Chapter 2 Assessing the Straight Line Fit 1. Testing for lack of fit In chapter 1, we introduced SLR model: Y=Bo+F,X+E => E(Y)=Fo+F,X. Question: Is the model adequate? / True relationship Replication. At Xi, Leve You, Yiz, --, Yini, i=1, ..., m, i.e., Y12 Y22 Yin, Yen, ... Young # total observations: $n = \sum_{i=1}^{m} n_i$, $m = \# distinct X's, <math>Var(Y_{ij}) = \sigma^2$

Deviation about the fitted live can be decomposed into.

$$e_{ij} = \lambda_{ij} - \hat{y}_{ij} = \lambda_{ij} - \hat{y}_{i}$$

= $(y_{ij} - \bar{y}_{i}) + (\bar{y}_{i} - \hat{y}_{i})$.

$$(\gamma_{ij} - \hat{\gamma}_i)^2 = (\gamma_{ij} - \bar{\gamma}_i)^2 + (\bar{\gamma}_i - \hat{\gamma}_i)^2 + 2(\gamma_{ij} - \bar{\gamma}_i)(\bar{\gamma}_i - \hat{\gamma}_i).$$

- Sum over i and j

$$= \sum_{i=1}^{m} \frac{1}{(x_i - x_i)^2} + \sum$$

$$\Rightarrow (df \text{ of } SS(pe)) = \sum_{i=1}^{m} (n_i - 1) = \sum_{i=1}^{m} n_i - m = n - m_i$$

Then, (of of SS(lof)) = (of of RSS) - (of of SS(pe))

$$=(n-2)-(n-m)=m-2.$$

Notes: (1) $SS(pe) = \sum_{i=1}^{m} \sum_{j=1}^{n_i} (y_{ij} - \overline{y_i})^2$ does not depend on the model.

(2) $SS(lof) = \sum_{i=1}^{m} n_i (\bar{y}_i - \hat{y}_i)^2$ depends on the model fitted and measures model lack of fit.

Modify ANOVA table to "break out" pure error and lack of fit 55.

Source of variation	df	55	MS
Regression	ì	SSreg	55reg/1 = 55reg
Residual	n-2	RS5	R55/(n-2)
& Lack of fit	M-5	SS(Lof)	55(lof)/m-2)
Pure error	n-m	55 (pe)	35(pe)/(n-m)
Total (corrected)	n-1	TSS	

Testing Ho: $Y = \beta_0 + \beta_1 X + E$ (A SLR model is adequate) vs. Ha: $Y \neq \beta_0 + \beta_1 X + E$ (A SLR model is inadequate).

Test statistic: F = MS(lof) Under Ho Fm-2, n-m.

Reject Ho if p-value = P(Fm-2, n-m = Fobs) < x or Fobs = Fm-2, n-m(1-2), where Fm-2, n-m (1-d) is the (1-d)th quantile of Fm-2, n-m.

Notes: (1) For the lack of fit test, we need at beast 3 distinct X values and replication at at least one X value (2) Analysis steps for data with at least 3 distinct X values and replication at at least one x value.

Test for lack of fit

Significant Stop the analysis of the model fitted and seek an appropriate model

not significant Check whether any

assumptions are violated

Seek ways to improve Conduct all analyses

the model

introduced in Chapter1

2. Check Model Assumptions

Model: Y: = Po+B, X; +Ei, i=1,2,...,n.

Model assumptions: (1) $E(E_i) = 0$,

- (2) Var(E) = 52 constant variance
- (3) E1, E2, ..., En are independent,

(4) Ei is normally distributed

€ E1, E2, ..., En iid N(0, 02).

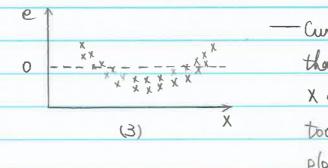
Since E_i is estimated by $e_i = Y_i - \hat{Y}_i$, we check the assumptions e_1, e_2, \cdots, e_n residuals.

Residual plots: Plot e vs. X; (on X axis)
or e; vs. ?; (=bo+b, X;).

Note: Since $\hat{\gamma}_i = b_0 + b_1 x_i$ is simply a livear function of x_i , the only real difference between the two types of residual plots is the scale on the horizontal axis. The pattern of points in the residual plots will be the same, and it is the pattern of points that is important, not the scale.

el	If model is correct, no pattern.
0 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -	- residuals are roughly uniformly
×××××	distributed about the horizontal
(I) X	line $e=0$.





- Curvature indicates a curved rather
them Cinear relationship between
X and Y. (Note: Sometimes it is
too subtle to pick up in the scatter
plot of Yi vs. Xi.)

- "Funnel" shape indicates non-constant variance (here variance increases with X).

Note: Read question and answer 1, 2, 3 on pages 63-67.

Assessing normality

Normal plot (Quantile - Quantile plot, i.e., Q-aplot)

- (1) Order residuals e, e, ..., en from the smallest to the largest to get the ordered residuals: ev, eu, ..., en.
- (2) Calculate the normal scores: $g_{(i)} = \overline{\Phi}^{-1}(\frac{i-\frac{1}{N}}{N})$, i=1,2,...n, where $\overline{\Phi}^{-1}(\cdot)$ is the inverse function of the standard normal distribution function $\overline{\Phi}(x) = P(Z \leq x) = \int_{-\infty}^{\infty} \frac{1}{\sqrt{2\pi}} e^{-\frac{3^2}{2}} dz$ (i.e., the $(\frac{i-\frac{1}{N}}{N})$ th quantile of N(0,1)). Thus, $\overline{\Phi}(g_{(i)}) = P(Z \leq g_{(i)}) = \frac{i-\frac{1}{N}}{N}$.

 (3) Plot the pairs $(g_{(i)}, e_{(i)})$, $(g_{(i)}, e_{(i)})$, ..., $(g_{(i)}, e_{(i)})$.

A substantial linear pattern in a normal plot indicates that the

normality assumption remains tenable. Otherwise, normality is suspect.

Note: The judgement as to whether a normal plot does or does not show a substantial linear pattern is somewhat subjective.

Test for normality

The Shapiro and Wilk test

Ho: e, ez, ..., en come from a normal population vs. (the normality assumption is tenable.)

Ha. e, ez, ..., en come from a non-normal population. (the normality assumption is violated)

Test statistic: $W = \frac{\left[\sum_{i=1}^{n} e_{(i)}\right]^{2}}{\sum_{i=1}^{n} e_{i}^{2}}$

Reject Ho if p-value & a.

Notes: 11 Residuals e, e, ..., en are not independent. However, the effect of correlations between residuals is usually negligible.

(2) When intercept is in model, $\Sigma e_i = 0 \iff \overline{e} = \overline{\Xi_i} e_i = 0$, Thus, there is need to check $\overline{e} = 0$.

Q: What if the SLR is inadequate or some assumptions are violated?

A: Transform data — Transformations, which are the focuses of Chapter 12 & 13.



Example 2.1: For the data given in problem F on page 99 (i.e., the data for HW #1),

X	4.7	5	5.2	5.2	5.9	4.7	5.9	5.2	5.3	5.9	5.6	5
Y	3	3	4	5	10	2	9	3	7	6	6	4

- (a) Test to determine whether it is adequate to fit the data by a straight line at $\alpha = 0.05$.
- (b) Conduct Shapiro and Wilk test for normality based on residuals using $\alpha = 0.05$.

Example 2.2: In a study, 15 American females aged 30-39 are randomly selected. The following data on X = height (in) and Y = weight (lb) are observed.

											68				
Y	113	115	118	121	124	128	131	134	137	141	145	150	153	159	164

Is the relationship between *X* and *Y* linear?