```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
from scipy import stats
import statsmodels.api as sm
from statsmodels.formula.api import ols
import warnings
warnings.filterwarnings('ignore')
# File paths
HIV FILE PATH = 'HIV data 2000-2023.csv'
POVERTY FILE PATH = 'multidimensional_poverty.xlsx'
# Set plotting style
plt.style.use('seaborn-v0 8-whitegrid')
sns.set palette("viridis")
# --- 1. Load and Clean HIV Data ---
print("Loading HIV data...")
try:
    df hiv = pd.read csv(HIV FILE PATH, encoding='latin-1')
    print(f"HIV data loaded successfully: {df hiv.shape} rows.")
    # Clean column names
    df hiv.columns = df hiv.columns.str.strip()
    # Filter for relevant indicator
    indicator code = 'HIV 0000000001' # People living with HIV
    df hiv = df hiv[df hiv['IndicatorCode'] == indicator code].copy()
    print(f"Filtered to HIV indicator data: {df_hiv.shape} rows.")
    # Extract numeric value from 'Value' column
    df hiv['Value'] = df hiv['Value'].astype(str).str.extract(r'^([^\
[]+)')
    df_hiv['Value'] = df_hiv['Value'].str.replace(' ',
'').<mark>str</mark>.replace(',', '')
    df hiv['Value'] = pd.to numeric(df hiv['Value'], errors='coerce')
    # Rename columns for clarity
    df hiv = df hiv.rename(columns={
        'SpatialDimValueCode': 'CountryCode',
        'Period': 'Year',
        'ParentLocationCode': 'RegionCode',
        'Value': 'HIV Cases'
    })
    # Drop rows with missing values in key columns
    df_hiv.dropna(subset=['HIV_Cases', 'Year', 'CountryCode',
'RegionCode'], inplace=True)
```

```
df hiv['Year'] = df hiv['Year'].astype(int)
    print(f"Cleaned HIV data: {df hiv.shape} rows,
{df hiv['CountryCode'].nunique()} countries")
    print(f"Year range: {df hiv['Year'].min()}-
{df_hiv['Year'].max()}")
except Exception as e:
    print(f"Error loading HIV data: {e}")
    raise
# --- 2. Load and Clean Poverty Data ---
print("\nLoading Poverty data...")
    # Read with header on second row
    df poverty = pd.read excel(POVERTY FILE PATH, header=1)
    # The first row contains the actual column names for the
deprivation columns
    deprivation cols = df poverty.iloc[0]
    # Create a mapping for renaming columns
    rename map = \{\}
    for i, col in enumerate(df poverty.columns):
        if i >= 9 and i <= 14: # Deprivation rate columns
            new name = str(deprivation cols[col]).replace(' (%)', '')
            rename map[col] = new name
    # Add main poverty measure
    if 'Multidimensional poverty headcount ratio (%)' in
df poverty.columns:
        rename map['Multidimensional poverty headcount ratio (%)'] =
'MPI Headcount'
    # Rename columns
    df poverty.rename(columns=rename map, inplace=True)
    # Also rename key columns
    df poverty.rename(columns={'Country code': 'CountryCode',
'Reporting year': 'Year'}, inplace=True)
    # Drop the first row (which contained the column names)
    df poverty = df poverty.iloc[1:].reset_index(drop=True)
    # Convert deprivation columns to numeric
    numeric cols = ['Year', 'Monetary', 'Educational attainment',
'Educational enrollment',
                   'Electricity', 'Sanitation', 'Drinking water',
'MPI Headcount'
```

```
for col in numeric cols:
        if col in df_poverty.columns:
            df poverty[col] =
pd.to numeric(df poverty[col].astype(str).str.replace('-',
'0').str.replace('%', ''),
                                          errors='coerce')
    df poverty['Year'] = df poverty['Year'].astype(int)
    print(f"Cleaned poverty data: {df poverty.shape} rows,
{df_poverty['CountryCode'].nunique()} countries")
    print(f"Year range: {df_poverty['Year'].min()}-
{df poverty['Year'].max()}")
except Exception as e:
    print(f"Error loading poverty data: {e}")
    raise
# --- 3. Global Top 75% Burden Analysis ---
print("\n--- Task 1: Global Top 75% Burden Analysis ---")
# Calculate total burden across all years by country
country burden = df hiv.groupby('CountryCode')
['HIV Cases'].sum().sort values(ascending=False)
country total = country burden.sum()
country cumulative = country burden.cumsum() / country total
# Find countries making up 75% of global burden
top countries = country cumulative[country cumulative <=</pre>
0.75].index.tolist()
# Get one more country if needed to pass 75%
if len(top_countries) > 0 and country_cumulative.loc[top_countries[-
111 < 0.75:
    next idx = list(country cumulative.index).index(top countries[-1])
+ 1
    if next idx < len(country cumulative):</pre>
        top countries.append(country cumulative.index[next idx])
# Get country names for these country codes
country names = df hiv[['CountryCode',
'Location']].drop_duplicates().set_index('CountryCode')
top_countries_with_names = [(code, country_names.loc[code, 'Location']
if code in country names.index else code)
                           for code in top_countries]
print(f"Top {len(top countries)} countries contribute to 75% of global
HIV burden:")
for i, (code, name) in enumerate(top_countries_with_names[:10]):
    print(f"{i+1}. {name} ({code})")
```

```
if len(top countries) > 10:
    print(f"...and {len(top countries) - 10} more countries")
# Filter data for visualization
df top global =
df hiv[df hiv['CountryCode'].isin(top countries)].copy()
# Create yearly trend
yearly trend = df top global.groupby('Year')
['HIV Cases'].sum().reset index()
# Visualization - directly display in notebook
plt.figure(figsize=(12, 7))
sns.lineplot(x='Year', y='HIV Cases', data=yearly trend, linewidth=3,
marker='o')
plt.title('HIV Cases Trend in Countries Contributing to 75% of Global
Burden', fontsize=16)
plt.xlabel('Year', fontsize=14)
plt.ylabel('Number of People Living with HIV', fontsize=14)
plt.xticks(yearly trend['Year'].unique()[::2]) # Show every other
plt.ticklabel format(style='plain', axis='y') # Don't use scientific
notation
plt.grid(True, alpha=0.3)
# Add trend annotation
if len(yearly_trend) > 1:
    start val = yearly trend.iloc[0]['HIV Cases']
    end_val = yearly_trend.iloc[-1]['HIV_Cases']
    percent change = ((end val - start val) / start val) * 100
    plt.annotate(f"{percent_change:.1f}% change from
{yearly_trend['Year'].min()} to {yearly_trend['Year'].max()}",
                xy=(0.5, 0.95), xycoords='axes fraction', ha='center',
fontsize=12,
                bbox=dict(boxstyle="round,pad=0.3", fc="white",
ec="gray", alpha=0.8))
plt.tight layout()
plt.show() # Display in notebook instead of saving
# --- 4. Regional Top 75% Burden Analysis ---
print("\n--- Task 2: Regional Top 75% Burden Analysis ---")
# Get region names
region names = df hiv[['RegionCode',
'ParentLocation']].drop duplicates().set index('RegionCode')
print("WHO Regions in the data:")
for code, name in region names.iterrows():
    print(f"- {code}: {name['ParentLocation']}")
```

```
# Analyze each region separately
regional top countries = {}
region trend data = pd.DataFrame()
for region code, region data in df hiv.groupby('RegionCode'):
    region name = region names.loc[region code, 'ParentLocation']
    print(f"\nAnalyzing region: {region_name} ({region_code})")
    # Calculate country burden within this region
    region country burden = region data.groupby('CountryCode')
['HIV Cases'].sum().sort values(ascending=False)
    region total = region country burden.sum()
    region cumulative = region country burden.cumsum() / region total
    # Find countries making up 75% of regional burden
    region top = region cumulative[region cumulative <=</pre>
0.751.index.tolist()
    # Get one more country if needed to pass 75%
    if len(region top) > 0 and region cumulative.loc[region top[-1]] <
0.75:
        next idx = list(region cumulative.index).index(region top[-1])
+ 1
        if next idx < len(region cumulative):
            region top.append(region cumulative.index[next idx])
    regional top countries[region code] = region top
    # Get country names
    top names = [(code, country_names.loc[code, 'Location'] if code in
country names.index else code)
                 for code in region top]
    print(f"Top {len(region top)} countries contribute to 75% of
{region name} burden:")
    for i, (code, name) in enumerate(top names[:5]):
        burden pct = (region country burden[code] / region total) *
100
        print(f"{i+1}. {name} ({code}): {burden pct:.1f}% of regional
burden")
    if len(top names) > 5:
        print(f"...and {len(top names) - 5} more countries")
    # Filter data for visualization and create yearly trend
    region filtered =
region data[region data['CountryCode'].isin(region top)].copy()
    region yearly = region filtered.groupby('Year')
['HIV Cases'].sum().reset index()
    region yearly['RegionCode'] = region code
```

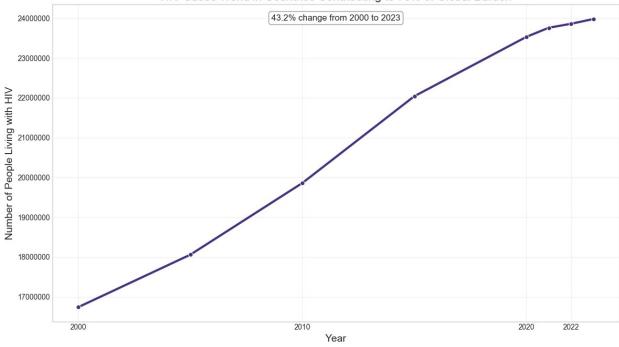
```
region yearly['Region'] = region name
    # Add to combined dataset
    region trend data = pd.concat([region trend data, region yearly])
# Visualization of regional trends - directly display in notebook
plt.figure(figsize=(14, 8))
sns.lineplot(x='Year', y='HIV_Cases', hue='Region',
data=region_trend_data, linewidth=2.5, marker='o')
plt.title('HIV Cases Trend by WHO Region (Top 75% Burden Countries)',
fontsize=16)
plt.xlabel('Year', fontsize=14)
plt.ylabel('Number of People Living with HIV', fontsize=14)
plt.xticks(region trend data['Year'].unique()[::2]) # Show every
other year
plt.ticklabel format(style='plain', axis='y') # Don't use scientific
notation
plt.grid(True, alpha=0.3)
plt.legend(title='WHO Region', fontsize=12)
plt.tight_layout()
plt.show() # Display in notebook instead of saving
# --- 5. HIV and Poverty Relationship Analysis ---
print("\n--- Task 3: HIV and Poverty Relationship Analysis ---")
# Merge datasets
print("Merging HIV and poverty datasets...")
df merged = pd.merge(
    df_hiv[['CountryCode', 'Year', 'HIV_Cases', 'Location',
'RegionCode']],
    df poverty,
    on=['CountryCode', 'Year'],
    how='inner'
)
print(f"Merged data: {df_merged.shape} rows,
{df merged['CountryCode'].nunique()} countries")
print(f"Years covered: {sorted(df merged['Year'].unique())}")
# Check if we have sufficient data for analysis
if df merged.shape[0] < 20:
    print("\nWARNING: Limited data available for regression
analysis.")
    print("Proceeding with descriptive analysis instead.")
# --- Correlation Analysis ---
# Get deprivation columns that are present in the data
deprivation cols = ['Monetary', 'Educational attainment', 'Educational
enrollment',
```

```
'Electricity', 'Sanitation', 'Drinking water',
'MPI Headcount']
available cols = [col for col in deprivation cols if col in
df merged.columns]
# Calculate correlations with HIV cases
correlations = []
for col in available cols:
    if df_merged[col].notna().sum() > 5: # Only if we have at least 5
data points
        corr, p value = stats.pearsonr(df merged['HIV Cases'],
df merged[col])
        correlations.append({
            'Factor': col,
            'Correlation': corr.
            'P-value': p value,
            'Sample Size': df merged[col].notna().sum()
        })
# Display correlation results
if correlations:
    print("\nCorrelations between HIV Cases and Poverty Factors:")
    corr df = pd.DataFrame(correlations).sort values('Correlation',
ascending=False)
    print(corr df)
    # Visualization of correlations - directly display in notebook
    plt.figure(figsize=(10, 6))
    bars = plt.barh(corr_df['Factor'], corr_df['Correlation'],
color=sns.color_palette("viridis", len(corr_df)))
    plt.axvline(x=0, color='black', linestyle='-', alpha=0.3)
    plt.xlabel('Pearson Correlation with HIV Cases', fontsize=14)
    plt.title('Correlation between HIV Cases and Poverty Factors',
fontsize=16)
    # Add significance markers
    for i, p in enumerate(corr df['P-value']):
        marker = '*' if p < 0.05 else 'ns'
        plt.text(corr df['Correlation'].iloc[i] * 1.05, i, marker,
fontsize=14)
    plt.grid(axis='x', alpha=0.3)
    plt.tight layout()
    plt.show() # Display in notebook instead of saving
# --- Simplified Regression Analysis ---
# If we have enough data points for at least one factor, run a simple
rearession
print("\nSimplified Regression Analysis:")
for col in available cols:
```

```
# Filter to rows with data for this column
    temp df = df merged[['HIV Cases', col]].dropna()
    if len(temp df) >= 10: # Only if we have at least 10 data points
        print(f"\nRegressing HIV Cases on {col}:")
        X = sm.add constant(temp df[col])
        model = sm.OLS(temp df['HIV Cases'], X).fit()
        print(model.summary().tables[1]) # Print the coefficients
table
        # Create scatter plot with regression line - directly display
in notebook
        plt.figure(figsize=(10, 6))
        sns.regplot(x=col, y='HIV_Cases', data=temp_df,
scatter_kws={'alpha':0.6}, line_kws={'color':'red'})
        plt.title(f'Relationship between HIV Cases and {col}',
fontsize=16)
        plt.xlabel(f'{col} (%)', fontsize=14)
        plt.ylabel('Number of People Living with HIV', fontsize=14)
        plt.grid(True, alpha=0.3)
        # Add regression equation
        slope = model.params[1]
        intercept = model.params[0]
        r2 = model.rsquared
        plt.annotate(f'y = {slope:..2f}x + {intercept:..2f} \setminus nR^2 =
{r2:.2f}',
                    xy=(0.05, 0.95), xycoords='axes fraction',
fontsize=12,
                    bbox=dict(boxstyle="round,pad=0.3", fc="white",
ec="gray", alpha=0.8))
        plt.tight layout()
        plt.show() # Display in notebook instead of saving
        print(f"Insufficient data for {col} regression
(n={len(temp df)})")
# --- Country-level Analysis for top HIV burden countries ---
print("\nCountry-level Analysis for Top HIV Burden Countries:")
# Get top 10 countries by total HIV burden
top10 countries = country burden.nlargest(10).index.tolist()
top10 with poverty = [c for c in top10 countries if c in
df_merged['CountryCode'].unique()]
if top10 with poverty:
    print(f"Found poverty data for {len(top10 with poverty)} of the
top 10 HIV burden countries")
```

```
# Create a summary table
    summary rows = []
    for country in top10_with_poverty:
        country data = df merged[df merged['CountryCode'] ==
country].iloc[0]
        row = {
            'Country': country data['Location'],
            'CountryCode': country,
            'HIV Cases': country data['HIV Cases'],
            'MPI Headcount': country data.get('MPI Headcount', np.nan)
        }
        # Add available deprivation factors
        for col in available cols:
            if col != 'MPI Headcount':
                row[col] = country data.get(col, np.nan)
        summary_rows.append(row)
    summary_df = pd.DataFrame(summary_rows)
    print("\nSummary of top HIV burden countries with poverty data:")
    print(summary df)
else:
    print("No poverty data available for top HIV burden countries")
print("\nAnalysis Complete")
Loading HIV data...
HIV data loaded successfully: (1552, 11) rows.
Filtered to HIV indicator data: (1552, 11) rows.
Cleaned HIV data: (1084, 11) rows, 144 countries
Year range: 2000-2023
Loading Poverty data...
Cleaned poverty data: (110, 16) rows, 110 countries
Year range: 2009-2022
--- Task 1: Global Top 75% Burden Analysis ---
Top 15 countries contribute to 75% of global HIV burden:
1. South Africa (ZAF)
2. Mozambique (MOZ)
3. Nigeria (NGA)
4. Kenya (KEN)
5. United Republic of Tanzania (TZA)
6. Zimbabwe (ZWE)
7. Uganda (UGA)
8. Zambia (ZMB)
9. Malawi (MWI)
10. Brazil (BRA)
...and 5 more countries
```





```
--- Task 2: Regional Top 75% Burden Analysis ---
```

WHO Regions in the data:

- AFR: Africa - AMR: Americas

- EMR: Eastern Mediterranean

- EUR: Europe

SEAR: South-East AsiaWPR: Western Pacific

Analyzing region: Africa (AFR)

Top 9 countries contribute to 75% of Africa burden:

- 1. South Africa (ZAF): 28.2% of regional burden
- 2. Mozambique (MOZ): 8.3% of regional burden
- 3. Nigeria (NGA): 8.2% of regional burden
- 4. Kenya (KEN): 6.6% of regional burden
- 5. United Republic of Tanzania (TZA): 6.4% of regional burden
- ...and 4 more countries

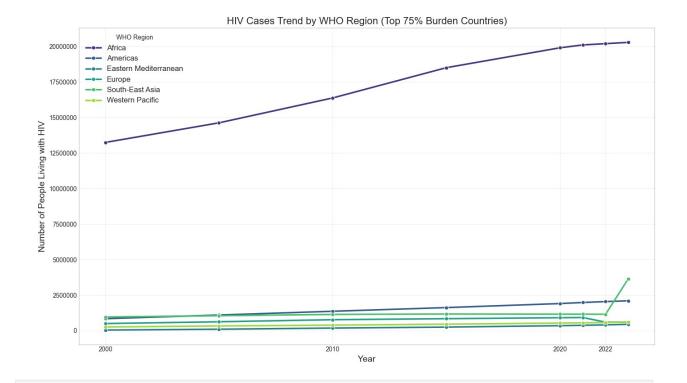
Analyzing region: Americas (AMR)

Top 7 countries contribute to 75% of Americas burden:

- 1. Brazil (BRA): 36.6% of regional burden
- 2. Mexico (MEX): 13.2% of regional burden
- 3. Colombia (COL): 8.6% of regional burden
- 4. Haiti (HTI): 6.1% of regional burden
- 5. Argentina (ARG): 5.2% of regional burden
- ...and 2 more countries

```
Analyzing region: Eastern Mediterranean (EMR)
Top 5 countries contribute to 75% of Eastern Mediterranean burden:
1. Pakistan (PAK): 46.2% of regional burden
2. Iran (Islamic Republic of) (IRN): 12.1% of regional burden
3. Sudan (SDN): 10.1% of regional burden
4. Egypt (EGY): 5.7% of regional burden
5. Morocco (MAR): 5.5% of regional burden
Analyzing region: Europe (EUR)
Top 7 countries contribute to 75% of Europe burden:
1. Ukraine (UKR): 19.4% of regional burden
2. France (FRA): 17.4% of regional burden
3. Spain (ESP): 14.8% of regional burden
4. Italy (ITA): 13.4% of regional burden
5. Portugal (PRT): 4.7% of regional burden
...and 2 more countries
Analyzing region: South-East Asia (SEAR)
Top 3 countries contribute to 75% of South-East Asia burden:
1. Thailand (THA): 39.3% of regional burden
2. Indonesia (IDN): 25.5% of regional burden
3. India (IND): 18.1% of regional burden
Analyzing region: Western Pacific (WPR)
Top 4 countries contribute to 75% of Western Pacific burden:
1. Viet Nam (VNM): 39.3% of regional burden
2. Philippines (PHL): 15.4% of regional burden
```

3. Cambodia (KHM): 14.4% of regional burden 4. Malaysia (MYS): 13.7% of regional burden



--- Task 3: HIV and Poverty Relationship Analysis ---

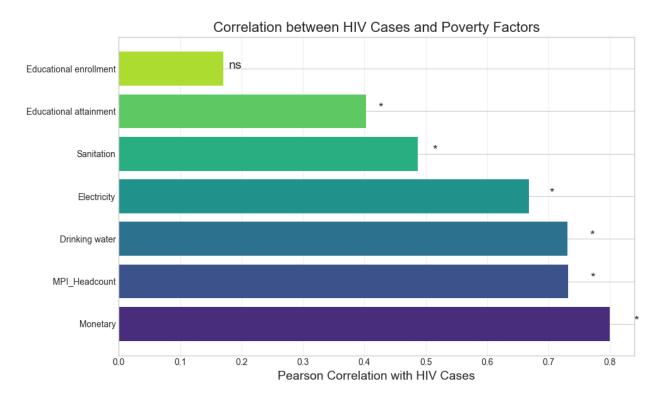
Merging HIV and poverty datasets...

Merged data: (39, 19) rows, 39 countries

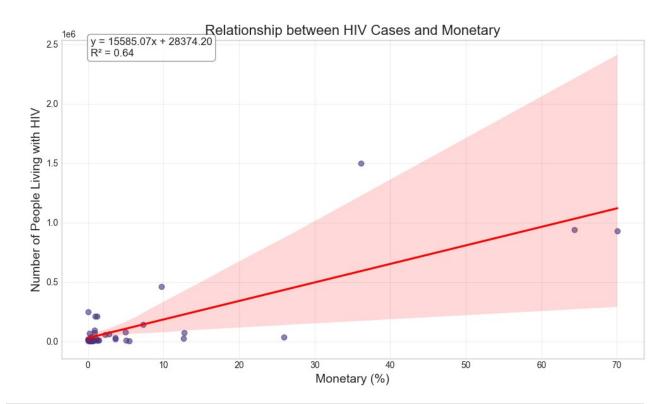
Years covered: [2010, 2015, 2022]

Correlations between HIV Cases and Poverty Factors:

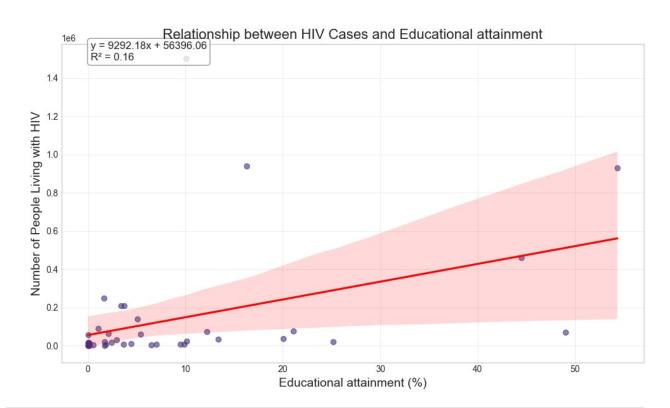
	Factor	Correlation	P-value	Sample Size
0	Monetary	0.799411	1.043874e-09	39
6	MPI_Headcount	0.731889	1.195944e-07	39
5	Drinking water	0.730925	1.266471e-07	39
3	Electricity	0.667747	3.419476e-06	39
4	Sanitation	0.487285	1.654122e-03	39
1	Educational attainment	0.402762	1.101882e-02	39
2	Educational enrollment	0.170370	2.997604e-01	39



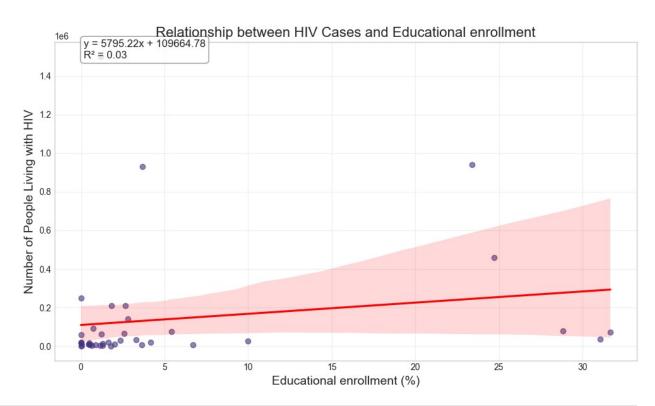
Simplified	l Regression A	nalysis:			
Regressing	HIV Cases or	Monetary:			
0.975]	coef	std err	t	P> t	[0.025
const 9.57e+04	2.837e+04	3.33e+04	0.853	0.399	-3.9e+04
Monetary 1.95e+04	1.559e+04	1925.559	8.094	0.000	1.17e+04
=======		=======	========		========



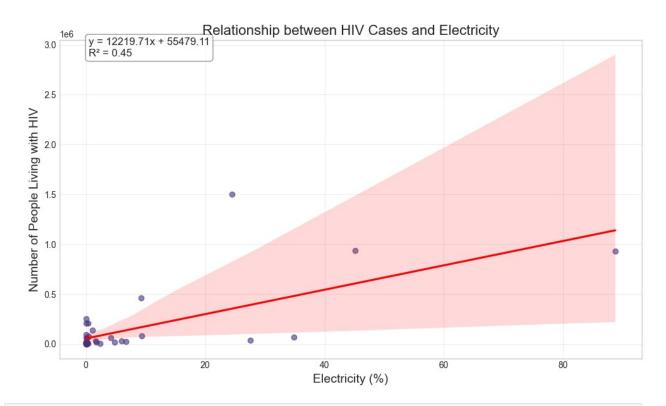
Regressing I	HIV Cases on	Educational	attainment:			==
[0.025	0.975]	coef	std err	t	P> t	
const 5.64e+04 Educational	1.69e+05	5.64e+04 9292.1781	5.57e+04 3471.634	1.013	0.318	-
2257.980 ========	1.63e+04 =========	=========	.========	=======		==



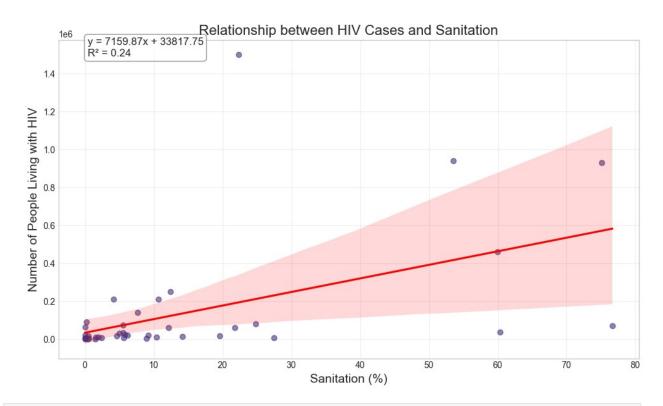
Regressing H	HIV Cases on	Educational	enrollment:	=======		==
[0.025	0.975]	coef	std err	t	P> t	
const 6694.628 Educational 5369.843	2.26e+05 enrollment 1.7e+04	1.097e+05 5795.2186	5.74e+04 5510.366	1.910 1.052	0.064 0.300	-
				=======		==



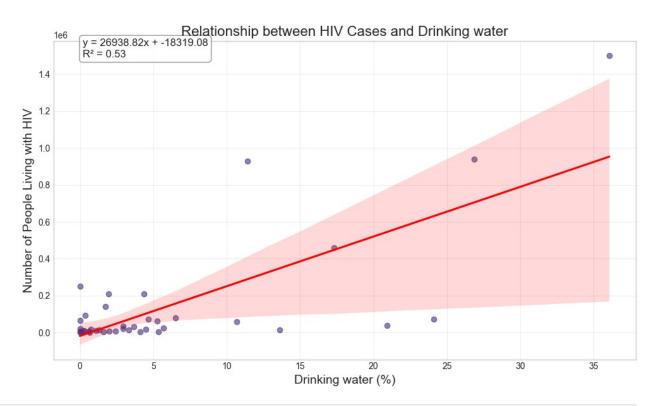
Regressing H	IV Cases on	Electricity: 	: -=======	=======	=========
=======					
	coef	std err	t	P> t	[0.025
0.975]					
const	5.548e+04	4.06e+04	1.368	0.180	-2.67e+04
1.38e+05					
Electricity	1.222e+04	2239.485	5.456	0.000	7682.086
1.68e+04					
========	========			======	
=======					



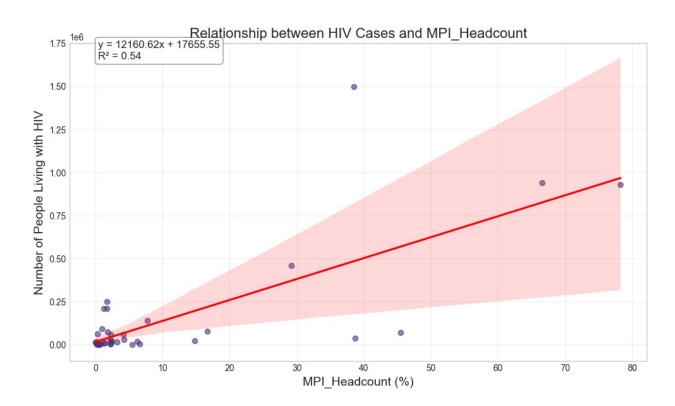
Regressing	HIV Cases or	Sanitation:	========		
======					
	coef	std err	t	P> t	[0.025
0.975]					
const	3.382e+04	5.4e+04	0.627	0.535	-7.55e+04
1.43e+05					
Sanitation	7159.8732	2109.388	3.394	0.002	2885.848
1.14e+04					
	========				
======					



Regressing HIV	Cases on Dri	inking water:		=======	========
========					
	coef	std err	t	P> t	[0.025
0.975]					
const	-1.832e+04	4.21e+04	-0.435	0.666	-1.04e+05
6.7e+04					
Drinking water	2.694e+04	4135.050	6.515	0.000	1.86e+04
3.53e+04					
========					



Regressing HIV	Cases on MF	PI_Headcount	:		
	=======		========		
	coef	std err	t	P> t	[0.025
0.975]					
const	1.766e+04	3.91e+04	0.452	0.654	-6.16e+04
9.69e+04 MPI Headcount	1.216e+04	1861.345	6.533	0.000	8389.173
1.59e+04	1.2106+04	1001.545	0.555	0.000	0509.175



		•	Burden Countr p 10 HIV burde	
Summary of to Country Cou O Kenya 1 Zambia 2 Malawi	intryCode HIV	/ Cases 0000.0 0000.0	66.506058	Monetary \ 36.146057 64.341974
Sanitation \ 0		Educatio	onal enrollmen 1.179968	
22.312516 1 53.505135	16.267821		23.398350	9 45.135146
2 75.137657	54.329389		3.686354	4 88.757396
Drinking w 0 36.06 1 26.84 2 11.46	60327 19246			
Analysis Comp	olete			