



# Lecture 5: Hypothesis testing with the classical linear model

# Assumption MLR6: Normality

$$u \sim N(0, \sigma^2)$$

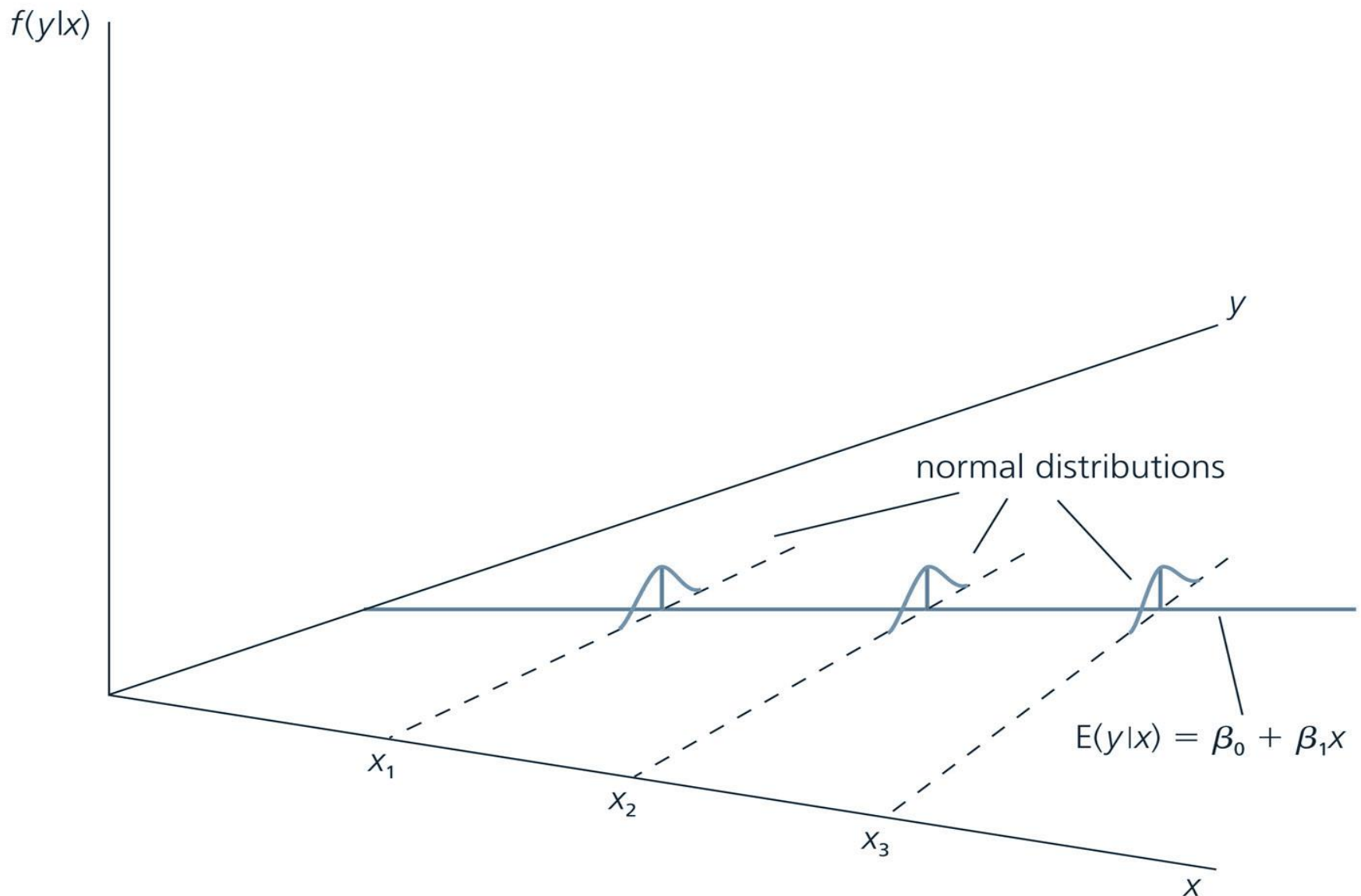
$$E(u \mid x_1, x_2, \dots, x_k) = E(u) = 0$$

$$Var(u \mid x_1, x_2, \dots, x_k) = Var(u) = \sigma^2$$

- MLR6 is not one of the Gauss-Markov assumptions. It's not necessary to assume the error is normally distributed in order to obtain the best linear unbiased estimator from OLS.
- MLR6 makes OLS the best unbiased estimator (linear or not), and allows us to conduct hypothesis tests.

**FIGURE 4.1**

**The homoskedastic normal distribution with a single explanatory variable.**



# Assumption MLR6: Normality

- But if  $Y$  takes on only  $n$  distinct values, for any set of values of  $X$ , the residual can take on only  $n$  distinct values.
  - Non-normal errors: we can no longer trust hypothesis tests
  - Heteroscedasticity
- With a dichotomous  $Y$ , run a logit or probit model
- With an ordered categorical  $Y$ , ordered probit/logit
- With an unordered categorical  $Y$ , multinomial probit/logit
- With non-negative integer counts, poisson or negative binomial models
- But in chapter 5 we'll see large sample size can overcome this problem.

# Assumption MLR6: Normality

- If we assume that the error is normally distributed conditional on the x's, it follows:

$$\hat{\beta}_j \sim N(\beta_j, \text{Var}(\hat{\beta}_j))$$

$$(\hat{\beta}_j - \beta_j) / \text{sd}(\hat{\beta}_j) \sim N(0,1)$$

- In addition, any linear combination of beta estimates is normally distributed, and multiple estimates are jointly normally distributed.

# Assumption MLR6: Normality

- In practice, beta estimates follow the t-distribution:

$$(\hat{\beta}_j - \beta_j) / se(\hat{\beta}_j) \sim t_{n-k-1}$$

- Where  $k$  is the number of slope parameters,  $k+1$  is the number of unknown parameters (including intercept),  $n$  is the sample size, and  $n-k-1$  is the total degrees of freedom.

# [ Hypothesis testing: ]

- 1) State null and research hypotheses
- 2) Select significance level
- 3) Determine critical value for test statistic (decision rule for rejecting null hypothesis)
- 4) Calculate test statistic
- 5) Either reject or fail to reject (not “accept” null hypothesis)

# [ Hypothesis testing:





# [ Hypothesis Testing, example ]

- Go back to state poverty and homicide rates.
- Two-tailed vs. one-tailed test, which should we do? How do we read the output differently for the two tests?

$$H_0 : \beta = 0$$

$$H_0 : \beta \leq 0$$

$$H_1 : \beta \neq 0$$

$$H_1 : \beta > 0$$

two-tailed

one-tailed

# [Hypothesis Testing, cont.]

- We typically use two-tailed tests when we have no *a priori* expectation about the direction of a specific relationship. Otherwise, we use a one-tailed test.
- With poverty and homicide, a one-tailed test is justifiable.
- Hypothesis tests and confidence intervals in Stata regression output report t-test statistics, but it is important to understand what they mean because we don't always want to use exactly what Stata reports.

# [Hypothesis Testing, cont.]

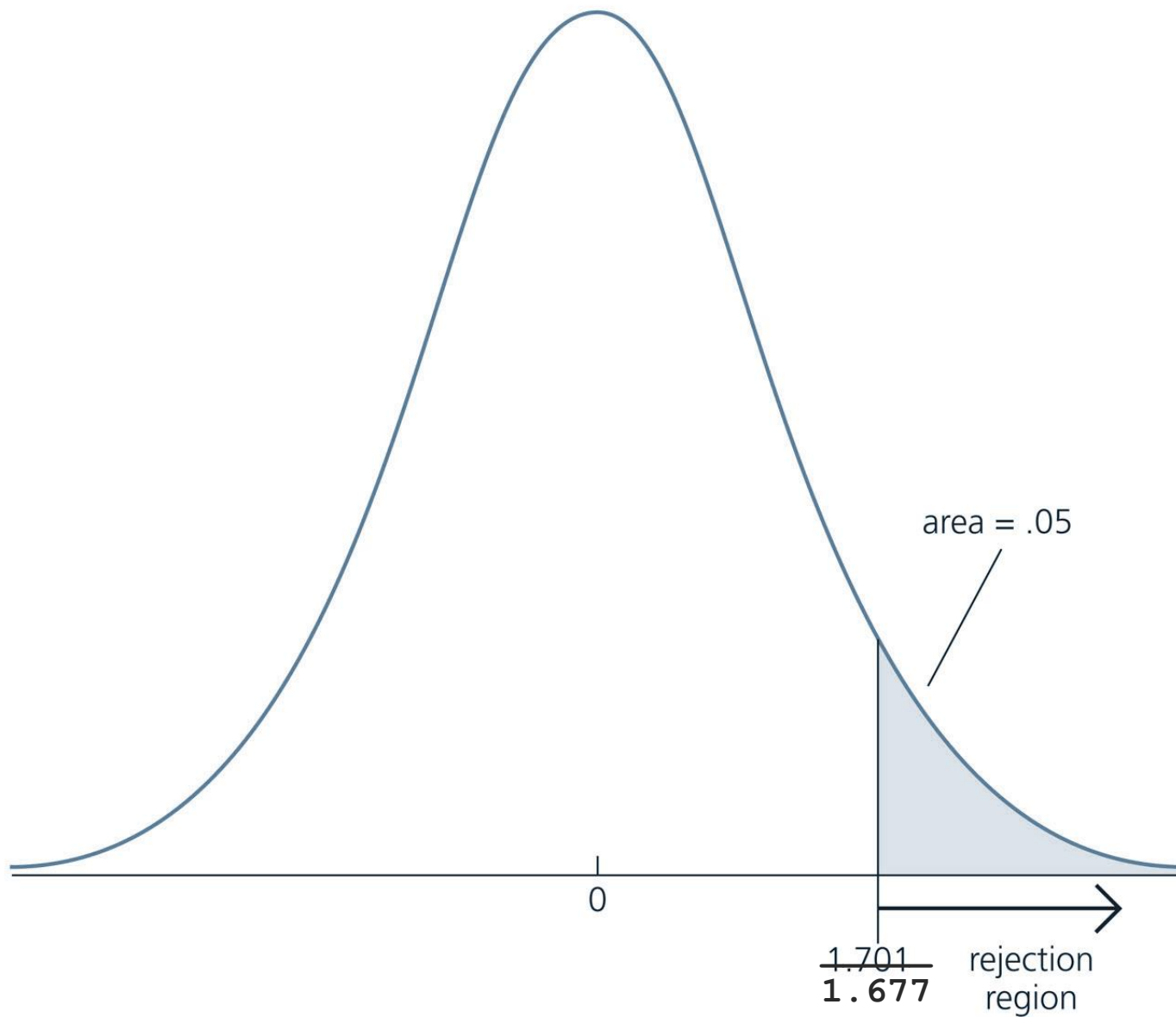
- The alpha level is the chance that you will falsely reject the null hypothesis, Type 1 error.
- Step 2: select alpha level
  - Don't always use .05 alpha level.
  - Consider smaller alphas for very large samples, or when it's particularly important that you don't falsely reject the null hypothesis.
  - Use larger alphas for very small samples, or if it's not a big deal to falsely reject the null.

# [Hypothesis Testing, cont.]

- Step 3: determine critical value. This depends on the test statistic distribution, the alpha level and whether it's a one or two-tailed test.
- In a one-tailed t-test, with an alpha of .05, and a large sample size ( $>120$ ), the critical value would be 1.64.
- But with 48 degrees of freedom ( $N-k-1$ ), the critical value is  $\sim 1.68$  (see Table 6.2, page 825).

**FIGURE 4.2**

5% rejection rule for the alternative  $H_1: \beta_j > 0$  with ~~28~~ **48**  $df$ .



# [Hypothesis Testing, cont.]

- To find critical t-statistics in Stata:
  - `. di invttail(48, .05)`
- You should look up these commands (ttail, invttail) and make sure you understand what they are doing. These are part of a larger class of density functions.

# [Hypothesis Testing, cont.]

- The test statistic is calculated as follows:

$$t_{\hat{\beta}} = \frac{\hat{\beta} - \beta_{H_0}}{\hat{\sigma}_{\hat{\beta}}}$$

- The null hypothesis value of beta is subtracted from our estimate and divided by its estimated standard error.
- This is compared to our pre-determined test statistic. If it's larger than 1.677, we reject the null.

# [Hypothesis Testing, cont.]

- Returning to the poverty and homicide rate example, we have an estimated beta of .475 and a standard error of .103. If our null hypothesis is:

$$H_0 : \beta \leq 0$$

Then the test statistic is:  $t.s. = \frac{.475 - 0}{.103} = 4.62$

- $4.62 > 1.677$ , so we reject the null hypothesis.



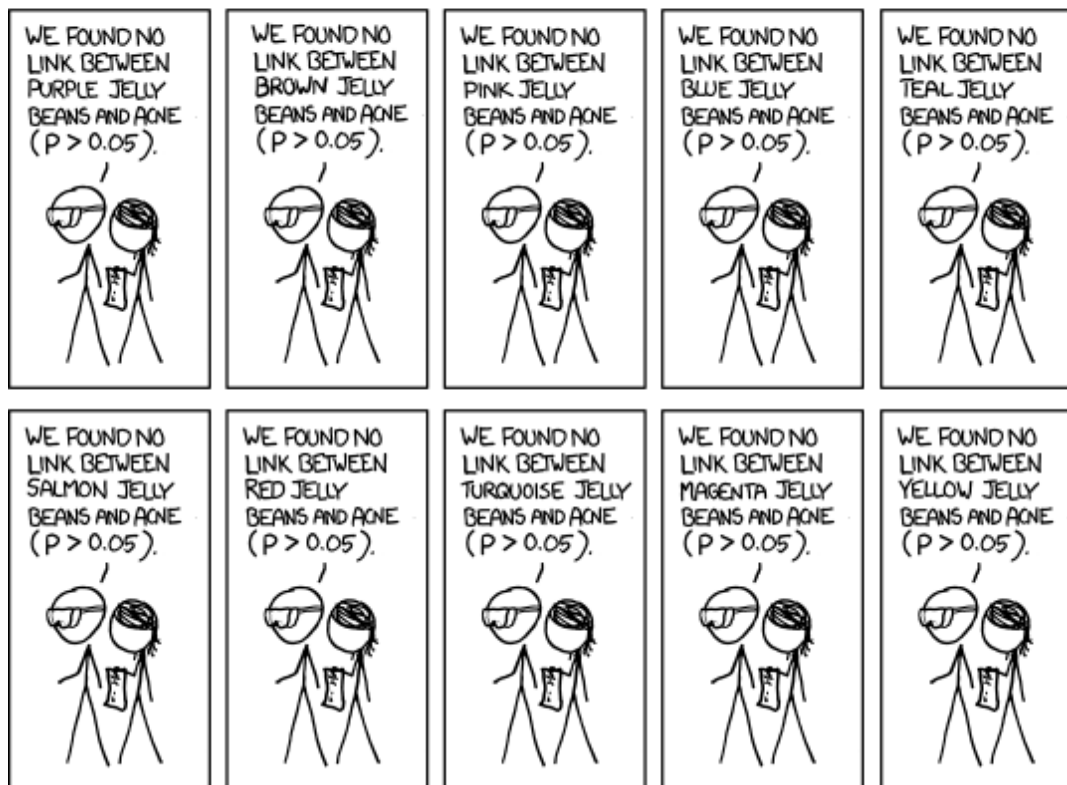
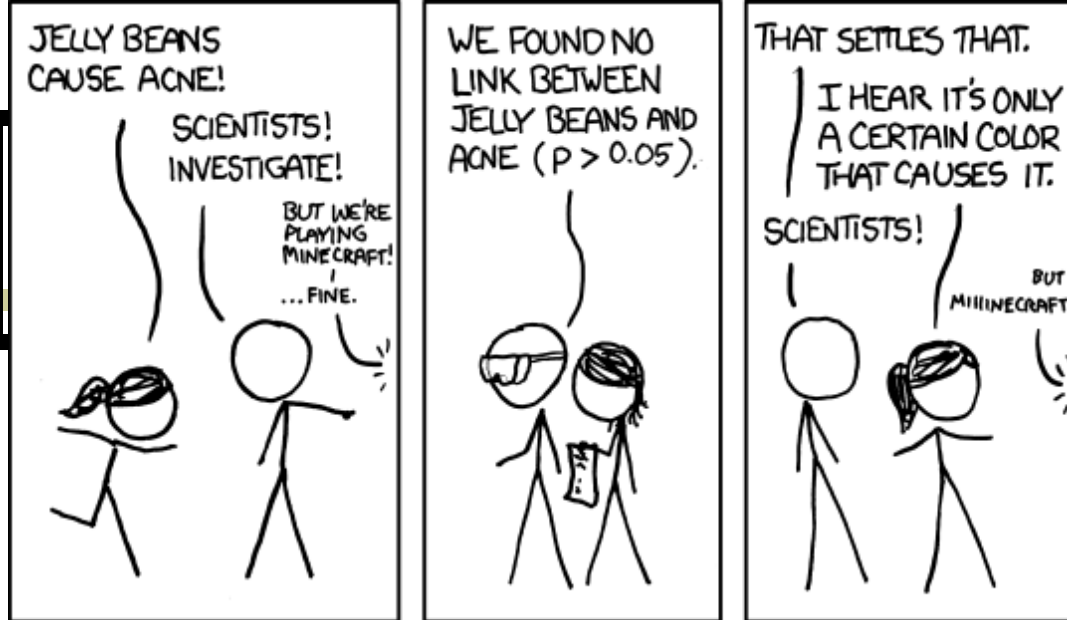
# [ Hypothesis Testing, cont. ]

- Stata also reports p-values in regression output. We would reject the null for any two-sided test where the alpha level is larger than the p-value. It's the area under the curve in a two-sided test.
- To find exact one-sided p values for the t-distribution in Stata:
  - `. di ttail(48,4.62)`
  - `.00001451`, so we would reject the null with any conventional alpha level

# [ Hypothesis Testing, warning ]

- Regression output always reports two-sided tests. You have to divide stata's outputted  $p$  values by 2 in order to get one-tailed tests, but make sure the coefficient is in the right direction!
- On the other hand, *ttail*, and *invttail* always report one-tailed values. Adjust accordingly.
- `Ttail & invttail` worksheet

# Learning



ORANGE JELLY BEANS AND ACNE ( $P > 0.05$ ).



RED JELLY BEANS AND ACNE ( $P > 0.05$ ).



ROSEBUD JELLY BEANS AND ACNE ( $P > 0.05$ ).



PURPLE JELLY BEANS AND ACNE ( $P > 0.05$ ).



YELLOW JELLY BEANS AND ACNE ( $P > 0.05$ ).



WE FOUND NO LINK BETWEEN GREY JELLY BEANS AND ACNE ( $P > 0.05$ ).



WE FOUND NO LINK BETWEEN TAN JELLY BEANS AND ACNE ( $P > 0.05$ ).



WE FOUND NO LINK BETWEEN CYAN JELLY BEANS AND ACNE ( $P > 0.05$ ).



WE FOUND A LINK BETWEEN GREEN JELLY BEANS AND ACNE ( $P < 0.05$ ).



WE FOUND NO LINK BETWEEN MAUVE JELLY BEANS AND ACNE ( $P > 0.05$ ).



WE FOUND NO LINK BETWEEN BEIGE JELLY BEANS AND ACNE ( $P > 0.05$ ).



WE FOUND NO LINK BETWEEN LILAC JELLY BEANS AND ACNE ( $P > 0.05$ ).



WE FOUND NO LINK BETWEEN BLACK JELLY BEANS AND ACNE ( $P > 0.05$ ).

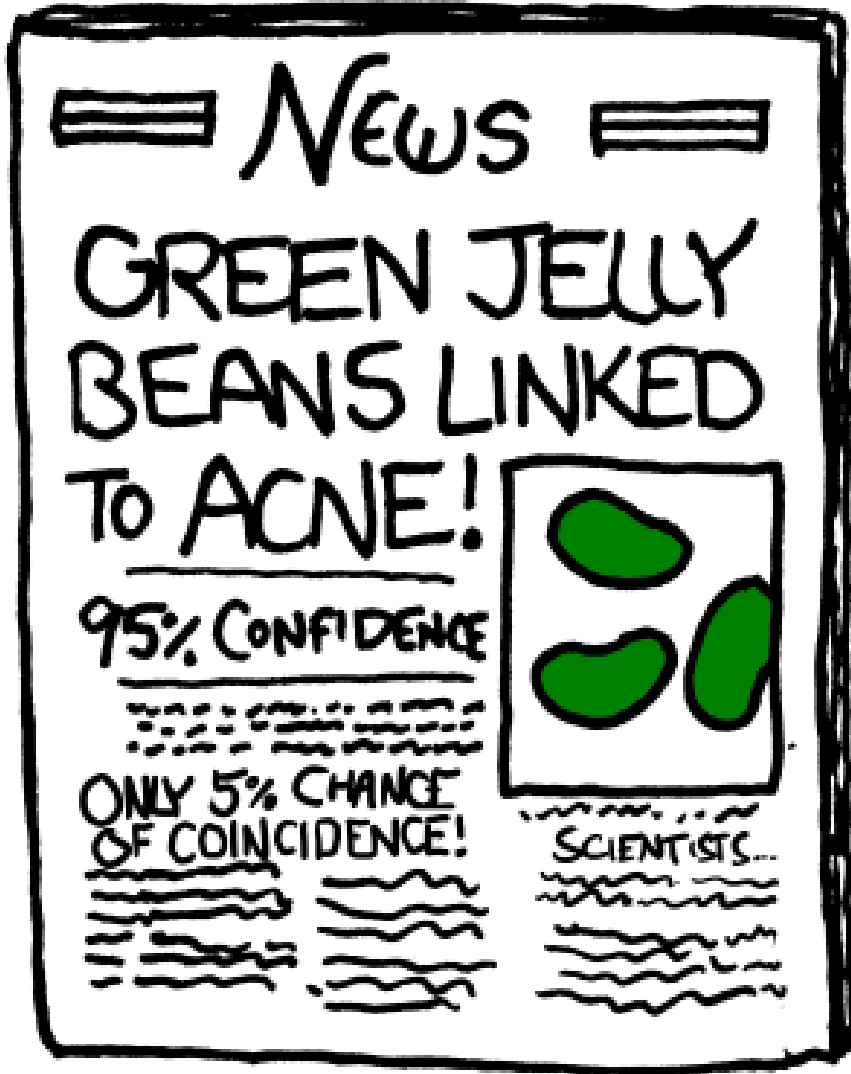


WE FOUND NO LINK BETWEEN PEACH JELLY BEANS AND ACNE ( $P > 0.05$ ).



WE FOUND NO LINK BETWEEN ORANGE JELLY BEANS AND ACNE ( $P > 0.05$ ).





- What went wrong?
- What are the chances of finding at least one statistically significant variable at  $p < .05$  when you are testing 20 variables?  

```
. di binomialtail(20,1,.05) = .64
```
- There's a 64% chance of having at least one "statistically significant" result.
- This is the problem of multiple comparisons. How can you correct for this?

■ The most common and simplest is the Bonferroni correction where you replace your original alpha level with  $\alpha/k$  where  $k$  is the number of comparisons you make.

```
. di binomialtail(20,1,.05/20)  
.04883012
```

# Confidence intervals

- Confidence intervals are related to hypothesis tests, but are interpreted much differently.

$$CI : \hat{\beta}_j \pm c \cdot se(\hat{\beta}_j)$$

- $c$  is the t-value needed to obtain the correct % confidence interval. The 97.5% one-sided t-value is needed for a 95% confidence interval.
- Confidence intervals are always two-sided.
- Given the sample data, the confidence interval tells us, with X% confidence, that the *true* parameter falls within a certain range.

# Confidence intervals

- Going back to the homicide rate and poverty example, the estimated parameter for poverty was .475 with a standard error of .103.
- The 95% confidence interval, reported by Stata is  $.475 \pm .103 * 2.01 = [.268, .682]$
- So, with 95% confidence, the population value for the effect of poverty on homicide is between those two numbers.
- The 99% confidence interval will be wider in order to have greater confidence that the true value falls within that range:
  - $.475 \pm .103 * 2.68 = [.199, .751]$

## Example 4.2 (p. 126-8): student performance and school size

- Hypotheses:  $H_0 : \beta_{enroll} \geq 0$   
 $H_1 : \beta_{enroll} < 0$
- Alpha: .05, one tailed, tcrit=-1.65
- Reject null hypothesis if t.s.<-1.65
- The estimated coefficient on enrollment, controlling for teacher compensation and staff:student ratio is -.00020 with a .00022 standard error.
- So the test statistic equals  $-.00020/.00022 = -.91$ , fail to reject null.
- Functional form can change our conclusions!  
When school size is logged, we do reject the null.



# [ Other hypotheses about $\beta$ ]

- We may want to test the hypothesis that  $\beta$  equals 1, or some other number besides zero. In this case, we proceed exactly as before, but t-statistic won't match the regression output. We subtract the hypothesized parameter size (now non-zero) from the parameter estimate before dividing by the standard error.

$$t_{\hat{\beta}} = \frac{\hat{\beta} - \beta_{H_0}}{\hat{\sigma}_{\hat{\beta}}}$$

- Stata, helpfully, will do this for us. After any regression type: “test varname=X”, inserting the appropriate variable name and null parameter value.
- Example 4.4, p. 130-131

# [ Linear combinations of $\beta$ s ]

- In section 4.4, Wooldredge goes through a detailed explanation of how to transform the estimated regression model in order to obtain  $se(\beta_1 + \beta_2)$ , which is necessary in order to directly test the hypothesis that  $\beta_1 + \beta_2 = 0$ .
- This method is correct, and it is useful to follow, I just prefer a different method after a regression model:
- “test  $x_1 + x_2 = 0$ ”, replacing  $x_1$  and  $x_2$  with your variable names.

# [ Testing multiple linear restrictions ]

- Restricted model: Multiple restrictions are imposed on the data. (e.g. linearity, additivity,  $X_j=0$ ,  $X_j=X_k$ ,  $X_j=3$ , etc.)
- Unrestricted model: At least one of the above assumptions is relaxed, often by adding an additional predictor to the model.
- To test the null hypothesis, we conduct an F-test:

# F-test for restricted/unrestricted models

$$F(k_{UR} - k_R, n - k_{UR}) = \frac{(SSR_R - SSR_{UR}) / (k_{UR} - k_R)}{SSR_{UR} / (n - k_{UR})}$$

- Where SSR refers to the residual sum of squares, and k refers to the number of regressors (including the intercept).



# [ F-test for restricted/unrestricted models, example ]

## Restricted model:

```
. reg homrate poverty
```

Source	SS	df	MS	Number of obs = 50		
Model	100.175656	1	100.175656	F( 1, 48)	=	21.36
Residual	225.109343	48	4.68977798	Prob > F	=	0.0000
				R-squared	=	0.3080
				Adj R-squared	=	0.2935
Total	325.284999	49	6.63846936	Root MSE	=	2.1656

homrate	Coef.	Std. Err.	t	P> t	[95% Conf. Interval]	
poverty	.475025	.1027807	4.62	0.000	.2683706	.6816795
_cons	-.9730529	1.279803	-0.76	0.451	-3.54627	1.600164

- **Why is this “restricted”? What restrictions are we imposing, and how might we test these?**



# F-test for restricted/unrestricted models, example

## Unrestricted model:

```
. reg homrate poverty gradrate het
```

Source	SS	df	MS	Number of obs	=	50
Model	183.012608	3	61.0042025	F( 3, 46)	=	19.72
Residual	142.272391	46	3.09287807	Prob > F	=	0.0000
Total	325.284999	49	6.63846936	R-squared	=	0.5626
				Adj R-squared	=	0.5341
				Root MSE	=	1.7587

	homrate	Coef.	Std. Err.	t	P> t	[95% Conf. Interval]	
	poverty	.3134171	.0922506	3.40	0.001	.1277263	.4991079
	gradrate	-.0518914	.0404837	-1.28	0.206	-.1333809	.0295981
	het	7.098508	2.174708	3.26	0.002	2.721047	11.47597
	_cons	2.357754	3.913269	0.60	0.550	-5.519249	10.23476

- Here, we have lifted the restriction that  $\beta_{\text{gradrate}} = \beta_{\text{het}} = 0$ . The F-test of this restriction is calculated as follows:



# F-test for restricted/unrestricted models, example

$$F(k_{UR} - k_R, n - k_{UR}) = \frac{(SSR_R - SSR_{UR}) / (k_{UR} - k_R)}{SSR_{UR} / (n - k_{UR})}$$

$$F(4 - 2, 50 - 4) = \frac{(225.1 - 142.3) / (4 - 2)}{142.3 / (50 - 4)}$$

$$F(2, 46) = 41.4 / 3.1 = 13.4, (p < .000)$$

- We can find the p-value in Stata using “di Ftail(2, 46, 13.4)” – or we can let Stata do all the calculations with “test gradrate het” after the unrestricted model. This is testing two restrictions jointly: gradrate=0 & het=0.

# [ F-test for restricted/unrestricted models, example ]

- This kind of test is appropriate when the difference between two models can be expressed as a set of restrictions or assumptions.
- It may take a little bit of imagination to recognize the “restrictions” in your restricted model.

$$y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \dots + \beta_j x_j + u$$

- Examples:
  - $\beta_{j+1} = 0$
  - the coefficient on the product of  $x_1$  and  $x_2$  is zero.





# [ F-test for restricted/unrestricted models, example

- One special type of restriction which is sometimes of interest in criminology, is that our models are the same across different groups. This follows the same logic, but is called a Chow test.



# [ F-test for restricted/unrestricted models, Chow test example ]

- The Chow test can be used in a couple different situations.
  - Completely different sets of data with the same variables
  - Sub-populations within one dataset.
- Either way, we compare the SSR from a regression model with the two sets of data (or groups) pooled (restricted model), to the summed SSR from two separate regression models (unrestricted).
- What is the restriction in the restricted model?

# [ F-test for restricted/unrestricted models, Chow test example ]

Unrestricted model (two groups):

$$Y = \alpha_1 + \beta_1 X_1 + \delta_1 X_2 + \dots + \gamma_1 X_k + \varepsilon$$

$$Y = \alpha_2 + \beta_2 X_1 + \delta_2 X_2 + \dots + \gamma_2 X_k + \varepsilon$$

Restricted model (pooled):

$$Y = \alpha + \beta X_1 + \delta X_2 + \dots + \gamma X_k + \varepsilon$$

$$\alpha_1 = \alpha_2, \beta_1 = \beta_2, \dots \quad \leftarrow \text{restrictions}$$



# F-test for restricted/unrestricted models, Chow test example

- Suppose we have a model for teen delinquency, but we think it differs for males and females. **Restricted model (note: we don't control for gender here):**

```
. reg dfreq1 age1 hisp black other msgrd sus1 r_wk biop1 smoke1
```

Source	SS	df	MS	Number of obs =	8669
Model	86926.9336	9	9658.54818	F( 9, 8659) =	56.05
Residual	1492077.55	8659	172.315227	Prob > F =	0.0000
Total	1579004.48	8668	182.1648	R-squared =	0.0551
				Adj R-squared =	0.0541
				Root MSE =	13.127

dfreq1	Coef.	Std. Err.	t	P> t	[95% Conf. Interval]	
age1	.0392229	.1006811	0.39	0.697	-.1581361	.2365818
hisp	.3504168	.4325393	0.81	0.418	-.497463	1.198297
black	-.8410179	.3773185	-2.23	0.026	-1.580652	-.1013839
other	-.3523527	.4795827	-0.73	0.463	-1.292449	.5877435
msgrd	-.347948	.0939261	-3.70	0.000	-.5320656	-.1638304
sus1	4.032407	.3474379	11.61	0.000	3.351346	4.713468
r_wk	.4253605	.1738242	2.45	0.014	.0846237	.7660973
biop1	-.7830546	.300954	-2.60	0.009	-1.372996	-.1931132
smoke1	3.773678	.3128116	12.06	0.000	3.160493	4.386864
_cons	2.279977	1.563863	1.46	0.145	-.785567	5.345521



# F-test for restricted/unrestricted models, Chow test example

## Unrestricted model, part 1:

```
. reg dfreq1 age1 hisp black other msgrd sus1 r_wk biop1 smoke1 if male==1
```

Source	SS	df	MS	Number of obs =	4436
Model	76722.9184	9	8524.76872	F( 9, 4426) =	30.13
Residual	1252212.9	4426	282.92203	Prob > F =	0.0000
Total	1328935.82	4435	299.647311	R-squared =	0.0577
				Adj R-squared =	0.0558
				Root MSE =	16.82

dfreq1	Coef.	Std. Err.	t	P> t	[95% Conf. Interval]	
age1	.1722392	.1807942	0.95	0.341	-.1822079	.5266863
hisp	.9256955	.778416	1.19	0.234	-.6003892	2.45178
black	-.9784988	.6809885	-1.44	0.151	-2.313577	.3565793
other	-.9274644	.86288	-1.07	0.283	-2.619141	.7642119
msgrd	-.322382	.165856	-1.94	0.052	-.6475428	.0027788
sus1	4.10308	.5883441	6.97	0.000	2.949631	5.256529
r_wk	.4572663	.3020877	1.51	0.130	-.1349767	1.049509
biop1	-1.566485	.5393016	-2.90	0.004	-2.623785	-.5091838
smoke1	5.485458	.5611064	9.78	0.000	4.385409	6.585507
_cons	.7287458	2.803031	0.26	0.795	-4.766596	6.224088



# F-test for restricted/unrestricted models, Chow test example

## Unrestricted model, part 2:

```
. reg dfreq1 age1 hisp black other msgrd sus1 r_wk biop1 smoke1 if male==0
```

Source	SS	df	MS	Number of obs =	4233
Model	12738.1839	9	1415.35377	F( 9, 4223) =	27.02
Residual	221189.499	4223	52.377338	Prob > F =	0.0000
Total	233927.682	4232	55.2759174	R-squared =	0.0545
				Adj R-squared =	0.0524
				Root MSE =	7.2372

dfreq1	Coef.	Std. Err.	t	P> t	[95% Conf. Interval]	
age1	-.0747234	.0793737	-0.94	0.347	-.2303376	.0808908
hisp	-.2843726	.3401383	-0.84	0.403	-.9512225	.3824774
black	-.5786616	.2963413	-1.95	0.051	-1.159646	.0023231
other	.1702421	.3771467	0.45	0.652	-.5691639	.909648
msgrd	-.1599254	.0776844	-2.06	0.040	-.3122276	-.0076232
sus1	2.685044	.3034377	8.85	0.000	2.090147	3.279942
r_wk	.1609845	.1428534	1.13	0.260	-.1190833	.4410524
biop1	-.2722414	.2388061	-1.14	0.254	-.7404268	.1959441
smoke1	2.155191	.2475283	8.71	0.000	1.669905	2.640476
_cons	2.556738	1.240103	2.06	0.039	.1254827	4.987992



# [ F-test for restricted/unrestricted models, Chow test example ]

- **Chow test proceeds as follows:**

$$F(k_{UR} - k_R, n - k_{UR}) = \frac{(SSR_R - SSR_{UR}) / (k_{UR} - k_R)}{SSR_{UR} / (n - k_{UR})}$$

$$F(20 - 10, 8669 - 20) = \frac{(1492078 - (1252212 + 221189)) / (20 - 10)}{(1252212 + 221189) / (8669 - 20)}$$

$$F(10, 8649) = \frac{18675 / 10}{1473402 / 8649} = 10.96, (p < .001)$$

- **Alternately, we could interact male with all other variables, run a fully interactive model, and . . .**



# F-test for restricted/unrestricted models, Chow test example

```
. reg dfreq1 age1 hisp black other msgrd sus1 r_wk biop1 smoke1 male magel mhisp mblack mother  
mmsgrd msus1 mr_wk mbiop1 msmoke1
```

Source	SS	df	MS	Number of obs =	8669
Model	105602.083	19	5558.00435	F( 19, 8649) =	32.63
Residual	1473402.4	8649	170.355232	Prob > F =	0.0000
Total	1579004.48	8668	182.1648	R-squared =	0.0669
				Adj R-squared =	0.0648
				Root MSE =	13.052

dfreq1	Coef.	Std. Err.	t	P> t	[95% Conf. Interval]	
age1	-.0747234	.1431472	-0.52	0.602	-.355326	.2058792
hisp	-.2843726	.6134251	-0.46	0.643	-1.486832	.9180869
black	-.5786616	.5344391	-1.08	0.279	-1.62629	.4689663
other	.1702421	.6801683	0.25	0.802	-1.16305	1.503534
. . .						
. . .						
mbiop1	-1.294243	.6005073	-2.16	0.031	-2.471381	-.1171058
msmoke1	3.330267	.623581	5.34	0.000	2.1079	4.552634
_cons	2.556738	2.236474	1.14	0.253	-1.827285	6.94076

```
. test male magel mhisp mblack mother mmsgrd msus1 mr_wk mbiop1 msmoke1
```

**F( 10, 8649) = 10.96 ←----- get the same answer!**

Prob > F = 0.0000



# [ F-test for restricted/unrestricted models, Chow test example ]

- We know that there are significant differences in average levels of delinquency between males and females.
- Part of the Chow test is that there is no difference in average levels between the two groups (same intercept).
- How would we test a modified Chow test where we allow males and females to have different levels of delinquency and just test if the effects of the covariates differ between the genders?



# [ F-test for restricted/unrestricted models, other uses ]

- This general test is used to calculate the overall F-statistic for every regression model. The restricted model is intercept only where all parameters are assumed to be zero.
- Interaction terms

# [ Stata's saved regression results ]

- After any regression:
  - “ereturn list” returns a list of all stored results
  - e(N): number of observations
  - e(mss): model sum of squares
  - e(df\_m): model degrees of freedom
  - e(rss): residual sum of squares
  - e(df\_r): residual degrees of freedom
  - e(F): F statistic
  - e(r2): r-squared
  - e(r2\_a): adjusted r-squared
  - e(rmse): root mean squared error

# [Next time:

Homework 6 Problems 4.2, 4.4, C4.6, C4.8

Answers posted – do not turn in.

Midterm: available today after class, due by 4:40pm 10/4,  
open to any non-interactive resource  
(books/notes/lectures/internet pages), but not other  
people.

Read: Wooldridge Chapter 5 (skim), Chapter 6