```
import os
import shutil
import pandas as pd
import numpy as np
import requests
from sklearn.model_selection import train_test_split
from lightgbm import LGBMRegressor
import shap
import matplotlib.pyplot as plt  # For visualizations
import seaborn as sns

supress_warnings = True


# Set seed for reproducibility
np.random.seed(42)
```

Data Loading and Preparation

```
import pandas as pd
import numpy as np
import requests
from io import BytesIO
import zipfile
import os

def download_csv(url, filename):
    print(f"Downloading {filename} ...")
    r = requests.get(url)
    r.raise_for_status()
    with open(filename, "wb") as f:
        f.write(r.content)
    print(f"Saved to {filename}")


places_url = "https://data.cdc.gov/api/views/cwsq-ngmh/rows.csv?acces
places_filepath = "/Users/sankates/workspace/MSAI/AI-391MCSML/PLACES_(

# Add check for file existence
if not os.path.exists(places_filepath):
    download_csv(places_url, places_filepath)
else:
    print(f"File already exists at {places_filepath}. Skipping downlo

places = pd.read_csv(places_filepath, dtype={'LocationID':'str'})
places = places.rename(columns={'LocationID': 'fips'})
```

```
File already exists at /Users/sankates/workspace/MSAI/AI-391MCSML/PLAC
```

```
# Drop unnecessary columns
places = places.drop(columns=['Year', 'DataSource', 'StateDesc', 'Data

# Display the first few rows of the dataframe
places.head()
```

	StateAbbr	CountyName	CountyFIPS	LocationName	Category	Measure	D
0	FL	Miami-Dade	12086	12086010025	Health Outcomes	Stroke among adults	
1	FL	Miami-Dade	12086	12086002709	Disability	Vision disability among adults	
2	FL	Miami-Dade	12086	12086007807	Disability	Vision disability among adults	
3	FL	Miami-Dade	12086	12086001206	Health Status	Frequent physical distress among adults	

```
places.info()

places.describe().T
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 3183048 entries, 0 to 3183047
Data columns (total 19 columns):
 #   Column                 Dtype
---  ------                 -----
 0   StateAbbr              object
 1   CountyName             object
 2   CountyFIPS             object
 3   LocationName           int64
 4   Category               object
 5   Measure                object
 6   Data_Value_Unit        object
 7   Data_Value_Type        object
 8   Data_Value             float64
 9   Low_Confidence_Limit   float64
 10  High_Confidence_Limit  float64
 11  TotalPopulation        int64
 12  TotalPop18plus         int64
 13  Geolocation            object
 14  fips                   object
 15  CategoryID             object
 16  MeasureId              object
 17  DataValueTypeID        object
 18  Short_Question_Text    object
dtypes: float64(3), int64(3), object(13)
memory usage: 461.4+ MB
```

	count	mean	std	min	
LocationName	3183048.0	2.781862e+10	1.601556e+10	1.001020e+09	1.2
Data_Value	3183048.0	2.569415e+01	2.296357e+01	2.000000e-01	9.1
Low_Confidence_Limit	3183048.0	2.346279e+01	2.192081e+01	2.000000e-01	8.0
High_Confidence_Limit	3183048.0	2.797654e+01	2.394928e+01	3.000000e-01	1.0
TotalPopulation	3183048.0	3.972090e+03	1.673262e+03	5.400000e+01	2.7
TotalPop18plus	3183048.0	3.094050e+03	1.273252e+03	5.000000e+01	2.1

```
# Ensure 'CountyFIPS' is treated as a string
places['CountyFIPS'] = places['CountyFIPS'].astype(str)
```

```
# Pivot the DataFrame to have separate columns for DIABETES and STROKI

places_filtered = places[
    places['MeasureId'].isin(["DIABETES", "STROKE"])
][['fips', 'CountyFIPS', 'Measure', 'Data_Value']]
places_pivot = places_filtered.pivot(index=['fips', 'CountyFIPS'], co
places_pivot = places_pivot.reset_index().rename_axis(None, axis=1)

places_pivot.head()
```

	fips	CountyFIPS	Diagnosed diabetes among adults	Stroke among adults
0	01001020100	1001	13.8	4.2
1	01001020200	1001	14.7	4.0
2	01001020300	1001	14.1	4.2
3	01001020400	1001	13.4	4.2
4	01001020501	1001	11.4	3.2

```
# Calculate total Data_Value by CountyFIPS and Measure
total_data_value_by_county_measure = places_filtered.groupby(['County
print(total_data_value_by_county_measure.head(10))
```

```
  CountyFIPS                          Measure  Data_Value
0      10001  Diagnosed diabetes among adults       537.3
1      10001              Stroke among adults       168.0
2      10003  Diagnosed diabetes among adults      1878.0
3      10003              Stroke among adults       512.3
4      10005  Diagnosed diabetes among adults       996.6
5      10005              Stroke among adults       323.6
6       1001  Diagnosed diabetes among adults       227.4
7       1001              Stroke among adults        66.5
8       1003  Diagnosed diabetes among adults       589.0
9       1003              Stroke among adults       172.1
```

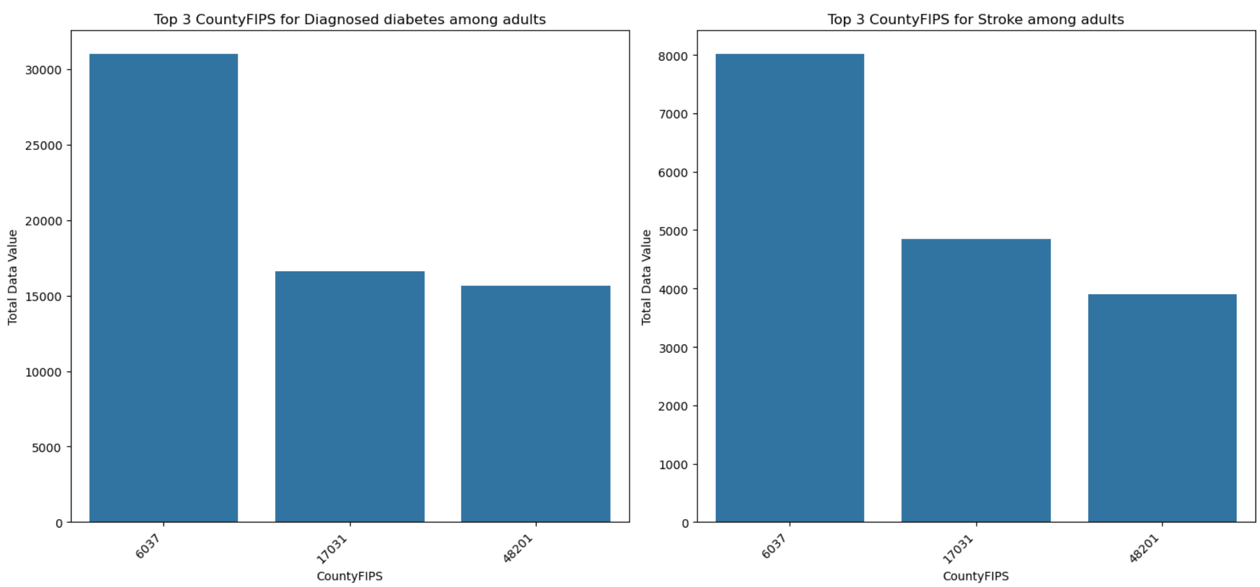
```
# Create dataset for 'Diagnosed diabetes among adults'
diabetes_data = total_data_value_by_county_measure[
    total_data_value_by_county_measure['Measure'] == "Diagnosed diabe
].copy()

# Create dataset for 'Stroke among adults'
stroke_data = total_data_value_by_county_measure[
```

```
    total_data_value_by_county_measure['Measure'] == "Stroke among adu
].copy()

# Prepare places dataset for merging (select relevant columns and drop
county_info = places[['CountyFIPS', 'StateAbbr', 'CountyName']].drop_(

# Merge diabetes_data with county_info
diabetes_data = pd.merge(diabetes_data, county_info, on='CountyFIPS',

# Merge stroke_data with county_info
stroke_data = pd.merge(stroke_data, county_info, on='CountyFIPS', how=

print("Diabetes Data Head:")
print(diabetes_data.head())
print("\nStroke Data Head:")
print(stroke_data.head())
```

```
Diabetes Data Head:
  CountyFIPS                          Measure  Data_Value StateAbbr  \
0      10001  Diagnosed diabetes among adults       537.3        DE
1      10003  Diagnosed diabetes among adults      1878.0        DE
2      10005  Diagnosed diabetes among adults       996.6        DE
3       1001  Diagnosed diabetes among adults       227.4        AL
4       1003  Diagnosed diabetes among adults       589.0        AL

   CountyName
0        Kent
1  New Castle
2      Sussex
3     Autauga
4     Baldwin

Stroke Data Head:
  CountyFIPS               Measure  Data_Value StateAbbr  CountyName
0      10001  Stroke among adults       168.0        DE        Kent
1      10003  Stroke among adults       512.3        DE  New Castle
2      10005  Stroke among adults       323.6        DE      Sussex
3       1001  Stroke among adults        66.5        AL     Autauga
4       1003  Stroke among adults       172.1        AL     Baldwin
```

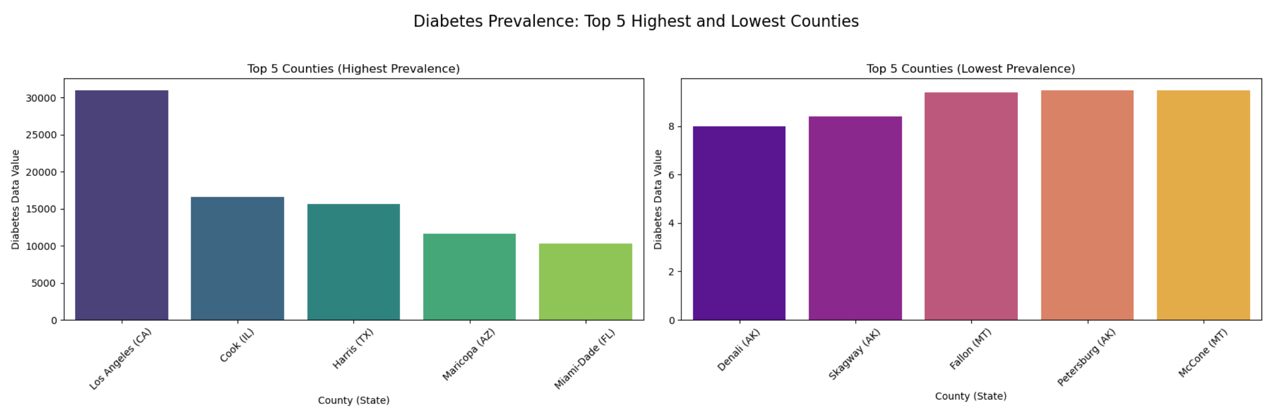
```
# Get unique measures
unique_measures = total_data_value_by_county_measure['Measure'].unique

plt.figure(figsize=(15, 7))

for i, measure in enumerate(unique_measures):
```

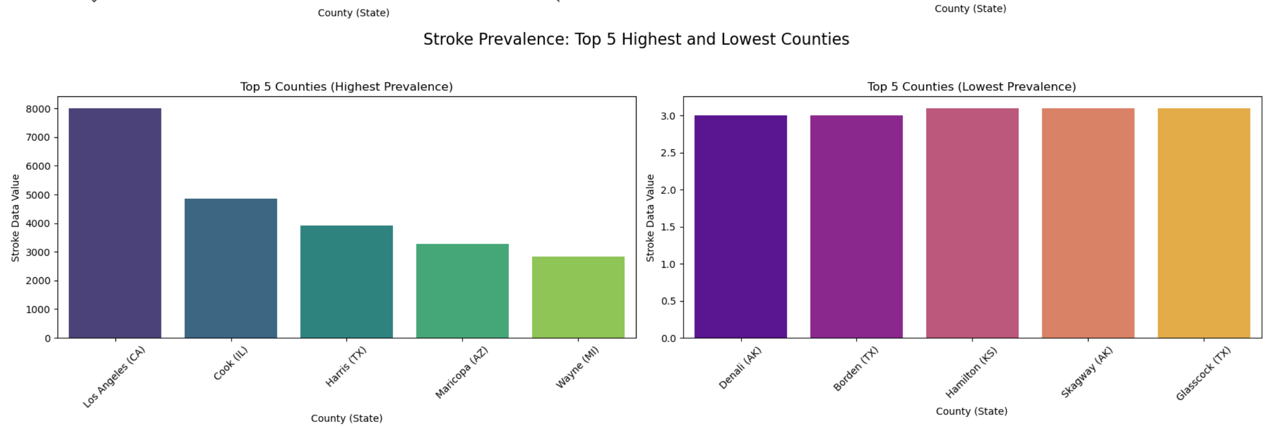
```
        # Filter data for the current measure
        measure_data = total_data_value_by_county_measure[
            total_data_value_by_county_measure['Measure'] == measure
        ]

        # Get top 3 CountyFIPS for the current measure
        top_3_counties = measure_data.nlargest(3, 'Data_Value')

        # Create a subplot for each measure
        plt.subplot(1, len(unique_measures), i + 1)
        sns.barplot(x='CountyFIPS', y='Data_Value', data=top_3_counties)
        plt.title(f'Top 3 CountyFIPS for {measure}')
        plt.xlabel('CountyFIPS')
        plt.ylabel('Total Data Value')
        plt.xticks(rotation=45, ha='right')

    plt.tight_layout()
    plt.show()
```



```
# Function to plot top 5 highest and lowest counties for a given measu

def plot_top_and_bottom_counties(df, measure_name, value_col='Data_Va
    # Sort for top 5 highest
    top_5_highest = df.nlargest(5, value_col)
    # Sort for top 5 lowest
    top_5_lowest = df.nsmallest(5, value_col)

    # Create combined label for x-axis
    top_5_highest['County_State'] = top_5_highest['CountyName'] + ' (
    top_5_lowest['County_State'] = top_5_lowest['CountyName'] + ' (' +

    fig, axes = plt.subplots(1, 2, figsize=(18, 6))
    fig.suptitle(f'{measure_name} Prevalence: Top 5 Highest and Lowest

    # Plot top 5 highest
    sns.barplot(
        ax=axes[0],
        x='County_State',
        y=value_col,
        data=top_5_highest,
        hue='County_State',  # Assign x to hue
        palette='viridis',
        legend=False  # Disable the legend for the same effect
    )
    axes[0].set_title('Top 5 Counties (Highest Prevalence)')
    axes[0].set_xlabel('County (State)')
    axes[0].set_ylabel(f'{measure_name} Data Value')
    axes[0].tick_params(axis='x', rotation=45)

    # Plot top 5 lowest
    sns.barplot(
        ax=axes[1],
```

```
            x='County_State',
            y=value_col,
            data=top_5_lowest,
            hue='County_State',  # Assign x to hue
            palette='plasma',
            legend=False  # Disable the legend for the same effect
        )
        axes[1].set_title('Top 5 Counties (Lowest Prevalence)')
        axes[1].set_xlabel('County (State)')
        axes[1].set_ylabel(f'{measure_name} Data Value')
        axes[1].tick_params(axis='x', rotation=45)

        plt.tight_layout(rect=[0, 0.03, 1, 0.95])
        plt.show()

    # Plot for Diabetes Data
    plot_top_and_bottom_counties(diabetes_data, 'Diabetes')

    # Plot for Stroke Data
    plot_top_and_bottom_counties(stroke_data, 'Stroke')
```





```
acs_vars = [
    "NAME", "B19013_001E", "B17001_002E", "B23025_005E",
    "B15003_022E", "B15003_023E", "B15003_024E", "B15003_025E",
    "B27001_017E"
]
acs_var_string = ",".join(acs_vars)
print(acs_var_string)
# acs_url = f"https://api.census.gov/data/2022/acs/acs5?get=NAME,B190
# download_csv(acs_url, "/Users/sankates/workspace/MSAI/AI-391MCSMLAC
```

```
NAME,B19013_001E,B17001_002E,B23025_005E,B15003_022E,B15003_023E,B1500
```

```
# Load ACS data
acs = pd.read_json("/Users/sankates/workspace/MSAI/AI-391MCSML/ACS_rav
acs.columns = acs.iloc[0]
acs = acs[1:]

acs['fips'] = acs['state'] + acs['county']

# Rename columns for clarity
acs = acs.rename(columns={
    "B19013_001E": "median_income",
    "B17001_002E": "poverty_count",
    "B23025_005E": "unemployed_count",
    "B27001_017E": "uninsured_count"
})

acs.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 3222 entries, 1 to 3222
Data columns (total 12 columns):
 #   Column            Non-Null Count  Dtype
---  ------            --------------  -----
 0   NAME              3222 non-null   object
 1   median_income     3222 non-null   object
 2   poverty_count     3222 non-null   object
 3   unemployed_count  3222 non-null   object
 4   B15003_022E       3222 non-null   object
 5   B15003_023E       3222 non-null   object
 6   B15003_024E       3222 non-null   object
 7   B15003_025E       3222 non-null   object
 8   uninsured_count   3222 non-null   object
 9   state             3222 non-null   object
 10  county            3222 non-null   object
 11  fips              3222 non-null   object
dtypes: object(12)
memory usage: 302.2+ KB
```

```
acs.head()
```

	NAME	median_income	poverty_count	unemployed_count	B15003_022E
1	Autauga County, Alabama	68315	6630	752	6726
2	Baldwin County, Alabama	71039	23445	3825	33474
	Barbour				

```
# ejs_url = "https://gaftp.epa.gov/EJSCREEN/2023/EJSCREEN_2023_USPR_Pu
# download_csv(ejs_url, "/Users/sankates/workspace/MSAI/AI-391MCSMLEJS

# with zipfile.ZipFile("EJSCREEN.zip", "r") as z:
#     z.extractall("ejscreen")

bg = pd.read_csv("/Users/sankates/workspace/MSAI/AI-391MCSML/EJSCREEN_

base_cols = ['ID','STATE_NAME','ST_ABBREV','CNTY_NAME','ACSTOTPOP']
missing_base = [c for c in base_cols if c not in bg.columns]
print(missing_base)

print(bg.info())
bg.head(5)
```

```
/var/folders/xv/jppz3tnj7z10dvcn0jp_xfk00000gp/T/ipykernel_60556/30873
  bg = pd.read_csv("/Users/sankates/workspace/MSAI/AI-391MCSML/EJSCREEN
[]
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 243022 entries, 0 to 243021
Columns: 229 entries, ID to Shape_Area
dtypes: float64(173), int64(3), object(53)
memory usage: 424.6+ MB
None
```

	ID	STATE_NAME	ST_ABBREV	CNTY_NAME	REGION	ACSTOTPOP	ACSI
0	10010201001	Alabama	AL	Autauga County	4	558.0	
1	10010201002	Alabama	AL	Autauga County	4	1307.0	
2	10010202001	Alabama	AL	Autauga County	4	548.0	
3	10010202002	Alabama	AL	Autauga County	4	1313.0	

```
# Pick candidate feature columns
candidate_features = [
    'PM25','OZONE','DSLPM','RSEI_AIR','PTRAF',
    'PNPL','PRMP','PWDIS','DWATER','NO2',
    'DEMOGIDX_2','DEMOGIDX_5',
    'PEOPCOLORPCT','LOWINCPCT','UNEMPPCT','LINGISOPCT','LESSHSPCT','UN
]

feature_cols = [c for c in candidate_features if c in bg.columns]
print("Using feature columns:", feature_cols)
```

```
Using feature columns: ['PM25', 'OZONE', 'DSLPM', 'RSEI_AIR', 'PTRAF',
```

```
# Aggregate block group data to county level

output_path = "/Users/sankates/workspace/MSAI/AI-391MCSML/EJSCREEN_cou

# Check if the file already exists
if os.path.exists(output_path):
    county_ejs = pd.read_csv(output_path)
    print(county_ejs.info())
    print(f"Loaded county_ejs from existing file: {output_path}")
else:
    # Ensure numeric
    for col in feature_cols + ['ACSTOTPOP']:
        bg[col] = pd.to_numeric(bg[col], errors='coerce')

    # Drop rows without population
    bg = bg[bg['ACSTOTPOP'] > 0].copy()

    group_cols = ['ST_ABBREV','STATE_NAME','CNTY_NAME']

    def weighted_mean(series, weights):
        mask = series.notna() & weights.notna() & (weights > 0)
        if not mask.any():
            return np.nan
        return np.average(series[mask], weights=weights[mask])

    grouped = bg.groupby(group_cols, as_index=False)

    records = []
    for keys, group in grouped:
        rec = {}
```

```
        # keys is tuple matching group_cols
        for k, name in zip(keys, group_cols):
            rec[name] = k
        rec['total_pop'] = group['ACSTOTPOP'].sum()
        for col in feature_cols:
            rec[col] = weighted_mean(group[col], group['ACSTOTPOP'])
        records.append(rec)

    county_ejs = pd.DataFrame(records)
    county_ejs.to_csv(output_path, index=False)
    print(f"Generated and saved county_ejs to: {output_path}")

county_ejs.head()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 3233 entries, 0 to 3232
Data columns (total 23 columns):
 #   Column        Non-Null Count  Dtype
---  ------        --------------  -----
 0   ST_ABBREV     3233 non-null   object
 1   STATE_NAME    3233 non-null   object
 2   CNTY_NAME     3233 non-null   object
 3   total_pop     3233 non-null   float64
 4   PM25          3109 non-null   float64
 5   OZONE         3109 non-null   float64
 6   DSLPM         3192 non-null   float64
 7   RSEI_AIR      3233 non-null   float64
 8   PTRAF         3222 non-null   float64
 9   PNPL          3230 non-null   float64
 10  PRMP          3230 non-null   float64
 11  PWDIS         3192 non-null   float64
 12  DWATER        3142 non-null   float64
 13  NO2           3222 non-null   float64
 14  DEMOGIDX_2    3233 non-null   float64
 15  DEMOGIDX_5    3222 non-null   float64
 16  PEOPCOLORPCT  3233 non-null   float64
 17  LOWINCPCT     3233 non-null   float64
 18  UNEMPPCT      3233 non-null   float64
 19  LINGISOPCT    3233 non-null   float64
 20  LESSHSPCT     3233 non-null   float64
 21  UNDER5PCT     3233 non-null   float64
 22  OVER64PCT     3233 non-null   float64
dtypes: float64(20), object(3)
memory usage: 581.1+ KB
None
Loaded county_ejs from existing file: /Users/sankates/workspace/MSAI/AI
```

	ST_ABBREV	STATE_NAME	CNTY_NAME	total_pop	PM25	OZONE	DSLPM	RSEI_

0	AK	Alaska	Aleutians East Borough	3407.0	NaN	NaN	NaN	18.79
1	AK	Alaska	Aleutians West Census Area	5219.0	NaN	NaN	NaN	3.63
2	AK	Alaska	Anchorage Municipality	290674.0	NaN	NaN	NaN	47.48

```
# Load FIPS lookup data

fips_lookup = pd.read_excel('/Users/sankates/workspace/MSAI/AI-391MCSM
print(fips_lookup.head())

# Rename columns in fips_lookup for easier merging
# Corrected column names based on available fips_lookup (from kernel s
fips_lookup = fips_lookup.rename(columns={'Name': 'STATE_NAME', 'fips

# Create the new dataset by merging county_ejs with fips_lookup
county_ejs_with_fips = pd.merge(
    county_ejs,
    fips_lookup[['STATE_NAME', 'CNTY_NAME', 'fips_from_lookup']],
    on=['STATE_NAME', 'CNTY_NAME'],
    how='left'
)

# Rename the merged fips column to 'fips'
county_ejs_with_fips = county_ejs_with_fips.rename(columns={'fips_fror

county_ejs_with_fips.tail(10)
```

```
   State FIPS Code  County FIPS Code       Area Name     Name  fips
0                1                 1  Autauga County  Alabama  1001
1                1                 3  Baldwin County  Alabama  1003
2                1                 5  Barbour County  Alabama  1005
3                1                 7     Bibb County  Alabama  1007
4                1                 9   Blount County  Alabama  1009
```

	ST_ABBREV	STATE_NAME	CNTY_NAME	total_pop	PM25	OZONE	I
3223	WY	Wyoming	Niobrara County	2460.0	4.460460	64.361420	0.0
3224	WY	Wyoming	Park County	29878.0	4.630895	60.448647	0.0

3225	WY	Wyoming	Platte County	8618.0	4.454283	65.295025	0.0
3226	WY	Wyoming	Sheridan County	31176.0	5.131052	58.859135	0.0
3227	WY	Wyoming	Sublette County	8801.0	3.551251	63.564417	0.0
3228	WY	Wyoming	Sweetwater County	42079.0	4.282689	63.228821	0.1
3229	WY	Wyoming	Teton County	23346.0	4.445018	61.689650	0.0

```
# Convert 'fips' column to int64, handling NaN values
# Fill NaN values with 0 before converting to int, as int type cannot
county_ejs_with_fips['fips'] = county_ejs_with_fips['fips'].fillna(0)

output_csv_path = "/Users/sankates/workspace/MSAI/AI-391MCSML/county_
county_ejs_with_fips.to_csv(output_csv_path, index=False)

print(f"DataFrame saved to {output_csv_path}")
print("Info of saved DataFrame with converted fips column:")
county_ejs_with_fips.info()
county_ejs_with_fips.head()
```

```
DataFrame saved to /Users/sankates/workspace/MSAI/AI-391MCSML/county_e
Info of saved DataFrame with converted fips column:
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 3233 entries, 0 to 3232
Data columns (total 24 columns):
 #   Column        Non-Null Count  Dtype
---  ------        --------------  -----
 0   ST_ABBREV     3233 non-null   object
 1   STATE_NAME    3233 non-null   object
 2   CNTY_NAME     3233 non-null   object
 3   total_pop     3233 non-null   float64
 4   PM25          3109 non-null   float64
 5   OZONE         3109 non-null   float64
 6   DSLPM         3192 non-null   float64
 7   RSEI_AIR      3233 non-null   float64
 8   PTRAF         3222 non-null   float64
 9   PNPL          3230 non-null   float64
 10  PRMP          3230 non-null   float64
 11  PWDIS         3192 non-null   float64
 12  DWATER        3142 non-null   float64
```

```
 13  NO2           3222 non-null   float64
 14  DEMOGIDX_2    3233 non-null   float64
 15  DEMOGIDX_5    3222 non-null   float64
 16  PEOPCOLORPCT  3233 non-null   float64
 17  LOWINCPCT     3233 non-null   float64
 18  UNEMPPCT      3233 non-null   float64
 19  LINGISOPCT    3233 non-null   float64
 20  LESSHSPCT     3233 non-null   float64
 21  UNDER5PCT     3233 non-null   float64
 22  OVER64PCT     3233 non-null   float64
 23  fips          3233 non-null   int64
dtypes: float64(20), int64(1), object(3)
memory usage: 606.3+ KB
```

	ST_ABBREV	STATE_NAME	CNTY_NAME	total_pop	PM25	OZONE	DSLPM	RSEI_
0	AK	Alaska	Aleutians East Borough	3407.0	NaN	NaN	NaN	18.79
1	AK	Alaska	Aleutians West Census Area	5219.0	NaN	NaN	NaN	3.63
2	AK	Alaska	Anchorage Municipality	290674.0	NaN	NaN	NaN	47.48

```
# Load Food Access Research Atlas data
food = pd.read_csv("/Users/sankates/workspace/MSAI/AI-391MCSML/Food A
#print(food.columns)
# CensusTract,State,County,Urban,Pop2010,OHU2010,GroupQuartersFlag,NUM

# Create county FIPS (first 5 digits of tract GEOID)
food['fips'] = food['CensusTract'].str[:5]

# Only use tracts with recorded population
food = food[food['Pop2010'] > 0]

# Functions for weighted averages
def weighted_mean(series, weights):
    mask = series.notna() & weights.notna() & (weights > 0)
    if not mask.any():
        return np.nan
    return np.average(series[mask], weights=weights[mask])

# Aggregate to county level
food_county = (
```

```
    food.groupby('fips')
        .apply(lambda g: pd.Series({
            # Count of low-income / low-access tracts
            'low_access_tracts': g['LILATracts_1And10'].fillna(0).sum

            # Percent of households with low vehicle access
            'pct_low_vehicle_access': weighted_mean(g['HUNVFlag'], g[

            # Poverty / SNAP weighted averages
            'poverty_rate': weighted_mean(g['PovertyRate'], g['Pop201
        }), include_groups=False)
        .reset_index()
)

food_county.head()
```

	fips	low_access_tracts	pct_low_vehicle_access	poverty_rate
0	10001	7.0	0.526215	13.881833
1	10003	19.0	0.239005	11.927730
2	10005	6.0	0.070628	11.873381
3	10010	5.0	0.449341	15.137584
4	10030	4.0	0.223543	10.947872

```
# Ensure 'fips' is numeric
food_county['fips'] = pd.to_numeric(food_county['fips'], errors='coer
print(food_county.nsmallest(5, 'fips'))
```

```
    fips  low_access_tracts  pct_low_vehicle_access  poverty_rate
0  10001                7.0                0.526215     13.881833
1  10003               19.0                0.239005     11.927730
2  10005                6.0                0.070628     11.873381
3  10010                5.0                0.449341     15.137584
4  10030                4.0                0.223543     10.947872
```

```
# Load ERS County Typology data
df = pd.read_csv("/Users/sankates/workspace/MSAI/AI-391MCSML/erscount

# Pivot Attribute → feature columns
rucc = df.pivot_table(
    index=["FIPStxt", "State", "County_Name", "Metro2023"],
    columns="Attribute",
    values="Value",
    aggfunc="first"
).reset_index()

# Clean up column names
rucc.columns.name = None
rucc = rucc.rename(columns={"FIPStxt": "fips"})


# Show result
rucc.head()
```

	fips	State	County_Name	Metro2023	High_Farming_2025	High_Governm
0	01001	AL	Autauga County	1	0	
1	01003	AL	Baldwin County	1	0	
2	01005	AL	Barbour County	0	0	
3	01007	AL	Bibb County	1	0	
4	01009	AL	Blount County	1	0	

```
from functools import reduce


# --- 1. Standardize 'fips' column and select relevant columns for ea

# Prepare rucc
rucc_standardized = rucc.copy()
# Ensure fips is numeric and int64, handle potential non-numeric valu
rucc_standardized['fips'] = pd.to_numeric(rucc_standardized['fips'], 
# Drop redundant state/county name columns as they will come from cou
```

```
rucc_standardized = rucc_standardized.drop(columns=['State', 'County_N

# Prepare food_county (fips is already int64 after previous steps)
food_county_standardized = food_county.copy()
food_county_standardized['fips'] = food_county_standardized['fips'].as

# Prepare county_ejs_with_fips (fips is already int64 after previous s
# This will serve as our base DataFrame for merging.
county_ejs_standardized = county_ejs_with_fips.copy()
county_ejs_standardized['fips'] = county_ejs_standardized['fips'].asty

# Prepare acs
acs_standardized = acs[['fips', 'median_income', 'poverty_count', 'un
acs_standardized['fips'] = pd.to_numeric(acs_standardized['fips'], er

# Prepare diabetes_data
diabetes_standardized = diabetes_data.copy()
diabetes_standardized = diabetes_standardized.rename(columns={'County
# Ensure fips is int64, handle potential non-numeric values by fillin
diabetes_standardized['fips'] = pd.to_numeric(diabetes_standardized['
# Select only fips and the new prevalence column
diabetes_standardized = diabetes_standardized[['fips', 'diabetes_prev

# Prepare stroke_data
stroke_standardized = stroke_data.copy()
stroke_standardized = stroke_standardized.rename(columns={'CountyFIPS
# Ensure fips is int64, handle potential non-numeric values by fillin
stroke_standardized['fips'] = pd.to_numeric(stroke_standardized['fips
# Select only fips and the new prevalence column
stroke_standardized = stroke_standardized[['fips', 'stroke_prev']]

# --- 2. List of DataFrames to merge, starting with county_ejs_with_f
dfs_to_merge = [
    county_ejs_standardized, # Base dataframe
    rucc_standardized,
    food_county_standardized,
    acs_standardized,
    diabetes_standardized,
    stroke_standardized
]

# --- 3. Perform the merge ---
data = reduce(lambda left, right: pd.merge(left, right, on='fips', ho

# Display head to confirm the merge result
```

```
print("Merged Data Head:")
data.head()
```

Merged Data Head:

	ST_ABBREV	STATE_NAME	CNTY_NAME	total_pop	PM25	OZONE	DSLPM	RSEI_
0	AK	Alaska	Aleutians East Borough	3407.0	NaN	NaN	NaN	18.79
1	AK	Alaska	Aleutians West Census Area	5219.0	NaN	NaN	NaN	3.63
2	AK	Alaska	Anchorage Municipality	290674.0	NaN	NaN	NaN	47.48
3	AK	Alaska	Bethel Census Area	18538.0	NaN	NaN	NaN	24.38

```
output_path = "/Users/sankates/workspace/MSAI/AI-391MCSML/data.csv"
data.to_csv(output_path, index=False)
print(f"DataFrame 'data' saved to {output_path}")
```

```
DataFrame 'data' saved to /Users/sankates/workspace/MSAI/AI-391MCSML/da
```

```
# Display info of the final merged DataFrame
print("Merged Data Info:")
data.info()
```

```
Merged Data Info:
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 3233 entries, 0 to 3232
Data columns (total 47 columns):
 #   Column                       Non-Null Count  Dtype
---  ------                       --------------  -----
 0   ST_ABBREV                    3233 non-null   object
 1   STATE_NAME                   3233 non-null   object
 2   CNTY_NAME                    3233 non-null   object
 3   total_pop                    3233 non-null   float64
 4   PM25                         3109 non-null   float64
 5   OZONE                        3109 non-null   float64
 6   DSLPM                        3192 non-null   float64
 7   RSEI_AIR                     3233 non-null   float64
```

```
 8   PTRAF                         3222 non-null   float64
 9   PNPL                          3230 non-null   float64
 10  PRMP                          3230 non-null   float64
 11  PWDIS                         3192 non-null   float64
 12  DWATER                        3142 non-null   float64
 13  NO2                           3222 non-null   float64
 14  DEMOGIDX_2                    3233 non-null   float64
 15  DEMOGIDX_5                    3222 non-null   float64
 16  PEOPCOLORPCT                  3233 non-null   float64
 17  LOWINCPCT                     3233 non-null   float64
 18  UNEMPPCT                      3233 non-null   float64
 19  LINGISOPCT                    3233 non-null   float64
 20  LESSHSPCT                     3233 non-null   float64
 21  UNDER5PCT                     3233 non-null   float64
 22  OVER64PCT                     3233 non-null   float64
 23  fips                          3233 non-null   int64
 24  Metro2023                     3095 non-null   float64
 25  High_Farming_2025             3095 non-null   float64
 26  High_Government_2025          3095 non-null   float64
 27  High_Manufacturing_2025       3095 non-null   float64
 28  High_Mining_2025              3095 non-null   float64
 29  High_Recreation_2025          3095 non-null   float64
 30  Housing_Stress_2025           3095 non-null   float64
 31  Industry_Dependence_2025      3095 non-null   float64
 32  Low_Employment_2025           3095 non-null   float64
 33  Low_PostSecondary_Ed_2025     3095 non-null   float64
 34  Nonspecialized_2025           3095 non-null   float64
 35  Persistent_Poverty_1721       3095 non-null   float64
 36  Population_Loss_2025          3095 non-null   float64
 37  Retirement_Destination_2025   3095 non-null   float64
 38  low_access_tracts             2786 non-null   float64
 39  pct_low_vehicle_access        2786 non-null   float64
 40  poverty_rate                  2785 non-null   float64
 41  median_income                 3095 non-null   object
 42  poverty_count                 3095 non-null   object
 43  unemployed_count              3095 non-null   object
 44  uninsured_count               3095 non-null   object
 45  diabetes_prev                 3094 non-null   float64
 46  stroke_prev                   3094 non-null   float64
dtypes: float64(39), int64(1), object(7)
memory usage: 1.2+ MB
```

```
data.head()
```

	ST_ABBREV	STATE_NAME	CNTY_NAME	total_pop	PM25	OZONE	DSLPM	RSEI_
0	AK	Alaska	Aleutians East Borough	3407.0	NaN	NaN	NaN	18.79
1	AK	Alaska	Aleutians West Census Area	5219.0	NaN	NaN	NaN	3.63
2	AK	Alaska	Anchorage Municipality	290674.0	NaN	NaN	NaN	47.48
3	AK	Alaska	Bethel Census Area	18538.0	NaN	NaN	NaN	24.38

```
data.shape
```

```
(3233, 47)
```

```
# Create a copy of the original 'data' DataFrame
data_cleaned = data.copy()

# 1. Change specified columns to int64
columns_to_convert_to_int = ['median_income', 'poverty_count', 'unemp

for col in columns_to_convert_to_int:
    # Convert to numeric, coercing errors to NaN
    data_cleaned[col] = pd.to_numeric(data_cleaned[col], errors='coer
    # Fill NaN values with 0 before converting to int64
    data_cleaned[col] = data_cleaned[col].fillna(0).astype('int64')

# 2. Drop specified columns
columns_to_drop = ['CNTY_NAME', 'STATE_NAME', 'ST_ABBREV']
data_cleaned = data_cleaned.drop(columns=columns_to_drop)

print("Info of the new data_cleaned DataFrame:")
data_cleaned.info()
print("\nHead of the new data_cleaned DataFrame:")
data_cleaned.head()
```

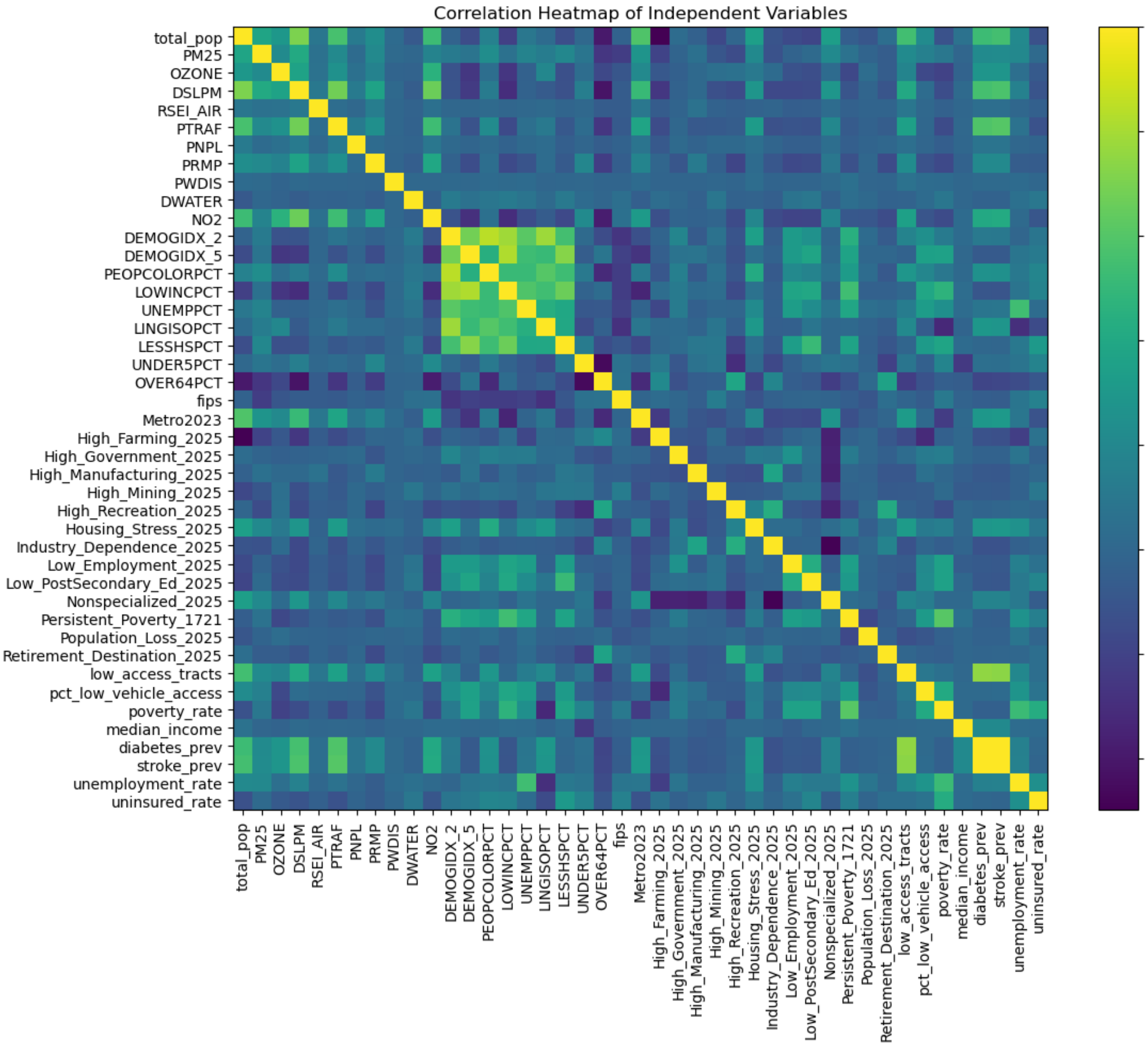
```
Info of the new data_cleaned DataFrame:
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 3233 entries, 0 to 3232
Data columns (total 44 columns):
 #   Column                         Non-Null Count  Dtype  
---  ------                         --------------  -----  
 0   total_pop                      3233 non-null   float64
 1   PM25                           3109 non-null   float64
 2   OZONE                          3109 non-null   float64
 3   DSLPM                          3192 non-null   float64
 4   RSEI_AIR                       3233 non-null   float64
 5   PTRAF                          3222 non-null   float64
 6   PNPL                           3230 non-null   float64
 7   PRMP                           3230 non-null   float64
 8   PWDIS                          3192 non-null   float64
 9   DWATER                         3142 non-null   float64
 10  NO2                            3222 non-null   float64
 11  DEMOGIDX_2                     3233 non-null   float64
 12  DEMOGIDX_5                     3222 non-null   float64
 13  PEOPCOLORPCT                   3233 non-null   float64
 14  LOWINCPCT                      3233 non-null   float64
 15  UNEMPPCT                       3233 non-null   float64
 16  LINGISOPCT                     3233 non-null   float64
 17  LESSHSPCT                      3233 non-null   float64
 18  UNDER5PCT                      3233 non-null   float64
 19  OVER64PCT                      3233 non-null   float64
 20  fips                           3233 non-null   int64  
 21  Metro2023                      3095 non-null   float64
 22  High_Farming_2025              3095 non-null   float64
 23  High_Government_2025           3095 non-null   float64
 24  High_Manufacturing_2025        3095 non-null   float64
 25  High_Mining_2025               3095 non-null   float64
 26  High_Recreation_2025           3095 non-null   float64
 27  Housing_Stress_2025            3095 non-null   float64
 28  Industry_Dependence_2025       3095 non-null   float64
 29  Low_Employment_2025            3095 non-null   float64
 30  Low_PostSecondary_Ed_2025      3095 non-null   float64
 31  Nonspecialized_2025            3095 non-null   float64
 32  Persistent_Poverty_1721        3095 non-null   float64
 33  Population_Loss_2025           3095 non-null   float64
 34  Retirement_Destination_2025    3095 non-null   float64
 35  low_access_tracts              2786 non-null   float64
 36  pct_low_vehicle_access         2786 non-null   float64
 37  poverty_rate                   2785 non-null   float64
 38  median_income                  3233 non-null   int64  
 39  poverty_count                  3233 non-null   int64  
 40  unemployed_count               3233 non-null   int64  
 41  uninsured_count                3233 non-null   int64  
 42  diabetes_prev                  3094 non-null   float64
 43  stroke_prev                    3094 non-null   float64
```

```
dtypes: float64(39), int64(5)
memory usage: 1.1 MB

Head of the new data_cleaned DataFrame:
```

	total_pop	PM25	OZONE	DSLPM	RSEI_AIR	PTRAF	PNPL	PRI
0	3407.0	NaN	NaN	NaN	18.795745	0.000000e+00	0.000000	2.3570
1	5219.0	NaN	NaN	NaN	3.631383	0.000000e+00	0.323449	0.1881
2	290674.0	NaN	NaN	NaN	47.484369	1.186345e+06	1.337817	0.4477
3	18538.0	NaN	NaN	NaN	24.384799	0.000000e+00	0.000000	0.0000
4	854.0	NaN	NaN	NaN	22.729112	0.000000e+00	0.000000	0.1925

5 rows × 44 columns

```
# Load merged dataset
df = data_cleaned.copy()

# Select only numeric columns for correlation
numeric_df = df.select_dtypes(include=[np.number])


numeric_df["poverty_rate"] = numeric_df["poverty_count"] / numeric_df
numeric_df["unemployment_rate"] = numeric_df["unemployed_count"] / nu
numeric_df["uninsured_rate"] = numeric_df["uninsured_count"] / numeri
numeric_df["total_pop"] = np.log1p(df["total_pop"])

# Drop poverty_count, unemployed_count, uninsured_count
numeric_df = numeric_df.drop(columns=["poverty_count", "unemployed_co

# Compute correlation matrix
corr = numeric_df.corr()

# Plot heatmap (matplotlib only, no specified colors)
plt.figure(figsize=(12, 10))
plt.imshow(corr, aspect='auto')
plt.colorbar()
plt.xticks(range(len(corr.columns)), corr.columns, rotation=90)
plt.yticks(range(len(corr.columns)), corr.columns)
plt.title("Correlation Heatmap of Independent Variables")

plt.tight_layout()
plt.show()
```


Correlation Heatmap of Independent Variables
total_pop
PM25
OZONE
DSLPM
RSEI_AIR
PTRAF
PNPL
PRMP
PWDIS
DWATER
NO2
DEMOGIDX_2
DEMOGIDX_5
PEOPCOLORPCT
LOWINCPCT
UNEMPPCT
LINGISOPCT
LESSHSPCT
UNDER5PCT
OVER64PCT
fips
Metro2023
High_Farming_2025
High_Government_2025
High_Manufacturing_2025
High_Mining_2025
High_Recreation_2025
Housing_Stress_2025
Industry_Dependence_2025
Low_Employment_2025
Low_PostSecondary_Ed_2025
Nonspecialized_2025
Persistent_Poverty_1721
Population_Loss_2025
Retirement_Destination_2025
low_access_tracts
pct_low_vehicle_access
poverty_rate
median_income
diabetes_prev
stroke_prev
unemployment_rate
uninsured_rate
1.0
0.8
0.6
0.4
0.2
0.0
−0.2
−0.4

```
# Targets
targets = ["diabetes_prev", "stroke_prev"]

ranked_results = {}

for target in targets:
    if target in corr.columns:
        ranked = corr[target].drop(labels=[target]).abs().sort_values
        ranked_results[target] = ranked

# Extract top 20 predictors for diabetes_prev
top_diabetes = ranked_results["diabetes_prev"].head(20)
top_diabetes
```

```
stroke_prev                0.994584
low_access_tracts          0.752232
PTRAF                      0.586347
DSLPM                      0.557147
total_pop                  0.530519
NO2                        0.405743
Metro2023                  0.296897
LINGISOPCT                 0.294815
Housing_Stress_2025        0.290966
OZONE                      0.283500
PEOPCOLORPCT               0.259983
PM25                       0.221053
median_income              0.210882
PRMP                       0.209355
OVER64PCT                  0.183075
Nonspecialized_2025        0.169826
unemployment_rate          0.153201
High_Farming_2025          0.120520
Industry_Dependence_2025   0.117146
DEMOGIDX_2                 0.108128
Name: diabetes_prev, dtype: float64
```

```
# Extract top 20 predictors for stroke_prev
top_stroke = ranked_results["stroke_prev"].head(20)
top_stroke
```

```
diabetes_prev               0.994584
low_access_tracts           0.737570
PTRAF                       0.604597
DSLPM                       0.577473
total_pop                   0.554268
NO2                         0.415541
Metro2023                   0.310801
Housing_Stress_2025         0.303543
LINGISOPCT                  0.286679
OZONE                       0.285590
PEOPCOLORPCT                0.257388
PM25                        0.223269
median_income               0.213146
PRMP                        0.207583
OVER64PCT                   0.178539
Nonspecialized_2025         0.173761
unemployment_rate           0.163062
High_Farming_2025           0.129321
Industry_Dependence_2025    0.117552
DEMOGIDX_2                  0.105260
Name: stroke_prev, dtype: float64
```

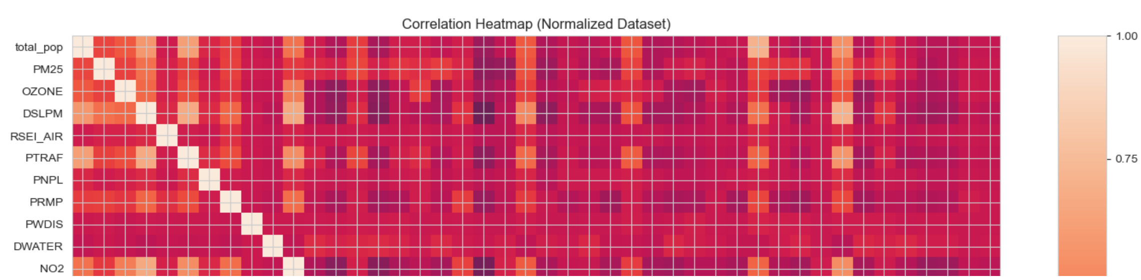
```
# Load merged dataset
df = data_cleaned.copy()

# Columns that represent raw counts
count_cols = [
    "poverty_count", "unemployed_count", "uninsured_count",
    "stroke_prev", "diabetes_prev", 'High_Manufacturing_2025', 'Low_Er
]

# Check existence
existing = [c for c in count_cols if c in df.columns]

# Create log-transformed population
if "total_pop" in df.columns:
    df["log_total_pop"] = np.log1p(df["total_pop"])
else:
    raise ValueError("total_pop column missing.")

# Create rates per 100k
for col in existing:
    df[col + "_rate"] = df[col] / df["total_pop"] * 100000

# Drop raw count columns safely
df_clean = df.drop(columns=existing)

# Save cleaned file
output_path = "/Users/sankates/workspace/MSAI/AI-391MCSML/data_normal:
df_clean.to_csv(output_path, index=False)
```

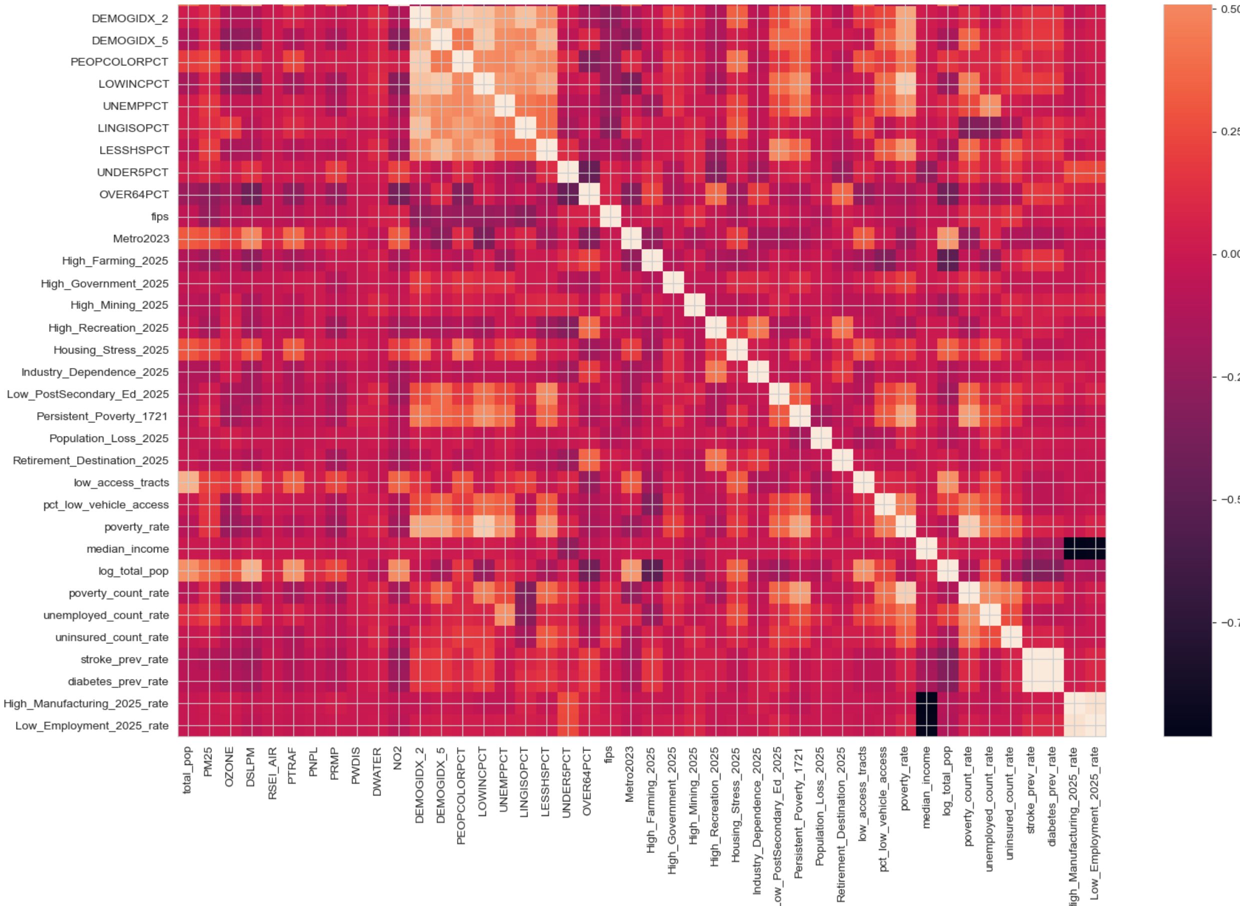
```
df_clean.head()
```

	total_pop	PM25	OZONE	DSLPM	RSEI_AIR	PTRAF	PNPL	PRMP
0	3407.0	NaN	NaN	NaN	18.795745	0.000000e+00	0.000000	2.357087
1	5219.0	NaN	NaN	NaN	3.631383	0.000000e+00	0.323449	0.188127
2	290674.0	NaN	NaN	NaN	47.484369	1.186345e+06	1.337817	0.447789
3	18538.0	NaN	NaN	NaN	24.384799	0.000000e+00	0.000000	0.000000
4	854.0	NaN	NaN	NaN	22.729112	0.000000e+00	0.000000	0.192515

5 rows × 45 columns

```
# Create heatmap of correlations in normalized dataset

# Select numeric columns only
numeric_df = df_clean.select_dtypes(include=[np.number])

# Drop specified column
if 'Nonspecialized_2025' in numeric_df.columns:
    numeric_df = numeric_df.drop(columns=['Nonspecialized_2025'])

# Compute correlation matrix
corr = numeric_df.corr()

# Plot heatmap
plt.figure(figsize=(16, 14))
plt.imshow(corr, aspect='auto')
plt.colorbar()
plt.xticks(range(len(corr.columns)), corr.columns, rotation=90)
plt.yticks(range(len(corr.columns)), corr.columns)
plt.title("Correlation Heatmap (Normalized Dataset)")
plt.tight_layout()
plt.show()
```




DEMOGIDX_2
DEMOGIDX_5
PEOPCOLORPCT
LOWINCPCT
UNEMPPCT
LINGISOPCT
LESSHSPCT
UNDER5PCT
OVER64PCT
fips
Metro2023
High_Farming_2025
High_Government_2025
High_Mining_2025
High_Recreation_2025
Housing_Stress_2025
Industry_Dependence_2025
Low_PostSecondary_Ed_2025
Persistent_Poverty_1721
Population_Loss_2025
Retirement_Destination_2025
low_access_tracts
pct_low_vehicle_access
poverty_rate
median_income
log_total_pop
poverty_count_rate
unemployed_count_rate
uninsured_count_rate
stroke_prev_rate
diabetes_prev_rate
High_Manufacturing_2025_rate
Low_Employment_2025_rate
total_pop
PM25
OZONE
DSLPM
RSEI_AIR
PTRAF
PNPL
PRMP
PWDIS
DWATER
NO2
0.50
0.25
0.00
−0.25
−0.50
−0.75

```
# Modeling script

from sklearn.model_selection import train_test_split
from sklearn.linear_model import LinearRegression, ElasticNet
from sklearn.ensemble import RandomForestRegressor, GradientBoostingR
from sklearn.metrics import mean_squared_error, r2_score, root_mean_s
from sklearn.preprocessing import StandardScaler
from sklearn.pipeline import Pipeline
from xgboost import XGBRegressor
from sklearn.metrics import mean_squared_error, r2_score


# ---------------------------------------------------
# 0. Load your merged dataset
# ---------------------------------------------------
df = df_clean.copy()

# targets (dependent variables)
y_diab = df["diabetes_prev_rate"]
y_stroke = df["stroke_prev_rate"]
```

```
# drop rows where either target is missing
mask = y_diab.notna() & y_stroke.notna()
df = df[mask].copy()
y_diab = y_diab[mask]
y_stroke = y_stroke[mask]



# Winsorize (cap at 99th percentile) as a quick fix
from scipy.stats import mstats
y_diab_winsor = mstats.winsorize(y_diab, limits=[0, 0.05])  # Cap top
y_stroke_winsor = mstats.winsorize(y_stroke, limits=[0, 0.05])

# ---------------------------------------------------
# 2. Define feature matrix X
# ---------------------------------------------------
drop_cols = set(["diabetes_prev_rate",
                              "stroke_prev_rate", "total_pop", "log_t
                              "fips"])  # fips is an ID, not a featur

numeric_cols = df.select_dtypes(include=[np.number]).columns
feature_cols = [c for c in numeric_cols if c not in drop_cols]

X = df[feature_cols]

# simple mean imputation for any remaining NaNs
X = X.fillna(X.mean())

# ---------------------------------------------------
# 3. Train–test split (shared for both targets)
# ---------------------------------------------------
X_train, X_test, yD_train, yD_test, yS_train, yS_test = train_test_sp
    X, y_diab_winsor, y_stroke_winsor, test_size=0.2, random_state=42
)

# ---------------------------------------------------
# 4. Helper to train + evaluate a model
# ---------------------------------------------------
def eval_model(model, X_tr, X_te, y_tr, y_te):
    model.fit(X_tr, y_tr)
    preds = model.predict(X_te)
    rmse = np.sqrt(mean_squared_error(y_te, preds))
    r2 = r2_score(y_te, preds)
    return rmse, r2
```

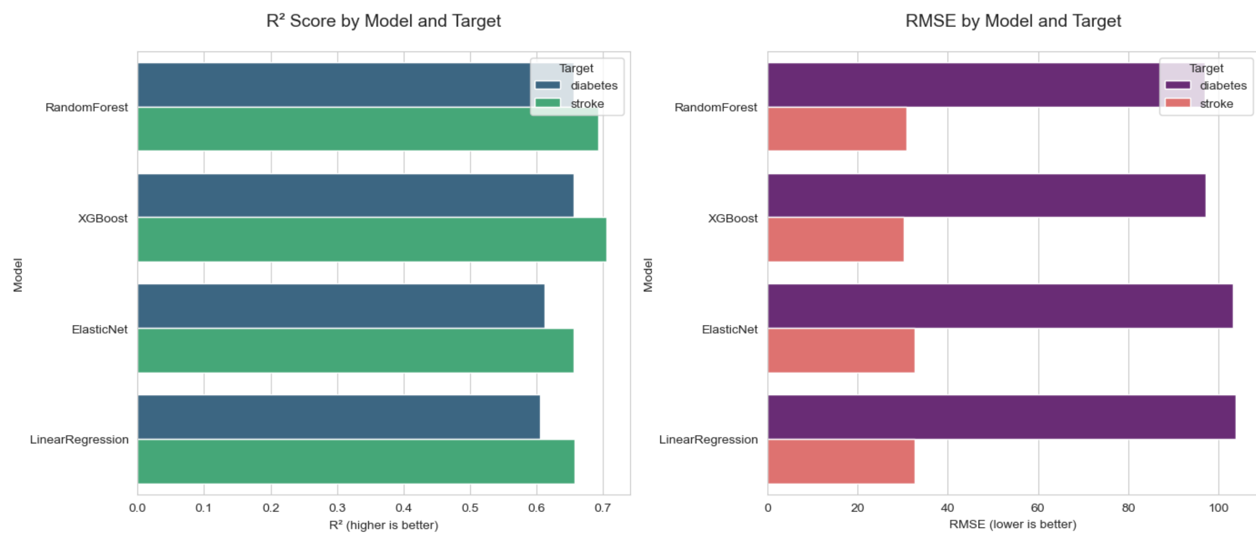
```
results = []

# ------------------------------------------------------
# 5. MODELS
# ------------------------------------------------------

# 5.1 Linear Regression (needs scaling)
lin_pipeline = Pipeline([
    ("scaler", StandardScaler()),
    ("linreg", LinearRegression())
])

results.append(["LinearRegression", "diabetes"] +
               list(eval_model(lin_pipeline, X_train, X_test, yD_trai
results.append(["LinearRegression", "stroke"] +
               list(eval_model(lin_pipeline, X_train, X_test, yS_trai

# 5.2 Random Forest (nonlinear, handles interactions)
rf = RandomForestRegressor(
    n_estimators=200,
    random_state=42,
    n_jobs=-1
)

results.append(["RandomForest", "diabetes"] +
               list(eval_model(rf, X_train, X_test, yD_train, yD_test
results.append(["RandomForest", "stroke"] +
               list(eval_model(rf, X_train, X_test, yS_train, yS_test

# 5.3 Gradient Boosting (you can swap in XGBoost if installed)
#gb = GradientBoostingRegressor(random_state=42)
gb = XGBRegressor(n_estimators=300, learning_rate=0.05, random_state=


results.append(["XGBoost", "diabetes"] +
               list(eval_model(gb, X_train, X_test, yD_train, yD_test
results.append(["XGBoost", "stroke"] +
               list(eval_model(gb, X_train, X_test, yS_train, yS_test

# 5.4 Elastic Net (L1 + L2 regularized linear model)
en_pipeline = Pipeline([
    ("scaler", StandardScaler()),
    ("enet", ElasticNet(alpha=0.1, l1_ratio=0.5,
                        random_state=42, max_iter=10000))
])
```

```
results.append(["ElasticNet", "diabetes"] +
               list(eval_model(en_pipeline, X_train, X_test, yD_train
results.append(["ElasticNet", "stroke"] +
               list(eval_model(en_pipeline, X_train, X_test, yS_train

# ----------------------------------------------------
# 6. Compare performance
# ----------------------------------------------------
results_df = pd.DataFrame(results,
                          columns=["Model", "Target", "RMSE", "R2"])

print(results_df.sort_values(["Target", "R2"], ascending=[True, False
```

```
              Model    Target        RMSE        R2
2      RandomForest  diabetes   97.033926  0.655837
4           XGBoost  diabetes   97.090497  0.655435
6        ElasticNet  diabetes  103.114787  0.611349
0  LinearRegression  diabetes  103.861457  0.605700
5           XGBoost    stroke   30.310563  0.704462
3      RandomForest    stroke   30.932333  0.692212
1  LinearRegression    stroke   32.652272  0.657033
7        ElasticNet    stroke   32.722188  0.655563
```

```
# Plotting model performance

# Make sure results_df exists
results_df = pd.DataFrame(results, columns=["Model", "Target", "RMSE",
results_df = results_df.sort_values(["Target", "R2"], ascending=[True,

# Set style
sns.set_style("whitegrid")
fig, axes = plt.subplots(1, 2, figsize=(14, 6), sharey=False)

# R² plot
sns.barplot(data=results_df, x="R2", y="Model", hue="Target", ax=axes[0
axes[0].set_title("R² Score by Model and Target", fontsize=14, pad=20)
axes[0].set_xlabel("R² (higher is better)")
axes[0].legend(title="Target")

# RMSE plot
sns.barplot(data=results_df, x="RMSE", y="Model", hue="Target", ax=axes
axes[1].set_title("RMSE by Model and Target", fontsize=14, pad=20)
axes[1].set_xlabel("RMSE (lower is better)")
axes[1].legend(title="Target")
```

```
axes[1].legend(title="Target")

plt.tight_layout()
plt.show()
```



Hyperparameter tuning for the top 2 models

```
# Random Forest hyperparameters
rf_param_dist = {
    "n_estimators": [100, 200, 400],
```

```
        "max_depth": [10, 15, 20, None],
        "max_features": ["sqrt", "log2", 0.3, 0.5, 0.7],
        "min_samples_split": [2, 5, 10],
        "min_samples_leaf": [1, 2, 4],
        "bootstrap": [True, False],
    }

    # XGBoost Boosting hyperparameters
    xgb_param_dist = {
        "n_estimators": [200, 400, 600, 1000],  # Higher for early stoppi
        "learning_rate": [0.01, 0.03, 0.05, 0.1],
        "max_depth": [2, 3, 4, 5],
        "min_child_weight": [1, 3, 5],  # Replace min_samples_leaf
        "gamma": [0, 0.1, 0.2],  # For split regularization (like min_sam
        "subsample": [0.6, 0.8, 1.0],
        "colsample_bytree": [0.6, 0.8, 1.0],  # Add this
    }


    from sklearn.model_selection import RandomizedSearchCV

    def tune_and_eval(name, estimator, param_dist, X_train, y_train, X_te
                      n_iter=25):
        search = RandomizedSearchCV(
            estimator,
            param_distributions=param_dist,
            n_iter=n_iter,
            scoring="r2",
            cv=3,
            random_state=42,
            n_jobs=-1,
            verbose=1,
        )
        search.fit(X_train, y_train)
        best_model = search.best_estimator_
        preds = best_model.predict(X_test)
        rmse = np.sqrt(mean_squared_error(y_test, preds))
        r2 = r2_score(y_test, preds)
        return {
            "name": name,
            "best_params": search.best_params_,
            "rmse": rmse,
            "r2": r2,
            "model": best_model,
        }
```

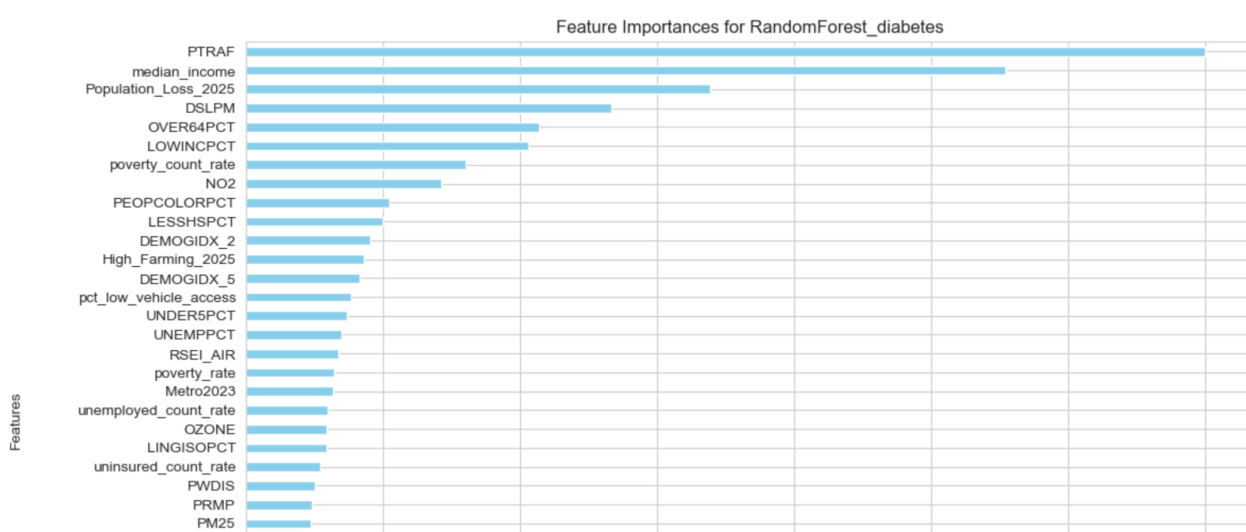
```
# Example: Tune Random Forest for diabetes_prev_rate
results = []

# ---- Diabetes models ----
rf_diab = tune_and_eval(
    "RandomForest_diabetes",
    RandomForestRegressor(random_state=42),
    rf_param_dist,
    X_train, yD_train, X_test, yD_test,
    n_iter=25
)
results.append(rf_diab)

gb_diab = tune_and_eval(
    "XGBoost_diabetes",
    XGBRegressor(random_state=42),
    xgb_param_dist,
    X_train, yD_train, X_test, yD_test,
    n_iter=25
)
results.append(gb_diab)

# ---- Stroke models ----
rf_stroke = tune_and_eval(
    "RandomForest_stroke",
    RandomForestRegressor(random_state=42),
    rf_param_dist,
    X_train, yS_train, X_test, yS_test,
    n_iter=25
)
results.append(rf_stroke)

gb_stroke = tune_and_eval(
    "XGBoost_stroke",
    XGBRegressor(random_state=42),
    xgb_param_dist,
    X_train, yS_train, X_test, yS_test,
    n_iter=25
)
results.append(gb_stroke)

# Display tuning results
for res in results:
    print(f"Model: {res['name']}")
```

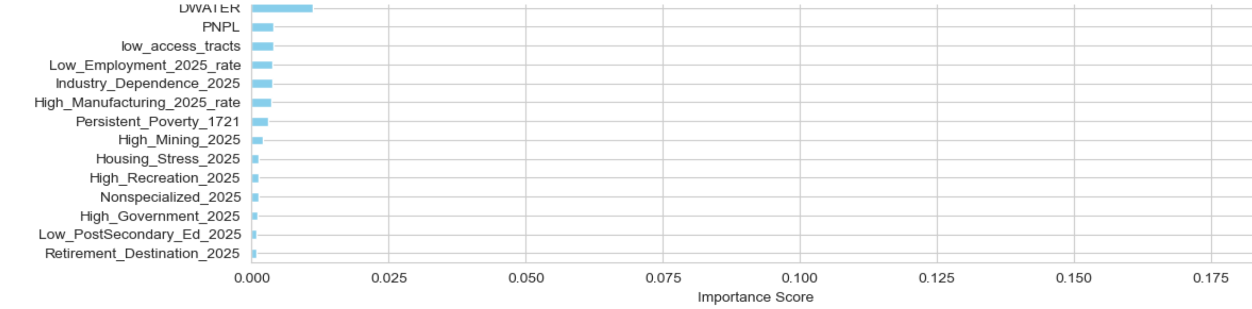
```
    print("Best Parameters:")
    for param, value in res['best_params'].items():
        print(f"  - {param}: {value}")
    print(f"R²: {res['r2']:.4f}, RMSE: {res['rmse']:.4f}")
    print("-" * 40)
```

```
Fitting 3 folds for each of 25 candidates, totalling 75 fits
Fitting 3 folds for each of 25 candidates, totalling 75 fits
Fitting 3 folds for each of 25 candidates, totalling 75 fits
Fitting 3 folds for each of 25 candidates, totalling 75 fits
Model: RandomForest_diabetes
Best Parameters:
  - n_estimators: 400
  - min_samples_split: 2
  - min_samples_leaf: 1
  - max_features: 0.3
  - max_depth: 15
  - bootstrap: False
R²: 0.6646, RMSE: 95.7949
----------------------------------------
Model: XGBoost_diabetes
Best Parameters:
  - subsample: 0.6
  - n_estimators: 1000
  - min_child_weight: 3
  - max_depth: 5
  - learning_rate: 0.01
  - gamma: 0.1
  - colsample_bytree: 0.8
R²: 0.6800, RMSE: 93.5707
----------------------------------------
Model: RandomForest_stroke
Best Parameters:
  - n_estimators: 400
  - min_samples_split: 2
  - min_samples_leaf: 1
  - max_features: 0.3
  - max_depth: 15
  - bootstrap: False
R²: 0.7036, RMSE: 30.3569
----------------------------------------
Model: XGBoost_stroke
Best Parameters:
  - subsample: 0.6
  - n_estimators: 1000
  - min_child_weight: 3
  - max_depth: 5
  - learning_rate: 0.01
```

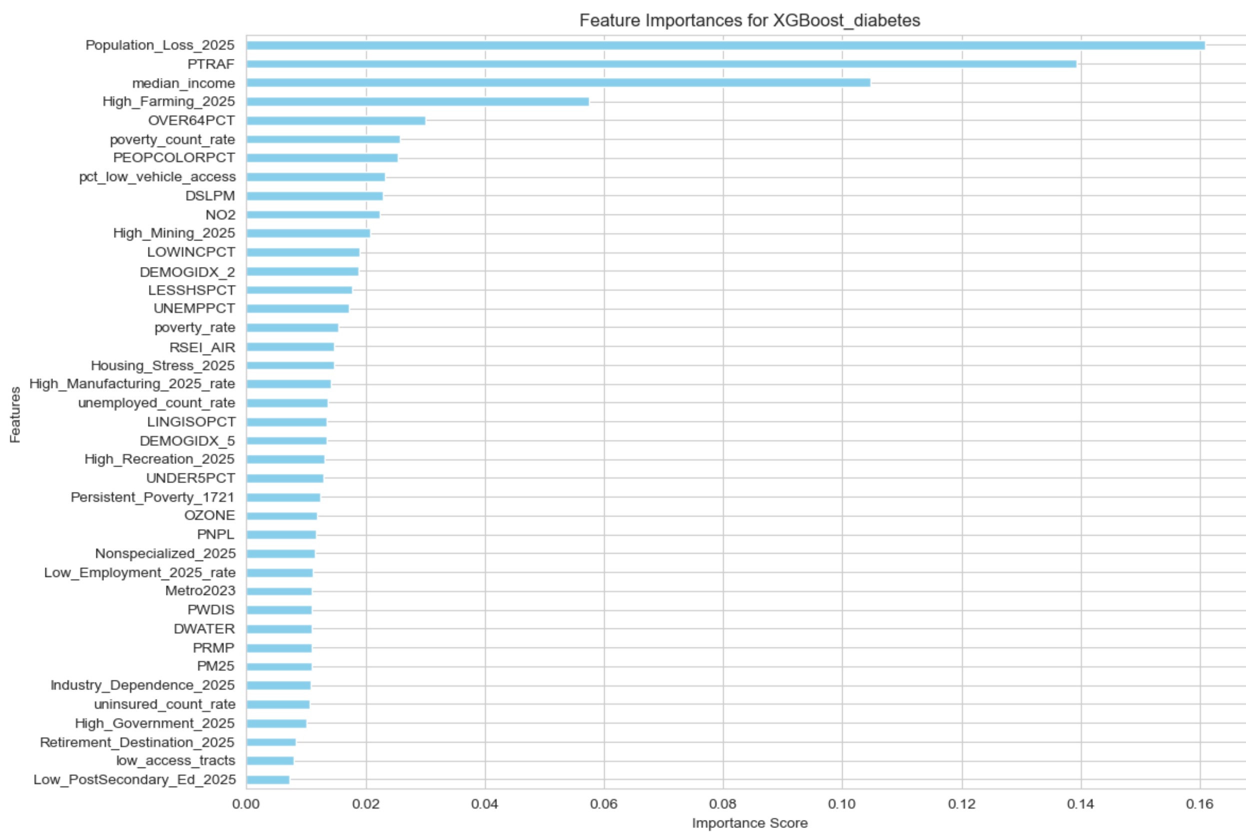
```
  - gamma: 0.1
  - colsample_bytree: 0.8
R²: 0.7176, RMSE: 29.6300
----------------------------------------
```

```
# Plot feature importances for the best models

for res in results:
    best_model = res['model']
    model_name = res['name']

    # Get feature importances as a sorted Series
    importances = pd.Series(
        best_model.feature_importances_,
        index=X.columns
    ).sort_values(ascending=False)  # Sort descending for top feature:

    # Plot
    plt.figure(figsize=(12, 8))  # Adjust size for readability
    importances.plot(kind='barh', color='skyblue')
    plt.title(f"Feature Importances for {model_name}")
    plt.xlabel("Importance Score")
    plt.ylabel("Features")
    plt.gca().invert_yaxis()  # Highest importance at the top
    plt.tight_layout()
    plt.show()

    # Optional: Print top 10 for quick view
    print(f"Top 10 Features for {model_name}:")
    print(importances.head(10))
    print("\n" + "-" * 50 + "\n")
```



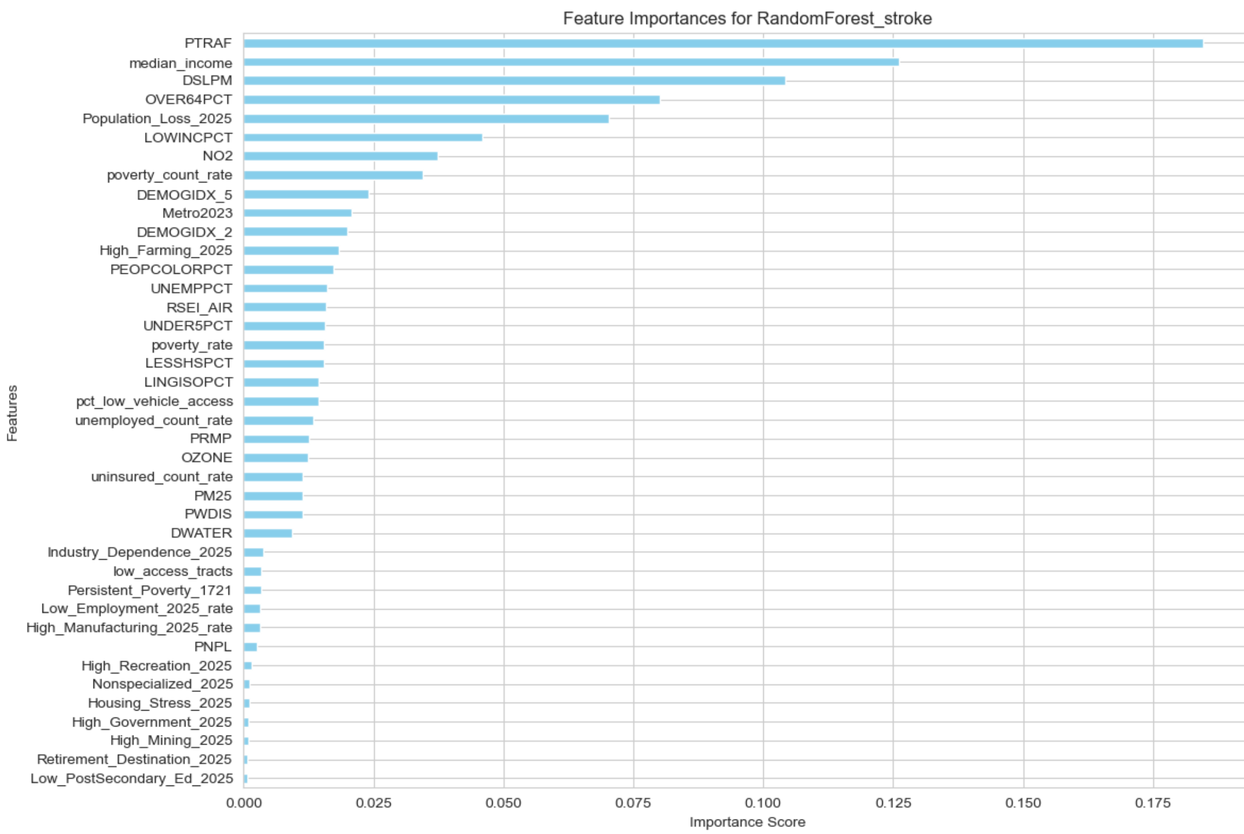



```
Top 10 Features for RandomForest_diabetes:
PTRAF                   0.174937
median_income           0.138520
Population_Loss_2025    0.084540
DSLPM                   0.066507
OVER64PCT               0.053423
LOWINCPCT               0.051559
poverty_count_rate      0.040006
NO2                     0.035530
PEOPCOLORPCT            0.026061
LESSHSPCT               0.024879
dtype: float64

--------------------------------------------------
```

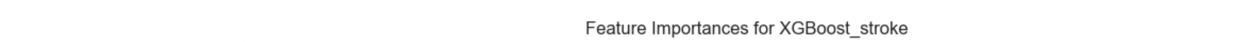


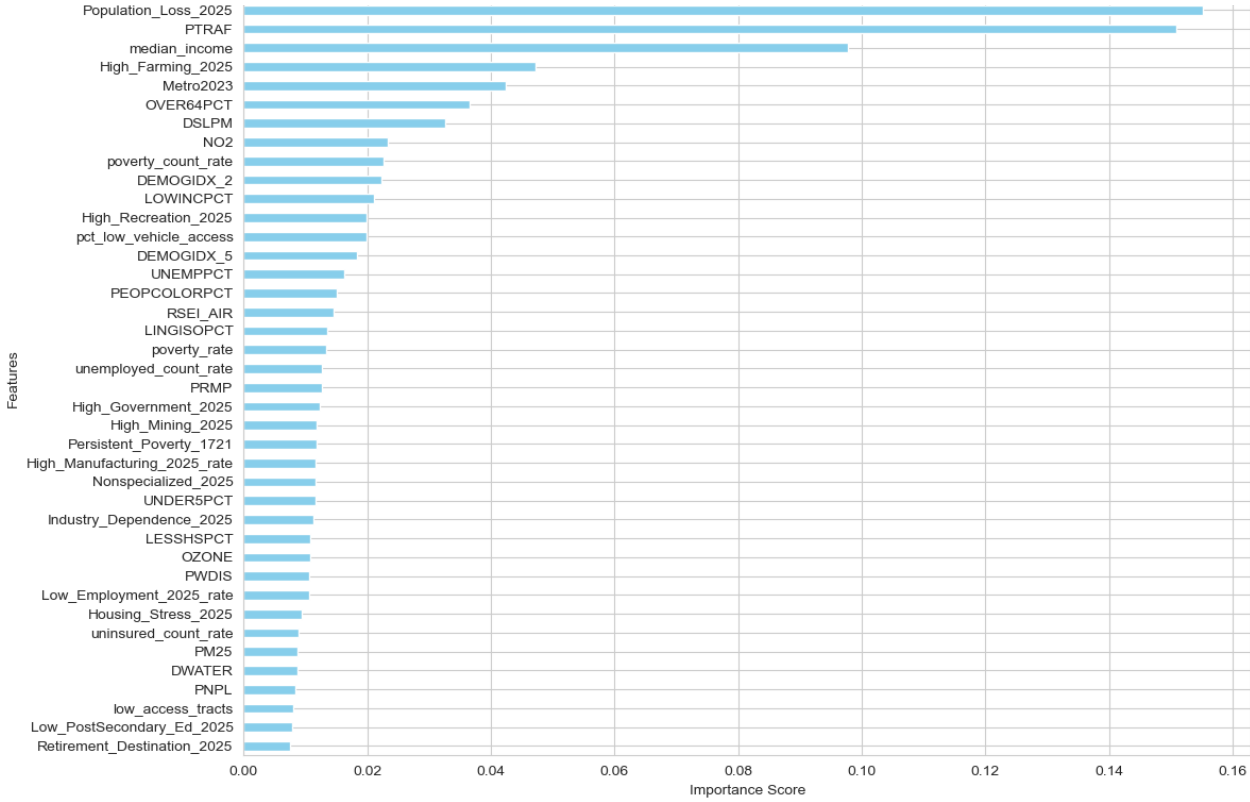

```
Top 10 Features for XGBoost_diabetes:
Population_Loss_2025      0.160859
PTRAF                     0.139243
median_income             0.104816
```

```
High_Farming_2025          0.057504
OVER64PCT                  0.030062
poverty_count_rate         0.025773
PEOPCOLORPCT               0.025360
pct_low_vehicle_access     0.023241
DSLPM                      0.022884
NO2                        0.022475
dtype: float32

--------------------------------------------------
```




```
Top 10 Features for RandomForest_stroke:
PTRAF                    0.184603
median_income            0.126162
DSLPM                    0.104185
OVER64PCT                0.080139
Population_Loss_2025     0.070341
LOWINCPCT                0.045969
NO2                      0.037371
poverty_count_rate       0.034504
DEMOGIDX_5               0.023977
Metro2023                0.020745
dtype: float64

--------------------------------------------------
```






```
Top 10 Features for XGBoost_stroke:
Population_Loss_2025    0.155176
PTRAF                   0.150960
median_income           0.097816
High_Farming_2025       0.047284
Metro2023               0.042388
OVER64PCT               0.036477
DSLPM                   0.032674
NO2                     0.023365
poverty_count_rate      0.022645
DEMOGIDX_2              0.022352
dtype: float32

--------------------------------------------------
```

```
# Summarize tuning results

summary = pd.DataFrame([
    {
        "Model": r["name"],
        "Target": "diabetes" if "diabetes" in r["name"] else "stroke"
        "RMSE": r["rmse"],
        "R2": r["r2"]
    }
    for r in results
])

print(summary.sort_values(["Target", "R2"], ascending=[True, False]))
```

```
                  Model    Target       RMSE        R2
1       XGBoost_diabetes  diabetes  93.570742  0.679965
0  RandomForest_diabetes  diabetes  95.794908  0.664570
3         XGBoost_stroke    stroke  29.629978  0.717585
2    RandomForest_stroke    stroke  30.356879  0.703558
```

```
from sklearn.ensemble import VotingRegressor

# Diabetes example (repeat for stroke with yS)
ensemble_diab = VotingRegressor(estimators=[
    ('xgb', results[1]['model']),  # Assuming results list order from
    ('rf', results[0]['model'])
])
ensemble_diab.fit(X_train, yD_train)  # Or full X/y for final model
preds_ens = ensemble_diab.predict(X_test)
rmse_ens = root_mean_squared_error(yD_test, preds_ens)
r2_ens = r2_score(yD_test, preds_ens)
print(f"Ensemble Diabetes: RMSE={rmse_ens:.2f}, R²={r2_ens:.4f}")
```

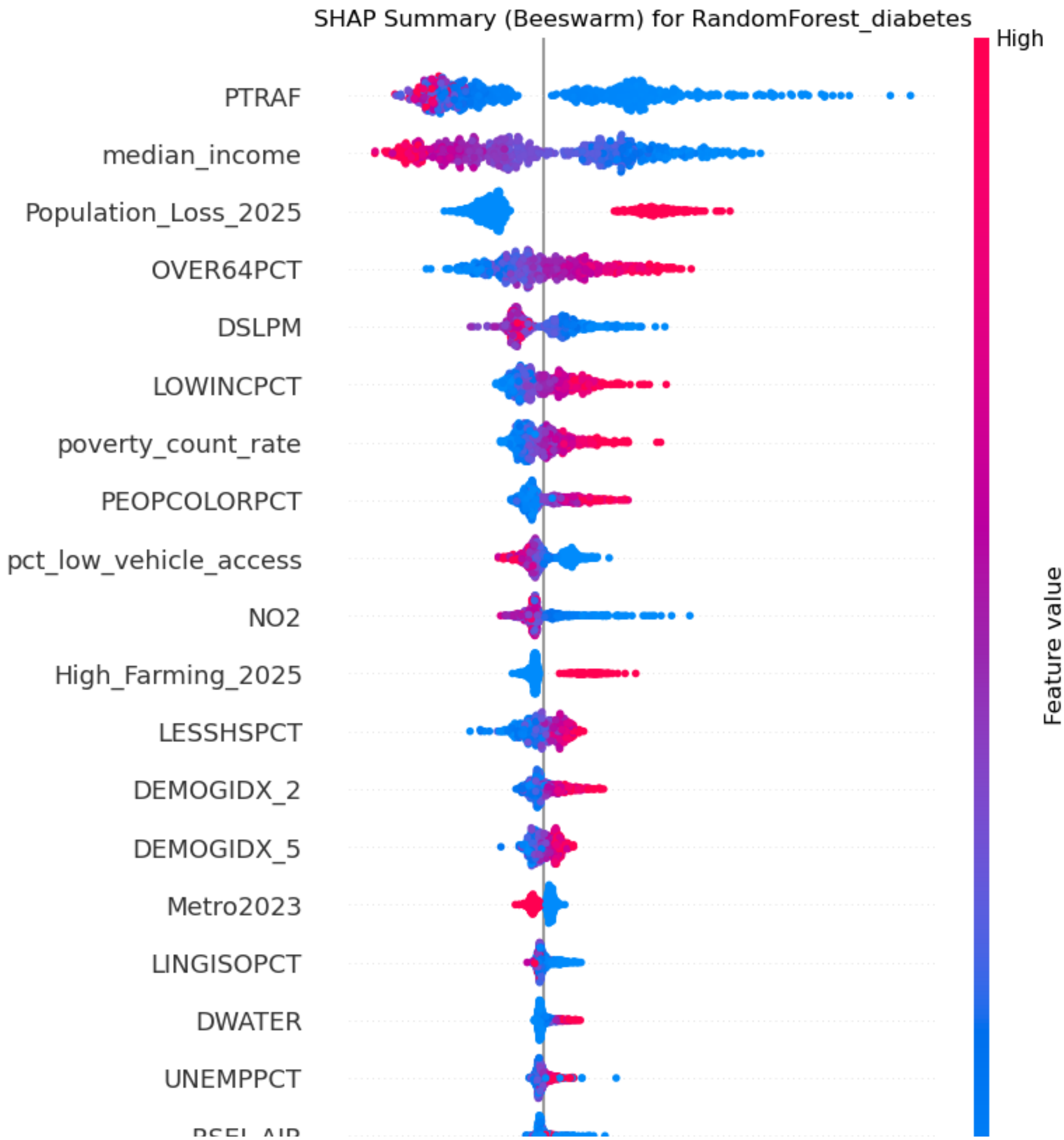
```
Ensemble Diabetes: RMSE=93.76, R²=0.6787
```

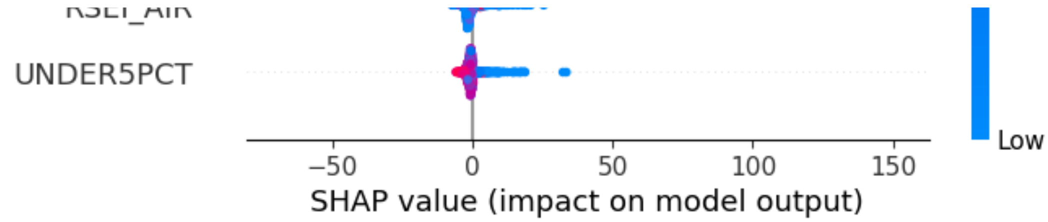
```
import shap
import matplotlib.pyplot as plt
import pandas as pd
import numpy as np

# Function to compute and plot SHAP for a model
def shap_analysis(model, model_name, X_data, top_features_only=False):
    # Use TreeExplainer for efficiency on tree models (RF or XGB)
```

```
        explainer = shap.TreeExplainer(model)
        shap_values = explainer.shap_values(X_data)

        # Summary plot: Shows global feature importance with direction (bee
        plt.figure()
        shap.summary_plot(shap_values, X_data, plot_type="dot", show=False)
        plt.title(f"SHAP Summary (Beeswarm) for {model_name}")
        plt.show()

        # Bar plot: Mean absolute SHAP values (global importance with magni
        plt.figure()
        shap.summary_plot(shap_values, X_data, plot_type="bar", show=False)
        plt.title(f"SHAP Mean Absolute Importance for {model_name}")
        plt.show()

        # If top_features_only=True, filter to top 10 from your lists
        if top_features_only:
            # Example: Limit to top 10 features (replace with your actual t
            top_indices = np.argsort(-np.abs(shap_values).mean(0))[:10]
            shap_values_top = shap_values[:, top_indices]
            X_top = X_data.iloc[:, top_indices] if isinstance(X_data, pd.Da
            shap.summary_plot(shap_values_top, X_top, show=False)
            plt.title(f"SHAP for Top 10 Features in {model_name}")
            plt.show()

        # Return SHAP values for further analysis (e.g., per county)
        return shap_values, explainer.expected_value  # Base value for pred

    # Run for each model (use X_test or a random subset for speed; e.g., X_
    # Ensure X_test has column names for better plots
    X_shap = X_test.copy()  # Or X for global view, but test set is better

    # Diabetes models
    rf_diab_shap, rf_diab_base = shap_analysis(results[0]['model'], "Random
    xgb_diab_shap, xgb_diab_base = shap_analysis(results[1]['model'], "XGBo

    # Stroke models
    rf_stroke_shap, rf_stroke_base = shap_analysis(results[2]['model'], "Ra
    xgb_stroke_shap, xgb_stroke_base = shap_analysis(results[3]['model'], "

    # Example: Dependence plot for a key feature (e.g., PTRAF's impact)
    shap.dependence_plot("PTRAF", xgb_diab_shap, X_shap, show=False)  # Sho
    plt.title("SHAP Dependence for PTRAF in XGBoost_diabetes")
    plt.show()
```

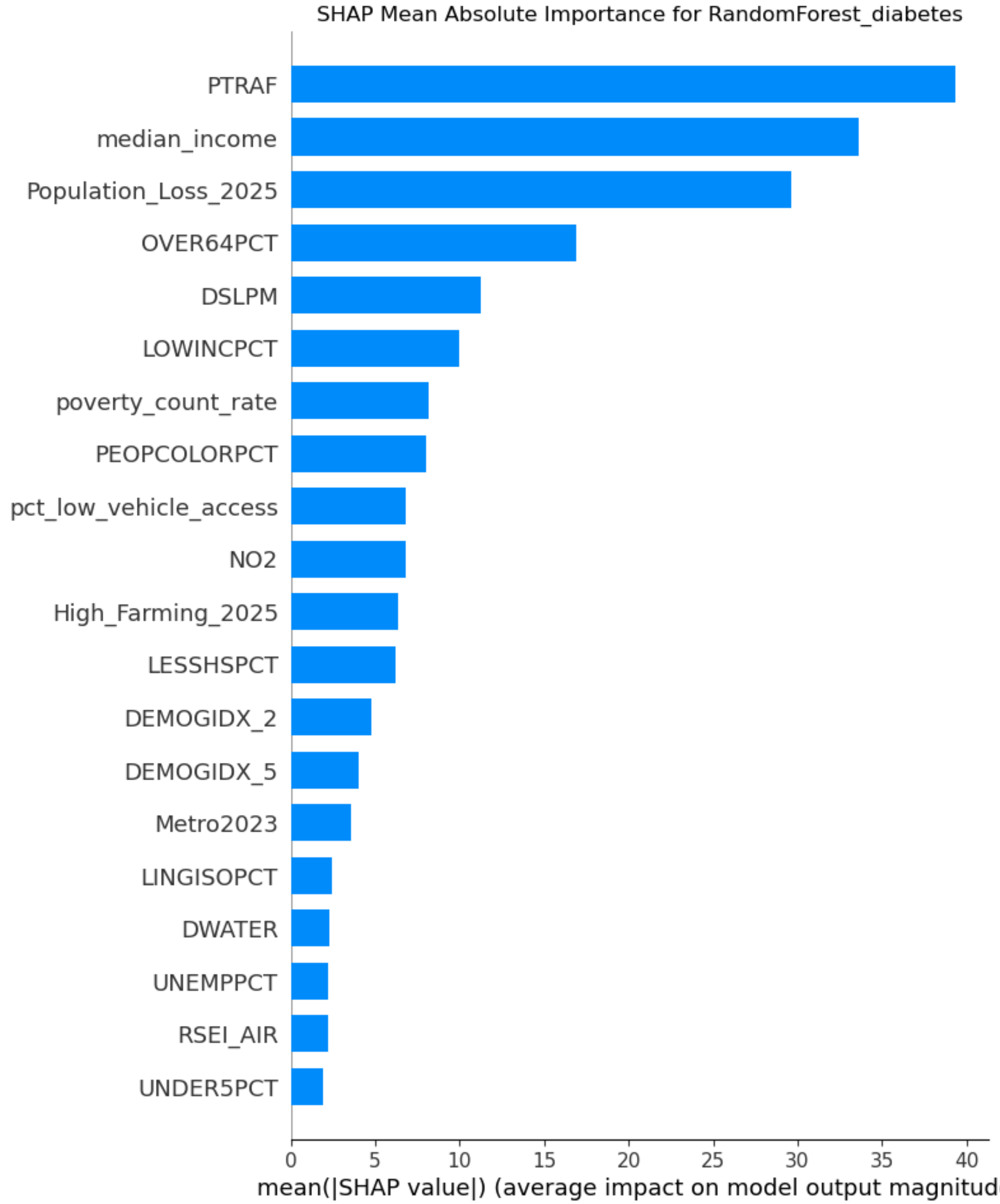
```
# Set matplotlib style to a white background theme (e.g., 'default' or
plt.style.use('default')  # 'default' typically gives white background;

# Optional: Local explanation for a specific county (row index in X_sha
# Get index of a county to explain based on FIPS
idx = data.index[data['fips'] == 6037] # Example FIPS for Los Angeles C
instance_idx = idx[0] if len(idx) > 0 else 0 # Use found index or defau
shap.initjs() # For interactive force plots
force_plot = shap.force_plot(xgb_diab_base, xgb_diab_shap[instance_idx,
display(force_plot) # In Jupyter, this shows an interactive plot
```

```
/var/folders/xv/jppz3tnj7z10dvcn0jp_xfk00000gp/T/ipykernel_60556/387051
  shap.summary_plot(shap_values, X_data, plot_type="dot", show=False)
```

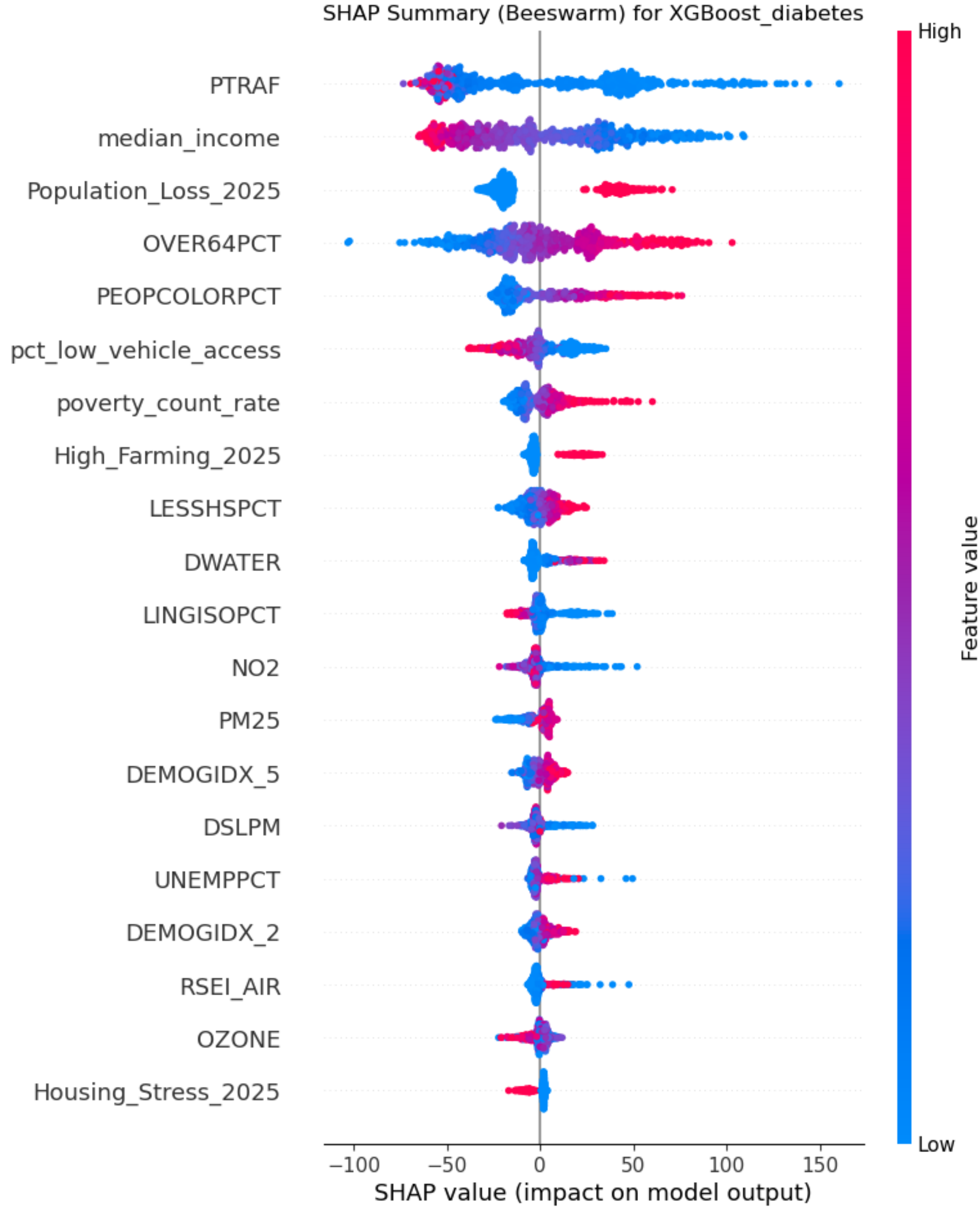




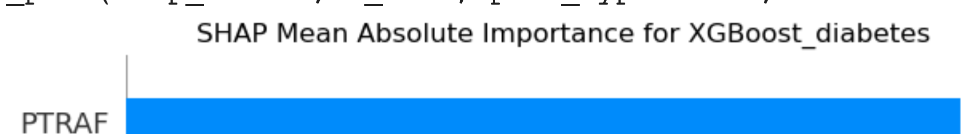

```
/var/folders/xv/jppz3tnj7z10dvcn0jp_xfk00000gp/T/ipykernel_60556/387051
  shap.summary_plot(shap_values, X_data, plot_type="bar", show=False)
```

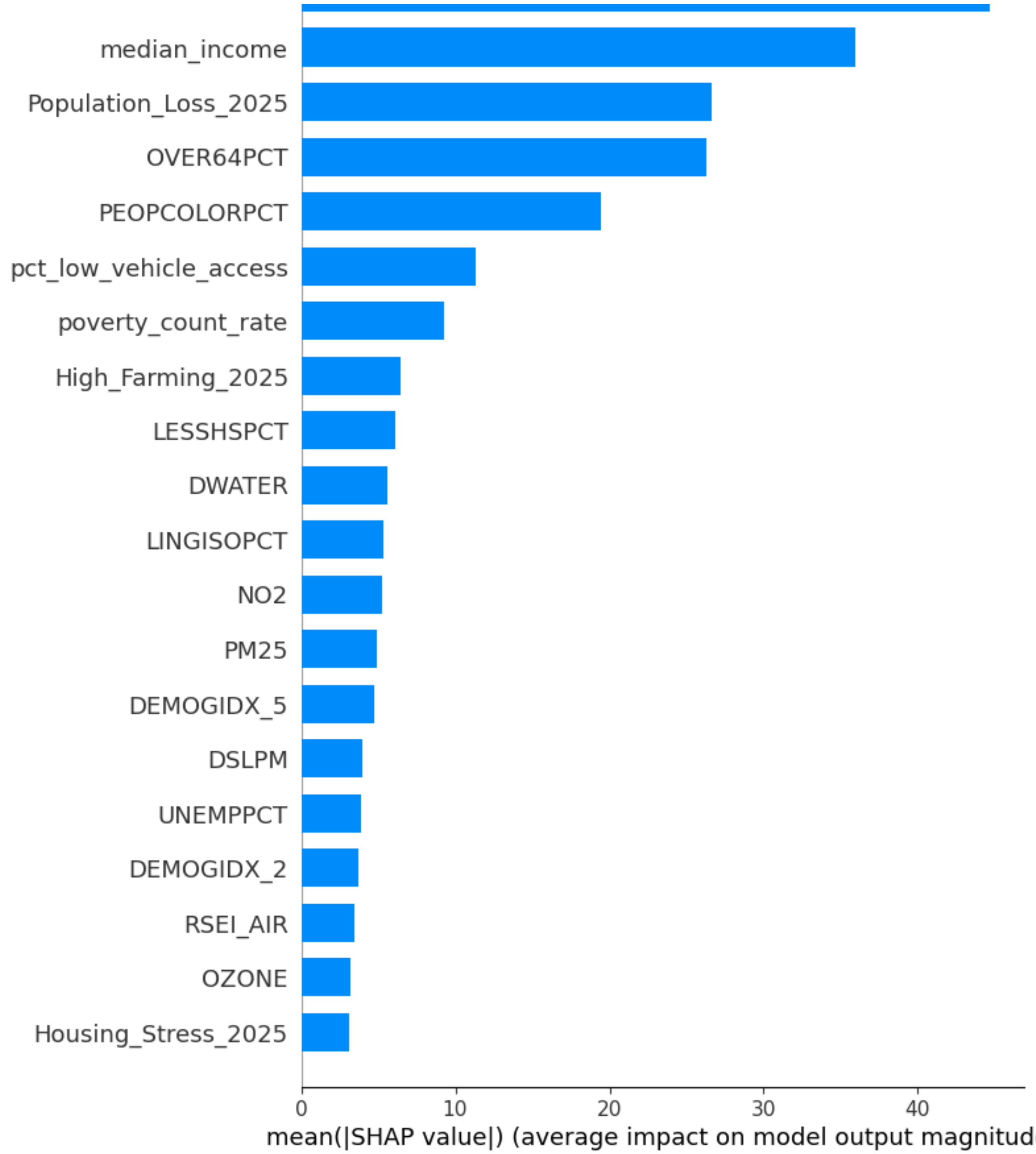


```
/var/folders/xv/jppz3tnj7z10dvcn0jp_xfk00000gp/T/ipykernel_60556/387051
  shap.summary_plot(shap_values, X_data, plot_type="dot", show=False)
```

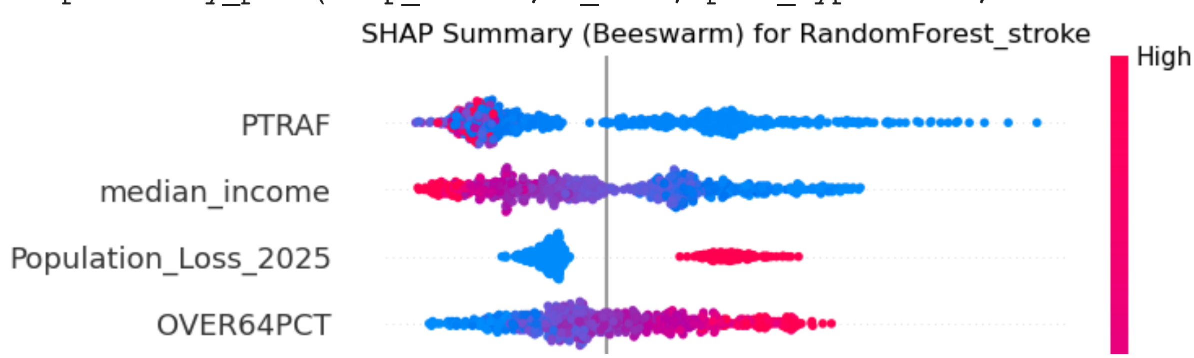


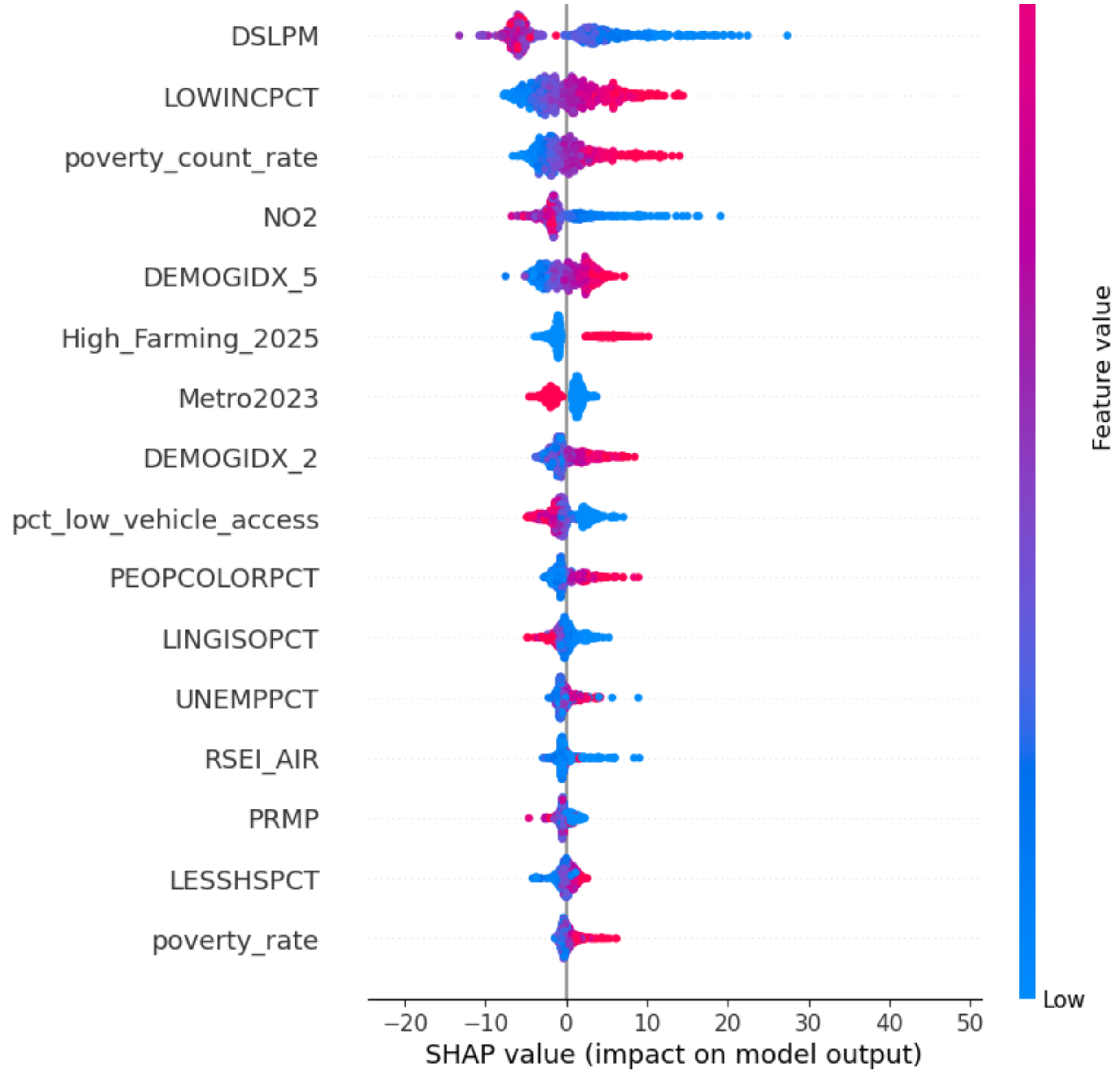

```
/var/folders/xv/jppz3tnj7z10dvcn0jp_xfk00000gp/T/ipykernel_60556/387051
  shap.summary_plot(shap_values, X_data, plot_type="bar", show=False)
```



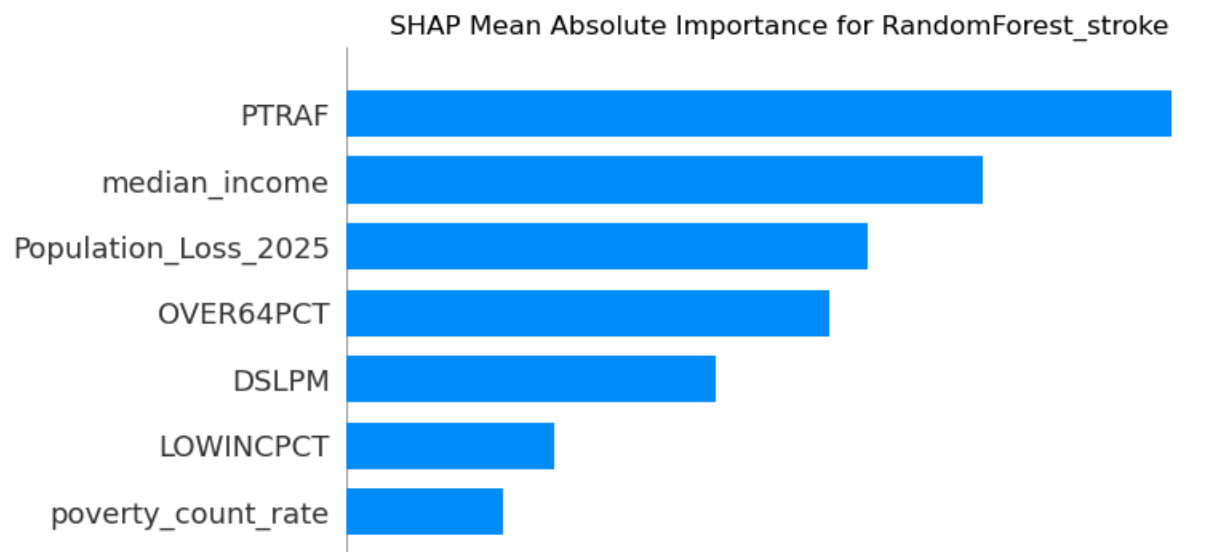


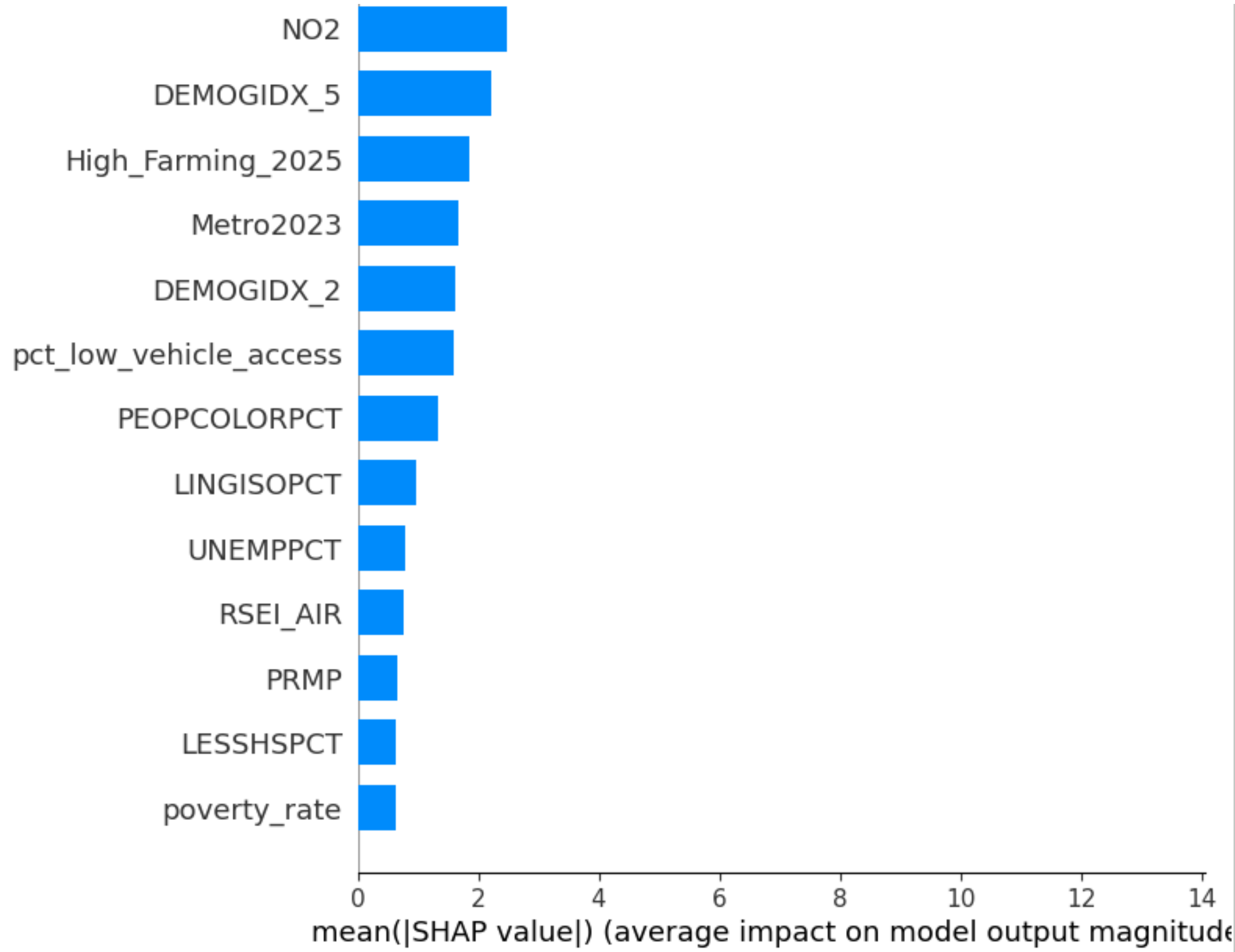

```
/var/folders/xv/jppz3tnj7z10dvcn0jp_xfk00000gp/T/ipykernel_60556/387051
  shap.summary_plot(shap_values, X_data, plot_type="dot", show=False)
```



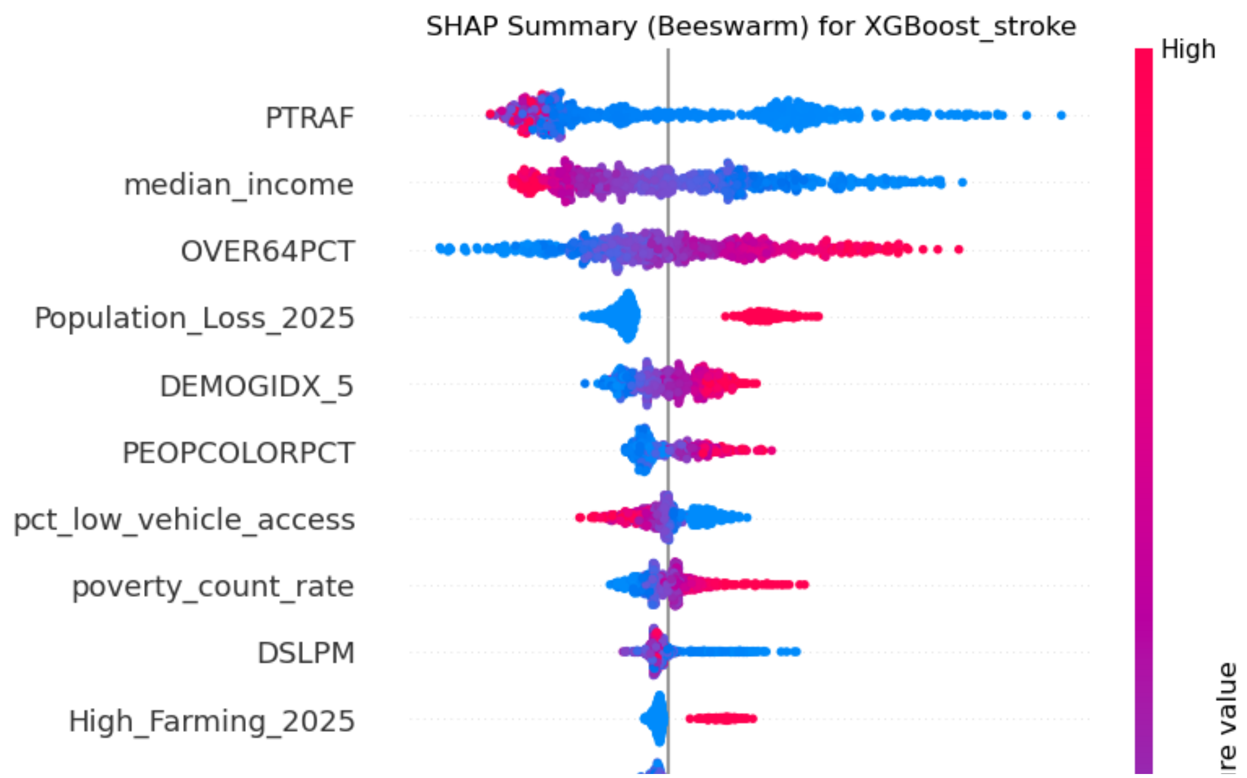


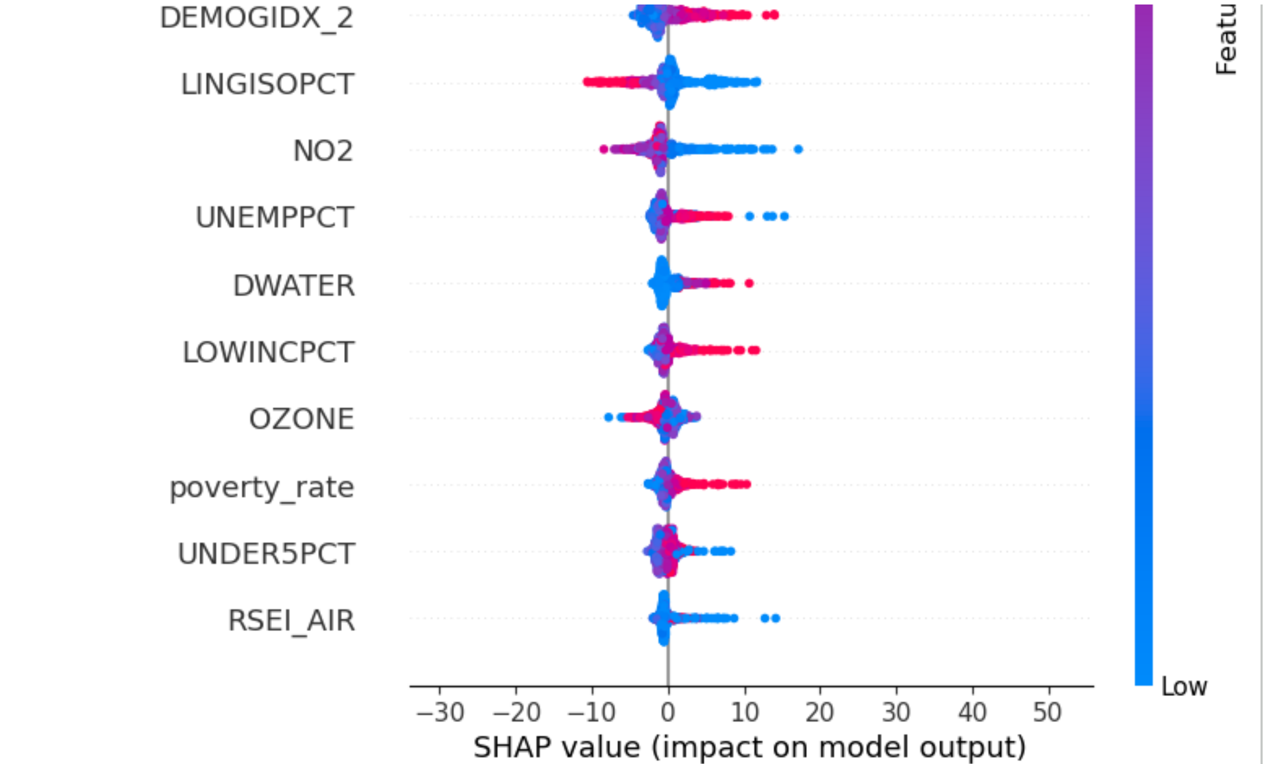

```
/var/folders/xv/jppz3tnj7z10dvcn0jp_xfk00000gp/T/ipykernel_60556/387051
  shap.summary_plot(shap_values, X_data, plot_type="bar", show=False)
```



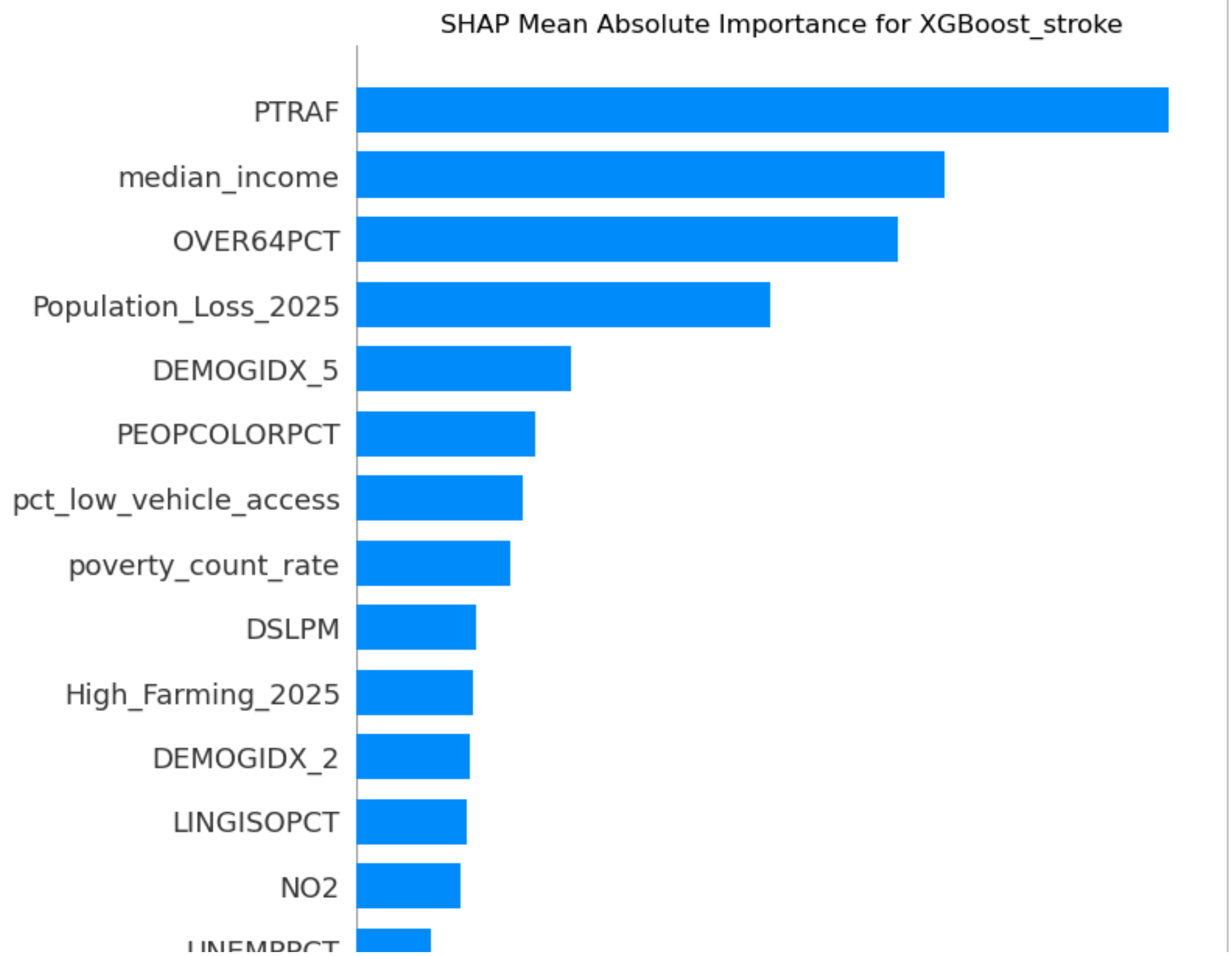


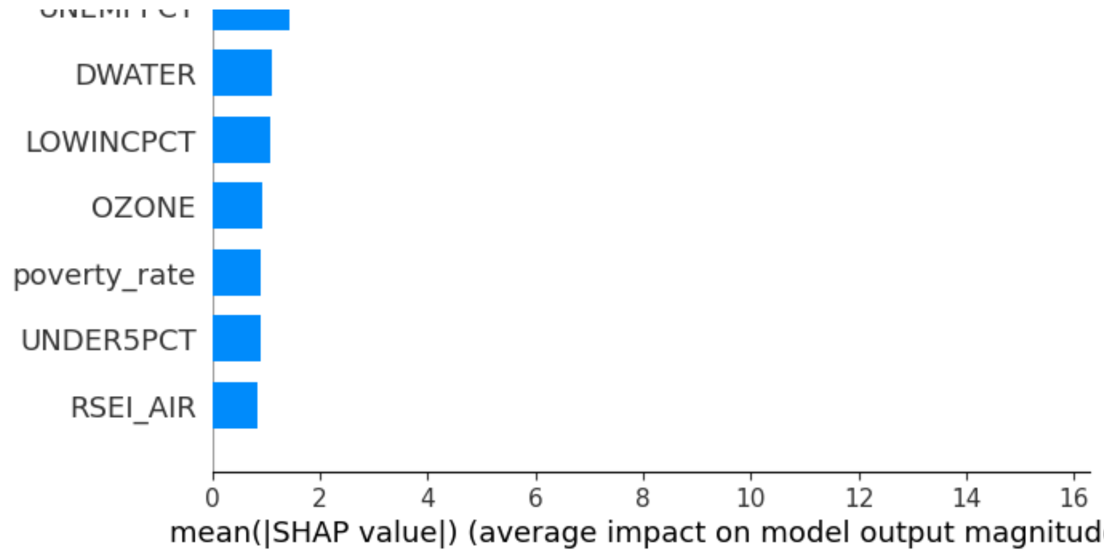

```
/var/folders/xv/jppz3tnj7z10dvcn0jp_xfk00000gp/T/ipykernel_60556/387051
  shap.summary_plot(shap_values, X_data, plot_type="dot", show=False)
```

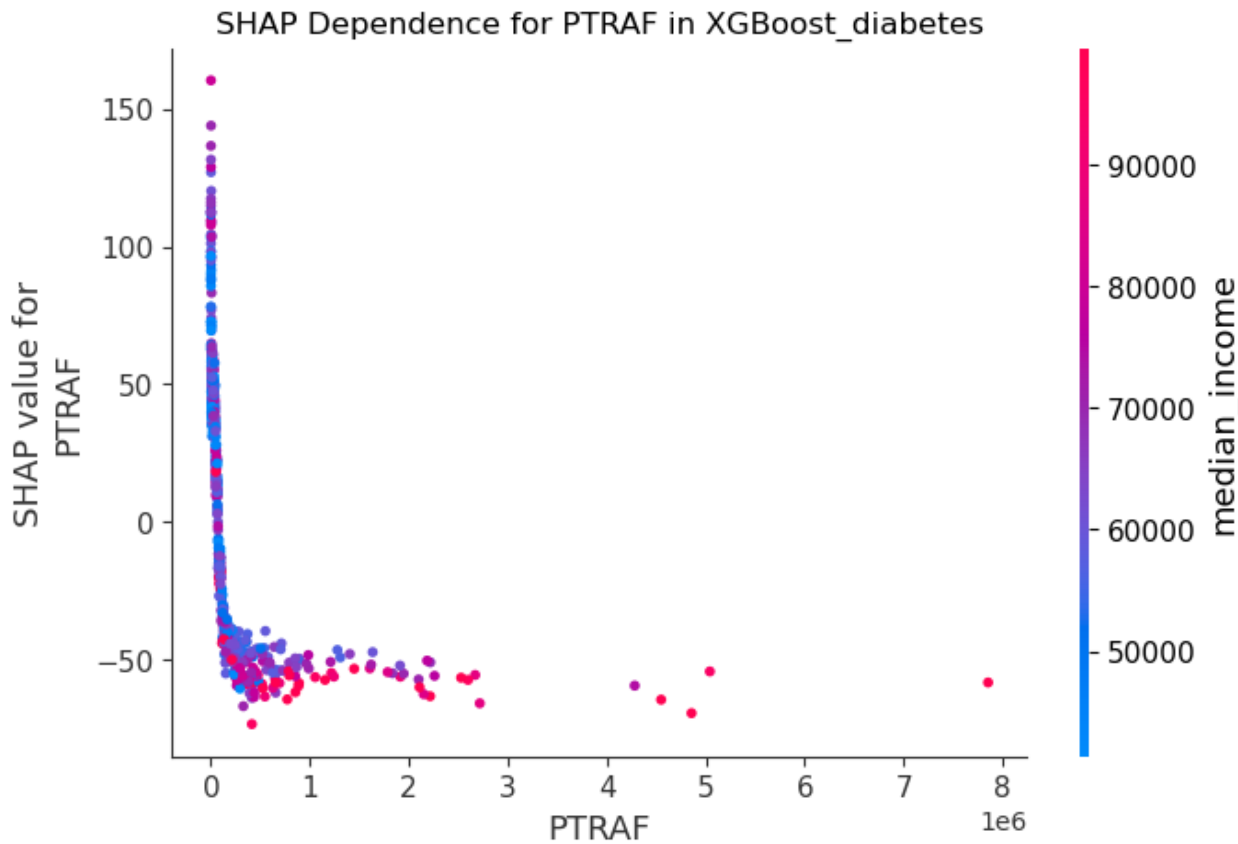


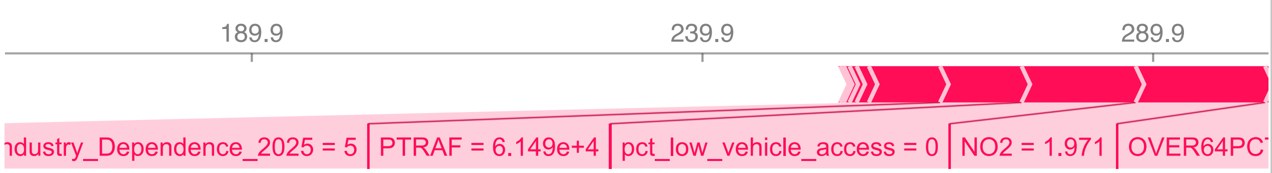



```
/var/folders/xv/jppz3tnj7z10dvcn0jp_xfk00000gp/T/ipykernel_60556/387051
  shap.summary_plot(shap_values, X_data, plot_type="bar", show=False)
```




UNEMPPCT
DWATER
LOWINCPCT
OZONE
poverty_rate
UNDER5PCT
RSEI_AIR
0
2
4
6
8
10
12
14
16
mean(|SHAP value|) (average impact on model output magnitude


SHAP Dependence for PTRAF in XGBoost_diabetes
SHAP value for PTRAF
150
100
50
0
−50
0
1
2
3
4
5
6
7
8
PTRAF
1e6
median_income
90000
80000
70000
60000
50000


189.9
239.9
289.9
ndustry_Dependence_2025 = 5
PTRAF = 6.149e+4
pct_low_vehicle_access = 0
NO2 = 1.971
OVER64PCT