

The Application of California School

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1 Introduction

This tutorial is to show how to estimate a multiple regression model and perform linear hypothesis testing. The application is about the test scores of the California school districts. We will use R to replicate the multiple regression with this data set in Chapter 6, and the hypothesis tests in Chapter 7.

Before running all R codes, we may first load all the packages.

```
library(AER)
library(foreign)
library(stargazer)
```

2 Reading the data and basic summary statistics

Let's first read the data into R and show some basic statistics.

Read the STATA file

Since the data is stored as an STATA file with the extension ".dta", we read the data using `read.dta()` in the library of `foreign`.

```
setwd("/Users/ztian/OneDrive/teaching/workshop/intro_org_RR/example")
classdata <- read.dta("./data/caschool.dta")
```

Summary

Upon reading the data, we often use `summary()` to see some basic statistics. Here we are not going to show summary statistics of all variables in the data set for the purpose of saving space, but only to select several variables of interest in Chapters 6 and 7, including test scores, `testscr`, student-teacher ratio, `str`, percentage of English learners, `el_pct`, expenditure per pupil, `expn_stu`, and percentage of students qualifying for free lunch, `meal_pct`.

```
summary(classdata[c("testscr", "str", "el_pct", "expn_stu", "meal_pct")])
```

testscr	str	el_pct	expn_stu	meal_pct
Min. :605.5	Min. :14.00	Min. : 0.000	Min. :3926	Min. : 0.00
1st Qu.:640.0	1st Qu.:18.58	1st Qu.: 1.941	1st Qu.:4906	1st Qu.: 23.28
Median :654.5	Median :19.72	Median : 8.778	Median :5215	Median : 41.75
Mean :654.2	Mean :19.64	Mean :15.768	Mean :5312	Mean : 44.71
3rd Qu.:666.7	3rd Qu.:20.87	3rd Qu.:22.970	3rd Qu.:5601	3rd Qu.: 66.86
Max. :706.8	Max. :25.80	Max. :85.540	Max. :7712	Max. :100.00

3 Plots

Create a matrix of scatterplots using plot

We can create several scatterplots displayed in one graph with a matrix form.

```
oldpar <- par(mfrow = c(2, 3))

plot(classdata$str, classdata$testscr, col = "red",
      main = "Student-teacher ratio vs test scores",
      xlab = "Student-teacher ratio", ylab = "Test scores")

plot(classdata$el_pct, classdata$testscr, col = "blue",
      main = "English learners vs test scores",
      xlab = "Percentage of English learners",
      ylab = "Test scores")

plot(classdata$expn_stu, classdata$testscr, col = "green3",
      main = "Expenditure per pupil vs test scores",
      xlab = "Expenditure per pupil",
      ylab = "Test scores")

plot(classdata$meal_pct, classdata$testscr, col = "maroon",
      main = "Free lunch vs test scores",
      xlab = "Percentage of students with free lunch",
      ylab = "Test scores")

plot(classdata$calw_pct, classdata$testscr, col = "darkorange1",
      main = "Public assistance vs test scores",
      xlab = "Percentage of students in public assistance",
      ylab = "Test scores")
```

```
par(oldpar)
```

We can see that the codes above have some parts that are repeated in each plotting command. So these repetitive work can be concisely written in **for** a loop. The basic syntax of a **for** loop is **for (var in seq) expr**.

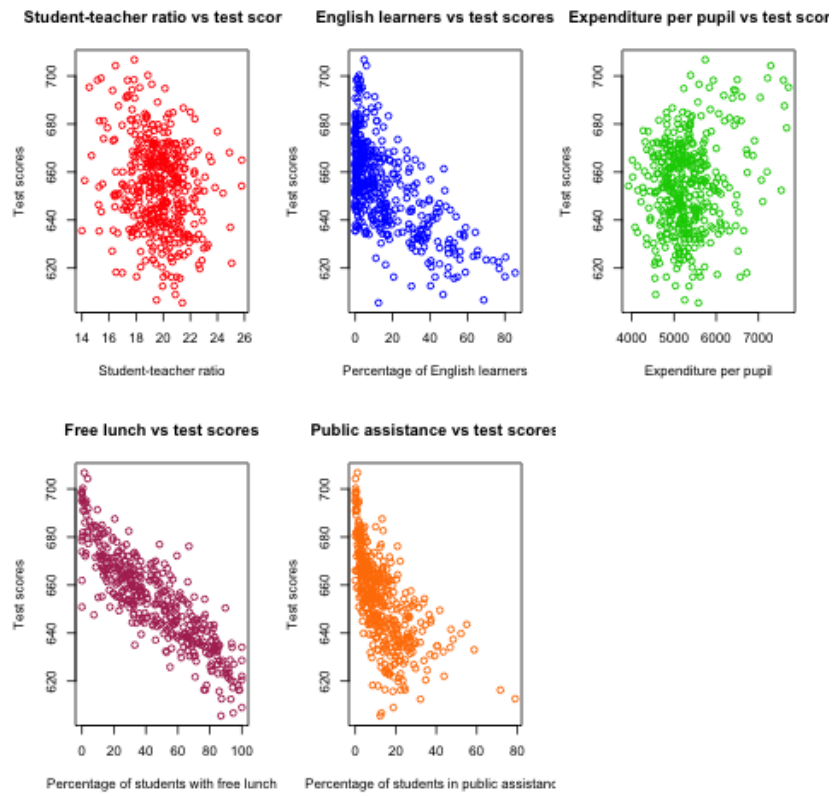


Figure 1: The scatterplots between several variables and test scores

```

xvars <- c("str", "el_pct", "expn_stu", "meal_pct", "calw_pct")
yvars <- c("testscr")

xlabels <- c("Student-teacher ratio", "Percentage of English learners",
             "Expenditure per pupil", "Percentage of students with free lunch",
             "Percentage of students in the public assistant program")
ylabels <- "Test scores"

titles <- c("student-teacher ratio vs test scores",
            "English learners vs test scores",
            "Expenditure per pupil vs test scores",
            "Free lunch vs test scores vs test scores",
            "public assistance vs test scores")
colors <- c("red", "green3", "blue", "maroon", "darkorange1")

op <- par(mfrow = c(2, 3))
for (i in seq(along=xvars)) {
  fm <- formula(paste(yvars, "~", xvars[i]))
  plot(fm, data = classdata, col = colors[i], main = titles[i],
       xlab = xlabels[i], ylab = ylabels)
}
par(op)

```

4 Estimation

Let us first replicate the regression results in Equation (7.19). The unit of the expenditure per pupil is dollars in the data set but it is in thousand dollars in regression. So we need to convert the unit in the data set by dividing `expn_stu` by 1000, which is done directly in the formula.

The OLS estimation

```
model.76 <- testscr ~ str + I(expn_stu / 1000) + el_pct
```

Notice the function `I()` in the formula. The arithmetic operations, `+`, `*`, `:`, `/`, and `^`, have special meanings in R's formula. Using the function `I()` protects the original arithmetic meanings of these operations from being interpreted in terms of a formula.

The regression estimation can be done with `lm()` and use `summary()` afterwards.

```
res.model.76 <- lm(model.76, data = classdata)
summary(res.model.76)
```

Call:

```
lm(formula = model.76, data = classdata)
```

Residuals:

	Min	1Q	Median	3Q	Max
	-51.340	-10.111	0.293	10.318	43.181

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	649.57795	15.20572	42.719	< 2e-16 ***
str	-0.28640	0.48052	-0.596	0.55149
I(expn_stu/1000)	3.86790	1.41212	2.739	0.00643 **
el_pct	-0.65602	0.03911	-16.776	< 2e-16 ***

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

Residual standard error: 14.35 on 416 degrees of freedom

Multiple R-squared: 0.4366, Adjusted R-squared: 0.4325

F-statistic: 107.5 on 3 and 416 DF, p-value: < 2.2e-16

We can extract some components in the reported results. Use `coef()` to get the coefficient estimates, `resid()` to get the residuals, and `fitted()` or `predict()` to get the fitted values. Alternatively, we can think the `lm` and `summary.lm` objects returned by `lm()` and `summary()` are the `list` object so that we can use the `"$"` operator to get each component of the lists. Below are some examples of extracting regression results.

```
# get some components of the results
bhat <- coef(res.model.76)
rsq <- summary(res.model.76)$r.squared
adj.rsq <- summary(res.model.76)$adj.r.squared
```

- Interpretation of the results

As for the coefficients

1. The intercept is 649.5779, which is significant at 1% significance level. It does not have real meaning in this application, just determining the position of the sample regression line crossing the vertical axis.
2. The coefficient on `str` is -0.2864, implying that increasing one more student per teacher would decrease test scores by 0.2864 unit. However, this estimated coefficient is not significant at the 10% level.
3. The coefficient on expenditure per pupil is 3.8679, significantly positive at the 5% level, implying that an increase in expenditure per pupil by one thousand dollars lead to an increase in test scores by 3.8679 unit.
4. The coefficient on the percentage of English learners is -0.656, significantly negative at the 1% level, implying that an increase in the percentage of English learners by one percent results in a decrease of test scores by 0.656.

Besides, the R^2 and \bar{R}^2 are 0.4366 and 0.4325, respectively. Overall, the model explains about 43% variation of test scores with the included explanatory variables, which is modest in the sense that a little more than half of the variation of test scores is not accounted for in the model.

The heteroskedasticity-consistent covariance matrix

Note that standard errors and t statistics reported by `summary()` are the homoskedasticity-only s.e. and t's. The heteroskedasticity-robust covariance matrix can be obtained by `vcovHC()` in the package of `sandwich`.

```
htvarm <- vcovHC(res.model.76, type = "HC1")
```

```
      238.960380157595    -6.66491920338914    -20.7034584893236     0.0818068203778049
    -6.66491920338933     0.232394197515306     0.40034628247013    -0.00244872476838095
    -20.7034584893232     0.400346282470112     2.49868335516912    -0.0102366018665727
    0.0818068203778026    -0.00244872476838084    -0.0102366018665727     0.00101024993508859
```

5 Hypothesis tests

Testing a single coefficient

Running `summary(res.model.76)` can give you t-statistics for all coefficients. However, as noted above, these t-statistics are the homoskedasticity-only t-statistics. We should use the heteroskedasticity-robust ones.

```
# homoskedasticity-only
```

```
coeftest(res.model.76)
```

```
# heteroskedasticity-robust, t distribution
```

```
cfptest.t <- coeftest(res.model.76, vcov = htvarm)
```

```
cfptest.t
```

```
# heteroskedasticity-robust, normal distribution
```

```
cfptest.n <- coeftest(res.model.76, vcov = htvarm, df = Inf)
```

```
cfptest.n
```

```
t test of coefficients:
```

```

              Estimate Std. Error  t value  Pr(>|t|)
(Intercept)  649.577947  15.205719  42.7193 < 2.2e-16 ***
str          -0.286399   0.480523  -0.5960  0.551489
I(expn_stu/1000)  3.867902  1.412122   2.7391  0.006426 **
el_pct       -0.656023   0.039106 -16.7755 < 2.2e-16 ***
---
```

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

t test of coefficients:

	Estimate	Std. Error	t value	Pr(> t)	
(Intercept)	649.577947	15.458343	42.0212	< 2e-16	***
str	-0.286399	0.482073	-0.5941	0.55277	
I(expn_stu/1000)	3.867902	1.580722	2.4469	0.01482	*
el_pct	-0.656023	0.031784	-20.6397	< 2e-16	***

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

z test of coefficients:

	Estimate	Std. Error	z value	Pr(> z)	
(Intercept)	649.577947	15.458343	42.0212	< 2e-16	***
str	-0.286399	0.482073	-0.5941	0.55245	
I(expn_stu/1000)	3.867902	1.580722	2.4469	0.01441	*
el_pct	-0.656023	0.031784	-20.6397	< 2e-16	***

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

We can see from the results above that

1. whether we use the homoskedasticity-only or heteroskedasticity-robust variance matrices does not affect the coefficient estimates because the calculation of these estimates does not involve the variance matrices.
2. Using the homoskedasticity-only or heteroskedasticity-robust variance matrices yields different standard errors and t-statistics. Even though the homoskedasticity-only standard errors of student-teacher ratios seems smaller than the heteroskedasticity-robust ones, we cannot say that the estimates with the homoskedasticity-only standard errors are more efficient or precise because we are using a wrong variance matrix in this case.
3. The p-values from t distribution and standard normal distribution are slightly different, given the corresponding t-statistics are identical in the two cases.

Testing joint hypotheses

- Zero restrictions Let's first test the joint zero restrictions.

$$H_0 : \beta_1 = 0, \beta_2 = 0 \text{ vs. } H_1 : \beta_1 \neq 0 \text{ or } \beta_2 \neq 0$$

We can use the function `linearHypothesis()` to test this and any linear hypotheses.

```
test1 <- linearHypothesis(res.model.76,
  c("str = 0", "I(expn_stu/1000) = 0"),
```

```

      vcov = htvvarm, test = "F")
test1
test1.F <- test1$F[2]
test1.p <- test1$"Pr(>F)"[2]

Linear hypothesis test

Hypothesis:
str = 0
I(expn_stu/1000) = 0

Model 1: restricted model
Model 2: testscr ~ str + I(expn_stu/1000) + el_pct

```

Note: Coefficient covariance matrix supplied.

```

      Res.Df Df      F    Pr(>F)
1        418
2        416  2 5.4337 0.004682 **
---

```

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

The F-statistic is 5.4337 with the p-value as 0.0047, which is less than 1%. Therefore, we can reject the null hypothesis at the 1% level.

Note that the F-statistic is computed with the heteroskedasticity-robust variance matrix and tested against a F distribution of (2, 416) degree of freedom.

- linear restrictions Let's test the following restriction,

$$H_0 : \beta_1 + \beta_2 = 0, H_1 : \beta_1 + \beta_2 \neq 0$$

We still use `linearHypothesis()`. But this time we use the argument `white.adjust` for which we specify "hc1" and test against a Chi-squared distribution with one degree of freedom. Therefore, what we get is a Wald statistic.

```

# b1 + b2 = 0
test2 <- linearHypothesis(res.model.76,
  c("str + I(expn_stu/1000) = 0"),
  white.adjust = "hc1", test = "Chisq")
test2
test2.x <- test2$Chisq[2]
test2.p <- test2$"Pr(>Chisq)"[2]

```

Linear hypothesis test

```

Hypothesis:
str + I(expn_stu/1000) = 0

```



```
Model 1: restricted model
Model 2: testscr ~ str + I(expn_stu/1000) + el_pct
```

Note: Coefficient covariance matrix supplied.

```
      Res.Df Df    Chisq Pr(>Chisq)
1         417
2         416   1 3.6319    0.05668 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The Wald statistic is 3.6319 and the p-value is 0.0567, which is less than 10% and greater than 5%. That means that the null hypothesis can be rejected at the 10% level but not at the 5% level. This result implies that the effects of hiring more teachers on test scores could be to some extent similar to increasing more expenditure per pupil.

The homoskedasticity-only F statistic can be computed without specifying `vcov` or `white.adjust`.

```
# homoskedasticity-only F
test2.hm <- linearHypothesis(res.model.76,
  c("str + I(expn_stu/1000) = 0"),
  test = "F")
test2.hm
```

Linear hypothesis test

```
Hypothesis:
str + I(expn_stu/1000) = 0
```

```
Model 1: restricted model
Model 2: testscr ~ str + I(expn_stu/1000) + el_pct
```

```
      Res.Df  RSS Df Sum of Sq      F Pr(>F)
1         417 86562
2         416 85700   1    862.09 4.1847 0.04142 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The homoskedasticity-only F test points to rejecting the null hypothesis at both 5% and 10% levels.

6 Control variables and model specifications

In this section we estimate different models for the application of test scores. The variable of interest is student-teacher ratios, *STR*. In the base specification, we include the percentage

of students who are English learners, *PctEL*, and the percentage of students who are eligible for free or subsidized lunch, *LchPct*, as control variables. An alternative control variable is the percentage of students who receive public assistance.

```
model1 <- lm(testscr ~ str, data = classdata)
model2 <- lm(testscr ~ str + el_pct, data = classdata)
model3 <- lm(testscr ~ str + el_pct + meal_pct, data = classdata)
model4 <- lm(testscr ~ str + el_pct + calw_pct, data = classdata)
model5 <- lm(testscr ~ str + el_pct + meal_pct + calw_pct, data = classdata)
```

We compute the heteroskedasticity-robust standard errors for the coefficients in all model specifications. The function `vcovHC` is used to get the heteroskedasticity-consistent covariance matrix (HCCM), in which we set the argument `type` to be `HC1`. The heteroskedasticity-robust standard errors of coefficients are the square roots of the diagonal elements of these HCCMs.

```
hccm1 <- vcovHC(model1, type = "HC1")
se1 <- sqrt(diag(hccm1))
```

```
hccm2 <- vcovHC(model2, type = "HC1")
se2 <- sqrt(diag(hccm2))
```

```
hccm3 <- vcovHC(model3, type = "HC1")
se3 <- sqrt(diag(hccm3))
```

```
hccm4 <- vcovHC(model4, type = "HC1")
se4 <- sqrt(diag(hccm4))
```

```
hccm5 <- vcovHC(model5, type = "HC1")
se5 <- sqrt(diag(hccm5))
```

Finally, the results for all models are displayed in Table (1) that replicates Table 7.1 in Chapter 7. To create a \LaTeX table, we use the function `stargazer`.

```
stargazer(model1, model2, model3, model4, model5,
  title = "Results of regressions of test scores and class size",
  covariate.labels = c("student-teacher ratio",
    "percent English learners",
    "percent eligible for subsidized lunch",
    "percent on public assistance"),
  dep.var.caption = "average test scores in the district",
  se = list(se1, se2, se3, se4, se5), df = FALSE,
  font.size = "small",
  header = FALSE,
  label = "table:tbl71")
```

Table 1: Results of regressions of test scores and class size

	average test scores in the district				
	testscr				
	(1)	(2)	(3)	(4)	(5)
student-teacher ratio	-2.280*** (0.519)	-1.101** (0.433)	-0.998*** (0.270)	-1.308*** (0.339)	-1.014*** (0.269)
percent English learners		-0.650*** (0.031)	-0.122*** (0.033)	-0.488*** (0.030)	-0.130*** (0.036)
percent eligible for subsidized lunch			-0.547*** (0.024)		-0.529*** (0.038)
percent on public assistance				-0.790*** (0.068)	-0.048 (0.059)
Constant	698.933*** (10.364)	686.032*** (8.728)	700.150*** (5.568)	697.999*** (6.920)	700.392*** (5.537)
Observations	420	420	420	420	420
R ²	0.051	0.426	0.775	0.629	0.775
Adjusted R ²	0.049	0.424	0.773	0.626	0.773
Residual Std. Error	18.581	14.464	9.080	11.654	9.084
F Statistic	22.575***	155.014***	476.306***	234.638***	357.054***

Note:

*p<0.1; **p<0.05; ***p<0.01

7 Appendix: R codes

```
library(AER)

# read the data files into R
# read the dta file
library(foreign)
classdata <- read.dta("caschool.dta")
head(classdata)
str(classdata)

summary(classdata[, c("testscr", "str", "el_pct", "expn_stu", "meal_pct")])

model.76 <- testscr ~ str + I(expn_stu / 1000) + el_pct
res.model.76 <- lm(model.76, data = classdata)
summary(res.model.76)

# scatterplot
oldpar <- par(mfrow = c(2, 2))

plot(classdata$str, classdata$testscr, col = "red",
      main = "student-teacher ratio vs test scores",
      xlab = "Student-teacher ratio", ylab = "Test scores")

plot(classdata$el_pct, classdata$testscr, col = "blue",
      main = "English learners vs test scores",
      xlab = "Percentage of English learners",
      ylab = "Test scores")

plot(classdata$expn_stu, classdata$testscr, col = "green",
      main = "Expenditure per pupil vs test scores",
      xlab = "Expenditure per pupil",
      ylab = "Test scores")

plot(classdata$meal_pct, classdata$testscr, col = "black",
      main = "Free lunch vs test scores",
      xlab = "Percentage of students with free lunch",
      ylab = "Test scores")

par(oldpar)

# do this in a loop
xvars <- c("str", "el_pct", "expn_stu", "meal_pct")
yvars <- c("testscr")
```

```

xlabels <- c("Student-teacher ratio", "Percentage of English learners",
            "Expenditure per pupil", "Percentage of students with free lunch")
ylabels <- "Test scores"

titles <- c("student-teacher ratio vs test scores",
            "English learners vs test scores",
            "Expenditure per pupil vs test scores",
            "Free lunch vs test scores")
colors <- c("red", "green3", "blue", "black")

op <- par(mfrow = c(2, 2))
for (i in seq(along=xvars)) {
  fm <- formula(paste(yvars, "~", xvars[i]))
  plot(fm, data = classdata, col = colors[i], main = titles[i],
       xlab = xlabels[i], ylab = ylabels)
}
par(op)

## # use pairs() or scatterplot.matrix() in car
## pairs(~ testscr +str + el_pct + expn_stu + meal_pct,
##       data = classdata)

## scatterplot.matrix(~ testscr +str + el_pct + expn_stu + meal_pct,
##                    data = classdata)

#####
###           estimation           ###
#####

model.76 <- testscr ~ str + I(expn_stu / 1000) + el_pct

res.model.76 <- lm(model.76, data = classdata)
summary(res.model.76)

# get some components of the results
bhat <- coef(res.model.76)
rsq <- summary(res.model.76)$r.squared
adj.rsq <- summary(res.model.76)$adj.r.squared

htvarm <- vcovHC(res.model.76, type = "HC1")

# application of the FWL theorem

```

```

# purge the effect of English learners and expenditure per pupil
mod.fwl1 <- lm(testscr ~ el_pct + I(expn_stu/1000), data = classdata)
mod.fwl2 <- lm(str ~ el_pct + I(expn_stu/1000), data = classdata)
mod.fwl3 <- lm(resid(mod.fwl1) ~ resid(mod.fwl2))

# test whether the FWL theorem works
# first check for the equality of the coefficient on str
if (abs(coef(res.model.76)[2] - coef(mod.fwl3)[2]) < 1.0e-10) {
  cat("The coefficient on str is the same.\n")
} else {
  cat("The FWL theorem fails? Check your step!\n")
}

# second check for the equality of residuals
if (all(abs(resid(mod.fwl3) - resid(res.model.76)) < 1.0e-10)) {
  cat("The residuals are all the same.\n")
} else {
  cat("The FWL theorem fails? Check your step!\n")
}

#####
###          hypothesis testing          ###
#####

# single coefficient test
# homoskedasticity-only
coeftest(res.model.76)

# heteroskedasticity-robust, t distribution
cftest.t <- coeftest(res.model.76, vcov = htvarm)

# heteroskedasticity-robust, normal distribution
cftest.n <- coeftest(res.model.76, vcov = htvarm, df = Inf)

# joint hypothesis
# b1 = 0, b2 = 0
test1 <- linearHypothesis(res.model.76,
  c("str = 0", "I(expn_stu/1000) = 0"),
  vcov = htvarm, test = "F")
test1
test1.F <- test1$F[2]
test1.p <- test1$"Pr(>F)"[2]

# b1 + b2 = 0

```

```

test2 <- linearHypothesis(res.model.76,
  c("str + I(expn_stu/1000) = 0"),
  white.adjust = "hc1", test = "Chisq")
test2
test2.x <- test2$Chisq[2]
test2.p <- test2$"Pr(>Chisq)"[2]

# homoskedasticity-only F
test2.hm <- linearHypothesis(res.model.76,
  c("str + I(expn_stu/1000) = 0"),
  test = "Chisq")
test2.hm

#####
## Control variables and model specifications ##
#####

# replicate Table 7.1
model1 <- lm(testscr ~ str, data = classdata)
model2 <- lm(testscr ~ str + el_pct, data = classdata)
model3 <- lm(testscr ~ str + el_pct + meal_pct, data = classdata)
model4 <- lm(testscr ~ str + el_pct + calw_pct, data = classdata)
model5 <- lm(testscr ~ str + el_pct + meal_pct + calw_pct, data = classdata)

hccm1 <- vcovHC(model1, type = "HC1")
se1 <- sqrt(diag(hccm1))

hccm2 <- vcovHC(model2, type = "HC1")
se2 <- sqrt(diag(hccm2))

hccm3 <- vcovHC(model3, type = "HC1")
se3 <- sqrt(diag(hccm3))

hccm4 <- vcovHC(model4, type = "HC1")
se4 <- sqrt(diag(hccm4))

hccm5 <- vcovHC(model5, type = "HC1")
se5 <- sqrt(diag(hccm5))

library(stargazer)
stargazer(model1, model2, model3, model4, model5,
  title = "Results of regressions of test scores and class size",
  covariate.labels = c("student-teacher ratio",
    "percent English learners",
    "percent eligible for subsidized lunch",

```

```
      "percent on public assistance"),  
dep.var.caption = "average test scores in the district",  
se = list(se1, se2, se3, se4, se5), df = FALSE,  
font.size = "small",  
label = "table:tbl71")
```