- 19 Modeling Problems Other Diagnostics
 - Non-Normality Residuals
 - False assumption of linearity between Y and any predictor.
- 1. When residuals suggest error term does not following.

 Normal Distribution:
 - · OLS method still has "BLUE" estimates
 for parameters

ca) problem: · Normality is needed to perform t test.

But when sample size is large, since Bx is a weighted sum (linear cumbination) of y1, --, yn, C.L.T. quaantees that it's approximately Normal distributed.

More commonly, a Mormality assurption is presented but is described as less important than other assumptions.

of regression models:

"only extreme departures of the distribution of I from normality yield spurious results"

- Kleinbaum et al.

(b) Detection:

- (i) Normal Probability Plot (Q-Q Plut)
 - resulting plut is approximately linear on chagnal of the plut suggests normality
- (ii) Tests for Normality.

There are many tests addressing normality using different hypothesis: Anderson-Darling, Shapiro-Walls, Ryan-Joiner, Kolmogonov-Smirnov, etc.

we will briefly discuss several things given in the summary table that indicate the normality/skewness of the dota:

- Skew: skewness of residuals measure for symmetry. Sample estimate of $E\left[\left(\frac{e_i}{\sigma}\right)^3\right]$: 3rd moment A distribution that is perfectly symmetric around the mean will have zero skewness
- * Kurtusis: tailshape of residuels measure for clustering sample estimate of $E\left[\left(\frac{ei}{T}\right)^4\right]$ Normal distribution has kurtusis = 0. Higher peaks leads to bigger kurtusis value.
- · Ombibus K-squencel Normality Test: combine Skenness and kuntosis.

K steet = $Z_1(q_1)^2 + Z_2(q_2)^2$ A

Skewners purposits

variable vorable

K steet ~ $\chi^2(z)$

Ho: Residuals are normally distributed

Hi: Residual are not normally distributed

Perent to: suggest residuals are not normally

disjimuted.

· Jorque-Bera Test: Similar to Omnibus, 7t's a test combining skewness and kurtusis

Ho: Regiduals are approx. normal $H_1: \text{ Residuals are not cluse to normal}$ $JB_{\text{Stat}} = \frac{\Lambda-P}{b} \left(\frac{q_1}{4} \right)^2 + \frac{1}{4} \left(\frac{q_2}{2} \right)^2 \right)$

JB stat ~ $\chi^{(2)}$ under Ho
injection suggest residuals are not normally
distributed.

Note*: JB test is vary sensitive to molliers.

(C) solutions:

- (i) Natural-log transformention on y: Ynew = (ny
- (ii) Dox-cox transformation on y: y-new = $\frac{y^{1}-1}{\lambda}$

Lean be estimated using bux cox junction in Python.

viii) When sample size is large, the skewners of data doesn't impact the model estimation or inference very much.

II. False assurption of linearing between I and any predictor.

When the linearity between I arel X durit seem valid,
there've verys to activat but me need to be extremely

coneful:

(i) go with notnear approach:

very complicated.

adding poly nomical terms: In MIR part,

Hadds to of parameters and colds multicolinearity.

be come unstable. — CH13. optional MUR case Estimation doesn't have analytical expressions anymore.

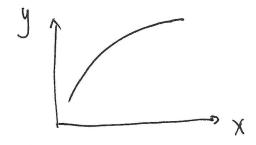
(ii) log-log transformation is powerful nithret losing inference

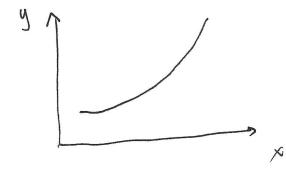
y-new= lny

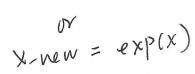
X-new= lnx

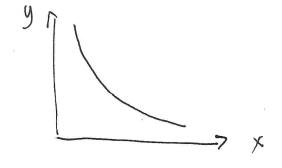
Ex: KC-house-data.

cili) Only transformation on X if non-linewing seems to be the only problem with the data









$$X-new = \frac{1}{x}$$

$$X-new = exp(-x)$$

II. Notes on adding interaction terms in the model.

We will stoot with two predictors:

The regression model for two predictors with Interaction effect is defined as:

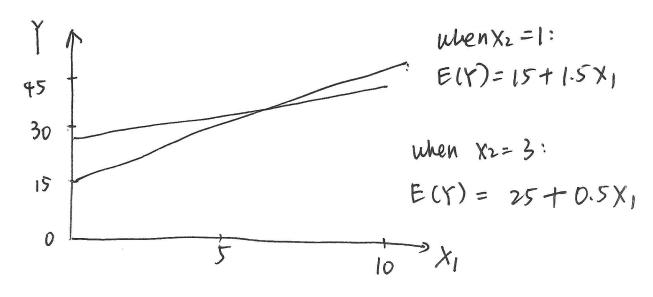
. When XI moveuse by 1 and X2 stay the said

$$E(Y_{1-X_{1}-X}) = \beta_{0} + \beta_{1} \times + \beta_{2} \times \lambda_{12} + \beta_{3} \times \cdot \times \lambda_{12} + \beta_{3} \times \cdot \lambda_{12} + \beta_{3} \times \lambda_{12} + \beta_{3$$

(2)-11): Change into) When X, increase by 1 unit

similarly: Chang mits) When X2 increase by 2 unit

For ex: E(y) = 10+2x,+5x2 0.5 X, X2



whith with different values of X2, the simport of X1 to Y changes.

- The estimation of is and testing one constructed the same as old for MIR without interactions but again we need to add interaction very causinsty:
 - (7) Instrease high multicolinearity
 - (2) When the number of predictors is high,
 the potiential number (2) of interaction
 terms is very high.

(3) In practice, we only add interaction terms

If we obtain knowleadge in advance that

Significant interaction may exist in the study.