

Lecture 11: AV plots, hypothesis testing and nested models

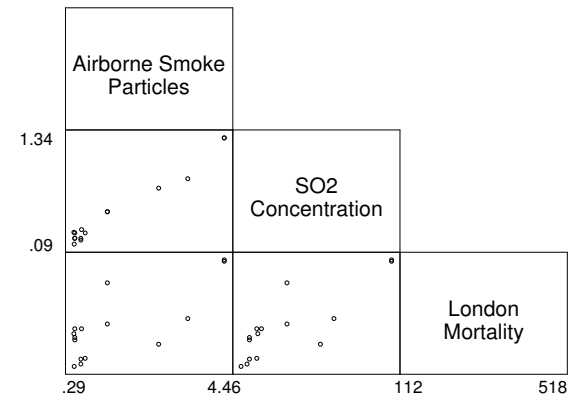
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1

Another Example: Mortality

Smoke, pollution & London mortality data



2

Mortality Example: Model

Let:

- Y = the daily mortality for London (*deaths*)
- X_1 = airborne smoke particles (mg/m^3) (*smoke*)
- X_2 = SO_2 (ppm) (*so2*)

Model:

- Systematic: $Y_i = \beta_0 + \beta_1(X_1 - 2) + \beta_2(X_2 - .5) + \varepsilon_i$
- Random: $\varepsilon_i \sim N(0, \sigma^2)$
 - Mortality is a linear function of the concentration of airborne smoke particles *AND* the SO_2 level

3

Mortality Example: Results

Model:

$$E(Y | X) = \beta_0 + \beta_1(X_1 - 2) + \beta_2(X_2 - .5)$$

Source	SS	df	MS	Number of obs = 15		
Model	205097.531	2	102548.765	F(2, 12) = 36.57		
Residual	33654.2025	12	2804.51687	Prob > F = 0.0000		
				R-squared = 0.8590		
				Adj R-squared = 0.8355		
Total	238751.733	14	17053.6952	Root MSE = 52.958		

deaths	Coef.	Std. Err.	t	P> t	[95% Conf. Interval]	
smokecenter	-220.3244	58.14314	-3.79	0.003	-347.0074	-93.64135
so2center	1051.816	212.5959	4.95	0.000	588.6096	1515.023
(Intercept)	174.7703	29.16174	5.99	0.000	111.2323	238.3083

4

Mortality Example

Inference: Overall F test

- Overall F-Test:
 - Are *ANY* of the covariates significant?
- $H_0: \beta_1 = \beta_2 = 0;$
- Fobs: (2,12) = 36.57;
- p-value = 0.0000
- Decision: At least one of the β 's are nonzero

5

Mortality Example

Coefficient inference: individual 95% C.I. & t-tests

- | | |
|--|--|
| β_0 <ul style="list-style-type: none"> $b_0 = 174.8$
95% CI: (111.2, 238.3) $H_0: \beta_0 = 0$ $t_{\text{obs}}: (12) = 5.99$ p-value = 0.000 | β_2 <ul style="list-style-type: none"> $b_2 = 1051.8$
95% CI: (588.6, 1515.0) $H_0: \beta_2 = 0$ $t_{\text{obs}}: (12) = 4.95$ p-value = 0.000
means p-value < 0.001 |
| β_1 <ul style="list-style-type: none"> $b_1 = -220.3$
95% CI: (-347.0, -93.6) $H_0: \beta_1 = 0$ $t_{\text{obs}}: (12) = -3.79$ p-value = 0.003 | |

6

Mortality Example

Parameter Estimates Interpretation

- b_0 : when smoke particles and SO_2 are at their average levels, (2 mg/m³, and 0.5 ppm respectively), the estimated mean number of deaths is 174.8 / day
- b_1 : the estimated mean mortality is 22 deaths/day lower on days when particles are 0.1 mg/m³ higher *if SO_2 is unchanged*
- b_2 : (*You do!*)

7

Mortality Example

Association between x and y

- The estimate for airborne smoke particles is $b_1 = -220$, implying that smoke particles and mortality have a *negative* relationship
 - i.e. an *increase* in smoke particles is associated with a *decrease* in mortality, after adjusting for SO_2 levels.

8

Mortality Example Negative Association??

- BUT WAIT!
- Look at the plot of *deaths vs smoke* presented previously. Shouldn't the relationship be *positive* instead?!
- Let's run Simple Linear Regressions (SLRs) of mortality on smoke & SO₂ and see what we get

9

SLR Models

- Y = the daily mortality for London (*deaths*)
- X_1 = airborne smoke particles (mg/m³) (*smoke*)
- X_2 = SO₂ (ppm) (*so2*)
- Smoke:
 - 1) $Y_i = \beta_0 + \beta_1(X_{1i} - 2) + \varepsilon_i$
 - 2) $\varepsilon_i \sim N(0, \sigma^2)$
- SO₂:
 - 1) $Y_i = \beta_0^* + \beta_1^*(X_{2i} - .5) + \varepsilon_i^*$
 - 2) $\varepsilon_i^* \sim N(0, \sigma^{2*})$

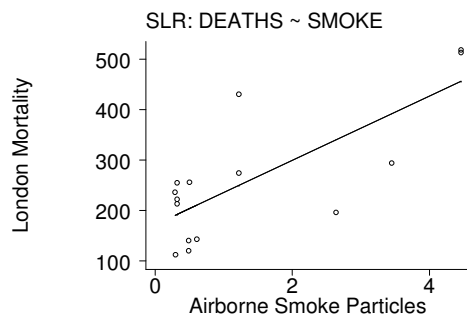
10

SLR: Deaths ~ Smoke

Parameter Estimates: $b_0 = 299.3$
 $b_1 = 63.8$ (*is positive?!!*)

Amount of variation described: $R^2 = SSM / SST = 57\%$

Residual Variability left over, (undescribed by this SLR):
 SSE = 1023002.216



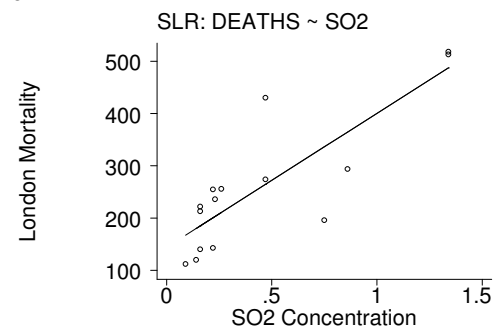
11

SLR: Death ~ SO₂

Parameter Estimates: $b_0 = 256.2$
 $b_1 = 272.2$

Amount of variation described: $R^2 = SSM / SST = 69\%$

Residual Variability left over, (undescribed by this SLR):
 SSE = 73924.6211



12

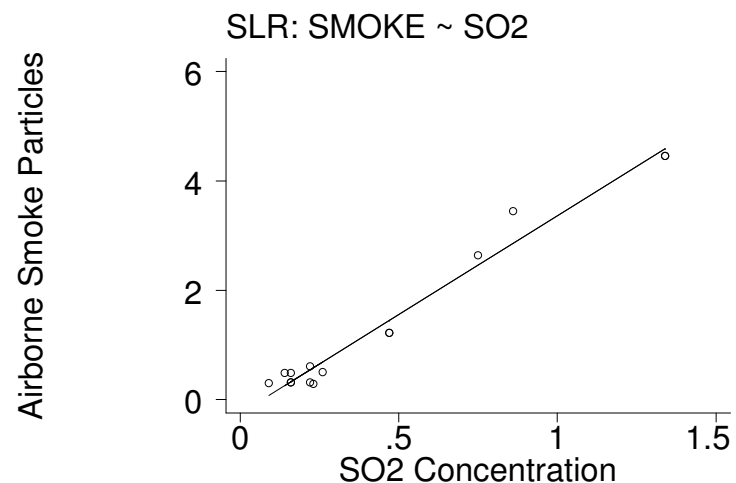
Confounding in this Example

Recall our parameter interpretations:

- β_1 = Expected change in mortality on days when particles are 0.1 mg/m³ higher *if SO₂ is unchanged*
- Suppose we examine the relationship between smoke particle concentrations and SO₂ levels, (SLR):

13

SLR: Smoke ~ SO₂



14

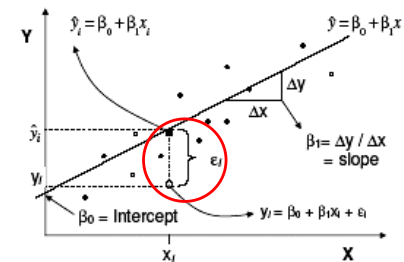
Confounding

- Smoke particle concentrations and SO₂ levels are highly related! How can we talk about *changing* smoke particle concentrations while *leaving SO₂ levels unchanged*??
- This is 'confounding'!
 - both covariates are related to the outcome and to each other
- Confounding is the reason we found differences between the SLR models and the MLR model
- We'll visualize this relationship using 'Added Variable Plots'

15

Recall Residuals: part "left over"

- Residuals are deviations (what's 'left over') in the response (Y) after removing what was expected given the predictor (X)
- The residuals are the part of Y that can't be predicted by X!



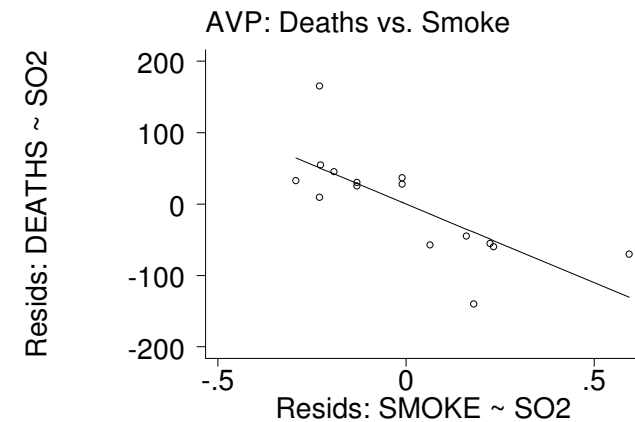
16

Adjusted Variable Plots Idea

- Explain all the signal we can in London daily mortality using SO_2 levels
- Explain all the signal we can in smoke particle concentrations using SO_2 levels
- Explain everything that's 'left over' in mortality with everything that's 'left over' in smoke particle concentrations. The slope of this line will be the MLR coefficient!

17

Mortality Example Adjusted Variable Plot



18

Recipe for AV plot

Recipe for obtaining the MLR slope for X_1 from an AV plot (adjusted for X_2):

1. Regress Y on X_2 , save residuals as: $R_{Y|X_2}$
2. Regress X_1 on X_2 , save residuals as: $R_{X_1|X_2}$
3. Plot $R_{Y|X_2}$ vs $R_{X_1|X_2}$ (Adjusted Variable Plot)

Regress $R_{Y|X_2}$ on $R_{X_1|X_2}$:

$$R_{Y|X_2} = \beta_0^* + \beta_1^* R_{X_1|X_2} + \varepsilon$$

19

Notes on AV Plots

- β_1^* is identical to the coefficient of X_1 from an MLR of Y on X_1 and X_2
- β_0^* (intercept) is always 0
- The AV Plot display may be misleading if Y and/or X_1 are not linearly related to the other predictors

20

AV Plot Recipe for Mortality Example

- Regress deaths on (centered) SO_2 , save residuals
 - Removes the effects of SO_2 on mortality
$$\text{Deaths} = 272 + 256 SO_{2c} + R_{Y|X2}$$
- Regress Smoke on SO_2 (both centered), save residuals
 - Removes the effects of SO_2 on smoke particles
$$\text{Smoke}_c = -.44 + 3.6 SO_{2c} + R_{X1|X2}$$
- Regress $R_{Y|X2}$ on $R_{X1|X2}$
 - regress deaths *adjusted for SO_2* on smoke particles *adjusted for SO_2*
- $R_{Y|X2} = 0.0 - 220 R_{X1|X2}$

21

AV plot interpretation

- Parameter from this last regression: $\beta_1^* = -220$ is the same as the related parameter from the MLR of deaths on smoke particles *and* SO_2
- $$\begin{aligned} E(\text{Deaths}) &= \beta_0 + \beta_1(\text{smoke}-2) + \beta_2(SO_2-.5) \\ &= 174.8 - 220(\text{smoke} - 2) + 1052(SO_2 - 0.5) \end{aligned}$$
- This helps in our interpretations of β_1 : the effect of airborne smoke particles on daily mortality after having removed (adjusted for) the effects of SO_2
 - This is what is usually meant by the term 'adjustment'

22

MLR and Scientific Inference

- The **single most important idea** today may be the realization that MLR can shift interpretations markedly!
- From SLR of the air pollution data:

$$E(\text{Deaths}) = 299 + 64(\text{smoke}-2)$$
 - Expected deaths **increase** by an estimated 64 per mg/m^3 increase in British smoke

23

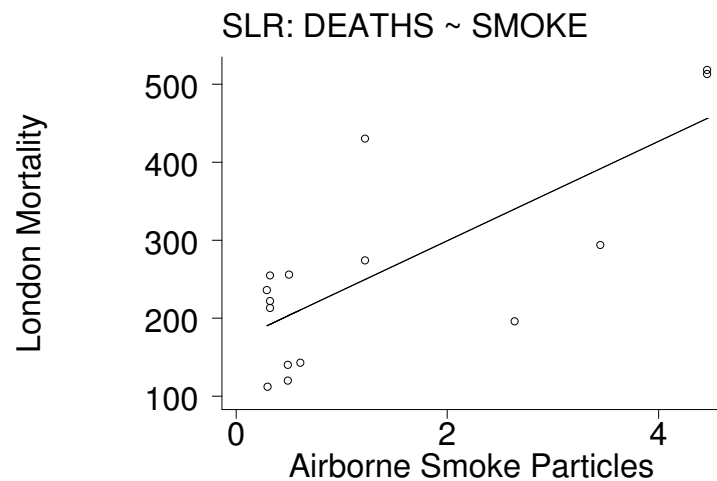
MLR and Scientific Inference

- From MLR of the air pollution data:

$$E(\text{Deaths}) = 174.8 - 220(\text{smoke}-2) + 1052(SO_2-.5)$$
 - Controlling for SO_2* , expected deaths **decrease** 220 per mg/m^3 of British smoke
- Interpretation and value of a regression coefficient depends critically on what other variables are in the model !!

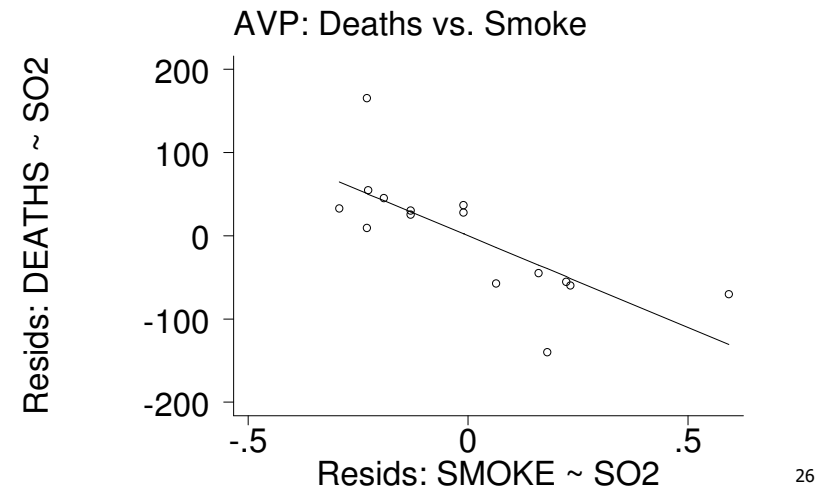
24

Simple Linear Regression



25

Multiple Linear Regression



26

Types of predictors in regression

- primary predictor
 - always in model
- other predictor(s)
 - can we improve prediction after adjusting for primary predictor?
 - interaction may be a component here
- potential confounder(s) (i.e., demographics)
 - only important if they change the effect of the primary predictor
 - commonly: age, gender, SES, race, etc...

27

Nested models

Definition: One model is nested within another if the **parent model** contains the 'original' set of variables and is *nested* within the **extended model** that contains the original set of variables plus additional variables

28

Nested models

Deciding whether to include variables

If the 'new variable(s)' are:

- another predictor(s)
 - assess with t-test in extended model if single variable
 - assess with F-test if two or more variables
- potential confounder(s)
 - compare CI of primary predictor in parent model to see whether new estimate of primary predictor coefficient is significantly different

29

Dataset

- Class health dataset
 - Outcome: number of credits
 - Primary predictor
 - housing (on or off campus)
 - Other predictors
 - health status (good/excellent or fair/poor)
 - year in school

30

Models

■ Parent Model (Model 1)

$$\hat{Y}_i = \hat{\beta}_0 + \hat{\beta}_1(\text{Housing}_i)$$

1 if on-campus
0 if off-campus

credits	Coef.	Std. Err.	t	P> t	[95% Conf. Interval]
housing	.1666667	.6761572	0.25	0.807	-1.228853 1.562187
(Intercept)	16.2	.5135783	31.54	0.000	15.14003 17.25997

■ Extended Model (Model 2)

$$\hat{Y}_i = \hat{\beta}_0 + \hat{\beta}_1(\text{Housing}_i) + \hat{\beta}_2(\text{Healthgood}_i)$$

1 if excellent/good
0 if fair/poor

credits	Coef.	Std. Err.	t	P> t	[95% Conf. Interval]
housing	.1541237	.6860262	0.22	0.824	-1.26503 1.573277
healthgood	.4139175	.7124214	0.58	0.567	-1.059838 1.887673
(Intercept)	15.9366	.6904955	23.08	0.000	14.5082 17.365

31

Comparing models 1 and 2

- Model 1 is nested in model 2
- Model 2 contains only one extra variable (healthgood), so use a t-test to decide whether to include healthgood
 - $p=0.567 > \alpha=0.05$ tests $H_0: \beta_2=0$
 - Fail to reject H_0
 - Conclude model 2 is no better than model 1

32

What if we add more than one variable?

- The t-test on each row only tests that variable *in the presence of everything else in the model*
- When more than one variable is added at a time, the t-test is not sufficient
 - The t-test only tests one variable at a time
 - Use the F-test instead to compare nested models that differ by more than one variable

33

When would more than one variable need to be added??

- Many modeling scenarios require adding more than one variable at once to go from the parent model to the extended model
- Commonly occurs when categorical variable needs to be added

34

Why do we need to specially code a categorical predictor?

- A categorical predictor (such as year in program) cannot be added as a single variable
 - If we add year (1, 2, 3, or 4) to the model in its original form, then software thinks it is a continuous predictor
 - As a continuous predictor, the difference in mean number of credits taken would be assumed to change by a constant amount for each additional year

35

Correct coding of a categorical predictor

- A categorical predictor should always be recoded as a set of dummy variables
 - Choose one category as the reference group
 - For each **other** category, create a dummy variable for membership in that category
 - You can have `R` do this automatically for you with the command `factor(mycatvar)` within your linear regression command

36

Example

- Year1 = reference group (no dummy variable for this group)
- Year2** = 1 for those in year 2, 0 else
- Year34** = 1 for those in yr 3/4, 0 else
 - very few observations, so categories were combined
- In in year 3: Year2=0, Year34=1
- For a first year: Year2=0, Year34=0

37

Model 3

$$\hat{Y}_i = \hat{\beta}_0 + \hat{\beta}_1(\text{Housing}_i) + \hat{\beta}_2(\text{Year2}_i) + \hat{\beta}_3(\text{Year34}_i)$$

credits	Coef.	Std. Err.	t	P> t	[95% Conf. Interval]
housing	-1.402299	.8537457	-1.64	0.115	-3.172859 .3682613
year2	.7068966	.7215468	0.98	0.338	-.7894999 2.203293
year34	-2.10197	1.087462	-1.93	0.066	-4.357228 .1532874
(Intercept)	17.34483	.9268436	18.71	0.000	15.42267 19.26698

- We cannot evaluate Year using the t-test for each row, because two variables are needed to define Year and the t tests are separate
- We must use an F-test to evaluate Year by comparing the residual sums of squares (RSS) in the parent model and in the nested model.

38

Comparing model RSS and Residual df

PARENT: MODEL 1

Source	SS	df	MS	
Model	.176282088	1	.176282088	Number of obs = 26
Residual	69.6333335	24	2.9013889	F(1, 24) = 0.06
Total	69.8096156	25	2.79238462	Prob > F = 0.8074

Adj R-squared = -0.0390
Root MSE = 1.7033

Annotations: RSS_{parent} points to .176282088; Residual df_{parent} points to 24.

EXTENDED: MODEL 3

Source	SS	df	MS	
Model	19.9853465	3	6.66178216	Number of obs = 26
Residual	49.8242691	22	2.26473951	F(3, 22) = 2.94
Total	69.8096156	25	2.79238462	Prob > F = 0.0555

Adj R-squared = 0.1890
Root MSE = 1.5049

Annotations: RSS_{extended} points to 19.9853465; Residual df_{extended} points to 22.

39

The F-test for nested models

H_0 : all new β 's=0 in population

H_A : at least one new β is not 0 in population

Numerator of F-statistic:

$$(RSS_{\text{parent}} - RSS_{\text{extended}})/(\text{number variables added})$$

Denominator of F-statistic:

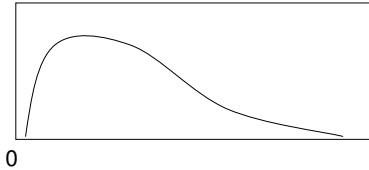
$$RSS_{\text{extended}}/(\text{residual df}_{\text{extended}})$$

$$F_{\text{obs}} = \frac{(69.6 - 49.8) / 3}{49.8 / 22} = 4.4$$

40

The F table

- Recall: the F distribution is very similar to the χ^2 distribution



- F distribution is automatically 2-sided (like χ^2)
- df change the shape of the F distribution (like χ^2), but now there are two sets of df: the numerator df and the denominator df

41

The F table

- numerator df: # of variables added = 2
- denominator df: residual $df_{\text{extended}} = 22$
- Using $\alpha=0.05$, find F_{cr}
 - Find quantile in R, using appropriate degrees of freedom

```
> qf(.05, 2, 22, lower.tail=F)
[1] 3.443357
```
- $F_{\text{cr}}=3.44 < F_{\text{obs}}=4.4$
- So, our p-value $< \alpha$

42

Conclusion using the F-test

- Reject H_0 :
conclude that adding year improves prediction after adjusting for housing
 - Notice:
both individual t tests were not statistically significant, but F test was still significant
 - Must always use F test to evaluate multiple X's at once

43

The F test: notes

- The F test *can* be used to compare any two nested models
- If only one variable is added, it's easier to compare the models using the t test for that variable
 - $t^2=F$ if one variable is added

44

The F test: how to in R

- Fit parent model
`fit.parent <- lm(y ~ x1 + x2)`
- Fit the extended model (parent model is nested within the extended model)
`fit.extend <- lm(y ~ x1 + x2 + x3 + x4)`
- Perform the F-test
`print(anova(fit.parent, fit.extend))`

Example output:

Analysis of Variance Table

Model 1: y ~ x1 + x2

Model 2: y ~ x1 + x2 + x3 + x4

	Res.Df	RSS	Df	Sum of Sq	F	Pr(>F)
1	650	110.65				
2	648	109.51	2	1.14	3.3718	0.03493 *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

45

Nested Models

- Comparing nested models
 - 1 new variable: use t test for that variable
 - 2+ new variables: use F test
- Categorical predictor
 - set one group as reference
 - create dummy variable for other groups
 - include/exclude all dummy variables
 - evaluate categorical predictor with F test

46

Lecture 11 Summary

- Hypothesis tests in linear regression
 - Overall F-test
 - Individual coefficient 95% CI and t-tests
- F-tests for nested models
- AV plots
 - visualizing the relationship between the outcome and a continuous predictor after adjusting for the effects of a third variable

47