Linear and logistic regression modeling, a case study with the NHANES data

This notebook introduces two statistical modeling techniques: linear regression and logistic regression. The focus here will be on fitting these two types of models to data, using Python statistical modeling libraries in the Jupyter notebook environment. As with several previous case studies in this course, here we will be analyzing the NHANES (https://www.cdc.gov/nchs/nhanes/index.htm) data, allowing us to illustrate the use of these two regression methods for addressing meaningful questions with actual data.

Note that the NHANES data were collected as a designed survey, and in general should be analyzed as such. This means that survey design information such as weights, strata, and clusters should be accounted for in any analysis using NHANES. But to introduce how linear and logistic regression are used with independent data samples, or with convenience samples, we will not incorporate the survey structure of the NHANES sample into the analyses conducted here.

As with our previous work, we will be using the Pandas (http://pandas.pydata.org) library for data management, the Numpy (http://www.numpy.org) library for numerical calculations, and the Statsmodels (http://www.statsmodels.org) library for statistical modeling.

We begin by importing the libraries that we will be using.

In [1]:

```
%matplotlib inline
import matplotlib.pyplot as plt
import seaborn as sns
import pandas as pd
import statsmodels.api as sm
import numpy as np
```

Next we will load the data. The NHANES study encompasses multiple waves of data collection. Here we will only use the 2015-2016 data. As with most data sets, there are some missing values in the NHANES files. While many of the methods demonstrated below would handle missing values automatically (at least in a crude way), here we drop up-front all rows with missing values in any of the key variables that we will use in this notebook.

In [2]:

```
# Read the 2015-2016 wave of NHANES data
da = pd.read_csv("nhanes_2015_2016.csv")

# Drop unused columns, and drop rows with any missing values.
vars = ["BPXSY1", "RIDAGEYR", "RIAGENDR", "RIDRETH1", "DMDEDUC2", "BMXBMI",
da = da[vars].dropna()
```

Linear regression

We will focus initially on regression models in which systolic blood pressure (https://en.wikipedia.org/wiki/Blood_pressure) (SBP) is the outcome (dependent) variable. That is, we will predict SBP from other variables. SBP is an important indicator of cardiovascular health. It tends to increase with age, is greater for overweight people (i.e. people with greater body mass index or BMI), and also differs among demographic groups, for example among gender and ethnic groups.

Since SBP is a quantitative variable, we will model it using linear regression. Linear regression is the most widely-utilized form of statistical regression. While linear regression is commonly used with quantitative outcome variables, it is not the only type of regression model that can be used with quantitative outcomes, nor is it the case that linear regression can only be used with quantitative outcomes. However, linear regression is a good default starting point for any regression analysis using a quantitative outcome variable.

Interpreting regression parameters in a basic model

We start with a simple linear regression model with only one covariate, age, predicting SBP. In the NHANES data, the variable BPXSY1 (https://wwwn.cdc.gov/Nchs/Nhanes/2015-2016/BPX_I.htm#BPXSY1) contains the first recorded measurement of SBP for a subject, and RIDAGEYR (https://wwwn.cdc.gov/Nchs/Nhanes/2015-2016/DEMO_I.htm#RIDAGEYR) is the subject's age in years. The model that is fit in the next cell expresses the expected SBP as a linear function of age:

In [3]:

```
model = sm.OLS.from_formula("BPXSY1 ~ RIDAGEYR", data=da)
result = model.fit()
result.summary()
```

Out[3]:

OLS Regression Results

Dep. Variable:	BPXSY1	**R-squared:**	0.207
Model:	OLS	**Adj. R-squared:**	0.207
Method:	Least Squares	**F-statistic:**	1333.
Date:	Thu, 11 Jul 2019	**Prob (F-statistic):**	2.09e-259
Time:	21:00:08	**Log-Likelihood:**	-21530.
No. Observations:	5102	**AIC:**	4.306e+04
Df Residuals:	5100	**BIC:**	4.308e+04
Df Model:	1		
Covariance Type:	nonrobust		

	coef	**std err**	**t**	**P>|t|**	**[0.025**	**0.975]**
Intercept	102.0935	0.685	149.120	0.000	100.751	103.436
RIDAGEYR	0.4759	0.013	36.504	0.000	0.450	0.501

Omnibus:	690.261	**Durbin-Watson:**	2.039
Prob(Omnibus):	0.000	**Jarque-Bera (JB):**	1505.999
Skew:	0.810	**Prob(JB):**	0.00
Kurtosis:	5.112	**Cond. No.**	156.

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

Much of the output above is not relevant for us, so focus on the center section of the output where the header begins with **coef**. This section contains the estimated values of the parameters of the regression model, their standard errors, and other values that are used to quantify the uncertainty in the regression parameter estimates. Note that the parameters of a regression model, which appear in the column labeled **coef** in the table above, may also be referred to as *slopes* or *effects*.

This fitted model implies that when comparing two people whose ages differ by one year, the older person will on average have 0.48 units higher SBP than the younger person. This difference is statistically significant, based on the p-value shown under the column labeled `P>|t|`. This means that there is strong evidence that there is a real association between between systolic blood pressure and age in this population.

SBP is measured in units of *millimeters of mercury*, expressed *mm/Hg*. In order to better understand the meaning of the estimated regression parameter 0.48, we can look at the standard deviation of SBP:

In [4]:

```
da.BPXSY1.std()
```

Out[4]:

```
18.486559500782416
```

The standard deviation of around 18.5 is large compared to the regression slope of 0.48. However the regression slope corresponds to the average change in SBP for a single year of age, and this effect accumulates with age. Comparing a 40 year-old person to a 60 year-old person, there is a 20 year difference in age, which translates into a `20 * 0.48 = 9.6` unit difference in average SBP between these two people. This difference is around half of one standard deviation, and would generally be considered to be an important and meaningful shift.

R-squared and correlation

In the case of regression with a single independent variable, as we have here, there is a very close correspondence between the regression analysis and a Pearson correlation analysis, which we have discussed earlier in course 2. The primary summary statistic for assessing the strength of a predictive relationship in a regression model is the *R-squared*, which is shown to be 0.207 in the regression output above. This means that 21% of the variation in SBP is explained by age. Note that this value is exactly the same as the squared Pearson correlation coefficient between SBP and age, as shown below.

In [5]:

```
cc = da[["BPXSY1", "RIDAGEYR"]].corr()
print(cc.BPXSY1.RIDAGEYR**2)
```

```
0.20715459625188243
```

There is a second way to interpret the R-squared, which makes use of the *fitted values* of the regression. The fitted values are predictions of the blood pressure for each person in the data set, based on their covariate values. In this case, the only covariate is age, so we are predicting each NHANES subject's blood pressure as a function of their age. If we calculate the Pearson correlation coefficient between the fitted values from the regression, and the actual SBP values, and then square this correlation coefficient, we see that we also get the R-squared from the regression:

In [6]:

```
cc = np.corrcoef(da.BPXSY1, result.fittedvalues)
print(cc[0, 1]**2)
```

```
0.20715459625186952
```

Thus, we see that in a linear model fit with only one covariate, the regression R-squared is equal to the squared Pearson correlation between the covariate and the outcome, and is also equal to the squared Pearson correlation between the fitted values and the outcome.

Adding a second variable

Above we considered a simple linear regression analysis with only one covariate (age) predicting systolic blood pressure (SBP). The real power of regression analysis arises when we have more than one covariate predicting an outcome. As noted above, SBP is expected to be related to gender as well as to age, so we next add gender to the model. The NHANES variable for gender is named RIAGENDR (https://wwwn.cdc.gov/Nchs/Nhanes/2015-2016/DEMO_I.htm#RIAGENDR)

We begin by creating a relabeled version of the gender variable:

In [7]:
```
# Create a labeled version of the gender variable
da["RIAGENDRx"] = da.RIAGENDR.replace({1: "Male", 2: "Female"})
```

Now we are ready to fit the linear model:

In [8]:
```
model = sm.OLS.from_formula("BPXSY1 ~ RIDAGEYR + RIAGENDRx", data=da)
result = model.fit()
result.summary()
```

Out[8]:
```
OLS Regression Results

       Dep. Variable:          BPXSY1           R-squared:      0.215
               Model:             OLS      Adj. R-squared:      0.214
              Method:   Least Squares         F-statistic:      697.4
                Date: Thu, 11 Jul 2019 Prob (F-statistic):  1.87e-268
                Time:        21:00:12      Log-Likelihood:    -21505.
   No. Observations:             5102                 AIC:  4.302e+04
        Df Residuals:            5099                 BIC:  4.304e+04
            Df Model:               2
     Covariance Type:       nonrobust

                        coef  std err        t  P>|t|  [0.025   0.975]
         Intercept  100.6305    0.712  141.257  0.000  99.234  102.027
 RIAGENDRx[T.Male]    3.2322    0.459    7.040  0.000   2.332    4.132
          RIDAGEYR    0.4739    0.013   36.518  0.000   0.448    0.499

       Omnibus:  706.732    Durbin-Watson:     2.036
 Prob(Omnibus):    0.000  Jarque-Bera (JB):  1582.730
          Skew:    0.818         Prob(JB):      0.00
      Kurtosis:    5.184         Cond. No.      168.


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

The syntax `RIDAGEYR + RIAGENDRx` in the cell above does not mean that these two variables are literally added together. Instead, it means that these variables are both included in the model as predictors of blood pressure (`BPXSY1`).

The model that was fit above uses both age and gender to explain the variation in SBP. It finds that two people with the same gender whose ages differ by one year tend to have blood pressure values differing by 0.47 units, which is essentially the same age parameter that we found above in the model based on age alone. This model also shows us that comparing a man and a woman of the same age, the man will on average have 3.23 units greater SBP.

It is very important to emphasize that the age coefficient of 0.47 is only meaningful when comparing two people of the same gender, and the gender coefficient of 3.23 is only meaningful when comparing two people of the same age. Moreover, these effects are additive, meaning that if we compare, say, a 50 year old man to a 40 year old woman, the man's blood pressure will on average be around 3.23 + 10*0.47 = 7.93 units higher, with the first term in this sum being attributable to gender, and the second term being attributable to age.

We noted above that the regression coefficient for age did not change by much when we added gender to the model. It is important to note however that in general, the estimated coefficient of a variable in a regression model will change when other variables are added or removed. The only circumstance in which a regresion parameters is unchanged when other variables are added or removed from the model is when those variables are uncorrelated with the variables that remain in the model.

Below we confirm that gender and age are nearly uncorrelated in this data set (the correlation of around -0.02 is negligible). Thus, it is expected that when we add gender to the model, the age coefficient is unaffected.

In [9]:

```
# We need to use the original, numerical version of the gender
# variable to calculate the correlation coefficient.
da[["RIDAGEYR", "RIAGENDR"]].corr()
```

Out[9]:

	RIDAGEYR	RIAGENDR
RIDAGEYR	1.000000	-0.021398
RIAGENDR	-0.021398	1.000000

Observe that in the regression output shown above, an R-squared value of 0.215 is listed. Earlier we saw that for a model with only one covariate, the R-squared from the regression could be defined in two different ways, either as the squared correlation coefficient between the covariate and the outcome, or as the squared correlation coefficient between the fitted values and the outcome. When more than one covariate is in the model, only the second of these two definitions continues to hold:

In [10]:

```
cc = np.corrcoef(da.BPXSY1, result.fittedvalues)
print(cc[0, 1]**2)
```

```
0.21478581086243784
```

Categorical variables and reference levels

In the model fit above, gender is a categorical variable, and only a coefficient for males is included in the regression output (i.e. there is no coefficient for females in the tables above). Whenever a categorical variable is used as a covariate in a regression model, one level of the variable is omitted and is automatically given a coefficient of zero. This level is called the *reference level* of the covariate. Here, the female level of the gender variable is the reference level. This does not mean that being a woman has no impact on blood pressure. It simply means that we have written the model so that female blood pressure is the default, and the coefficient for males (3.23) shifts the blood pressure by that amount for males only.

We could alternatively have set 'male' to be the reference level, in which case males would be the default, and the female coefficient would have been around -3.23 (meaning that female blood pressure is 3.23 units lower than the male blood pressure).

When using a categorical variable as a predictor in a regression model, it is recoded into "dummy variables" (also known as "indicator variables"). A dummy variable for a single level, say `a`, of a variable `x`, is a variable that is equal to `1` when `x=a` and is equal to `0` when `x` is not equal to `a`. These dummy variables are all included in the regression model, to represent the variable that they are derived from.

Statsmodels, like most software, will automatically recode a categorical variable into dummy variables, and will select a reference level (it is possible to override this choice, but we do not cover that here). When interpreting the regression output, the level that is omitted should be seen as having a coefficient of 0, with a standard error of 0. It is important to note that the selection of a reference level is arbitrary and does not imply an assumption or constraint about the model, or about the population that it is intended to capture.

A model with three variables

Next we add a third variable, body mass index (BMI), to the model predicting SBP. BMI (https://en.wikipedia.org/wiki/Body_mass_index) is a measure that is used to assess if a person has healthy weight given their height. BMXBMI (https://wwwn.cdc.gov/Nchs/Nhanes/2015-2016/BMX_I.htm#BMXBMI) is the NHANES variable containing the BMI value for each subject.

```
In [11]: model = sm.OLS.from_formula("BPXSY1 ~ RIDAGEYR + BMXBMI + RIAGENDRx", data=
         result = model.fit()
         result.summary()
```

```
Out[11]: OLS Regression Results

                Dep. Variable:          BPXSY1           R-squared:      0.228
                       Model:              OLS      Adj. R-squared:      0.228
                      Method:    Least Squares         F-statistic:      502.0
                        Date: Thu, 11 Jul 2019  Prob (F-statistic):  8.54e-286
                        Time:         21:00:15      Log-Likelihood:    -21461.
            No. Observations:             5102                 AIC:  4.293e+04
                Df Residuals:             5098                 BIC:  4.296e+04
                    Df Model:                3
             Covariance Type:        nonrobust

                            coef   std err        t   P>|t|   [0.025   0.975]
                Intercept  91.5840    1.198   76.456   0.000   89.236   93.932
         RIAGENDRx[T.Male]  3.5783    0.457    7.833   0.000    2.683    4.474
                  RIDAGEYR  0.4709    0.013   36.582   0.000    0.446    0.496
                    BMXBMI  0.3060    0.033    9.351   0.000    0.242    0.370

                 Omnibus: 752.325     Durbin-Watson:    2.040
           Prob(Omnibus):   0.000  Jarque-Bera (JB): 1776.087
                    Skew:   0.847          Prob(JB):     0.00
                Kurtosis:   5.343         Cond. No.      316.


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

Not surprisingly, BMI is positively associated with SBP. Given two subjects with the same gender and age, and whose BMI differs by 1 unit, the person with greater BMI will have, on average, 0.31 units greater systolic blood pressure (SBP). Also note that after adding BMI to the model, the coefficient for gender became somewhat greater. This is due to the fact that the three covariates in the model, age, gender, and BMI, are mutually correlated, as shown next:

In [12]:

```
da[["RIDAGEYR", "RIAGENDR", "BMXBMI"]].corr()
```

Out[12]:

	RIDAGEYR	RIAGENDR	BMXBMI
RIDAGEYR	1.000000	-0.021398	0.023089
RIAGENDR	-0.021398	1.000000	0.080463
BMXBMI	0.023089	0.080463	1.000000

Although the correlations among these three variables are not strong, they are sufficient to induce fairly substantial differences in the regression coefficients (e.g. the gender coefficient changes from 3.23 to 3.58). In this example, the gender effect becomes larger after we control for BMI - we can take this to mean that BMI was masking part of the association between gender and blood pressure. In other settings, including additional covariates can reduce the association between a covariate and an outcome.

Visualization of the fitted models

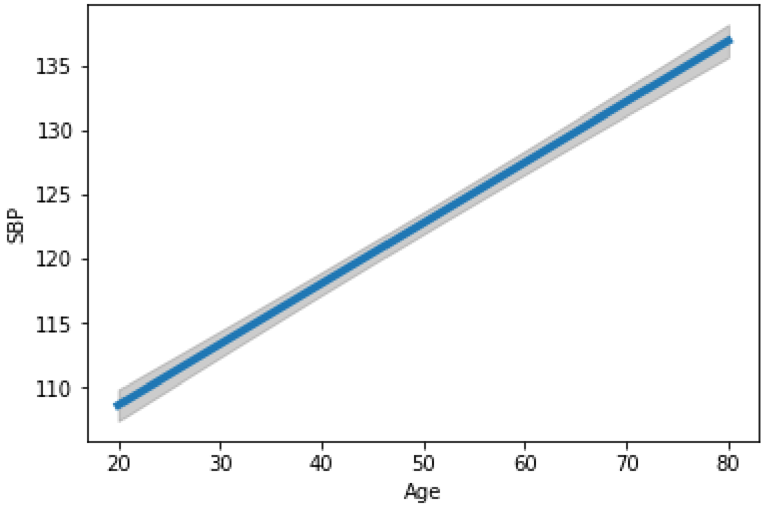
In this section we demonstrate some graphing techniques that can be used to gain a better understanding of a regression model that has been fit to data.

We start with plots that allow us to visualize the fitted regression function, that is, the mean systolic blood pressure expressed as a function of the covariates. These plots help to show the estimated role of one variable when the other variables are held fixed. We will also plot 95% *simultaneous confidence bands* around these fitted lines. Although the estimated mean curve is never exact based on a finite sample of data, we can be 95% confident that the true mean curve falls somewhere within the shaded regions of the plots below.

This type of plot requires us to fix the values of all variables other than the independent variable (SBP here), and one independent variable that we call the *focus variable* (which is age here). Below we fix the gender as "female" and the BMI as 25. Thus, the graphs below show the relationship between expected SBP and age for women with BMI equal to 25.

In [13]:

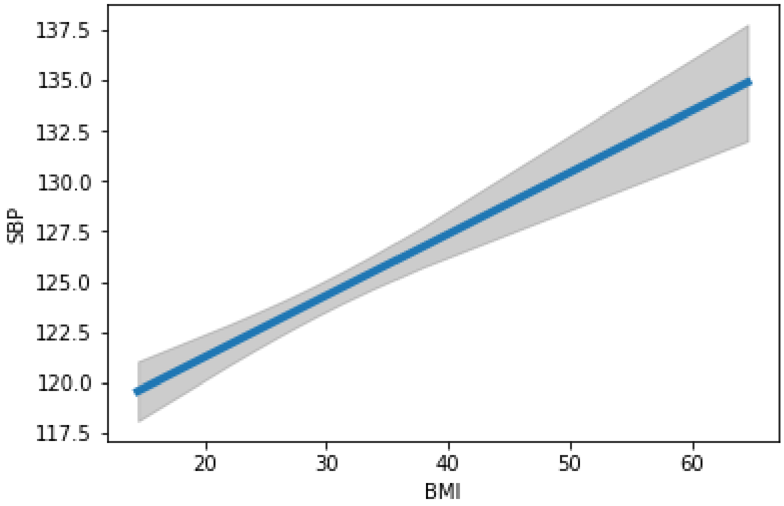
```
from statsmodels.sandbox.predict_functional import predict_functional

# Fix certain variables at reference values.  Not all of these
# variables are used here, but we provide them with a value anyway
# to prevent a warning message from appearing.
values = {"RIAGENDRx": "Female", "RIAGENDR": 1, "BMXBMI": 25,
          "DMDEDUC2": 1, "RIDRETH1": 1, "SMQ020": 1}

# The returned values are the predicted values (pr), the confidence bands (
# and the function values (fv).
pr, cb, fv = predict_functional(result, "RIDAGEYR",
                values=values, ci_method="simultaneous")

ax = sns.lineplot(fv, pr, lw=4)
ax.fill_between(fv, cb[:, 0], cb[:, 1], color='grey', alpha=0.4)
ax.set_xlabel("Age")
_ = ax.set_ylabel("SBP")
```



The analogous plot for BMI is shown next. Here we fix the gender as "female" and the age at 50, so we are looking at the relationship between expected SBP and age for women of age 50.

In [14]:

```
del values["BMXBMI"] # Delete this as it is now the focus variable
values["RIDAGEYR"] = 50
pr, cb, fv = predict_functional(result, "BMXBMI",
                values=values, ci_method="simultaneous")

ax = sns.lineplot(fv, pr, lw=4)
ax.fill_between(fv, cb[:, 0], cb[:, 1], color='grey', alpha=0.4)
ax.set_xlabel("BMI")
_ = ax.set_ylabel("SBP")
```



The error band for BMI is notably wider than the error band for age, indicating that there is less certainty about the relationship between BMI and SBP compared to the relationship between age and SBP.

The discussion so far has primarily focused on the mean structure of the population, that is, the model for the average SBP of a person with a given age, gender, and BMI. A regression model can also be used to assess the *variance structure* of the population, that is, how much and in what manner the observations deviate from their mean. We will focus on informal, graphical methods for assessing this.

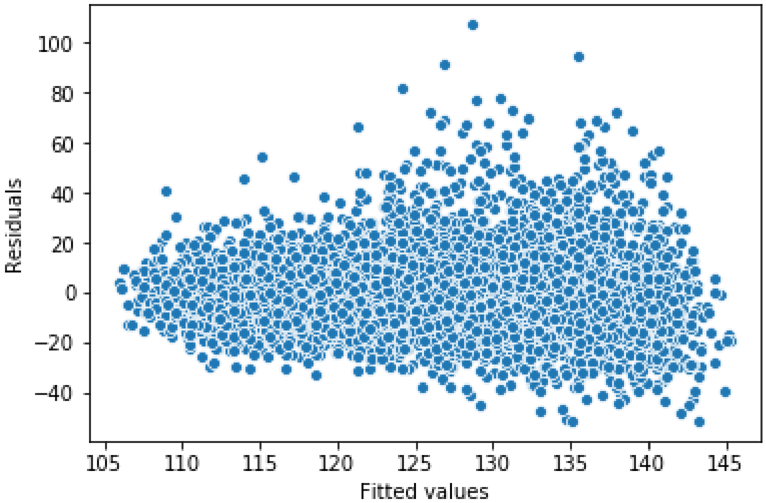
To begin with, we plot the residuals against the fitted values. Recall that the fitted values are the estimated means for each observation, and the residuals are the difference between an observation and its fitted mean. For example, the model may estimate that a 50 year old female will have on average an SBP of 125. But a specific 50 year old female may have a blood pressure of 110 or 150, for example. The fitted values for both of these women are 125, and their residuals are -15, and 25, respectively.

The simplest variance pattern that we can see in a linear regression occurs when the points are scattered around the mean, with the same degree of scatter throughout the range of the covariates. When there are multiple covariates, it is hard to assess whether the variance is uniform throughout this range, but we can easily check for a "mean/variance relationship", in which there is a systematic relationship between the variance and the mean, i.e. the variance either increases or decreases systematically with the mean. The plot of residuals on fitted values is used to assess whether such a mean/variance relationship is present.

Below we show the plot of residuals on fitted values for the NHANES data. It appears that we have a modestly increasing mean/variance relationship. That is, the scatter around the mean blood pressure is greater when the mean blood pressure itself is greater.

In [15]:

```
pp = sns.scatterplot(result.fittedvalues, result.resid)
pp.set_xlabel("Fitted values")
_ = pp.set_ylabel("Residuals")
```

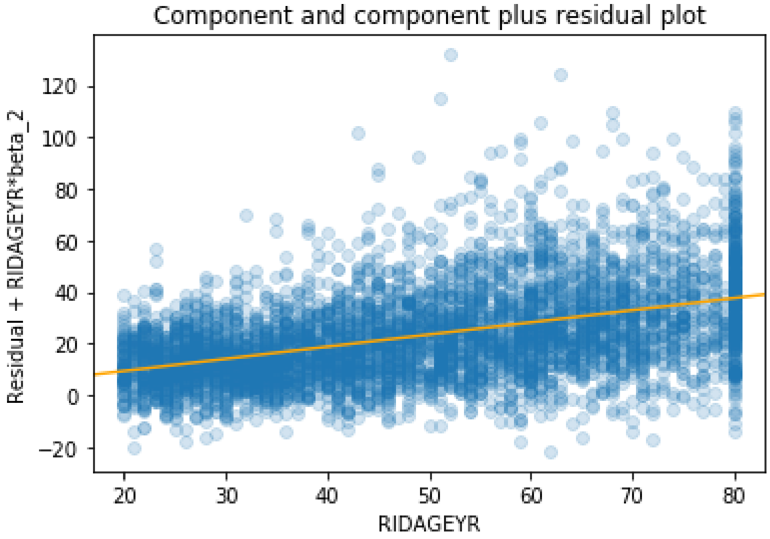


A "component plus residual plot" or "partial residual plot" is intended to show how the data would look if all but one covariate could be fixed at reference values. By controlling the values of these covariates, all remaining variation is due either to the "focus variable" (the one variable that is left unfixed, and is plotted on the horizontal axis), or to sources of variation that are unexplained by any of the covariates.

For example, the partial residual plot below shows how age (horizontal axis) and SBP (vertical axis) would be related if gender and BMI were fixed. Note that the origin of the vertical axis in these plots is not meaningful (we are not implying that anyone's blood pressure would be negative), but the differences along the vertical axis are meaningful. This plot implies that when BMI and gender are held fixed, the average blood pressures of an 80 and 18 year old differ by around 30 mm/Hg. This plot also shows, as discussed above, that the deviations from the mean are somewhat smaller at the low end of the range compared to the high end of the range. We also see that at the high end of the range, the deviations from the mean are somewhat right-skewed, with exceptionally high SBP values being more common than exceptionally low SBP values.

In [16]:

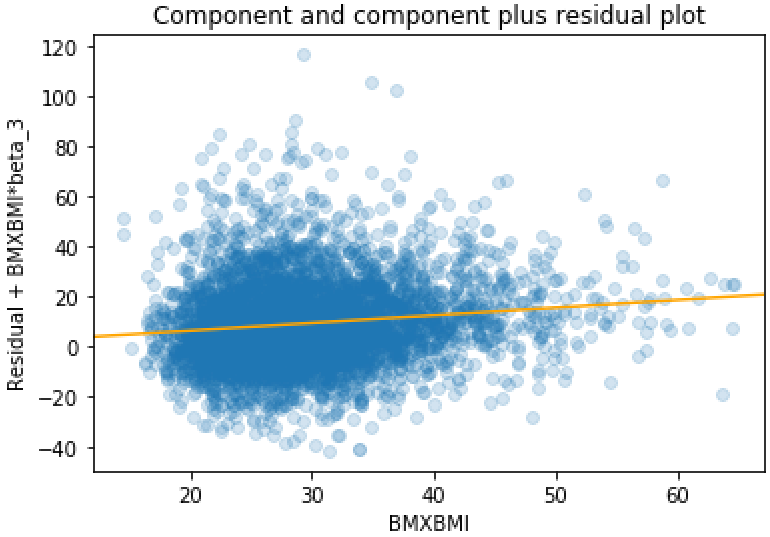
```
# This is not part of the main Statsmodels API, so needs to be imported sep
from statsmodels.graphics.regressionplots import plot_ccpr

ax = plt.axes()
plot_ccpr(result, "RIDAGEYR", ax)
ax.lines[0].set_alpha(0.2) # Reduce overplotting with transparency
_ = ax.lines[1].set_color('orange')
```



Next we have a partial residual plot that shows how BMI (horizontal axis) and SBP (vertical axis) would be related if gender and age were fixed. Compared to the plot above, we see here that age is more uniformly distributed than BMI. Also, it appears that there is more scatter in the partial residuals for BMI compared to what we saw above for age. Thus there seems to be less information about SBP in BMI, although a trend certainly exists.

In [17]:

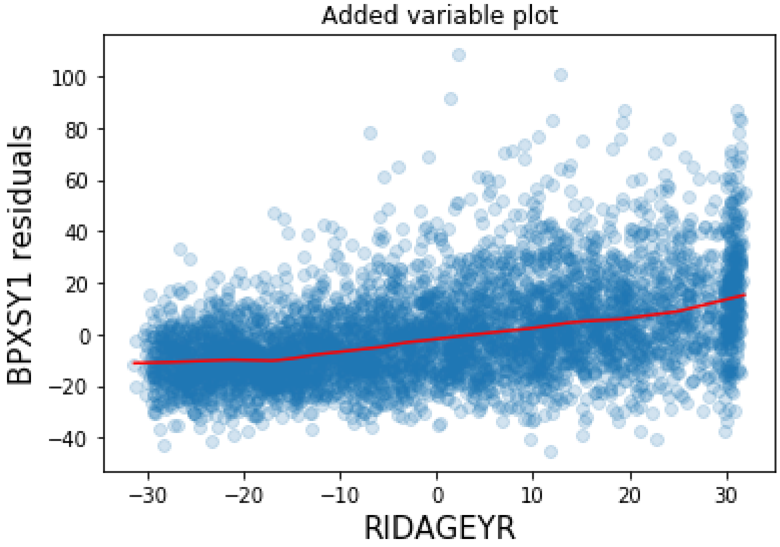
```
ax = plt.axes()
plot_ccpr(result, "BMXBMI", ax)
ax.lines[0].set_alpha(0.2)
ax.lines[1].set_color("orange")
```



Another important plot used for understanding a regression model is an "added variable plot". This is a plot that may reveal nonlinearity in the relationship between one covariate and the outcome. Below, we create an added variable plot for age as a predictor of SBP. Note that the two variables being plotted (age and blood pressure) have been centered. The scale of the variables is unchanged, but the origin has been translated to zero. The red line is an estimte of the relationship between age and blood pressure. Unlike the relationship in the model, it is not forced to be linear, and there is in fact a hint that the shape is slightly flatter for the first 15 years or so of age. This would imply that blood pressure increases slightly more slowly for people in theie 20s and early 30s, then begins increasing faster after that point.

In [18]:

```
# This is not part of the main Statsmodels API, so needs to be imported sep
from statsmodels.graphics.regressionplots import add_lowess

# This is an equivalent way to fit a linear regression model, it needs to b
# done this way to be able to make the added variable plot
model = sm.GLM.from_formula("BPXSY1 ~ RIDAGEYR + BMXBMI + RIAGENDRx", data=
result = model.fit()
result.summary()

fig = result.plot_added_variable("RIDAGEYR")
ax = fig.get_axes()[0]
ax.lines[0].set_alpha(0.2)
_ = add_lowess(ax)
```



Logistic regression

We now turn to regression models for *binary* outcome variables, meaning an outcome that can take on only two distinct values. For illustration, we will work with the NHANES variable [SMQ020 (https://wwwn.cdc.gov/Nchs/Nhanes/2015-2016/SMQ_I.htm#SMQ020)](https://wwwn.cdc.gov/Nchs/Nhanes/2015-2016/SMQ_I.htm#SMQ020), which asks whether a person has smoked at least 100 cigarettes in their lifetime (if this is the case, we say that the person has a "smoking history"). Below we create a version of this variable in which smoking and non-smoking are coded as 1 and 0, respectively, and rare responses like *don't know* and *refused to answer* are coded as missing values.

In [19]:

```
da["smq"] = da.SMQ020.replace({2: 0, 7: np.nan, 9: np.nan})
```

Odds and log odds

Logistic regression provides a model for the *odds* of an event happening. Recall that if an event has probability `p`, then the odds for this event is `p/(1-p)`. The odds is a mathematical transformation of the probability onto a different scale. For example, if the probability is 1/2, then the odds is 1.

To begin, we look at the odds of alcohol use for women and men separately.

In [20]:

```
c = pd.crosstab(da.RIAGENDRx, da.smq).apply(lambda x: x/x.sum(), axis=1)
c["odds"] = c.loc[:, 1] / c.loc[:, 0]
c
```

Out[20]:

smq	0.0	1.0	odds
RIAGENDRx			
Female	0.680197	0.319803	0.470162
Male	0.467453	0.532547	1.139252

We see that the probability that a woman has ever smoked is substantially lower than the probability that a man has ever smoked (30% versus 51%). This is reflected in the odds for a woman smoking being much less than 1 (around 0.47), while the odds for a man smoking is around 1.14.

It is common to work with *odds ratios* when comparing two groups. This is simply the odds for one group divided by the odds for the other group. The odds ratio for smoking, comparing males to females, is around 2.4. In other words, a man has around 2.4 times greater odds of smoking than a woman (in the population represented by these data).

In [21]:

```
c.odds.Male / c.odds.Female
```

Out[21]:

```
2.423105552613186
```

It is conventional to work with odds on the logarithmic scale. To understand the motivation for doing this, first note that the neutral point for a probability is 0.5, which is equivalent to an odds of 1 and a log odds of 0. Populations where men smoke more than women will have odds between 1 and infinity, with the exact value depending on the magnitude of the relationship between the male and female smoking rates. Populations where women smoke more than men would have odds falling between 0 and 1.

We see that the scale of the odds statistic is not symmetric. It is usually arbitrary in which order we compare two groups -- we could compare men to women, or compare women to men. An odds of 2 (men have twice the odds of smoking as women) is equivalent in strength to an odds of 1/2 (women have twice the odds of smoking as men). Taking the log of the odds centers the scale at zero, and symmetrizes the interpretation of the scale.

To interpret the log odds when comparing two groups, it is important to remember the following facts:

- A probability of 1/2, an odds of 1, and a log odds of 0 are all equivalent.

- A positive log odds indicates that the first group being compared has greater odds (and greater probability) than the second group.
- A negative log odds indicates that the second group being compared has greater odds (and greater probability) than the first group.
- The scale of the log odds statistic is symmetric in the sense that a log odds of, say, 2, is equivalent in strength to a log odds of -2 (but with the groups swapped in terms of which has the greater probability).

If you know that the log odds when comparing two groups is a given value, say 2, and you want to report the odds, you simply exponentiate the log odds to get the odds, e.g. `exp(2)` is around 7.4. Note however that you cannot recover the individual probabilities (or their ratio) from an odds ratio.`

Below we show the log odds for smoking history status of females and males in the NHANES data. The fact that the log odds for females is negative reflects that fact that substantially less than 50% of females have a history of smoking. The log odds for males is closer to 0, consistent with around half of males having a history of smoking.

In [22]:

```
c["logodds"] = np.log(c.odds)
c
```

Out[22]:

smq	0.0	1.0	odds	logodds
RIAGENDRx				
Female	0.680197	0.319803	0.470162	-0.754679
Male	0.467453	0.532547	1.139252	0.130371

A basic logistic regression model

Now that we have a clear understanding of log odds statistics, we will fit a logistic regression. The dependent variable (outcome) of this initial model is smoking status, and the only covariate is gender. Thus, we are looking at gender as a predictor of smoking status. We fit the model using the `GLM` function, where `GLM` stands for *Generalized Linear Model*. Logistic regression is one type of GLM, a class which also includes many other regression methods such as Poisson regression that we do not discuss further here. As with linear regression, logistic models also include an intercept parameter, but we are not focusing on that parameter now.

```
In [23]: model = sm.GLM.from_formula("smq ~ RIAGENDRx", family=sm.families.Binomial(
         result = model.fit()
         result.summary()
```

```
Out[23]:
Generalized Linear Model Regression Results

  Dep. Variable:              smq   No. Observations:        5094
          Model:              GLM       Df Residuals:        5092
   Model Family:         Binomial           Df Model:           1
  Link Function:            logit              Scale:      1.0000
         Method:             IRLS     Log-Likelihood:     -3350.6
           Date: Thu, 11 Jul 2019           Deviance:      6701.2
           Time:         21:00:26      Pearson chi2:     5.09e+03
 No. Iterations:                4   Covariance Type:    nonrobust

                         coef  std err        z  P>|z|  [0.025  0.975]
         Intercept    -0.7547    0.042  -18.071  0.000  -0.837  -0.673
RIAGENDRx[T.Male]      0.8851    0.058   15.227  0.000   0.771   0.999
```

To see the connection between logistic regression and the log odds statistic, note that the logistic regression coefficient for male gender is exactly equal to the difference between the log odds statistics for males and females:

```
In [24]: c.logodds.Male - c.logodds.Female
```

```
Out[24]: 0.8850500036644218
```

This relationship will always hold when conducting a logistic regression with a single binary covariate.

In general, a logistic regression model will have multiple covariates that may not be binary, but there is still an important connection between logistic regression and odds ratios. In this more general setting, we will use a more general type of odds ratio, which we will explore further next.

Adding additional covariates

As with linear regression, we can include multiple covariates in a logistic regression. Below we fit a logistic regression for smoking status using age (RIDAGEYR) and gender as covariates.

In [25]:

```
model = sm.GLM.from_formula("smq ~ RIDAGEYR + RIAGENDRx", family=sm.familie
result = model.fit()
result.summary()
```

Out[25]:

```
Generalized Linear Model Regression Results

   Dep. Variable:              smq   No. Observations:      5094
           Model:              GLM      Df Residuals:      5091
    Model Family:         Binomial          Df Model:         2
   Link Function:            logit             Scale:    1.0000
          Method:             IRLS    Log-Likelihood:   -3296.6
            Date: Thu, 11 Jul 2019          Deviance:    6593.2
            Time:         21:00:28     Pearson chi2:   5.10e+03
  No. Iterations:                4   Covariance Type: nonrobust

                          coef  std err        z  P>|z|  [0.025  0.975]
         Intercept     -1.6166    0.095  -16.985  0.000  -1.803  -1.430
 RIAGENDRx[T.Male]      0.8920    0.059   15.170  0.000   0.777   1.007
          RIDAGEYR      0.0172    0.002   10.289  0.000   0.014   0.021
```

Adding age to the model leads to a very small shift in the gender parameter (it changed from 0.885 to 0.892). In general, regression coefficients can change a lot when adding or removing other variables from a model. But in this case the change is quite minimal. This fitted model suggests that older people are more likely to have a history of smoking than younger people. The log odds for smoking increases by 0.017 for each year of age. This effect is additive, so that comparing two people whose ages differ by 20 years, the log odds of the older person smoking will be around 0.34 units greater than the log odds for the younger person smoking, adn the odds for the older person smoking will be around `exp(0.34) = 1.4` times greater than the odds for the younger person smoking.

The greater prevalence of smoking history among older people could be partly due to the definition of smoking status that we are using here -- an older person has had more time to smoke 99 cigarettes than a younger person. However most people who smoke begin when they are young, and the smoking rate in the US has been slowly declining for several decades. Thus, it is likely that the increased smoking levels in older people are driven primarily by real shifts in behavior.

As with linear regression, the roles of age and gender in the logistic regression model can be seen as being additive, but here the additivity is on the scale of log odds, not odds or probabilities. If we compare a 30 year old female to a 50 year old male, the log odds for the male being a smoker are `0.89 + 0.34 = 1.23` units greater than the log odds for the female being a smoker. The value of 0.89 in this expression is the change attributable to gender, and the value of 0.34 is the change attributable to age. Again, we can exponentiate to convert these effects from the log odds scale to the odds scale. Since `exp(0.89 + 0.34) = exp(0.89)*exp(0.34) = 2.44*1.41` we can state that male gender is associated with a 2.44 fold increase in the odds of smoking, and 20 years of age is associated with a 1.41 fold increase in the odds for smoking. These two effects are multiplied when discussing the odds, so a 50 year old man has `exp(1.23) = 3.42` fold greater odds of smoking than a 30 year old woman.

In this logistic regression model with two covariates, the coefficients for age and gender both have interpretations in terms of *conditional log odds*. This generalizes the interpretation of a logistic regression coefficient in terms of marginal log odds that we discussed above. When there are two or more covariates in a logistic regression model, we always need to think in terms of conditional, not marginal log odds.

Specifically, the coefficient of around 0.89 for male gender impacts the conditional log odds in the sense that when comparing a male to a female at a fixed age, the male will have 0.89 units greater log odds for smoking than the female. This relationship holds within any age (i.e. it holds among all people of age 30, and among all people of age 70). In this sense, it is a *conditional* coefficient because it is only interpretable when holding the other variables in the model fixed. Similarly, the coefficient of around 0.02 for age holds within a gender. Comparing two females whose ages differ by one year, the older female has 0.02 units greater log odds for smoking than the younger female. This same contrast holds for males.

A logistic regression model with three predictors

Next we fit a logistic regression model, again for smoking, including educational attainment as a predictor. The educational attainment in NHANES is called DMDEDUC2 (https://wwwn.cdc.gov/Nchs/Nhanes/2015-2016/DEMO_I.htm#DMDEDUC2), and we will recode it so that the meaning of the levels becomes more clear. We will call the recoded variable `DMDEDUC2x` .

In [26]:

```
# Create a labeled version of the educational attainment variable
da["DMDEDUC2x"] = da.DMDEDUC2.replace({1: "lt9", 2: "x9_11", 3: "HS", 4: "S
                                      5: "College", 7: np.nan, 9: np.nan})

model = sm.GLM.from_formula("smq ~ RIDAGEYR + RIAGENDRx + DMDEDUC2x", famil
result = model.fit()
result.summary()
```

Out[26]:

```
Generalized Linear Model Regression Results

  Dep. Variable:              smq   No. Observations:       5093
         Model:               GLM       Df Residuals:       5086
  Model Family:          Binomial           Df Model:          6
 Link Function:             logit              Scale:     1.0000
        Method:              IRLS     Log-Likelihood:    -3201.2
          Date:  Thu, 11 Jul 2019           Deviance:     6402.4
          Time:          21:00:29      Pearson chi2:    5.10e+03
No. Iterations:                 4    Covariance Type:  nonrobust

                                coef  std err        z  P>|z|  [0.025  0.975]
                   Intercept  -2.3060   0.114  -20.174  0.000  -2.530  -2.082
          RIAGENDRx[T.Male]   0.9096   0.060   15.118  0.000   0.792   1.028
            DMDEDUC2x[T.HS]   0.9434   0.090   10.521  0.000   0.768   1.119
   DMDEDUC2x[T.SomeCollege]   0.8322   0.084    9.865  0.000   0.667   0.998
           DMDEDUC2x[T.lt9]   0.2662   0.109    2.438  0.015   0.052   0.480
         DMDEDUC2x[T.x9_11]   1.0986   0.107   10.296  0.000   0.889   1.308
                   RIDAGEYR   0.0183   0.002   10.582  0.000   0.015   0.022
```

We see that the "Female" level of the gender variable, and the "College" level of the educational attainment variable are the reference levels, as they are not shown in the output above. We have discussed the gender and age variables above, but the educational attainment variable is new for us. All non-reference coefficients for the educational attainment are positive, while the `College` coefficient, as the reference coefficient, is exactly zero. Thus, we see that people with a college degree have the lowest rate of smoking, followed by people with less than 9 years of schooling, then (after a large gap) people with some college, then people with a high school degree (and no college), and finally (with the greatest rate of smoking), people with 9-11 years of schooling. The overall story here is that smoking rates are much lower for people who graduated from college or did not start high school, presumably for very different reasons. On the other hand, people with some high school, people who completed high school, and people who began but did not complete college have much higher rates of smoking. The odds ratio between the former and the latter group depends on the specific subgroups being compared, but can be almost `3 = exp(1.09)`.

As noted above when we were discussing linear regression, it is important to remember that a coefficient in a logistic regression are "conditional" on the other variables being held fixed. For example, the log odds ratio of 1.09 between people with 9-11 years of schooling and people who completed college applies only when comparing people with the same age and gender.

Visualization of the fitted models

Visualization of fitted logistic regression models is more challenging than visualization of fitted linear models, but is still worth pursuing. We can begin by plotting the fitted proportion of the population that smokes, for various subpopulations defined by the regression model. We will focus here on how the smoking rate varies with age, so we restrict the population to female college graduates.

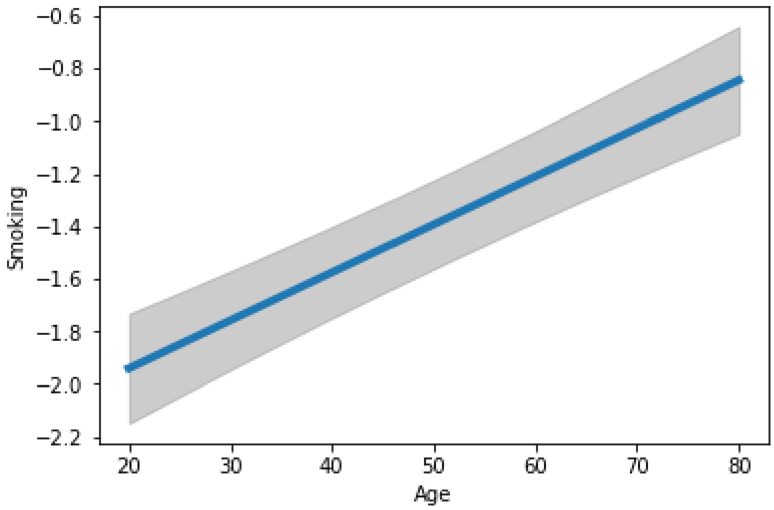
The following plot shows the fitted log odds (or logit) probability for the smoking outcome as a function of age. The grey band is a simultaneous 95% simultaneous confidence band, as discussed above in the case of a linear model.

In [27]:

```
values = {"RIAGENDRx": "Female", "RIAGENDR": 1, "BMXBMI": 25,
          "DMDEDUC2": 1, "RIDRETH1": 1, "SMQ020": 1,
          "DMDEDUC2x": "College", "BPXSY1": 120}

pr, cb, fv = predict_functional(result, "RIDAGEYR",
                values=values, ci_method="simultaneous")

ax = sns.lineplot(fv, pr, lw=4)
ax.fill_between(fv, cb[:, 0], cb[:, 1], color='grey', alpha=0.4)
ax.set_xlabel("Age")
ax.set_ylabel("Smoking")
```

Out[27]:

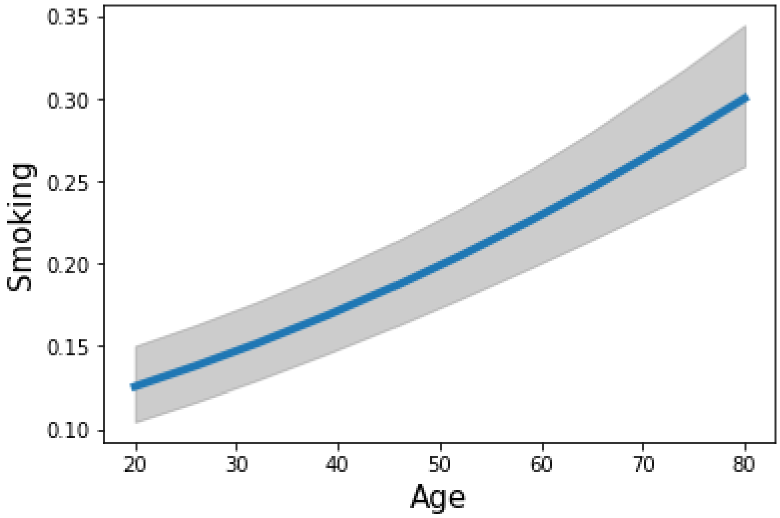
```
Text(0,0.5,'Smoking')
```



We can display the same plot in terms of probabilities instead of in terms of log odds. The probability can be obtained from the log odds using the relationship `p = 1 / (1 + exp(-o))` where `o` is the log odds. Note that while the age and log odds are linearly related, age has a curved relationship with probability. This is necessary since probabilities must remain between 0 and 1, a linear relationship would eventually exit this interval.

```
In [28]: pr1 = 1 / (1 + np.exp(-pr))
         cb1 = 1 / (1 + np.exp(-cb))
         ax = sns.lineplot(fv, pr1, lw=4)
         ax.fill_between(fv, cb1[:, 0], cb1[:, 1], color='grey', alpha=0.4)
         ax.set_xlabel("Age", size=15)
         ax.set_ylabel("Smoking", size=15)
```

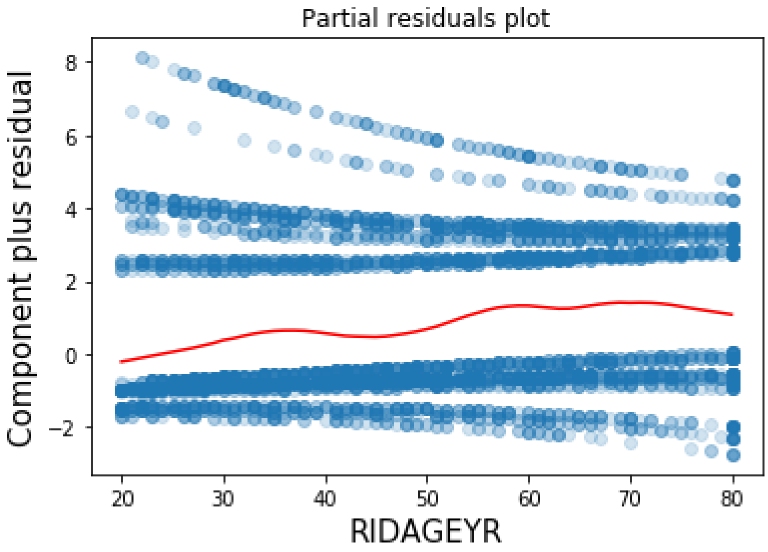
```
Out[28]: Text(0,0.5,'Smoking')
```



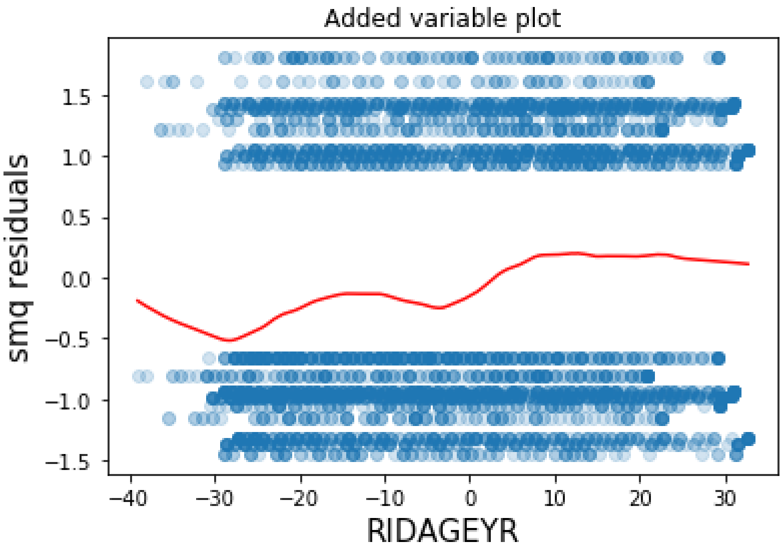
Next we turn to diagnostic plots that are intended to reveal certain aspects of the data that may not be correctly captured by the model. The three plots below are intended to reveal any curvature in the mean relationship between the outcome and one of the covariates. We used the partial regression plotting technique above for this same purpose when working with linear models.

In the case of logistic regression, the three techniques demonstrated below can identify major discrepancies between the fitted model and the population, but evidence for small discrepancies is not reliable unless the sample size is very large. The CERES technique has the strongest theoretical support. Taken at face value, the plots below suggest that smoking rates may rise slightly faster for people between the ages of 20 and 35, and again for people between the ages of 50 and 60, with a period of minimal increase between these age intervals. This would contradict the perfectly linear model for age (on the log odds scale) that we have specified in our model. These plotting techniques can be useful at identifying possible opportunities for future analysis with additional data, but do not identify features that can be claimed with high confidence using the present data.

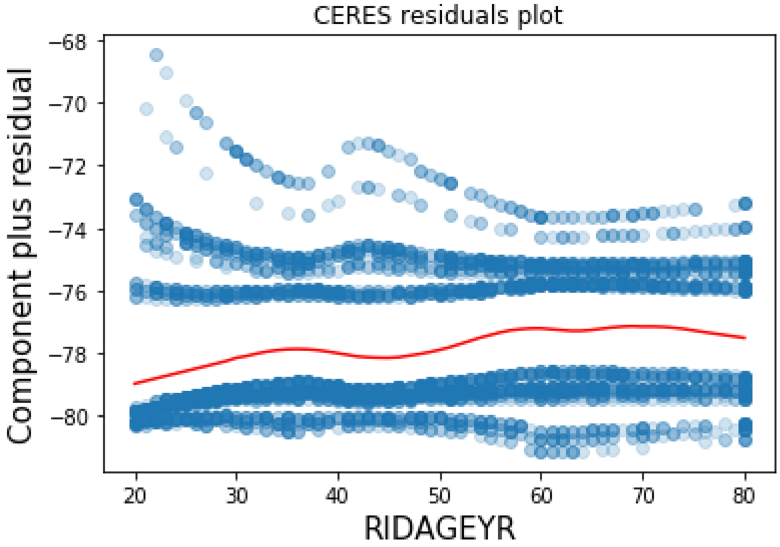
In [29]:
```
fig = result.plot_partial_residuals("RIDAGEYR")
ax = fig.get_axes()[0]
ax.lines[0].set_alpha(0.2)

_ = add_lowess(ax)
```



In [30]:
```
fig = result.plot_added_variable("RIDAGEYR")
ax = fig.get_axes()[0]
ax.lines[0].set_alpha(0.2)
_ = add_lowess(ax)
```



In [31]:
```
fig = result.plot_ceres_residuals("RIDAGEYR")
ax = fig.get_axes()[0]
ax.lines[0].set_alpha(0.2)
_ = add_lowess(ax)
```


CERES residuals plot
Component plus residual
RIDAGEYR