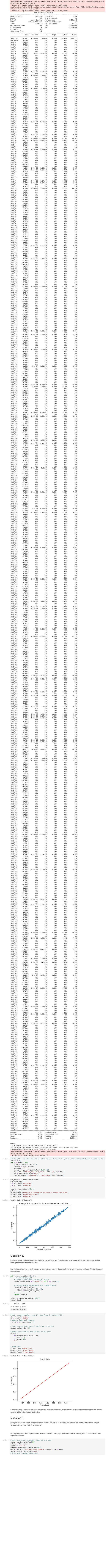
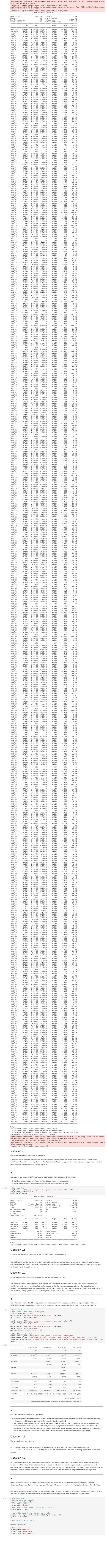
	<pre>import statsmodels.formula.api as sm import statsmodels.api as smf from stargazer.stargazer import Stargazer</pre>
	Background The Health Inequality Project uses 1.4 billion observations on income from tax records covering the U.S. population from 1999-20 to construct income-mortality gradients for each geographic region in the United States. The resulting datasets are publicly available at healthinequality.org. The map below shows life expectancy at age 40 for men in the bottom quartile of the income distribution for each commuting zor in the United States.
	in the United States. In this problem set, you will use these data to quantify the determinants of life expectancy for these low income men. The extract the data set, healthinequality.dta, is described below and posted on the course website. Source: The Health Inequality Project (Chetty, Stepner, Abraham, Lin, Scuderi, Turner, Bergeron, and Cutler 2016) Data Description
	Data DescriptionFile: healthinequality.dtaThe data consist of $n = 590$ U.S. commuting zones with populations larger than 25,000 in 2000. Commuting zones are geographical aggregations of counties that are similar to metro areas but cover the entire U.S., including rural areas.For more details on the construction of the variables included in this data set, please see Chetty, Stepner, Abraham, Lin, Scuderi, Turner, Bergeron, and Cutler (2016), which is posted on the course website.VariableDefinitionUnitsMeaczCommuting Zone ID n/a n/a
	czame Commuting Zone Name n/a n/a stateabbrv 2-letter state name (U.S. postal code) n/a
6]: 6]:	# Read dataset into a pandas dataframe health = pd.read_stata("healthinequality.dta") # Display first 5 rows of data health.head() cz czname fips stateabbrv cur_smoke bmi_obese exercise life_exp 0 100
	Please submit your Problem Set on Canvas. Your submission should include two files: 1. This notebook as a .ipynb file with your code and answers to questions 2. A .pdf version of this notebook. TODO: Provide general instructions on converting .ipynb to pdf Questions Note: Short answers should be very succinct. Show your work and intuition clearly: credit is given for explanations and not just having the correct answer
.7]:	Use the starter script files to help you get started on this question. The R^2 regression diagnostic statistic measures how much of the variance in the dependent variable can be explained $linearly$ by the covariates in the regression. It equals the ratio between the explained sum of squares and the total sum of squares in a regression: $R^2 = \frac{\sum_{i=1}^n (\hat{Y}_i - \hat{\vec{Y}})^2}{\sum_{i=1}^n (Y_i - \hat{Y})^2}$ In a simple bivariate regression, it equals the square of the correlation coefficient between the dependent variable and the single independent variable. 1. Estimate a regression of life_exp on cur_smoke. Explain in words what the coefficient on cur_smoke means. 2. What is the R^2 of this regression? Does the R^2 tell us whether the regression does a good job of fitting the data? If not, what does it tell us? 3. Now generate a random variable that is independent of both life_exp and cur_smoke. Run a regression of life_exp an intercept, cur_smoke, and the random variable that you generated. What happens to the R^2 ? 4. Now generate a total of 588 random variables that are independent of each other, life_exp and cur_smoke. Regress life_exp on an intercept, cur_smoke, and the 588 random variables that you generated. What happens to the R^2 ? Discuss briefly. 5. Explain (d) using the following simple non-trivial example: with N = 2 observations, what happens if we run a regression with intercept and one explanatory variable? 6. Now generate a total of 589 random variables. Regress life_exp on an intercept, cur_smoke, and the 589 independent random variable that you generated. What happens? 7. Use the residual regression formula to explain (f). # Your Code Here # 1. Regression of life_exp on cur_smoke mod_1 = sm.ols("life_exp ~ cur_smoke", data=health) res_1 = mod_1.fit(cov_type='HtC2')
	Dep. Variable: life_exp R-squared: 0.121 Model: 0LS Adj. R-squared: 0.119 No. Observations: 590 F-statistic: 43.65 Covariance Type: HC2 Prob (F-statistic): 8.81e-11
	Cur_smoke -7.4460 1.127 -6.607 0.000 -9.655 -5.237 Notes: [1] Standard Errors are heteroscedasticity robust (HC2) Question 1. We estimate the average effect of the fraction of people in a commuting zone that currently smokes in the bottom quartile of the national income distribution on life expecantcy to be -7.446 years. Our coefficient cur_smoke can be explained as the fraction of people in commuting zone *CZ* that currently smokes in the bottom quartile of the income distribution. Question 2. What is the R2 of this regression? The R^2 of this regression is 0.121. Does the R2 tell us whether the regression does a good job of fitting the data? the R^2 does generally not tell us if the regression does a good job of fitting the data, we can see that by plotting the estimated regression line vs the data to see if our estimate is a good or bad. If not, what does it tell us? Generelly the R^2 tells how much of the variance in our dependent variable is explained by our model.
2]:	<pre>Question 3. # Find number of rows def random_variables(x): N = health.shape[0] # Create column names like rand_5, rand_6 random_column_names = [f"rand_{i}" for i in range(x)] # Create a new dataframe with just random columns random_df = pd.DataFrame(np.random.random(size=(N, x)), columns=random_column_names) # Join old and new dataframes new_df = pd.concat([health, random_df], axis=1) return new_df frame = random_variables(1)</pre>
	<pre># 2. Regression of life_exp on cur_smoke, one random variable mod_2 = sm.ols("life_exp ~ cur_smoke + rand_0",data=frame) res_2 = mod_2.fit(cov_type='HC2') print(res_2.summary(slim=True)) OLS Regression Results ====================================</pre>
	No. Observations: 590 F-statistic: 21.82 Covariance Type: HC2 Prob (F-statistic): 7.21e-10
	What happens to \mathbb{R}^2 ? Nothing. \mathbb{R}^2 is a measure of how much of the variance in the dependent variable is explained by our model, since we are simply adding one random variable we would expect that there be not much change to the \mathbb{R}^2 besides a minor increase. An increase because we now have a random variable with random data, that could explain some of the variance in the dependent variable. Question 4.
	Now generate a total of 588 random variables. What happens to R^2 ? we can simply call the helper function as defined before to create 588 random variables, and then run our regression. Answer: We find that our R^2 now is 1.00 meaning that our model explains the variance in our dependent variable. Why? Essential we have created enough random variables with random data, that some are correlated with our dependent variable, and so we explained all the variance in our dependent variable with our model.
: :	<pre>frame = random_variables(588) columns = frame.columns seperator = "+" string = seperator.join(columns[8:]) mod_3 = sm.ols(f"life_exp ~ cur_smoke + {string}", data=frame) res_3 = mod_3.fit(cov_type='HC2') print(res_3.summary())</pre>





Out[17]:	Smoking 81 80 79 78 90 77 77 77 77 77 77 77 77 77
In [32]:	# Let's plot the regression plots -> e.g. the residuals linear_model = sm.ols("life_exp ~ cur_smoke", data=health).fit(cov_type='HC2') fig = smf.graphics.plot_regress_exog(linear_model, "cur_smoke") fig.tight_layout(pad=1.0) eval_env: 1 Regression Plots for cur_smoke Y and Fitted vs. X Residuals versus cur_smoke
	80 80 0.0 0.2 0.4 cur_smoke Partial regression plot Eagle 2.5 0.0 0.0 0.2 0.4 cur_smoke CCPR Plot 2.5 0.0 0.0 0.2 0.4 cur_smoke CURSPORT A cur_smoke CURSPORT CURSPORT A cur_smoke CU
	Sample Code This sequence allows you to import all necessary libraries for this problem set: import pandas as pd import numpy as np import matplotlib import statsmodels.formula.api as sm # Uncomment the line below if using Google Colab: # !pip install stargazer
	<pre>from stargazer.stargazer import Stargazer Reads in data and displays first 5 rows in dataset. We add an intercept column because Python does not automatically add a constant to regressions like Stata and R: # Read dataset into a pandas dataframe health = pd.read_stata("healthinequality.dta") # Display first 5 rows of data health.head() Estimates regression of yvar on an intercept and xvar1, with HC2 heteroskedasticity-robust standard errors. cov_type="HC2" corresponds to HC2 cov_type="HC1" corresponds to HC1 mod = sm.ols("yvar ~ xvar", data=health) res = mod.fit(cov_type="HC2")</pre>
	<pre># print results: res.summary(slim=True) Create x columns of random variables and add them to a new dataframe # Find number of rows N = health.shape[0] # Create column names like rand_5, rand_6 random_column_names = [f"rand_{i}" for i in range(x)] # Create a new dataframe with just random columns random_df = pd.DataFrame(np.random.random(size=(N, x)), columns=random_column_names) # Join old and new dataframes new df = pd.concat([health_random_df]_axis=1)</pre>
	<pre>new_df = pd.concat([health, random_df], axis=1) # Extra hint: look at the python "join" function to # create a string out of the list of variable names Create regression table with custom column labels # Estimate Regressions: mod1 = sm.ols("yvar1 ~ xvar1 + xvar2 + xvar3", data=health) res1 = mod.fit(cov_type="HC2") mod2 = sm.ols("yvar1 ~ xvar1 + xvar2", data=health) res2 = mod.fit(cov_type="HC2") mod3 = sm.ols("yvar2 ~ xvar2 + xvar3", data=health</pre>
	<pre>data=health) res3 = mod.fit(cov_type="HC2") # Create Table table = Stargazer(models) # Label columns # This list of 1s should be the same length as the # number of columns table.custom_columns(["yvar1", "yvar1", "yvar2"], seperators=[1, 1, 1]) # Display table table Calculate residuals from regression of variable yvar on variables xvar1 and xvar2 # Estimate Regressions: mod1 = sm.ols(</pre>
	<pre>"yvar ~ xvar1 + xvar2", data=health) res1 = mod.fit(cov_type="HC2") # Find residuals residuals = res1.resid Draw a scatter plot of variable x1 against variable y1 and add a line best fit # Sets up space for graphing fig, ax = plt.subplots(1, 1) # Plots scatter plot (size of points is set by s=3) ax.scatter(x1, y1, s=3) # Adds a line best fit for the data to the plot ax.plot(*np.polynomial.Polynomial.fit(x1, y1, 1</pre>
	<pre>).linspace(2), "r-") # Label axes ax.set_title("Graph Title") ax.set_xlabel("X Axis Label") ax.set_ylabel("Y Axis Label")</pre>