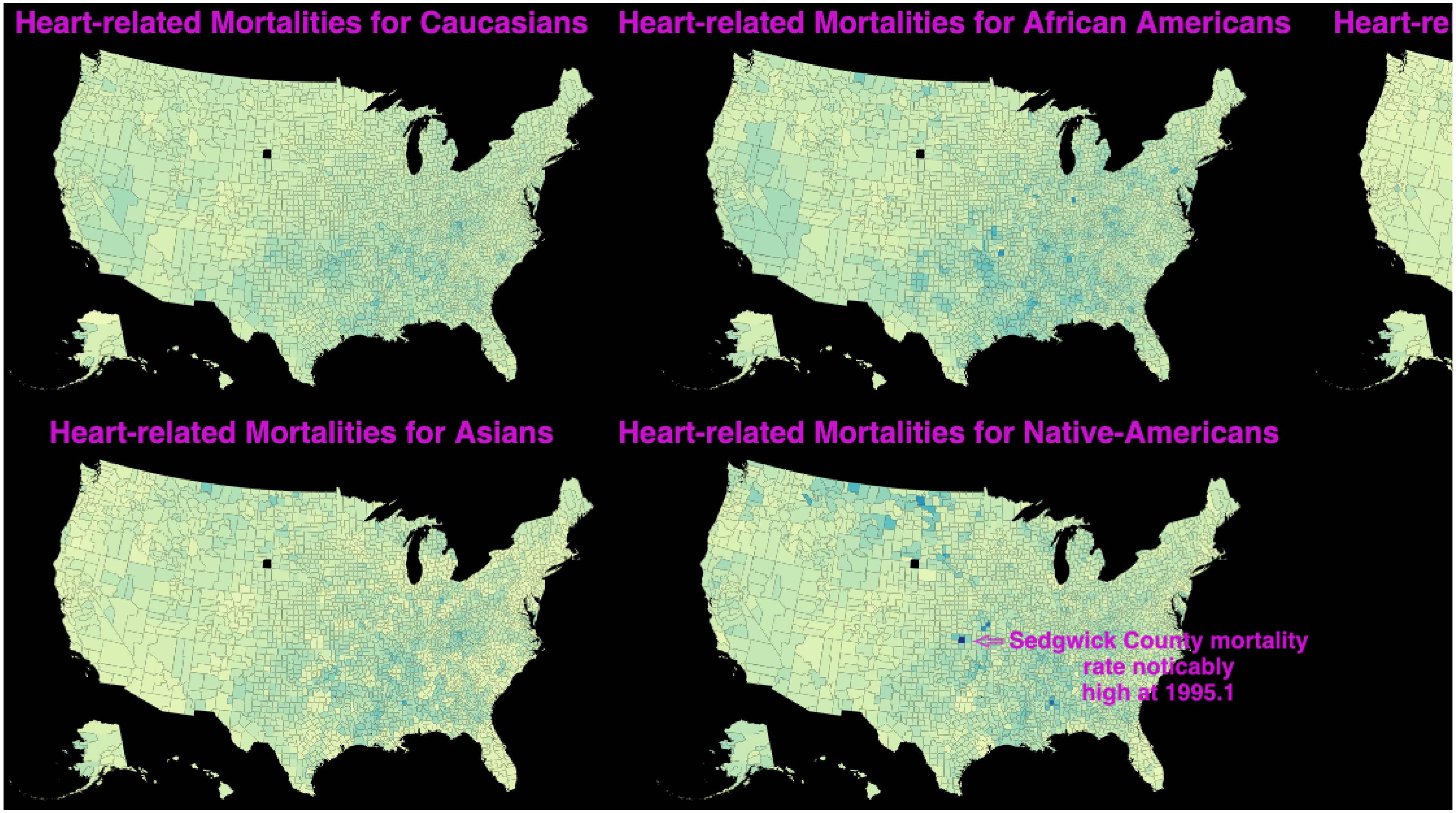
```
mortality_histogram(df_mortality_county_imputed_short_just_gender, 'Gender', 'Heart-related Mortalities by Gender',.4).configure_axis(
    titleFontSize=18,labelFontSize=14,titleColor=range_[3]
    ).configure_title(fontSize=22).configure_legend(titleFontSize=14,labelFontSize=14,titleColor=range_[3])
```



The histograms for genders corroborates what we found in the choropleth maps, in that it seems that males predominantly have higher cardiovascular disease mortality rates than females.

Next, let's visualize the mortality rates while accounting for race/ethnicity, again using choropleth maps.

```
((create_choropleth('Heart-related Mortalities for Caucasians', df_mortality_short_county_white) | \
    create_choropleth('Heart-related Mortalities for African Americans', df_mortality_short_county_black) | \
    create_choropleth('Heart-related Mortalities for Hispanics', df_mortality_short_county_hispanic)
    ) & \
    (create_choropleth('Heart-related Mortalities for Asians', df_mortality_short_county_asian) | \
    create_choropleth('Heart-related Mortalities for Native-Americans', df_mortality_short_county_native_american)\
    + alt.Chart().mark_text(text='Sedgwick County mortality\n rate noticably\n high at 1995.1',lineBreak='\n',fontSize=20,fontWeight='bold',x=430,y=160,c
    + alt.Chart().mark_point(shape='arrow',angle=270,size=500,x=285,y=160,color=range_[3])
    )
).configure_legend(titleFontSize=20,labelFontSize=20,titleColor=range_[3]).configure_title(fontSize=26)
```


Heart-related Mortalities for Caucasians
Heart-related Mortalities for African Americans
Heart-rel
Heart-related Mortalities for Asians
Heart-related Mortalities for Native-Americans
⇦ Sedgwick County mortality rate noticably high at 1995.1

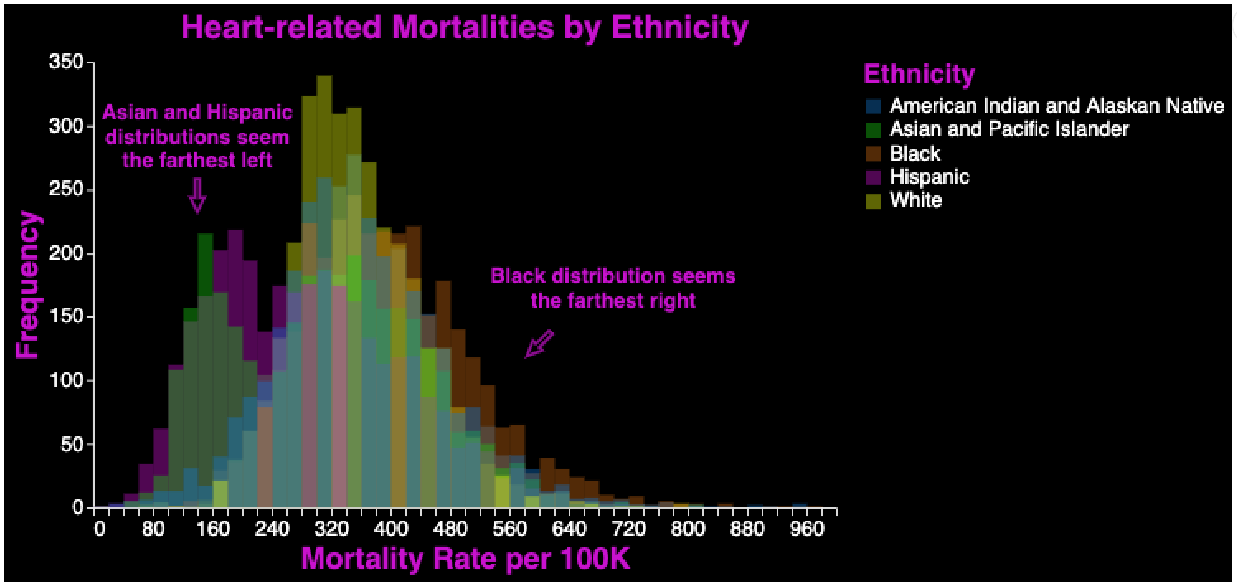
```
#looking up info for Sedgwick County out of curiosity. Commented out to make notebook concise.

#df_mortality_short_county_native_american['Mortality Rate per 100K'].idxmax()
#df_mortality.iloc[18005]
```

It's not particularly easy to tell any major differences, but it seems that the mortality rates for African-Americans are slightly higher than the rest of the ethnicities. There are some clusters of counties for Native Americans that seem pretty high as well. These could possibly be Native American reservations, however this is pure speculation.

As for large general clusters, the story is similar here: For all race/ethnicity categories, the south-eastern region of the US has the highest mortality rate caused by heart disease.

In order to get a better look at the mortality rates for each ehtnicity, let's visualize the histograms for mortality rates with respect to ethnicity.

```
(mortality_histogram(df_mortality_county_imputed_short_just_race, 'Ethnicity', 'Heart-related Mortalities by Ethnicity', opacity=.4) \
    + alt.Chart().mark_text(text='Black distribution seems \nthe farthest right',lineBreak='\n',fontSize=14,fontWeight='bold',x=350,y=145,color=range_[3]
    + alt.Chart().mark_point(shape='arrow',angle=225,color=range_[3],size=500,x=300,y=190)
    + alt.Chart().mark_text(text='Asian and Hispanic\n distributions seem\n the farthest left',lineBreak='\n',fontSize=14,fontWeight='bold',x=70,y=35,col
    + alt.Chart().mark_point(shape='arrow',angle=180,color=range_[3],size=500,x=70,y=90)
 ).configure_axis(titleFontSize=20,labelFontSize=14,titleColor=range_[3],gridColor='black'
 ).configure_title(fontSize=22
 ).configure_legend(titleFontSize=18,titleColor=range_[3],labelFontSize=14,labelLimit=250)
```



So it is fairly messy, but we can tell from the chart that the distributions for Hispanics and Asians peak at lower mortality rates than the distributions for the other ethnicities. The White distribution peaks around the middle while the Black distribution seems to be the furthest overall to the right. This seems to be in accordance with the choropleth maps.

Now let's test if gender and/or race/ethnicity is statistically significant at a P-value of 5% when we use a linear regression model to control for these variables as well as states. We apply one-hot encoding for all categorical variables of interest.

```
def get_model_results(model, filter_out_with_name_contains=None):
  """
  Formats the results of a fitted model with features statistically significant at a P-value of 5%.

  :param model: Fitted model.
  :param filter_out_with_name_contains: Whether to drop features from the output if the name of the feature contains this text.

  :return: Model results formatted as a dataframe.
  """
  model_summary = model.summary()
  results_as_html = model_summary.tables[1].as_html()
  df = pd.read_html(results_as_html, header=0, index_col=0)[0]
  df.index.name = 'Feature'
  if filter_out_with_name_contains:
    df = df.loc[~df.index.str.contains(filter_out_with_name_contains)]
  df=df.loc[~df.index.str.contains('const')]
  return df[df['P>|t|'] <= 0.05]
```

```
df_mortality_county_imputed_short_no_overall_one_hot = pd.get_dummies(df_mortality_county_imputed_short_no_overall, columns=['Gender', 'Ethnicity', 'Stat

#Let's standardize the columns due to different variable types
input_columns = [col for col in df_mortality_county_imputed_short_no_overall_one_hot.columns if col.startswith('State') or\
                 col.startswith('Ethnicity') or col.startswith('Gender')
                 ]
df_mortality_county_imputed_short_no_overall_one_hot[input_columns] = StandardScaler().fit_transform(df_mortality_county_imputed_short_no_overall_one_hot

#Let's get our X and y dataframes and add a constant to the X dataframe
df_mortality_county_imputed_short_no_overall_one_hot_x = df_mortality_county_imputed_short_no_overall_one_hot[input_columns]
df_mortality_county_imputed_short_no_overall_one_hot_y = df_mortality_county_imputed_short_no_overall_one_hot['Mortality Rate per 100K']
df_mortality_county_imputed_short_no_overall_one_hot_x = sm.add_constant(df_mortality_county_imputed_short_no_overall_one_hot_x)

#Renaming columns for table visualization
df_mortality_county_imputed_short_no_overall_one_hot_x=df_mortality_county_imputed_short_no_overall_one_hot_x.rename({'Gender_Male':'Gender: Male',
    'Ethnicity_Asian and Pacific Islander':'Ethnicity: Asian/Pacific Islander','Ethnicity_Black':'Ethnicity: Black','Ethnicity_Hispanic':'Ethnicity: Hisp
    'Ethnicity_White':'Ethnicity: White'
    },axis=1
    )


df_mortality_model = sm.OLS(df_mortality_county_imputed_short_no_overall_one_hot_y, df_mortality_county_imputed_short_no_overall_one_hot_x).fit()
get_model_results(df_mortality_model, 'State') # getting results back, while dropping the rows that account for each state so output is concise'''
```

Feature	coef	std err	t	P>|t|	[0.025	0.975]
Gender: Male	35.3828	0.603	58.638	0.00	34.200	36.566
Ethnicity: Asian/Pacific Islander	-14.6600	0.763	-19.207	0.00	-16.156	-13.164
Ethnicity: Black	13.7744	0.763	18.047	0.00	12.278	15.270
Ethnicity: Hispanic	-19.5108	0.763	-25.563	0.00	-21.007	-18.015
Ethnicity: White	-1.9569	0.763	-2.564	0.01	-3.453	-0.461

Note: We filter out the independent variables for each state to make the output concise.

Model coefficients suggest that gender and race/ethnicity are both statistically significant. Notably, males have a positive coefficient of almost 71, and African Americans have a positive coefficient of around 34.

We'll do more analysis on these and other variables from the survey dataset. For now let's move on to our next goal, which is to examine the correlation between personal income and cardiovascular disease mortalities. We'll do this by creating a pivot table from the income dataset with personal income per capita, total personal income, and population number as columns.

```
df_income_short_pivot = df_income_short.pivot_table('2019', ['GeoFIPS'], 'Description'
).reset_index().set_axis(['GeoFIPS', 'personal_income_per_capita','personal_income', 'population'], axis=1)

df_income_short_pivot.head()
```

	GeoFIPS	personal_income_per_capita	personal_income	population
0	0	56003.000000	1.848933e+10	3.300956e+08
1	1000	43407.000000	2.172375e+08	5.003725e+06
2	1001	42925.666667	2.503001e+06	5.829167e+04
3	1003	48331.000000	1.098884e+07	2.271433e+05
4	1005	35002.333333	8.811507e+05	2.518167e+04

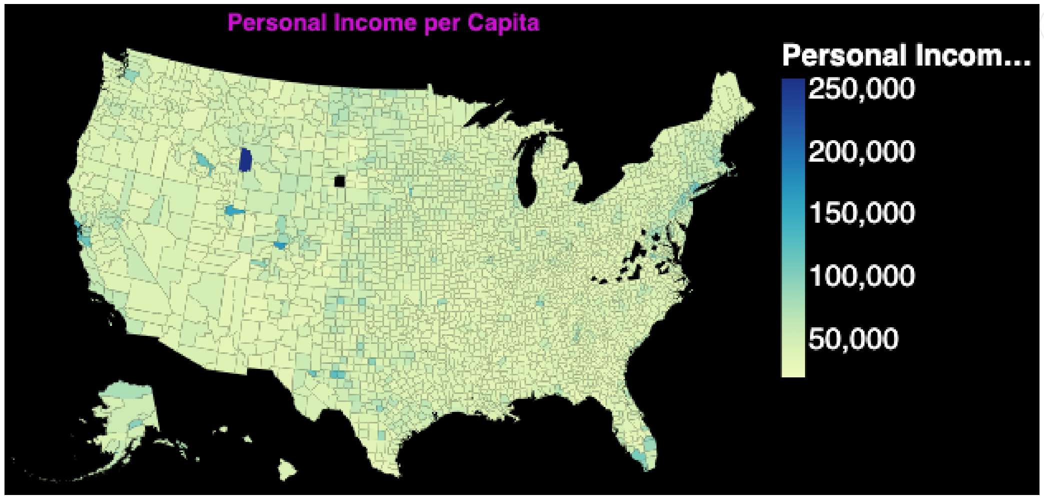
Let's join the mortality and income data using the location identifier.

```
df_mortality_with_income = pd.merge(df_mortality_county_imputed_short_overall, df_income_short_pivot, how='inner', left_on='locationid', right_on='GeoFIF
    {'personal_income_per_capita':'Personal Income per Capita'},axis=1
    )
df_mortality_with_income.head()
```

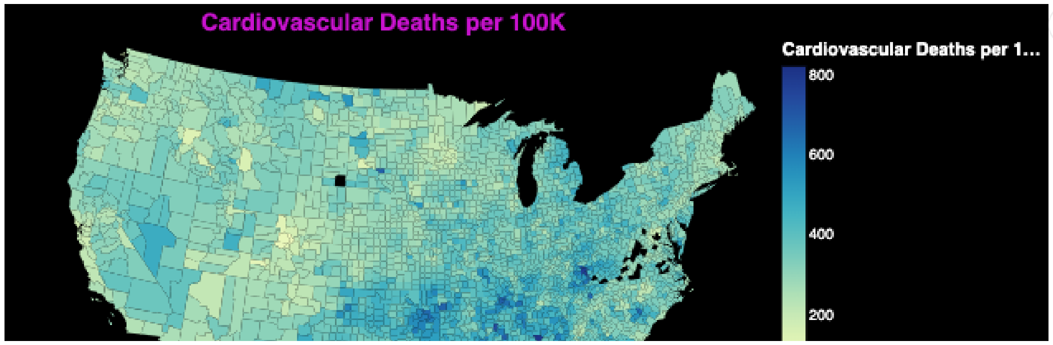
	State	County	geographiclevel	Mortality Rate per 100K	Gender	Ethnicity	locationid	y_lat	x_lon	GeoFIPS	Personal Income per Capita	personal_income	populatio
0	AK	Aleutians East	County	182.400	Overall	Overall	2013	55.442393	-161.959930	2013	57873.666667	1.967377e+05	3400.00000
1	AK	Aleutians West	County	172.600	Overall	Overall	2016	53.648343	-166.917533	2016	60098.333333	3.161803e+05	5262.00000
2	AK	Anchorage	County	255.600	Overall	Overall	2020	61.159145	-149.104559	2020	66530.333333	1.945064e+07	292376.33333
3	AK	Bethel	County	343.400	Overall	Overall	2050	60.923648	-159.753262	2050	44762.333333	8.325020e+05	18597.33333
4	AK	Bristol Bay	County	269.825	Overall	Overall	2060	58.753496	-156.694662	2060	135254.666667	1.184193e+05	876.33333

Is there a correlation between deaths and income? First, let's look at the choropleth map of personal income per capita and compare it with the choropleth map of mortalities. (Note: these were not included in our final report)

```
create_choropleth('Personal Income per Capita', df_mortality_with_income, legend_title='Personal Income per Capita', data_col='Personal Income per Capita
    ).configure_legend(titleFontSize=12).configure_title(fontSize=16).configure_legend(titleFontSize=20,labelFontSize=20)
```



```
create_choropleth('Cardiovascular Deaths per 100K', df_mortality_with_income, legend_title='Cardiovascular Deaths per 100K', data_col='Mortality Rate per
    ).configure_legend(titleFontSize=12).configure_title(fontSize=16)
```


Cardiovascular Deaths per 100K
Cardiovascular Deaths per 1...
800
600
400
200

It might not be immediately evident upon first glance, but upon further inspection it seems as though the counties with less income may have higher mortality rates, but these maps alone are insufficient, and of course there may be confounding variables.

Let's create a scatterplot of these two variables to see if we can find any interesting patterns. We will also create a line of best fit using polynomial regression.

Note: The chart below is interactive. Place your cursor to get more information about the data point or use your mouse to zoom in and out.

```
chart=alt.Chart(df_mortality_with_income).mark_circle(size=40,opacity=.5).encode(
    x=alt.X('Personal Income per Capita', title='Personal Income per capita'),
    y=alt.Y('Mortality Rate per 100K', title='Mortality Rate per 100K'),
    tooltip=['State', 'County', 'Ethnicity', 'Personal Income per Capita'],
    color=alt.value(range_[0])
).properties(
    width=800,
    height=400,
    title='Personal Income per Capita vs. Cardiovascular Disease Mortalities'
).interactive()

X=df_mortality_with_income[['Personal Income per Capita']] #Using double brackets so that X will be a dataframe, not series.
y=df_mortality_with_income['Mortality Rate per 100K']

poly_feats=PolynomialFeatures(degree=3)
Xpoly=poly_feats.fit_transform(X)
polyreg=LinearRegression()
polyreg.fit(Xpoly,y)
```