Multiple Linear Regression: Categorical Predictors

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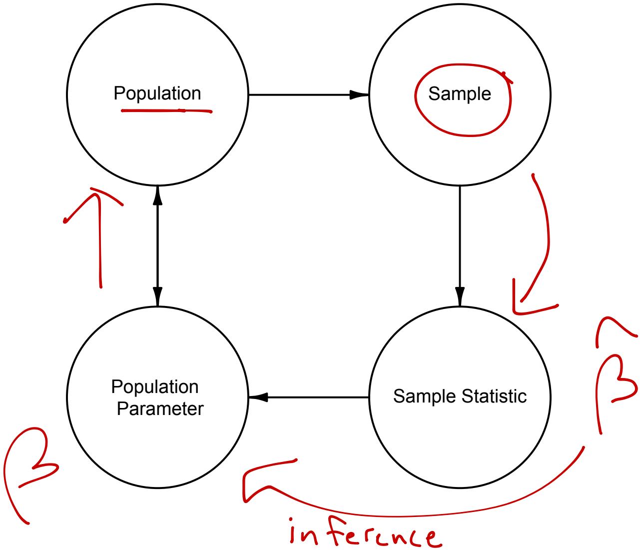
This material is part of the ***statsTeachR*** *project*

Today's Lecture

- Sampling distribution of $\hat{\boldsymbol{\beta}}$
- Confidence intervals
- Hypothesis tests for individual coefficients
- Global tests

Circle of Life



Statistical inference

- We have LSEs $\hat{\beta}_0, \hat{\beta}_1, \ldots$; we want to know what this tells us about $\beta_0, \beta_1, \ldots$.
- Two basic tools are confidence intervals and hypothesis tests
  - Confidence intervals provide a plausible range of values for the parameter of interest based on the observed data
  - Hypothesis tests ask how probable are the data we gathered under a null hypothesis about the data generating distribution

$$Y_i \sim \underset{\substack{\| \\ 0}}{\beta_0} + \underset{\substack{\| \\ 0}}{\beta_1} X_i + \underset{\underline{\sigma^2}}{\varepsilon_i}$$

Motivation

How can we draw **inference** about each of these parameters and relationships that our model is encoding?

```
mlr1 <- lm(disease ~ airqual + crowding + nutrition + smoking, d
summary(mlr1)$coef

##              Estimate Std. Error t value  Pr(>|t|)
## (Intercept) 11.86333   2.578819   4.600 1.316e-05
## airqual      0.25788   0.026799   9.623 1.165e-15
## crowding     1.11113   0.102037  10.889 2.404e-18
## nutrition   -0.03278   0.007954  -4.122 8.095e-05
## smoking      4.96093   1.085292   4.571 1.475e-05
```

t-stats

p-vals

Motivation

- Can we say anything about whether the effect of `airquality` is "significant" after adjusting for other variables?
- Can we say whether adding `airquality` improves the fit of our model?
- Can we compare this model to a model with ~~only~~ `crowding`, `nutrition` and `smoking`?

Sampling distribution

If our usual assumptions are satisfied and $\epsilon \overset{iid}{\sim} \mathrm{N}\left[0, \sigma^2\right]$ then

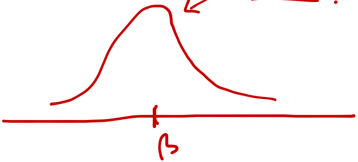
$$\hat{\boldsymbol{\beta}} \sim \mathrm{N}\left[\boldsymbol{\beta}, \sigma^2(\mathbf{X}^T\mathbf{X})^{-1}\right].$$ - MVNormal

$$\hat{\beta}_j \sim \mathrm{N}\left[\boldsymbol{\beta}, \sigma^2\underline{(\mathbf{X}^T\mathbf{X})^{-1}_{jj}}\right].$$

jjth entry of cov matrix

- This will be used later for inference.
- Even without Normal errors, asymptotic Normality of LSEs is possible under reasonable assumptions.

Normal!



Sampling distribution

For real data we have to estimate σ^2 as well as $\boldsymbol{\beta}$.

- Recall our estimate of the error variance is

$$\hat{\sigma^2} = \frac{RSS}{n-p-1} = \frac{\sum_i (y_i - \hat{y}_i)^2}{n-p-1}$$

- With Normally distributed errors, it can be shown that

$$(n-p-1)\frac{\hat{\sigma^2}}{\sigma^2} \sim \chi^2_{n-p-1}$$

Testing procedure

Calculate the probability of the observed data (or more extreme data) under a null hypothesis.

- Often $H_0 : \beta_1 = 0$ and $H_a : \beta_1 \neq 0$
- Set type I error rate
  $\alpha = P$(falsely rejecting a true null hypothesis) $= .05$
- Calculate a test statistic assuming the null hypothesis is true
- Compute a p-value =

$$P(\text{As or more extreme test statistic} | H_0)$$

- Reject or fail to reject H_0

Individual coefficients

For individual coefficients

- We can use the test statistic

in R

$$T = \boxed{\frac{\hat{\beta}_j - \beta_j}{\widehat{se}(\hat{\beta}_j)} = \frac{\hat{\beta}_j - \beta_j}{\sqrt{\hat{\sigma}^2(\mathbf{X}^T\mathbf{X})^{-1}_{jj}}}} \sim t_{n-p-1}$$

- For a two-sided test of size α, we reject if

$$|T| > t_{1-\alpha/2,n-p-1}$$

in R

- The p-value gives $\boxed{P(t_{n-p-1} > T_{obs}|H_0)}$

Note that t is a symmetric distribution that converges to a Normal as $n-p-1$ increses.

Back to the example

$\hat{\beta}_{std} = \frac{\hat{\beta}}{sd(x)}$

```
summary(mlr1)

##
## Call:
## lm(formula = disease ~ airqual + crowding + nutrition + smoking,
##     data = dat)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -8.130 -2.183 -0.572  1.941 13.326
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 11.86333    2.57882    4.60  1.3e-05 ***
## airqual      0.25788    0.02680    9.62  1.2e-15 ***
## crowding     1.11113    0.10204   10.89  < 2e-16 ***
## nutrition   -0.03278    0.00795   -4.12  8.1e-05 ***
## smoking      4.96093    1.08529    4.57  1.5e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.64 on 94 degrees of freedom
## Multiple R-squared:  0.866, Adjusted R-squared:  0.861
## F-statistic:  152 on 4 and 94 DF,  p-value: <2e-16
```

$1.2e^{-15} = 1.2 \times 10^{-15}$

Individual coefficients: CIs

Alternatively, we can construct a confidence interval for β_j

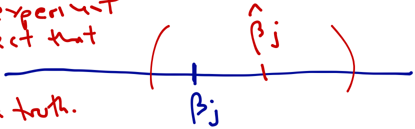
- A confidence interval with coverage $(1-\alpha)$ is given by

$$\hat{\beta}_j \pm \overbrace{t_{1-\alpha/2,n-p-1}}^{\sim 2}\widehat{se}(\hat{\beta}_j)$$

- Assuming all the standard assumptions hold,

$$(1-\alpha) = P(LB < \beta_j < UB)$$

$1-\alpha\%$ Our CI for $\hat{\beta}_j$ is (LB, UB), if we repeated this experiment we would expect that 95% of our CIs would cover the truth.



Back to the example

$\frac{\alpha}{2}, 1 - \alpha/2$

```
cbind(coef(mlr1), confint(mlr1))

##                           2.5 %   97.5 %
## (Intercept) 11.86333  6.74303 16.98364
## airqual      0.25788  0.20467  0.31109
## crowding     1.11113  0.90853  1.31372
## nutrition   -0.03278 -0.04858 -0.01699
## smoking      4.96093  2.80606  7.11580
```

Inference for linear combinations

Sometimes we are interested in making claims about $c^T\boldsymbol{\beta}$ for some c.

C^T 3×1

$[1\ 1\ 0] \begin{bmatrix} \beta_0 \\ \beta_1 \\ \beta_2 \end{bmatrix}$

- Define $H_0 : c^T\boldsymbol{\beta} = c^T\boldsymbol{\beta}_0$ or $H_0 : c^T\boldsymbol{\beta} = 0$
- We can use the test statistic

$$T = \frac{c^T\hat{\boldsymbol{\beta}} - c^T\boldsymbol{\beta}}{\widehat{se}(c^T\hat{\boldsymbol{\beta}})} = \frac{c^T\hat{\boldsymbol{\beta}} - c^T\boldsymbol{\beta}}{\sqrt{\hat{\sigma}^2 c^T(\mathbf{X}^T\mathbf{X})^{-1}c}}$$

$H_0: \beta_0 + \beta_1 = 0$

- This test statistic is asymptotically Normally distributed
- For a two-sided test of size α, we reject if

$$|T| > z_{1-\alpha/2}$$

Inference about multiple coefficients

Our model contains multiple parameters; often we want to perform multiple tests:

$$\begin{aligned} H_{01}: \beta_1 &= 0 \\ H_{02}: \beta_2 &= 0 \\ \vdots &= \vdots \\ H_{0k}: \beta_k &= 0 \end{aligned}$$

where each test has a size of α

- For any individual test, $P(\text{reject } H_{0i} | H_{0i}) = \alpha$

Inference about multiple coefficients

What about

$$P(\text{reject at least one } H_{0i} | \text{all } H_{0i} \text{are true}) \cancel{= \alpha}$$

$$Pr(\text{reject 1 test} \mid H_0 \text{ true}) = \alpha$$

Family-wise error rate

FWER

Family-wise error rate

perform
k tests

To calculate the FWER

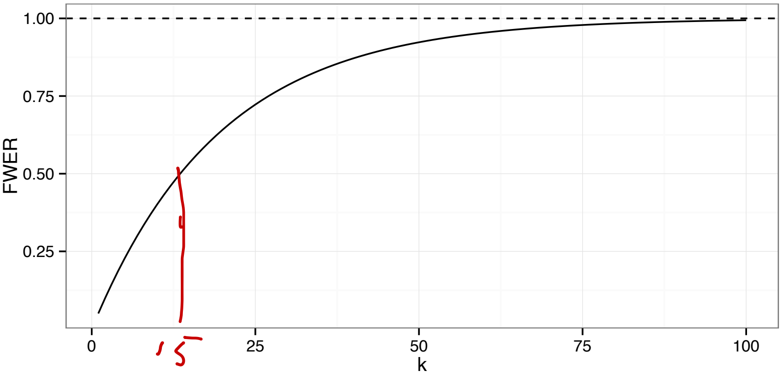
- First note $P(\text{no rejections}|\text{all } H_{0i} \text{are true}) = (1-\alpha)^k$
- It follows that

$$\begin{aligned} \text{FWER} &= P(\text{at least one rejection}|\text{all } H_{0i} \text{are true}) \\ &= 1-(1-\alpha)^k \end{aligned}$$

Family-wise error rate

$$\text{FWER} = 1 - (1 - \alpha)^k$$

```r
alpha <- 0.05
k <- 1:100
FWER <- 1 - (1 - alpha)^k
qplot(k, FWER, geom = "line") + geom_hline(yintercept = 1, lty = 2)
```



Addressing multiple comparisons

Three general approaches

- Do nothing in a reasonable way
  - Don't trust scientifically implausible results
  - Don't over-emphasize ~~isolated~~ findings
- Correct for multiple comparisons
  - Often, use the Bonferroni correction and use $\alpha_i = \alpha/k$ for each test
  - Thanks to the Bonferroni inequality, this gives an overall $FWER \leq \alpha$

very conservative

- Use a global test

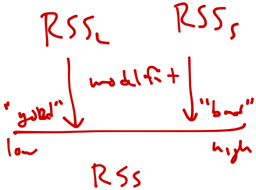
Global tests

Compare a smaller "null" model to a larger "alternative" model

- Smaller model must be nested in the larger model
- That is, the smaller model must be a special case of the larger model
- For both models, the *RSS* gives a general idea about how well the model is fitting
- In particular, something like

$$\frac{RSS_S - RSS_L}{RSS_L}$$

compares the relative *RSS* of the models



Nested models

- These models are nested:

$$\beta_2 = \beta_3 = \beta_4 = 0$$

$$\begin{aligned} \text{Smaller} &= \text{Regression of } Y \text{ on } X_1 \\ \text{Larger} &= \text{Regression of } Y \text{ on } \underline{X_1, X_2, X_3, X_4} \end{aligned}$$

- These models are not:

$$\begin{aligned} \text{Smaller} &= \text{Regression of } Y \text{ on } X_2 \\ \text{Larger} &= \text{Regression of } Y \text{ on } X_1, X_3 \end{aligned}$$

Global F tests

- Compute the test statistic

$$F_{obs} = \frac{(RSS_S - RSS_L)/(df_S - df_L)}{RSS_L/df_L}$$

- If H_0 (the null model) is true, then $F_{obs} \sim F_{df_S - df_L, df_L}$
- Note $df_s = n - p_S - 1$ and $df_L = n - p_L - 1$
- We reject the null hypothesis if the p-value is above α, where

$$\text{p-value} = P(F_{df_S - df_L, df_L} > F_{obs})$$

Global F tests

There are a couple of important special cases for the F test

- The null model contains the intercept only
  - When people say ANOVA, this is often what they mean (although all F tests are based on an analysis of variance)
- The null model and the alternative model differ only by one term
  - Gives a way of testing for a single coefficient
  - Turns out to be equivalent to a two-sided t-test: $t^2_{df_L} \sim F_{1,df_L}$

Lung data: multiple coefficients simultaneously

You can test multiple coefficients simultaneously using the F test

```
mlr_null <- lm(disease ~ nutrition, data = dat)
mlr1 <- lm(disease ~ nutrition + airqual + crowding + smoking, data = dat)
anova(mlr_null, mlr1)
        S       L

## Analysis of Variance Table
##
## Model 1: disease ~ nutrition
## Model 2: disease ~ nutrition + airqual + crowding + smoking
##   Res.Df  RSS Df Sum of Sq   F Pr(>F)
## 1     97 9193
## 2     94 1248  3      7945 199 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Lung data: single coefficient test

The F test is equivalent to the t test when there's only one parameter of interest

```
mlr_null <- lm(disease ~ nutrition, data = dat)
mlr1 <- lm(disease ~ nutrition + airqual, data = dat)
anova(mlr_null, mlr1)

## Analysis of Variance Table
##
## Model 1: disease ~ nutrition
## Model 2: disease ~ nutrition + airqual
##   Res.Df  RSS Df Sum of Sq    F  Pr(>F)
## 1     97 9193
## 2     96 5970  1      3223 51.8 1.3e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

summary(mlr1)$coef

##             Estimate Std. Error t value  Pr(>|t|)
## (Intercept)  37.6254    2.43946   15.42 9.946e-28
## nutrition    -0.0347    0.01692   -2.05 4.307e-02
## airqual       0.3611    0.05016    7.20 1.347e-10
```

Today's Big Ideas

- Inference for multiple linear regression models