**Testing for heteroscedasticity:**

Breusch-Pagan / Cook-Weisberg test for heteroscedasticity

Ho: Constant variance Variables: fitted values of (whatever the variable is):

Chi2 = 21.41

Prob > chi2 = 0.000

Breusch-Pagan / Cook-Weisberg tests the null hypothesis that the error variances are all equal versus the alternative that the error variances are a multiplicative function of one or more variables. For example, in the default form of the hettest command shown above, the alternative hypothesis states that the error variances increase (or decrease) as the predicted values of Y increase, e.g. the bigger the predicted value of Y, the bigger the error variance is.

A large chi-square would indicate that heteroscedasticity was present. In the hypothetical example above, the chi-square value was large and the p-value is small, indicating heteroskedasticity was present

**Testing for omitted Variables:**

Ramsey RESET test (ovtest)

Ho: model has no omitted variables

F(3, 42) = 0.22

Prob > F = 0.8805

In the case above, the p value of the reset test is 0.88 indicating that the model has no omitted variables, hence the model is properly specified.

If P value is significant level at 5%, we reject the null hypothesis which states that the functional form is correctly specified. Thus, there is functional form misspecification.

**Testing for omitted Autocorrelation:**

Durbin–Watson statistic: dwstat

**Normality Test:**

Normality test: swilk



The null hypothesis is that the distribution of the residuals is normal, here the p-value is 0.64 (way over the usual 0.05 threshold) therefore we failed to reject the null. We conclude then that residuals are normally distributed.

**K-density Test- kernel density graph**

A main assumption of the regression model (OLS) that guarantee the validity of all tests (p, t and F) is that residuals behave ‘normal’.

If residuals do not follow a ‘normal’ pattern then you should check for omitted variables, model specification, linearity, functional forms. In sum, you may need to reassess your model/theory. In practice normality does not represent much of a problem when dealing with really big samples.

