Advanced Linear Regression Modeling and ANOVA

In the general linear regression framework we saw that we can test individual regression coefficients in the model for statistical significance using the coefficient t-tests. This approach is most useful when one of the effects, such as a treatment effect, is of primary interest, and other variables are included as covariate adjustments. There is a danger, however, in doing multiple tests when we have more than one varable in the model. By doing so we can inflate the false positive rate, increasing the chance of detecting nonexistent results purely by increasing the number of tests performed.

Analysis of variance (ANOVA) gives us a way to counteract this effect, by testing all effects simultaneously to see if *any* variable is significant. It also lies behind the interpretation of R^2 as the proportion of variance explained by the model.

The strategy is to compare the full model with a constrained, null, model in which the set of parameters we wish to test are zeroed out or constrained. The change in residual sum of squares forms the basis for constructing an F test for the null hypothesis that the constrained model is correct.

As special cases we consider:

- F test for the regression
- Oneway ANOVA when the explanatory variable is categorical, i.e., the k sample design
- Testing a subset of variables in multiple linear regression

Relevant libraries and functions:

- pandas.DataFrame.groupby
- statsmodels.api
- statsmodels.formula.api
- statsmodels.formula.api.ols
- statsmodels.regression.linear_model
- RegressionResults.compare_f_test

Multiple Linear Regression Models *with Interaction Effects*

Example 1: Geographic analysis of melanoma mortality

Mortality rates from skin cancer are available from the CDC. Early studies of the relation between exposure to sunlight and melanoma, a type of skin cancer investigated the relation between mortality from skin cancer and geographic location in degrees latitude (how far north or south); Elwood et al. (1974). In this study, each state is represented by the latitude of its largest city. Mortality rates are age-standardized and expressed in rates per 1 million population.

DESCRIPTIVE ANALYTICS: Is there a relationship between state melanoma state mortality rate, latitude, and whether the state is on the coast *in the sample*?

In [9]:

```python
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns; sns.set()
```

Import and explore the data

In [10]:

```python
skin = pd.read_csv("skin.txt",
                   delim_whitespace=True)
display(skin.shape, skin.head())
```

```
(49, 4)
```

	state	latitude	mortality	ocean
0	AL	33.0	219	1
1	AZ	34.5	160	0
2	AR	35.0	170	0
3	CA	37.5	182	1
4	CO	39.0	149	0

Are there any missing values?

Check if any missing values using the pandas notna() and all() functions. notna() returns True if a value is not missing and False if missing. all() returns True only if all elements n a column are True. It returns False if any element is False.

In [22]:

```
skin.notna()
```

Out[22]:

	state	latitude	mortality	ocean
0	True	True	True	True
1	True	True	True	True
2	True	True	True	True
3	True	True	True	True
4	True	True	True	True
5	True	True	True	True
6	True	True	True	True
7	True	True	True	True
8	True	True	True	True
9	True	True	True	True
10	True	True	True	True
11	True	True	True	True
12	True	True	True	True
13	True	True	True	True
14	True	True	True	True
15	True	True	True	True
16	True	True	True	True
17	True	True	True	True
18	True	True	True	True
19	True	True	True	True
20	True	True	True	True
21	True	True	True	True
22	True	True	True	True
23	True	True	True	True
24	True	True	True	True
25	True	True	True	True
26	True	True	True	True
27	True	True	True	True
28	True	True	True	True
29	True	True	True	True
30	True	True	True	True
31	True	True	True	True
32	True	True	True	True
33	True	True	True	True

	state	latitude	mortality	ocean
34	True	True	True	True
35	True	True	True	True
36	True	True	True	True
37	True	True	True	True
38	True	True	True	True
39	True	True	True	True
40	True	True	True	True
41	True	True	True	True
42	True	True	True	True
43	True	True	True	True
44	True	True	True	True
45	True	True	True	True
46	True	True	True	True
47	True	True	True	True
48	True	True	True	True

In [11]:

```
skin.notna().all()
```

Out[11]:

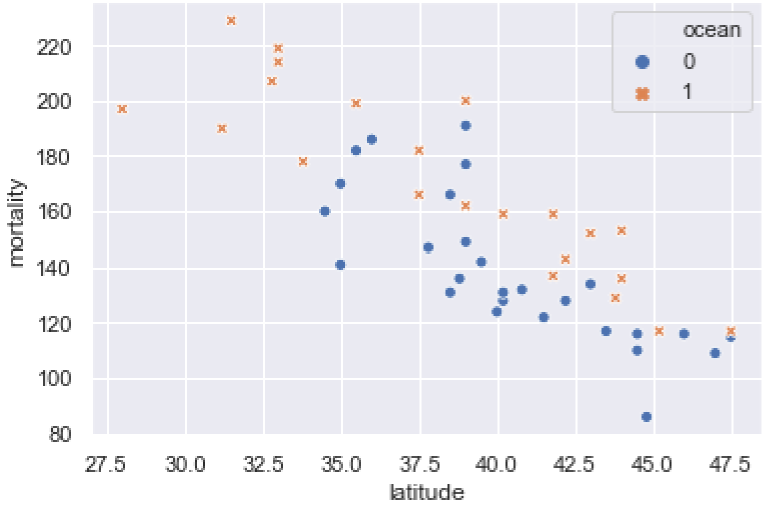
```
state          True
latitude       True
mortality      True
ocean          True
dtype: bool
```

Looks clean.

Let's view a scatter plot of mortality versus latitude. How can we also incorporate 'ocean', a binary indicator variable in the plot? One way is to color each state's data point by whether or not it is an ocean state. In the seaborn scatterplot function the 'style' and 'hue' arguments do this.

In [12]:

```python
sns.scatterplot(x='latitude', y='mortality',
                style='ocean',
                hue='ocean',
                data=skin)
plt.show()
```



Describe the relationship between the state melanoma mortality rate, the state latitude, and whether the state is on the coast.

MODELING: How can we fit a model that predicts state melanoma mortality rate with: a.) latitude, b.) whether it is on the coast, and c.) the interaction of being on the coast and latitude?

Modeling: Setting up the model and interpreting the coefficients

Let's fit a regression model that includes latitude, the ocean coastal indicator, and a possible interaction between these two variables. Mathematically, this model has the form:

$$\text{Expected Mortality Rate} = \beta_0 + \beta_1 * \text{latitude} + \beta_2 * \text{ocean} + \beta_3 * \text{latitude} * \text{ocean}$$

The interaction is expressed as the product of 'latitude' and the 0-1 value for 'ocean'. How can we interpret this? It creates two regression lines, one for ocean=0 (the reference line), and one for ocean=1:

$$\text{ocean=0:} \qquad \text{Expected Mortality Rate} = \beta_0 + \beta_1 * \text{latitude}$$

$$\text{ocean=1:} \qquad \text{Expected Mortality Rate} = (\beta_0 + \beta_2) + (\beta_1 + \beta_3) * \text{latitude}$$

The interaction term in the model means that the dependence of the mortality rate on latitude is modified by whether or not the state touches the ocean. By fitting the model we can test the difference coefficients.

In the python statsmodels formula package, the interaction is included as 'latitude:ocean'.

What does β_0 represent in words in this model?

What does $\beta_0 + \beta_2$ represent in words in this model?

What does β_1 represent in words in this model?

What does β_2 represent in words in this model?

What does β_3 represent in words in this model?

What does $\beta_1 + \beta_3$ represent in words in this model?

Checking Conditions (nothing new)

In [13]:

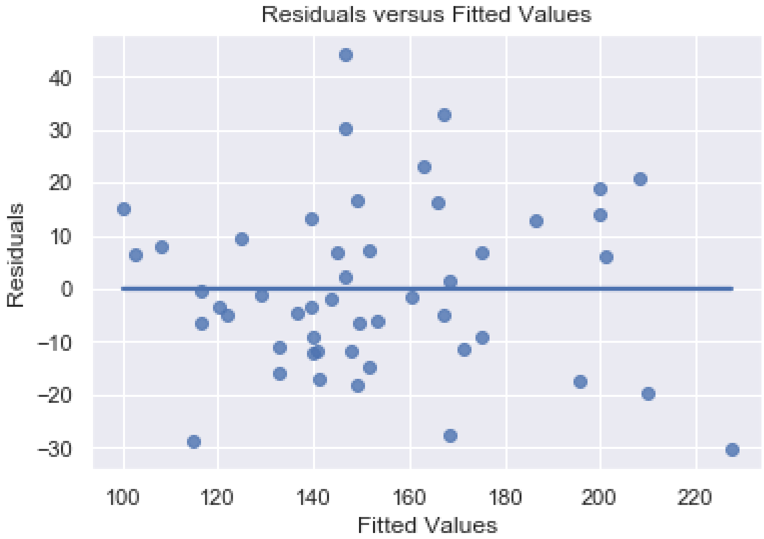
```
import statsmodels.api as sm
import statsmodels.formula.api as smf
```

In [14]:

```
# create the fitted model object
mod1 = smf.ols('mortality ~ latitude + ocean + latitude*ocean',
               data=skin).fit()
```

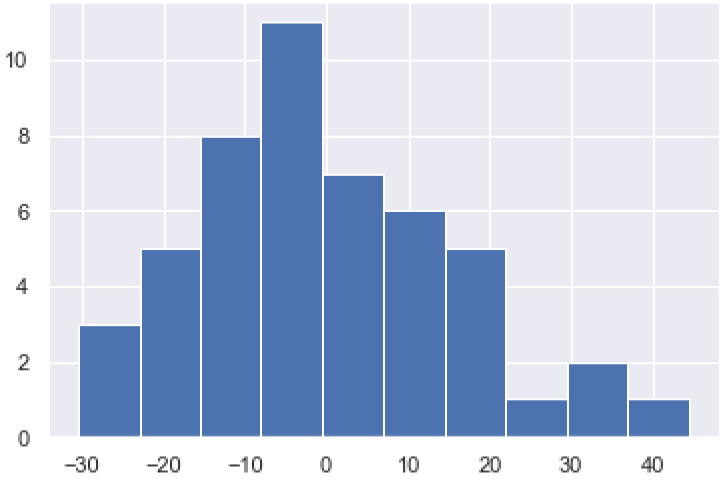
In [15]:

```python
# residual plot for inital check on the model fit
sns.regplot(x=mod1.fittedvalues, y=mod1.resid, ci=None)
plt.xlabel('Fitted Values')
plt.ylabel('Residuals')
plt.title('Residuals versus Fitted Values')
plt.show()
```



In [16]:

```python
plt.hist(mod1.resid)
plt.show()
```



Are the linear regression conditions met?

Model Summary and More Interpretation

Now let's have a look at the model summary.

```
In [8]:   mod1.summary()
```

```
Out[8]:
OLS Regression Results

       Dep. Variable:        mortality          R-squared:     0.770
               Model:              OLS      Adj. R-squared:     0.754
              Method:    Least Squares         F-statistic:     50.11
                Date: Mon, 30 Mar 2020  Prob (F-statistic):  2.17e-14
                Time:         10:27:53      Log-Likelihood:   -205.02
   No. Observations:               49                 AIC:     418.0
        Df Residuals:               45                 BIC:     425.6
            Df Model:                3
     Covariance Type:        nonrobust

                    coef  std err        t   P>|t|    [0.025    0.975]
     Intercept  360.5495   35.498   10.157   0.000   289.052   432.047
      latitude   -5.4853    0.874   -6.274   0.000    -7.246    -3.724
         ocean   20.6501   43.988    0.469   0.641   -67.946   109.246
latitude:ocean   -0.0055    1.101   -0.005   0.996    -2.224     2.213

        Omnibus:  2.149      Durbin-Watson:     2.049
 Prob(Omnibus):  0.342  Jarque-Bera (JB):     1.576
           Skew:  0.437           Prob(JB):     0.455
       Kurtosis:  3.085           Cond. No.  1.00e+03


Warnings:
[1] Standard Errors assume that the covariance matrix of the errors is correctly specified.
[2] The condition number is large, 1e+03. This might indicate that there are
strong multicollinearity or other numerical problems.
```

Fitting the Model with the Output

Based on the results in the summary, we see that the estimated model has the form:

$$\text{mortality} = 360.55 - 5.49 * \text{latitude} + 20.65 * \text{ocean} - 0.0055 * \text{latitude} * \text{ocean}.$$

In order to interpret the results, it is important to be able to extract the form of the model from the summary tables.

Interpret the slopes and coefficients of this model:

Inference - Using MULTIPLE Coefficient t-tests

What can we say about the relationship between melanoma mortality rate, latitude, being on the coast, and the relationship between latitude and being on the coast for a much LARGER POPULATION of regions?

The coefficient t tests indicate that latitude is highly statistically signficant with p < 0.001. Neither ocean nor the latitude x ocean interaction appears to be significant based on their coeffiicent t tests.

False Positive Rate

In a previous unit we discussed how the **p-value** is calculated.

What the p-value *represents* is a PROBABILITY:

- of a sample statistic that is at least as suspicious (in favor of the alternative hypothesis) than the one we observed
- in which we assume that the null hypothesis is true.

Ex:

How we interpret the p-value is as follows:

- if $p - value < \alpha$, then we reject Ho.
- if $p - value \geq \alpha$, then we fail to reject Ho.

Ex:

Determining the False Positive Rate of a Test

There are four possible combinations of 1.) hypothesis test conclusions and 2.) actual states of reality that can exist with a hypothesis test.

We call the **false positive rate** of a hypothesis test the **percentage of cases** in which:

1. the **null hypothesis was *actually* true**, BUT
2. our ***conclusion* said to reject the null hypothesis.**

Ex: Let's say we use a **significance level** $\alpha = 0.05$ for the hypothesis test $H_0 : \beta_1 = 0; H_a : \beta_1 \neq 0$. Suppose our null hypothesis is actually true. What is the probability that we will randomly select a sample statistic $\hat{\beta}_1$ in which we will incorrectly reject the null hypothesis in our conclusion?

Relationship between the False Positive Rate and the Significance Level α of a Hypothesis Test.

False positive rate = α

Ex: Suppose we conducted the following three hypothesis tests, eaching using a significance level of α.

- $H_0: \beta_1 = 0; H_a: \beta_1 \neq 0$
- $H_0: \beta_2 = 0; H_a: \beta_2 \neq 0$
- $H_0: \beta_3 = 0; H_a: \beta_3 \neq 0$

What is the probability that at least one of our three hypothesis tests was a false positive?

How can we test all three coefficents at the same time and control the false positive rate?

F test for regression

Considering the preceding example, with three regression variables in the model, how can we perform a test of the following hyptheses?

HYPOTHESES:

$$H_0: \beta_1 = \beta_2 = \beta_3 = 0 \qquad H_A: \text{at least one of } \beta_1, \beta_2, \beta_3 \neq 0$$

The key is to compare the residual sum of square with and without these variables in the model. As in the preceding section, let's use the general notation:

X_1	X_2	X_3	Y
x_{11}	x_{12}	x_{13}	y_1
x_{21}	x_{22}	x_{23}	y_2
$\vdots$	$\vdots$	$\vdots$	$\vdots$
x_{n1}	x_{n2}	x_{n3}	y_n

THEORY:

We compare the full three variable model with the null model without *any* explanatry variables. The null model still includes the intercept if the full model does. The fitted values, residual sums of squares, and *degrees of freedom (df)* for these models are as follows:

Full model: $\hat{y}_i = \hat{\beta}_0 + \hat{\beta}_1 x_{i1} + \hat{\beta}_2 x_{i2} + \hat{\beta}_3 x_{i3}$ $\qquad SSE = \sum_{i=1}^{n} (y_i - \hat{y}_i)^2$

$$df = n - 3 - 1 = n - 4$$

Null model: $\hat{y}_{0i} = \bar{y}$ $\qquad SST = \sum_{i=1}^{n} (y_i - \bar{y})^2$

$$df = n - 1$$

here SSE refers to the **residual sum of squares**, and SST refers to the residual sum of squares for the null model, sometimes called the **total sum of squares** for the response.

The sum of squares accounted for by the regression is the difference, which has $df_{diff} = (n - 1) - (n - 3 - 1) = 3$ degrees of freedom in this case:

$$SSReg = SST - SSE = \sum_{i=1}^{n} (\hat{y}_i - \bar{y})^2$$

where the second equality of this last equation can be shown using the normal equations solved by the least squares estimates.

The regression sum of squares is ≥ 0 because the null model is the special case of the full model where the explantory coefficients equal 0. Consequently, the minimized sum of square residuals cannot be smaller for the null model than for the full model. (The more options you add, the smaller the minimum can be).

TEST STATISTIC:

Assuming the full model is correctly specified, i.e. that there are no missing variables, and assuming Gaussian noise terms in the model, we can calculate the following test statistic for our hypotheses:

$$F = \frac{SSReg/p}{SSE/(n-p-1)}$$

It provides a test of the null model H_0 versus versus the full model expressed by H_A.

A random variable with this representation is said to have an **F distribution with p and n-p-1 degrees of freedom**. in the context of our example, n=49, p=3, so the F test statistic has degrees of freedom 3 and 49-3-1 = 45.

P-VALUE

Given F for our model, we can compute the p-value using the **scipy.stats.f** function in python.

p-value = 1-f.cdf(teststatistic, dfn=p, dfd=n-p-1)

Relation between F-statistic denominator and variance of the full model

It is also worth observing at this point that the denominator of the F test statistic provides an unbiased estimator of the full model error variance:

$$\hat{\sigma}^2 = \frac{SSE}{n - p - 1}.$$

Relation between R-squared and F

Both F and R^2 depend on RSS and SST. They can be related to each other as follows. First, recall that

$$R^2 = \frac{SST - SSE}{SST}$$

Therefore F can be rewritten in terms of R_2 as

$$F = \frac{(SST - SSE)/p}{SST/(n - p - 1)} = \left(\frac{SST}{SSE}\right)\left(\frac{SST - SSE}{SST}\right)\left(\frac{n - p - 1}{p}\right)$$

$$= \left(\frac{n - p - 1}{p}\right)\left(\frac{R^2}{1 - R^2}\right)$$

In other words, the higher the "proportion of variance explained" (R^2), the larger the value for F and vice versa, for a given model and sample size.

F test for Model: Geographic analysis of melanoma mortality

The F value appears in the first tabe of the model summary underneath the R-squared statistic. The table also displays the p-value "Prob(F-statistic)" and degrees of freedom for the model and residuals.

1. Set up the hypotheses that answer the research question: is there sufficient evidence to suggest that at least one of the population slopes is non-zero.

2. Find the test statistic for these hypotheses.

3. What distribution is this test statistic an observation from?

4. Find the p-value for these hypotheses.

5. Make a conclusion.

In [21]:

```
mod1.summary()
```

Out[21]:

```
OLS Regression Results

      Dep. Variable:        mortality          R-squared:     0.770
             Model:              OLS      Adj. R-squared:     0.754
            Method:     Least Squares         F-statistic:     50.11
              Date:  Sun, 18 Oct 2020  Prob (F-statistic):  2.17e-14
              Time:          20:44:16      Log-Likelihood:   -205.02
  No. Observations:                49                 AIC:     418.0
      Df Residuals:                45                 BIC:     425.6
          Df Model:                 3
   Covariance Type:         nonrobust

                     coef  std err       t   P>|t|   [0.025   0.975]
      Intercept  360.5495   35.498  10.157   0.000  289.052  432.047
       latitude   -5.4853    0.874  -6.274   0.000   -7.246   -3.724
          ocean   20.6501   43.988   0.469   0.641  -67.946  109.246
 latitude:ocean   -0.0055    1.101  -0.005   0.996   -2.224    2.213

         Omnibus:  2.149    Durbin-Watson:     2.049
  Prob(Omnibus):  0.342  Jarque-Bera (JB):     1.576
            Skew:  0.437          Prob(JB):     0.455
        Kurtosis:  3.085          Cond. No.  1.00e+03


Warnings:
[1] Standard Errors assume that the covariance matrix of the errors is correctly specified.
[2] The condition number is large, 1e+03. This might indicate that there are
strong multicollinearity or other numerical problems.
```

We see that F= 50.11 with degrees of freedom 3 and 45. The p-value is essentially zero, so there is no question the model is signficant. At least one of the explanatory variables is needed in the model.

Let's confirm the p-value by direct calculation.

In [10]:

```
import numpy as np
from scipy.stats import f
```

In [11]:

```python
pvalue= 1 - f.cdf(50.11, dfn=3, dfd=45)
pvalue
```

Out[11]:

```
2.1649348980190553e-14
```

Theory: Nondirectional nature of F test

Notice that we only use the right hand tail in this calculation. This is because the F test is already a nondirectional test of deviations from the null hypothesis, and we reject H_0 for large values only, no for small values.

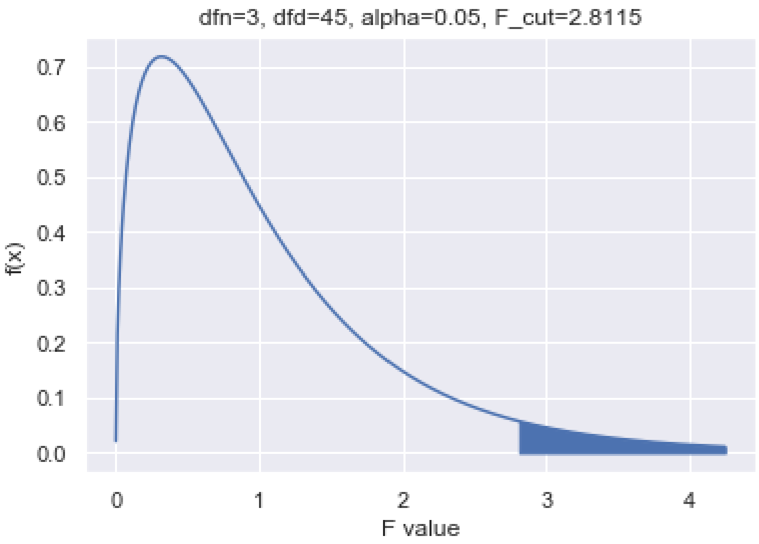
$$F - statistic = \frac{(SST - SSE)/p}{SST/(n - p - 1)}$$

$$p - value = P(F_{p, n-p-1} > F - statistic)$$

Graph of the F distribution and cutoff for hypothetical level α test of H_0.

In [12]:

```python
alpha = 0.05
Fvalue = 9.87
dfn, dfd = 3, 45
# alpha cutoff value
Fcut = f.ppf(1-alpha, dfn, dfd)
# set up for probability density curve
x = np.linspace(0.0001, f.ppf(0.99, dfn, dfd), 400)
plt.plot(x, f.pdf(x, dfn, dfd))
plt.xlabel('F value')
plt.ylabel('f(x)')
# Construct the title based on input data
degn = 'dfn=' + str(dfn)
degd = 'dfd=' + str(dfd)
alph = 'alpha=' + str(alpha)
fcut = 'F_cut=' + str(round(Fcut, 4))
comma = ', '
plt.title(degn+comma+degd+comma+alph+comma+fcut)
# add shaded areas whose probability we need
xfval = np.linspace(Fcut, f.ppf(0.99, dfn, dfd), 100)
plt.fill_between(xfval, 0, f.pdf(xfval, dfn, dfd), color='b')
plt.show()
```



One-Way ANOVA (Analysis of Variance) Model

Example 2: Analysis of the Relationship between Age and Political Affiliation

A very common special case of linear regression models is when there is one categorical explanatory variable, and the goal is to determine if the **mean response** is significantly different between categories of the explanatory variable.

This is an extension of two-sample analysis where we have one categorical exaplanatory variable, such as website version A versus B, and we compare them based on a quantitifed outcome. The ANOVA approach lets us compare K > 2 categories at the same time.

In [17]:

```
import zipfile as zp
zf = zp.ZipFile('Feb17-public.zip')
missing_values = ["NaN", "nan", "Don't know/Refused (VOL.)"]
pew = pd.read_csv(zf.open('Feb17public.csv'),
                  na_values=missing_values)[['age', 'party']].dropna()
pew.head()
```

Out[17]:

	age	party
0	80.0	Independent
1	70.0	Democrat
2	69.0	Independent
3	50.0	Republican
4	70.0	Democrat

In [18]:

```
pew['party'].value_counts()
```

Out[18]:

```
Democrat                   527
Independent                525
Republican                 367
No preference (VOL.)        41
Other party (VOL.)           5
Name: party, dtype: int64
```

Let's rename the party categories so they are easier to label in graphs. We can do this as follows.

In [19]:

```
# rename categories so they display better
party = pd.Categorical(pew['party'])
party.rename_categories({'Democrat': 'Dem',
                         'Independent': 'Ind',
                         'Republican': 'Rep',
                         'No preference (VOL.)': 'No_Pref',
                         'Other party (VOL.)': 'Other'
                        }, inplace=True)
pew['party']=party
```

In [16]:

```
pew['party'].value_counts()
```

Out[16]:

```
Dem        527
Ind        525
Rep        367
No_Pref     41
Other        5
Name: party, dtype: int64
```

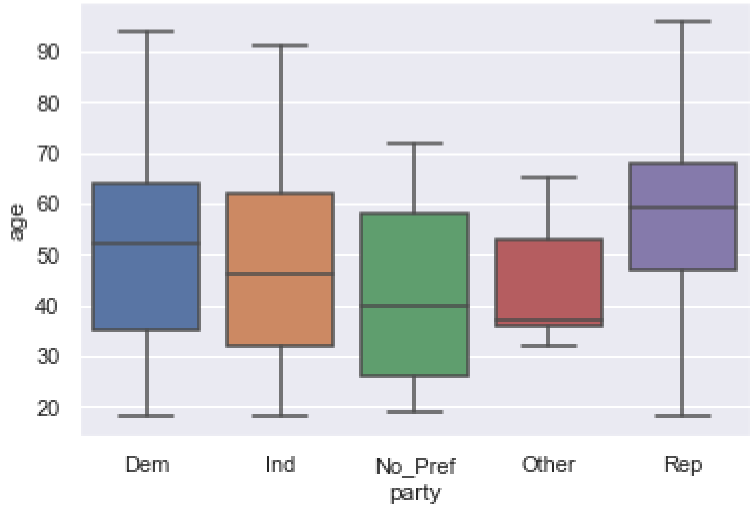
DESCRIPTIVE ANALYTICS: Is there a relationship between political affiliation and age *in the sample*?

Visualization

With several groups we can use side by side boxplots to visualize the age distributions.

In [20]:

```
sns.boxplot(x='party', y='age', data=pew)
plt.show()
```



Summary statistics

Using Pandas **groupby()** function to get summary statistics for each political affiliation

In [18]:

```
# within group means
pew.groupby('party').mean()
```

Out[18]:

	age
party	
Dem	50.499051
Ind	46.807619
No_Pref	43.146341
Other	44.600000
Rep	56.776567

In [19]:

```python
# within group sample standard deviations
pew.groupby('party').std()
```

Out[19]:

```
               age
party
Dem      17.687279
Ind      17.517144
No_Pref  17.062475
Other    13.939153
Rep      16.885801
```

In [20]:

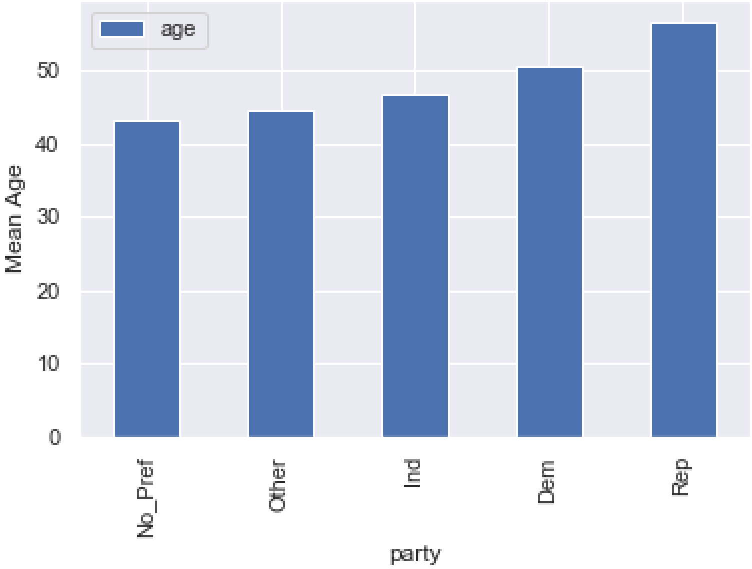
```python
# within group sample sizes
pew.groupby('party').count()
```

Out[20]:

```
         age
party
Dem      527
Ind      525
No_Pref   41
Other      5
Rep      367
```

In [21]:

```
pew.groupby('party').mean().sort_values(by='age').plot.bar()
plt.ylabel('Mean Age')
plt.show()
```



INFERENCE: Is there sufficient evidence to suggest that at least one pair of political party affiliations have mean ages (out of all adults living in the US) that differ?

HYPOTHESES

H_0: $\mu_{Dem} = \mu_{Ind} = \mu_{Other} = \mu_{No_{pref}} = \mu_{Rep}$

H_A: At least one pair of groups whose population mean values are different from each other.

One way to make a conclusion about these hypotheses.

THEORY: USE REGRESSION MODELING TO CONDUCT INFERENCE on $H_0: \mu_1 = \mu_2 = \ldots \mu_p$

Are there significant mean age differences between the different self-reported party affiliations? We can fit a one-way anova model with 5 categories of 'party'. The ols function will encode the categorical party affiliatoin variable into a series of 0/1 indicator variables. One category will be the reference category. Sometimes this is called reference cell coding.

In [22]:

```
agemod = smf.ols('age ~ party', data=pew).fit()
agemod.summary()
```

Out[22]:

```
OLS Regression Results

      Dep. Variable:               age          R-squared:      0.052
             Model:                OLS      Adj. R-squared:      0.049
            Method:      Least Squares         F-statistic:      19.82
              Date:   Mon, 30 Mar 2020   Prob (F-statistic):   6.66e-16
              Time:           10:27:55      Log-Likelihood:    -6261.1
 No. Observations:               1465                 AIC:  1.253e+04
      Df Residuals:              1460                 BIC:  1.256e+04
          Df Model:                 4
   Covariance Type:         nonrobust

                      coef   std err        t   P>|t|    [0.025   0.975]
        Intercept  50.4991     0.758   66.618   0.000    49.012   51.986
      party[T.Ind]  -3.6914     1.073   -3.440   0.001    -5.796   -1.587
  party[T.No_Pref]  -7.3527     2.821   -2.606   0.009   -12.887   -1.818
    party[T.Other]  -5.8991     7.819   -0.754   0.451   -21.237    9.439
      party[T.Rep]   6.2775     1.183    5.306   0.000     3.957    8.598

        Omnibus:  130.613      Durbin-Watson:     1.725
  Prob(Omnibus):    0.000   Jarque-Bera (JB):    40.798
           Skew:   -0.017           Prob(JB):  1.38e-09
       Kurtosis:    2.183           Cond. No.      19.0


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

Fit this linear regression model

Interpretation of the model: equivalence of reference cell and cell means models

Notice that the 'Intercept' in the model above equals the sample mean age for Democrats. In this case Democrats are the reference category. The other coefficients are incremental adjustments for other parties versus Democrats.

Example: Coding of Republicans and non Republicans.

$$\text{party[T.Rep]} = \begin{cases} 1, & \text{if 'party'} = \text{'Rep'} \\ 0, & \text{if 'party'} \neq \text{'Rep'} \end{cases}$$

The effective model for Republicans is that the mean age is

$$50.4991 + 6.2775 = 56.7766.$$

This is equal to the sample mean age for Republicans.

In [23]:

```
# Check calculation
50.4991 + 6.2775
```

Out[23]:

```
56.7766
```

The same relation holds for all the other groups. In other words, for the k group model, the fitted value for each observation is equal to the sample mean for the group that individual is from.

Coding of all groups

Overall the numerical coding of the binary X variables for different groups is as follows:

Party	party[T.Ind]	party[T.No_Pref]	party[T.Other]	party[T.Rep]
Dem	0	0	0	0
Ind	1	0	0	0
No_Pref	0	1	0	0
Other	0	0	1	0
Rep	0	0	0	1

TEST STATISTIC

What is the f-statistic and corresponding p-value for this linear regression that we just fitted?

What hypotheses does this f-statistic allow you to make a conclusion about? Use the p-value to make a conclusion for these hypotheses.

THEORY/RELATIONSHIP: This f-statistic also allows for you to make a conclusion about the following.

$H_0: \quad \mu_{Dem} = \mu_{Ind} = \mu_{Other} = \mu_{No_pref} = \mu_{Rep}$

H_A: At least one pair of groups whose population mean values are different from each other.

Use the p-value to make a conlusion for these hypotheses.

The F test is highly significant (F = 19.82, p < 0.001) <α=0.05.

- So we reject the null hypothesis.
- Thus there are significant differences in mean age across the self-reported party affiliations.

THEORY IN GENERAL:

Suppose you have a dataset with a single catgorical variable X with p levels and a numerical variable Y

X	Y
x_1	y_1
x_2	y_2
$\vdots$	$\vdots$
x_n	y_n

Then you can set up a linear regression equation $Y = \beta_0 + \beta_1 X_{level1} + \beta_2 X_{level2} + \ldots + \beta_{p-1} X_{levelp-1}$.

If this is the case, then you test the following two sets of hypotheses:

$H_0 : \mu_{level1} = \mu_{level2} = \ldots = \mu_{levelp-1} = \mu_{levelp}$

H_A: at least one pair of levels have means that are different.

$H_0 : \beta_{level1} = \beta_{level2} = \ldots = \beta_{levelp-1} = \beta_{levelp-1} = 0$

H_A: at least one $\beta_i \neq 0$ for i=1,2,..,p-1

and test them with the same F-statistic (test statistic) and corresponding p-value:

$F - statistic = \frac{(SST - SSE)/p}{SST/(n-p-1)}$

$p - value = P(F_{p,n-p-1} > F - statistic)$

Comments:

- In the linear model results we can see that 4 0/1 indicator variables were generated for each party versus the reference party (Democrats). The F test for the regression is a test of the party differences, with 4 and 1460 degrees of freedom. The coefficient estimates are mean age adjustments for each party versus the mean for Democrats.
- A key assumption for validity of the F test here is that the response variable (age) has the same variance within each group. The box plot above suggests this is a reasonable assumption in the IQR, a measure of spread is similar in each group.

THEORY JUST FOR SIMPLE LINEAR REGRESSION: Relation between F test for model and t test for slope

The simplest regression model is when there is only one explanatory varible. In this case, we can work out explicit expressions for the least squares estimates and standard errors. Also, in this case, it turns out that the F test for the regression is equivalent to the two-sided t test for the regression coefficient.

Example 3: Analysis between the relationship of animal brain weight and body weight.

In [24]:

```
brain = pd.read_csv('brain.csv')
brain.head(10)
```

Out[24]:

	species	bodykg	braing
0	African elephant	6654.000	5712.0
1	African giant pouched rat	1.000	6.6
2	Arctic Fox	3.385	44.5
3	Arctic ground squirrel	0.920	5.7
4	Asian elephant	2547.000	4603.0
5	Baboon	10.550	179.5
6	Big brown bat	0.023	0.3
7	Brazilian tapir	160.000	169.0
8	Cat	3.300	25.6
9	Chimpanzee	52.160	440.0

Give the population linear regression equation.

Set up the hypotheses to test the whether the slope β_1 is non-zero individually (learned from unit 9), using the t-statistic and p-value that evaluate these hypotheses.

In [25]:

```python
brain_mod = smf.ols('np.log10(braing) ~ np.log10(bodykg)',
                    data=brain).fit()
brain_mod.summary().tables[1]
```

Out[25]:

	coef	std err	t	P>|t|	[0.025	0.975]
Intercept	0.9271	0.042	22.227	0.000	0.844	1.011
np.log10(bodykg)	0.7517	0.028	26.409	0.000	0.695	0.809

Set up the hypotheses to test the whether "at least one" of the slopes in this linear regression is non-zero (learned in this unit 10), using the F-statistic and p-value that evaluate these hypotheses.

In [26]:

```
brain_mod.summary().tables[0]
```

Out[26]:

OLS Regression Results

Dep. Variable:	np.log10(braing)	**R-squared:**	0.921
Model:	OLS	**Adj. R-squared:**	0.919
Method:	Least Squares	**F-statistic:**	697.4
Date:	Mon, 30 Mar 2020	**Prob (F-statistic):**	9.84e-35
Time:	10:27:56	**Log-Likelihood:**	-12.626
No. Observations:	62	**AIC:**	29.25
Df Residuals:	60	**BIC:**	33.51
Df Model:	1		
Covariance Type:	nonrobust		

In [27]:

```
print('F value: ', brain_mod.fvalue)
print('Square of t value for slope coef: ', brain_mod.tvalues[1]**2)
```

```
F value:  697.4200360590312
Square of t value for slope coef:  697.4200360590308
```

We see that the square root of coefficient t statistic for 'np.log10(bodykg) equals the F statistic for the regression.

THEORY IN GENERAL (Relationship between f-statistic and t-statistic in a simple linear regression).

In a simple linear regression there is only one slope β_1.

- **Hypotheses the same:** Therefore the hypotheses that are tested with the f-statistic and the t-statistic are the same.
- **Test Statistics the same:** It also happens that the value of the f-statistic and the t-statistic are the same.
- **p-values the same:** It also happens that the p-value that corresponds to the f-statistic is equal to the p-value that corresponds to the t-statistic.

Extension: F test for comparing two regression models

The F test for the regression is a special case of a general method for comparing two regression models, a full model and a reduced model. The F test for the model takes the reduced model to be the one that has no explanatory variables, just the intercept. The more general testing problem is to compare two **nested models**, where the smaller model is a special case of the larger model, and the null hypothesis is that the smaller model is adequate for describing the data.

Example 1 (again): Relationship between melanoma mortality rate and state a.) latitude, b.) being on the coast, and c.) interaction of being on the coast and latitude.

Question: Is there evidence to suggest that b.) being on the coast and c.) interaction of being on the coast and latitude are needed to explain melanoma mortality rate?

Definitions: Nested Models

Here we compare two models:

Full Model:

$$\text{Expected Mortality Rate} = \beta_0 + \beta_1 * \text{latitude} + \beta_2 * \text{ocean} + \beta_3 * \text{latitude} * \text{ocean}$$

Reduced Model:

$$\text{Expected Mortality Rate} = \beta_0 + \beta_1 * \text{latitude}$$

Nested Model Hypotheses:

To compare these models we consider the hypotheses:

H_0: $\beta_2 = \beta_3 = 0$

H_A: $\beta_2 \neq 0$ or $\beta_3 \neq 0$

Operationally we can test for the difference between the two models by fitting both models and comparing the difference in residual sums of squares using an F test. Suppose we compare two models and the reduced model is obtained by zeroing out q of the parameters. Then we can organize the computations as follows.

Definitions

The "Full Model" has p+q parameters

$\hat{y} = \hat{\beta}_0 + \hat{\beta}_1 x_1 + \ldots + \hat{\beta}_p x_p + \hat{\beta}_{p+1} x_{p+1} + \ldots + \hat{\beta}_{p+q} x_{p+q}$

$df_1 = n - (p + q) - 1$

$SSE_1 = \sum_{i=1}^{n} (y_i - \hat{y}_i)^2$

The "Reduced Model" has p parameters (the q from the "full model" have been deleted).

$\hat{y}_0 = \hat{\beta}_0 + \hat{\beta}_1 x_1 + \ldots + \hat{\beta}_p x_p$

$df_0 = n - p - 1$

$SSE_0 = \sum_{i=1}^{n} (y_i - \hat{y}_{0i})^2$

TEST STATISTIC: F-Statistic for the Nested Model Hypotheses

We compute the F statistic as follows:

$$F_{diff} = \frac{SS_{diff}/(df_{diff})}{SSE_1/df_1} = \frac{(SSE_0 - SSE_1)/q}{SSE_1/(n-p-1)}$$

DEGREES OF FREEDOM: For the Nested Model Hypotheses

If H_0 (the reduced model) is correct, then F_{diff} has an F distribution

- q degrees of freedom and
- $n-p-1$ degrees of freedom.

In our example, n=49, p = 3, q=2, and the degrees of freedom for F are 2 and 49-3-1=45.

The statsmodels.regression.linear_model function .compare_f_test is one implementation of this test.

Main Question: Given that we have fit a model for predicting melanoma mortality rate with latitude, is there evidence to suggest that at least one of the slopes of b.) being on the ocean and c.) the interaction of being on the ocean are non-zero in the full model?

Formulate the hypotheses to test this.

Find the test statistic (f-statistic) that evaluates these hypotheses.

What distribution is this test statistic an observation from?

Find the p-value that evaluates these hypotheses and make a conclusion.

In [28]:

```
# The two fitted models we wish to compare
# mod 1 is the full model
# mod 0 is the restricted model (null hypothesis)
mod1 = smf.ols('mortality ~ latitude + ocean + latitude*ocean',
               data=skin).fit()
mod0 = smf.ols('mortality ~ latitude', data=skin).fit()
```

In [29]:

```
import statsmodels.regression.linear_model as lm
```

In [30]:

```
f, p, df = mod1.compare_f_test(mod0)
pd.DataFrame({'f': [f], 'pvalue': [p], 'df_diff': [df]})
```

Out[30]:

	f	pvalue	df_diff
0	8.769251	0.000608	2.0

We reject the null hypothesis that the 'ocean' main effect and interaction can be removed from the model. Ocean contiguity is a signficant factor.

THEORY: What is the relationship between: a.) the F-

statistic in comparing a full model to a reduced model where just one slope is added and b.) the t-statistic in this "added slope" in the full model?

Another Question: Given that we have fit a model for predicting melanoma mortality rate with a.) latitude and b.) being on the ocean, is there evidence to suggest that the slope of c.) the interaction of being on the ocean are non-zero in the full model is non-zero?

Formulate the hypotheses to test this.

Find the test statistic (f-statistic) that evaluates these hypotheses.

What distribution is this test statistic an observation from?

Find the p-value that evaluates these hypotheses and make a conclusion.

Interaction model versus additive model

We can also compare the larger model to the additive model that removes the interaction between ocean and latitude.

In this case we compare:

Full Model:

$$\text{Expected Mortality Rate} = \beta_0 + \beta_1 * \text{latitude} + \beta_2 * \text{ocean} + \beta_3 * \text{latitude} * \text{ocean}$$

Reduced Model:

$$\text{Expected Mortality Rate} = \beta_0 + \beta_1 * \text{latitude} + \beta_2 * \text{ocean}$$

In [31]:

```
mod1 = smf.ols('mortality ~ latitude + ocean + latitude*ocean',
               data=skin).fit()
mod01 = smf.ols('mortality ~ latitude + ocean',
                data=skin).fit()
f1, p1, df1 = mod1.compare_f_test(mod01)
pd.DataFrame({'f': [f1], 'pvalue': [p1], 'df_diff': [df1]})
```

Out[31]:

	f	pvalue	df_diff
0	0.000025	0.996013	1.0

Here we see that F is very small and the p-value is large, so we fail to reject. The simpler additive model is adequate for these data.

EQUIVALENT QUESTION: In the full model (which uses a.) latitude, b.) being on the coast, and c.) the interaction of being on the coast and latitude to predict melanoma mortality rate), is there evidence to suggest the interaction slope $\beta_3 \neq 0$?

Formulate the hypotheses to test this.

Find the test statistic (f-statistic) that evaluates these hypotheses.

What distribution is this test statistic an observation from?

Find the p-value that evaluates these hypotheses and make a conclusion.

In [32]:

```
mod1.summary().tables[1]
```

Out[32]:

	coef	std err	t	P>|t|	[0.025	0.975]
Intercept	360.5495	35.498	10.157	0.000	289.052	432.047
latitude	-5.4853	0.874	-6.274	0.000	-7.246	-3.724
ocean	20.6501	43.988	0.469	0.641	-67.946	109.246
latitude:ocean	-0.0055	1.101	-0.005	0.996	-2.224	2.213

What is the relationship between the f-statistic and the t-statistic of these last two hypothesis test?

What is the relationship between the p-value of these last two hypothesis test?

In [33]:

```
# check using results above
t_interact = -0.005
F_interact = 0.000025
print("t squared: "+str(t_interact**2)+", F: "+ str(F_interact))
```

```
t squared: 2.5e-05, F: 2.5e-05
```

In [34]:

```python
# Final model summary
mod01.summary().tables[1]
```

Out[34]:

	coef	std err	t	P>|t|	[0.025	0.975]
Intercept	360.6905	21.498	16.778	0.000	317.417	403.964
latitude	-5.4888	0.526	-10.437	0.000	-6.547	-4.430
ocean	20.4304	4.825	4.234	0.000	10.718	30.143

In this case the F test is equivalent to the coefficient t test for the interaction ocean:latitude.

THEORY: What is the relationship between: a.) the F-statistic in comparing a full model to a reduced model where just one slope is added and b.) the t-statistic in this "added slope" in the full model?

Test Statistic Relationship

$$F_{diff} = t^2_{coef}$$

p-value Relationship

(same)

$p - value = P(F_{q,n-p-1} > F_{diff}) = 2P(t_{n-(p+q)-1} < t_{coef}) = p - value$

Conclusions

- In the final model we see that a parallel regressions model is adequate. It implies that the mortality rate tends to decrease by -5.5 per 1 million for each increase of 1% latitude, on average. The 95% confidence interval for this effect is (-6.547, -4.430) per million.

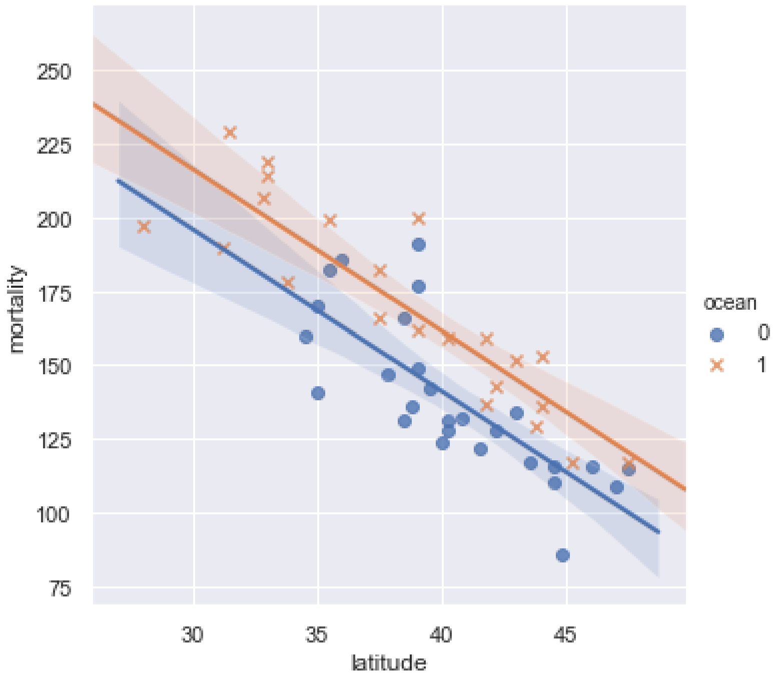
- The model also implies that being near an ocean is associated with an additional 20 per million in annual mortality. The 95% confidence interval for this effect is (10.7, 30.143) per million.

DESCRIPTIVE ANALYTICS

Let's redo the scatter plot of the data using the final model, adding the individual regression lines to the scatter plot. We plot for mortality versus latitude separating ocean versus non-ocean. We can see that the individual regression lines computed separtely for each group are very nearly parallel.

In [35]:

```
sns.lmplot(x="latitude", y="mortality", hue="ocean",
           data=skin, markers=["o", "x"])
plt.show()
```



PREDICTIVE ANALYTICS: What does the model predict for Illinois?

Let's extract the latitude for Illinois ad compare the model prediction with the observed rate.

In [36]:

```
skin[skin["state"]=="IL"]
```

Out[36]:

	state	latitude	mortality	ocean
11	IL	40.0	124	0

Predict the melanoma mortality rate for Illinois by hand.

#### Predict the melanoma mortality rate with Python function.

In [37]:

```
mod01.predict(exog=dict(latitude=40, ocean=0))
```

Out[37]:

```
0    141.139538
dtype: float64
```

In [38]:

```
# Compare direct calculation

360.6905 - 5.4888*40 + 20.4304*0
```

Out[38]:

```
141.13849999999996
```

Assessing the Residual for a Prediction

We see that the observed rate in Illinois was below the predicted rate by about 17 per million. Compare this with the residual standard error for the model, which is an estimate of the individual standard deviations:

In [39]:

```
# Extract mean square for residuals;
# Its square root is an estimate of the sigma for
# the random errors in the model
rstd = np.sqrt(mod01.mse_resid)
rstd
```

Out[39]:

```
16.38995028338583
```

We see that Illinois is well within 2 estimated standard deviations of the regression line, so it is consistent with the overall trend in the data.

One-way ANOVA as a test between two models

Using the full model/reduced model framework, if we take the reduced model to be the null model with an interccept only, then we recover the F test for the regression. This gives another way to perform the F test for the one way ANOVA model.

Pew example revisited

We previously imported and cleaned the 'party' and 'age' fields from the Pew Research Survey, saving them in the data frame 'pew'.

We fit the full model and null model (regression on the constant '1'):

In [40]:

```python
# Full model
agemod = smf.ols('age ~ party', data=pew).fit()
# Null model
agemod0 = smf.ols('age ~ 1', data=pew).fit()
```

Here are the coefficient estimates for the full model:

In [41]:

```python
agemod.params
```

Out[41]:

```
Intercept           50.499051
party[T.Ind]        -3.691432
party[T.No_Pref]    -7.352710
party[T.Other]      -5.899051
party[T.Rep]         6.277516
dtype: float64
```

In contrast, the null model has only one coefficient:

In [42]:

```python
agemod0.params
```

Out[42]:

```
Intercept    50.522867
dtype: float64
```

Having fit these nested models we can now test the null model against the unconstrained model

In [43]:

```python
f_party, p_party, df_party = agemod.compare_f_test(agemod0)
pd.DataFrame({'f': [f_party],
              'pvalue': [p_party],
              'df_diff': [df_party]})
```

Out[43]:

	f	pvalue	df_diff
0	19.818566	6.659457e-16	4.0

Comparing this result with F test for the regression for the uncontrained model we see that they produce the same result.

The advantage of the using compare_f_test is we explicitly control what is being tested.

References

Elwood JM, Lee JAH, Walter SD, Mo T, Green AES (1974). Relationship of melanoma and other skin cancer mortality to latitude and ultraviolet radiation in the United States and Canada. International Journal of Epidemiology, Vol. 3, No. 4, pp. 325-332.